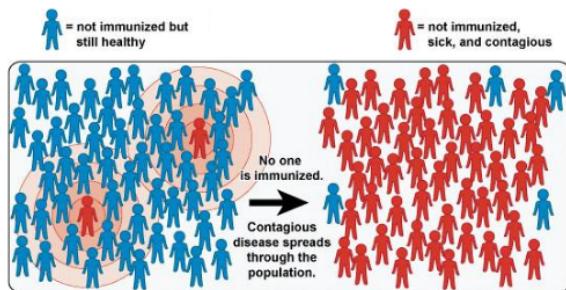


Modeling Infectious Disease

BIS20Q

Lecture 2



Starting w/ simple model
app'able to lots of stuff



Class discussion forum?

Discord

Quick Review

- Building bigmat
- Operations on matrices

Building bigmat

for loops

```
bigmat = ones zero(10,10); initializing matrix w/ 0s. easier to Δ  
for i=1:10 if replace all, don't have to Δ  
    for start w/ ls  
    bigmat(i,:) = (1:10) + (i-1); vector adds to #  
end Scratch  
also keeps past  
assignments from  
interfering
```

Operations on Matrices

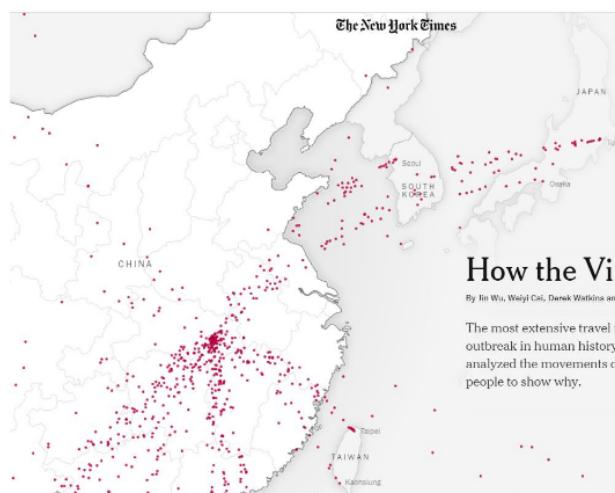
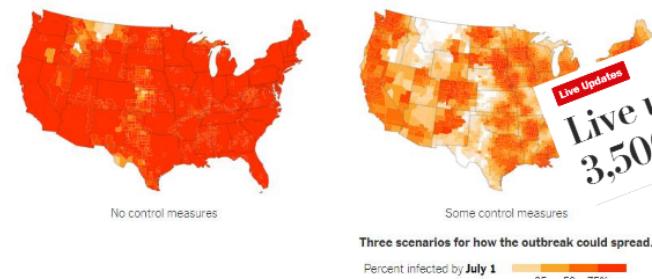
```
mat3 = mat1 .* mat2;
```

```
triangle = (bigmat >= 10);
```

```
mat2 = sin(mat1);
```

Coronavirus Could Overwhelm U.S. Without Urgent Action, Estimates Say

By James Glanz, Lauren Leatherby, Matthew Bloch, Mitch Smith, Larry Buchanan, Jin Wu and Nicholas Bogel-Burroughs March 20, 2020



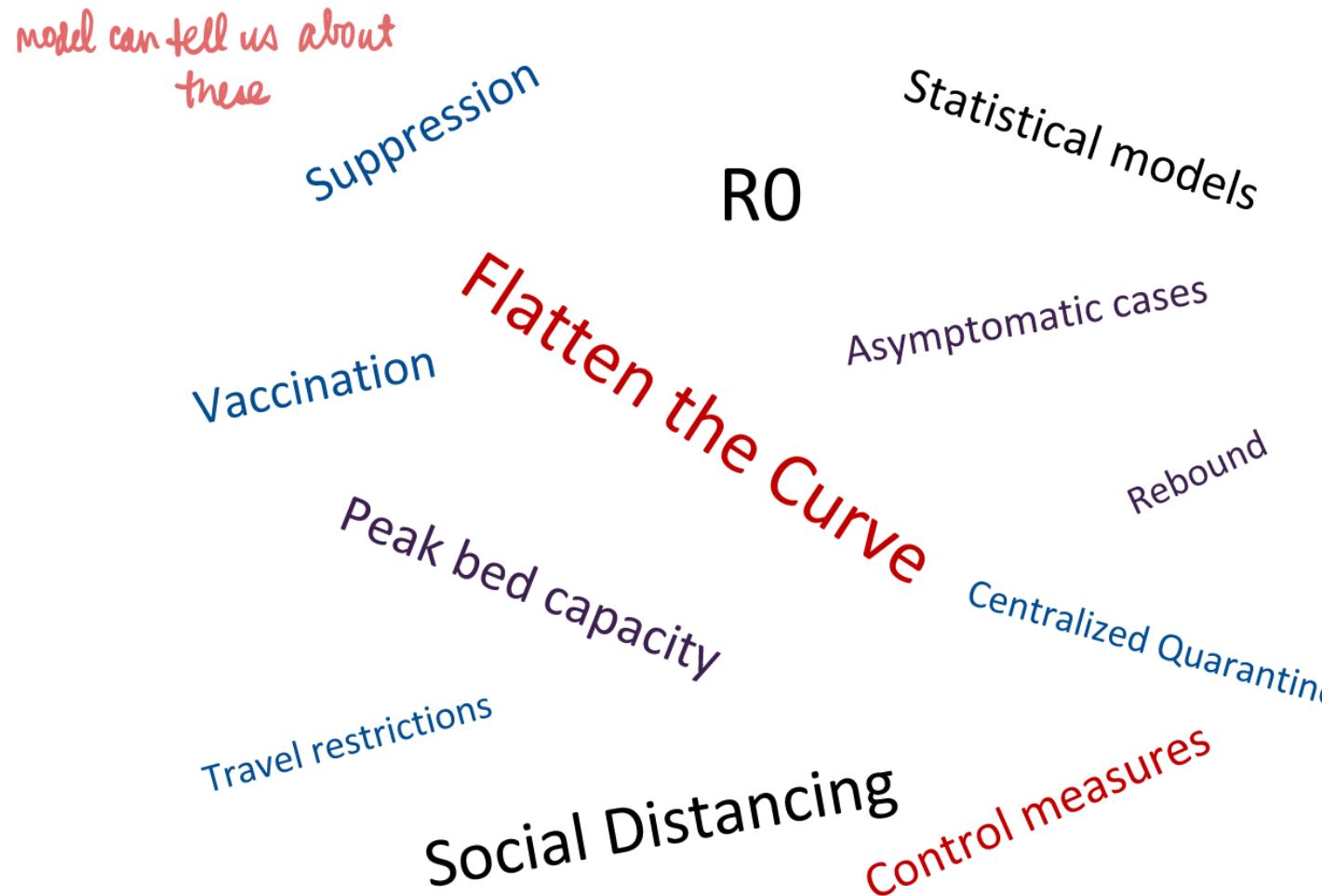
Live updates: New York coronavirus deaths surpass 3,500; confirmed cases nationwide top 300,000

HEALTH • CORONAVIRUS

White House turns to statistical models for coronavirus forecast

BY RICARDO ALONSO-ZALDIVAR, LAURAN NEERGAARD, AND THE ASSOCIATED PRESS

March 31, 2020 8:30 AM EST



Outline

- 1) Dynamic features of outbreaks
- 2) What is the basic reproduction number R_0 and why is it so important?
- 3) Essential core of model of disease dynamics:
the Susceptible-Infectious-Recovered (SIR) model

Pandemics in History



Plague of Athens, 430-427 BC

- Killed ~1/4 of the city's population

Black Plague, 1347-1351 *bubonic!*

- Killed 30-60% of Europe's population
- Fleas acted as the vector



Native American epidemics, 1518-1830's

- Smallpox and other diseases
- May have killed 90% of native Americans

Spanish flu (H1N1), 1918-1920

- Infected 1/3 of world population

Recent outbreaks

- Ebola, Zika, SARS, MERS

Without strong control measures, can affect large fractions of population

Recent Outbreaks and Scares

- Ebola
- Zika
- SARS
- West Nile
- HIV
- HPV
- Malaria
- SARS-CoV-2

Different:

Transmission rates - *person to person*

Transmission routes - *how transmitted*

Mortality rates

Recovery rates - *how long ppl sick*

Can model all of these

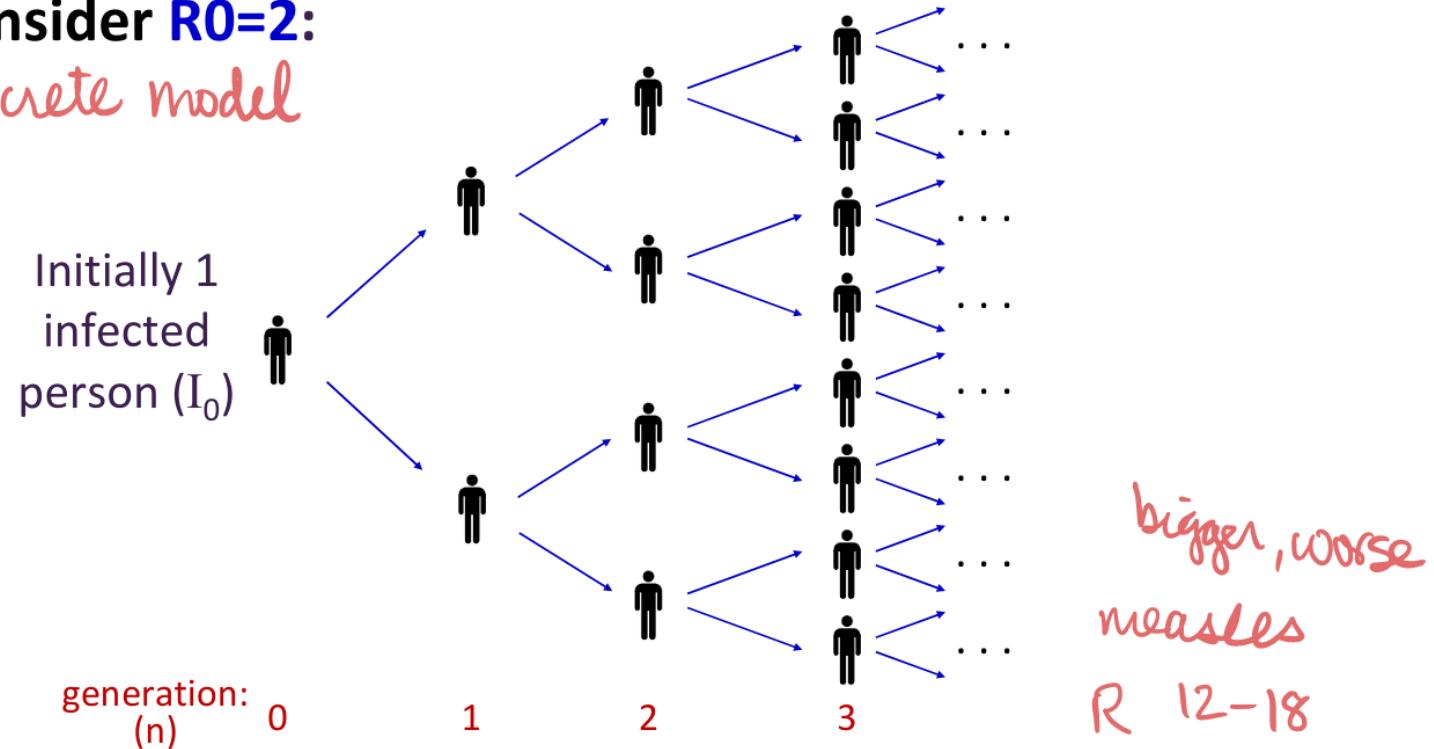
Key Concept: The “basic reproduction number” R_0

R_0 = average # of people that each infected person infects,
in a nearly entirely susceptible population

Why is this number so important?

Ex: $R_0 = 2$ Infected $\begin{matrix} \nearrow & \nwarrow \\ & \downarrow \\ \downarrow & \downarrow \end{matrix}$ exponential growth

Consider $R_0=2$:
discrete model



$$I(n) = (\# \text{ new infections in generation } n) = (1)(2)^n = I_0 R_0^n$$

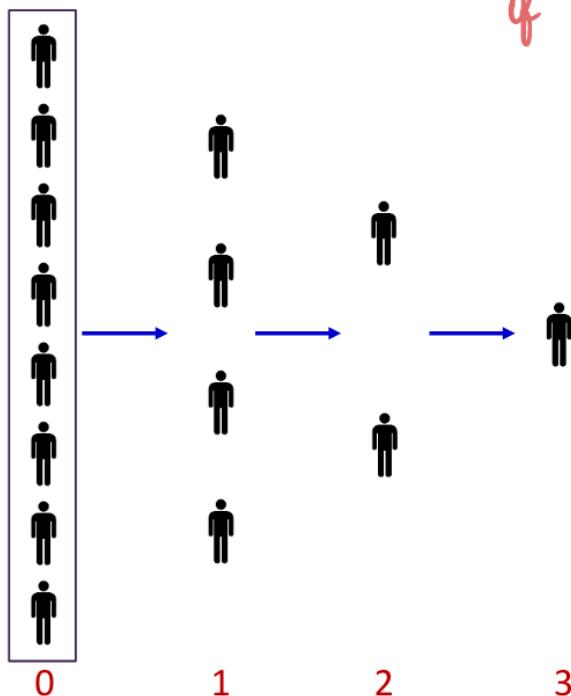
Grows exponentially fast – outbreak!!!

if $R_0 \geq 1$, grows exp.

Consider $R_0=1/2$:

Initially 8 infected people (I_0)

generation:
(n)



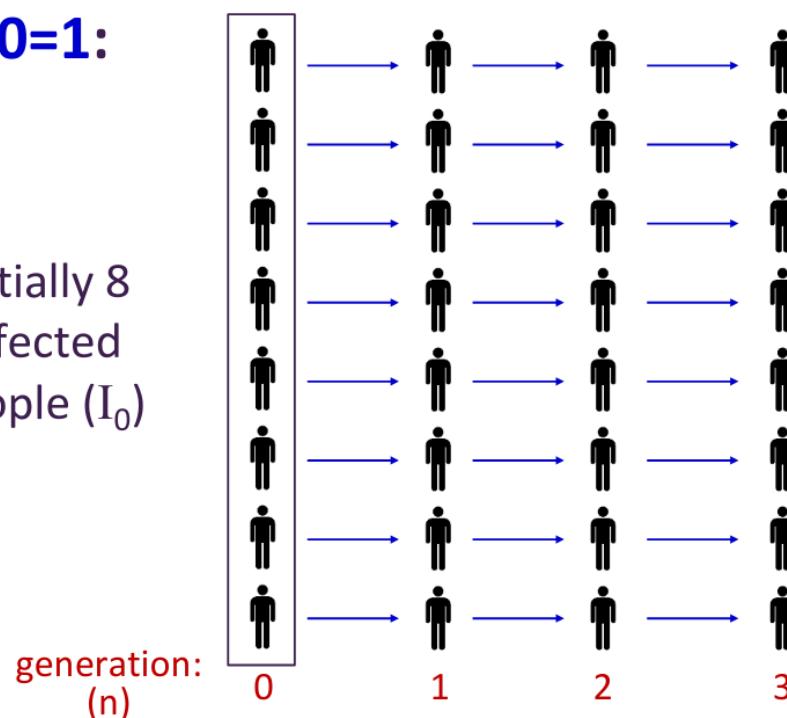
if $R_0 < 1$, decays

$$I(n) = (\# \text{ new infections in } n^{\text{th}} \text{ generation}) = (8)(\frac{1}{2})^n = I_0 R_0^n$$

Decays exponentially fast – rapid recovery!

Consider $R_0=1$:

Initially 8 infected people (I_0)



$$I(n) = (\# \text{ new infections in } n^{\text{th}} \text{ generation}) = (8)(1)^n = I_0 R_0^n$$

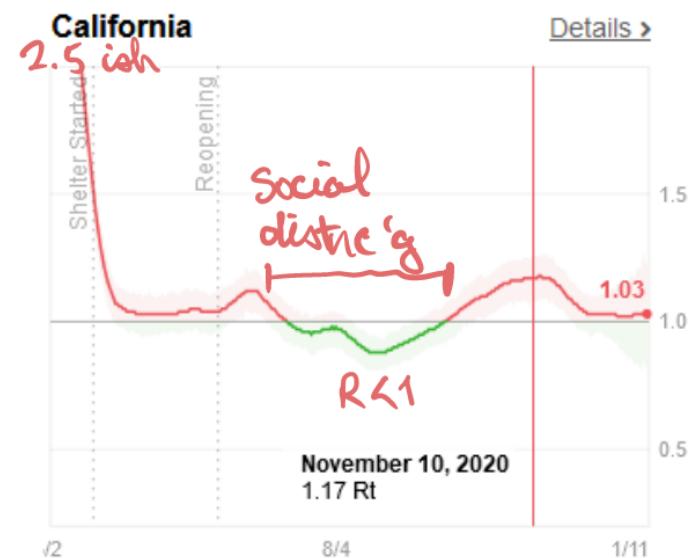
No change: borderline between growth and decay

R_{eff} or R_t measures transmission rates dynamically

R_0 is init rate - later can Δ

- R_t can change over time, depending on behavior, immunity and other conditions

$R=1$ flat spread rate



How do we model outbreaks?

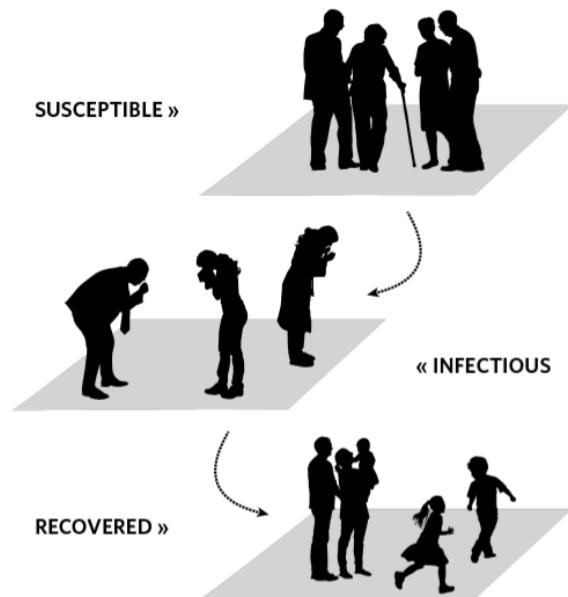
- We want units of time, not generations
- Time passes continuously, not in discrete steps
- We want flexibility to add to our model as we investigate it

Modeling Infectious Disease

3 subpops:

- Susceptible
- Infected
- Recovered

never goes backwards



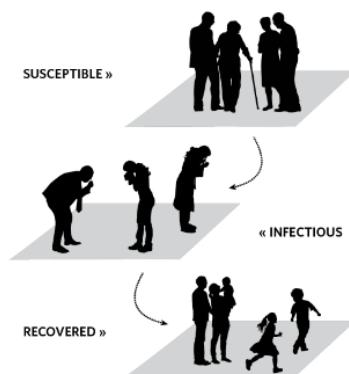
SIR model

SIR Model



Rate of infection – proportional to S and I

Rate of recovery – proportional to I



What should be the differential equations?

SIR Model

how does
Susceptible pop Δ
over time?



S = fraction of population susceptible

I = fraction of population currently infected

R = fraction of population recovered (and immune)

$$\begin{aligned}\frac{dS}{dt} &= -bIS \quad \text{reducing if } S \uparrow - bIS \text{ cd } \uparrow \text{ also if virus mutates} \\ \frac{dI}{dt} &= bIS - gI \quad \text{infected ppl} \\ \frac{dR}{dt} &= gI \quad \text{recovered}\end{aligned}$$

To write these equations:

For each species (variable) in your model, you should identify all the ways it can be **produced** and all the ways it can be **removed**.

Putting it in MATLAB

Populations and rate constants

Lines starting with “`%%`”
define the start of a new
“block” of code

Lines starting with “`%`”
are comments that are
ignored by MATLAB

```
1 %% Block 1 - Annotation of molecular species for SIR model
2
3 % Populations:
4 % 1: Susceptible
5 % 2: Infected
6 % 3: Resistant
7
8
9 %% Block 2 - Rate constants
10 % Kinase
11 - b=2;    % Transmission Rate
12 - g=1;    % Recovery Rate
13
```

Differential Equations

```
14 %% Block 3 - Define the differential equations
15 - tspan = 0:0.25:50;
16 - dy = @(t,y) [-b*y(1)*y(2);           t=time b=trans rate
17      b*y(1)*y(2) - g*y(2);           g=reco rate
18      g*y(2)];
19
```

dy is a “**function handle**.”

- After you define it, you can use it just like a built-in function.
- The “@” character tells MATLAB you are defining a function handle.
- This function takes two inputs (t and y), and it returns a 3 x1 vector as an output.

Custom functions

“function handle.”

- After you define it, you can use it just like a built-in function.
- The “@” character tells MATLAB you are defining a function handle.

```
func = @(x) x^2 + x + 1;  
func(7)
```

```
y=7; func(y)
```

input

Differential Equations

```
14 %% Block 3 - Define the differential equations
15 tspan = 0:0.25:50;
16 dy = @(t,y) [-b*y(1)*y(2);           ←
17          b*y(1)*y(2) - g*y(2);       ←
18          g*y(2)];                   ←
19
```

$$\frac{dS}{dt} = -bIS$$

$$\frac{dI}{dt} = bIS - gI$$

$$\frac{dR}{dt} = gI$$

**What do you need to solve a set of differential equations?
(or to go from equations to a simulated output)**

Simulate

need init cond to do

```
9    %% Block 2 - Rate constants
10   % Kinase
11   b=2;    % Transmission Rate
12   g=1;    % Recovery Rate
13
14   %% Block 3 - Define the differential equations
15   tspan = 0:0.25:50;
16   dy = @(t,y) [-b*y(1)*y(2);
17           b*y(1)*y(2) - g*y(2);
18           g*y(2)];
19
20   %% Block 4 - Define the initial conditions and solve the differential equations
21   % Define the initial conditions
22   y0 = [0.999 .001 0]; % S I R
23
24   % Solve the differential equations
25   [t,y] = ode45(dy,tspan,y0);
```

Initial Conditions

ode45 = MATALB built-in function for integrating differential equations

takes 3 inputs - time , eqs, init cond

Model Output in MATLAB

```
--  
24 % Solve the differential equations  
25 [t,y] = ode45(dy,tspan,y0);  
--
```

- t stores time
- y stores the outputs for S, I, and R
- y is a matrix and you can think of it as a big data table

t		
323x1 double		
1	0	
2	1	
3	2	
4	3	
5	4	
6	5	
7	6	
8	7	
9	8	
10	9	
11	10	
12	11	
13	12	
14	13	
15	14	
16	15	
17	16	
18	17	
19	18	
20	19	
21	20	

y		
323x3 double		
1	S	2
2	I	R
1	1.0000	1.0000e-06
2	1.0000	1.2976e-06
3	1.0000	1.6842e-06
4	1.0000	2.1851e-06
5	1.0000	2.8342e-06
6	1.0000	3.6776e-06
7	1.0000	4.7729e-06
8	1.0000	6.3715e-06
9	1.0000	8.5169e-06
10	1.0000	1.1073e-05
11	1.0000	1.4048e-05
12	1.0000	1.7599e-05
13	1.0000	2.2026e-05
14	1.0000	2.7777e-05
15	0.9999	3.5445e-05
16	0.9999	4.5769e-05
17	0.9999	5.9633e-05
18	0.9999	7.8070e-05
19	0.9998	1.0225e-04
20	0.9998	1.3351e-04
21	0.9997	1.7343e-04

Plot the results

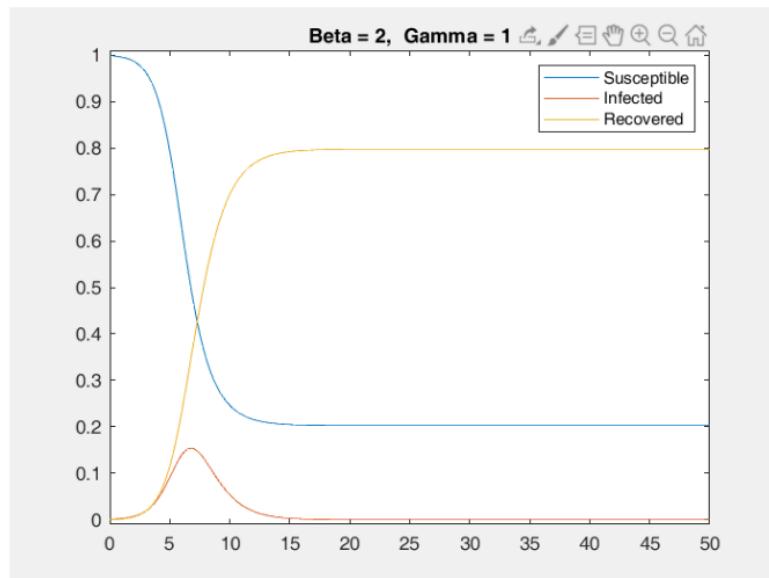
```
-->
27 %% Block 5 - Plot the results
28 - plot(t,y);
29 - ylim([-0.01 1.01]);
30 - legend({'Susceptible','Infected','Recovered'});
31 - title(['Beta = ' num2str(b) ', Gamma = ' num2str(g)]);
```

Why are the results so different?

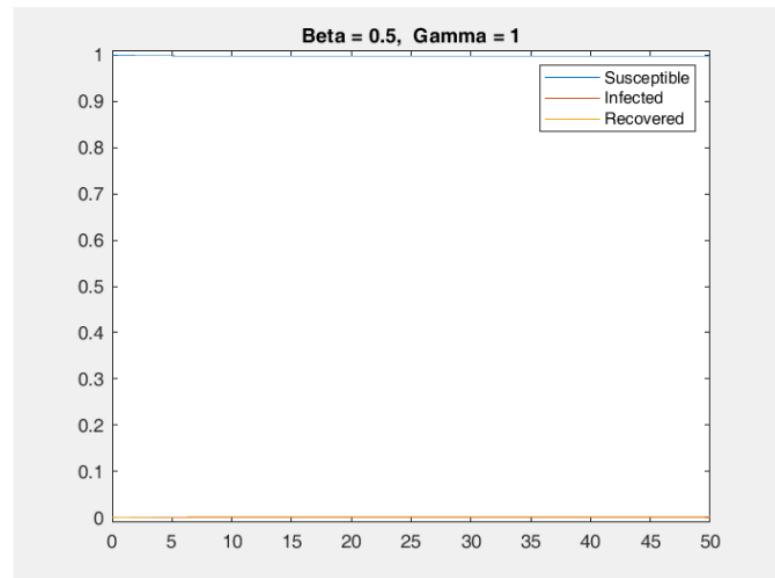
>1

R₀ is diff

<1

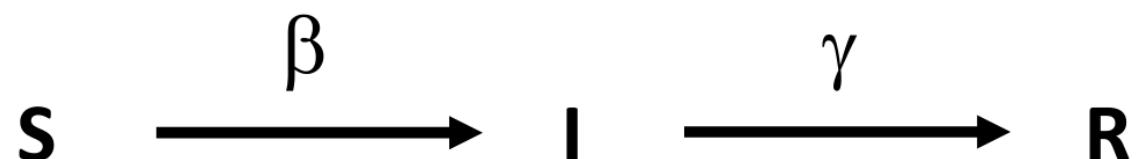


80% of population gets infected



Almost no one

SIR Model



$$\frac{dS}{dt} = -bIS$$

$$\frac{dI}{dt} = bIS - gI$$

R_0 if $R_0 = 1$, flat rate
if > 0 , spreads exp

$$\frac{dR}{dt} = gI$$

R_0 measures reproductive power

$$\frac{dI}{dt} = bIS - gI = 0 \longrightarrow \frac{bS}{g} = 1 = R_0$$

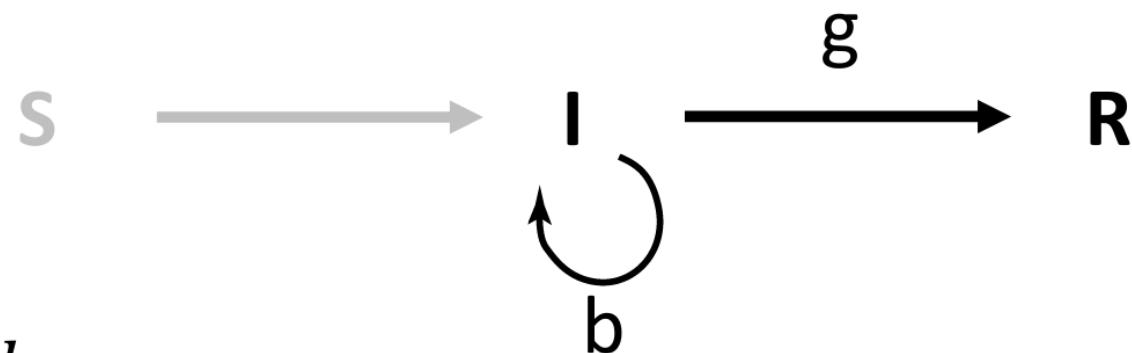
At the beginning of a potential epidemic, $S=1$ — everyone's 100% susceptible
Therefore:

$$R_0 = \frac{b}{g} > 1 \longrightarrow \text{Number of infections will rise. Outbreak.}$$

$$R_0 = \frac{b}{g} < 1 \longrightarrow \text{Number of infections will fall. No outbreak.}$$

What does R_0 represent?

At the beginning of a potential epidemic, $S=1$



$$R_0 = \frac{b}{g}$$

R_0 is the average number of new infections that each old infection gives rise to (in an entirely susceptible population).

Values of R_0 for well-known diseases

Disease	Transmission	R_0
Measles	Airborne	12–18
Diphtheria	Saliva	6–7
Smallpox	Airborne droplet	5–7
Polio	Fecal-oral route	5–7
Rubella	Airborne droplet	5–7
Mumps	Airborne droplet	4–7
HIV/AIDS <i>g v. sml</i>	Sexual contact	2–5
Pertussis	Airborne droplet	5.5 ^[2]
SARS	Airborne droplet	2–5 ^[3]
Influenza (1918 pandemic strain)	Airborne droplet	2–3 ^[4]
Ebola (2014 Ebola outbreak)	Bodily fluids	1.5–2.5 ^[5]

*spreads slower
- delayed symps*

Adapting the Model



$$\frac{dS}{dt} = -bIS$$

$$\frac{dI}{dt} = bIS - gI$$

$$\frac{dR}{dt} = gI$$

How would you change the model to account for vaccination?

Have a v pop - $S \rightarrow V$, $S \rightarrow I$
 $V \rightarrow I$ $R = 0.2R_0$

How would you change the model to account for social distancing?

Shd affect β - depends on time