

Special Lecture: Modeling Disease Spread with Differential Equations

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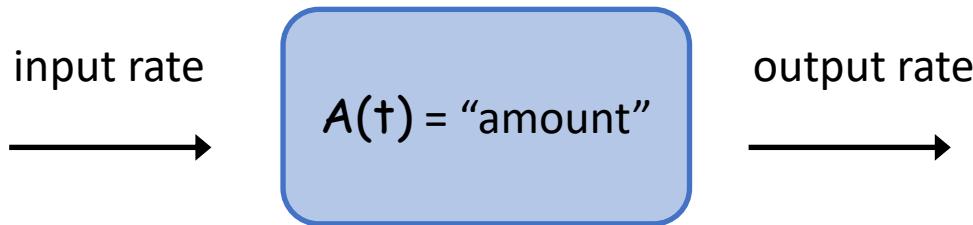
MATH 33LA (ODEs & Linear Algebra)
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EPIDEMIOLOGY

- “Epidemiology” is the study of **epidemics**: the phenomenon of infectious diseases spreading rapidly through a population.
- Understanding epidemiology is vital to avoiding **pandemics**, where a disease has become widespread (e.g., across the globe).
- Epidemiologists use mathematical models (as well as many other tools) to help predict the behavior of a given epidemic.
- Since it would be too difficult to model the interaction of every possible host and disease factor, **compartmental models** are extremely useful.

COMPARTMENTAL MODELS

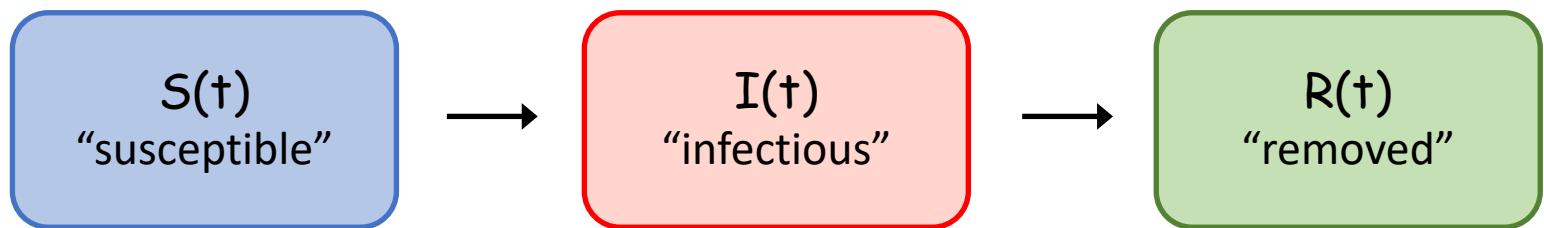
- Many complicated processes can be broken down into distinct stages, so the entire system can be modeled more simply by describing the interactions between each stage instead.
- Such models are called **compartmental** and can be graphically depicted using **block diagrams**.



- So far, the population models we have studied only involve one compartment, with a single input (birth) and output (death), but an epidemic involves multiple stages. See Sections (3.2) and (5.5) for more examples of compartmental models.

SIR Model

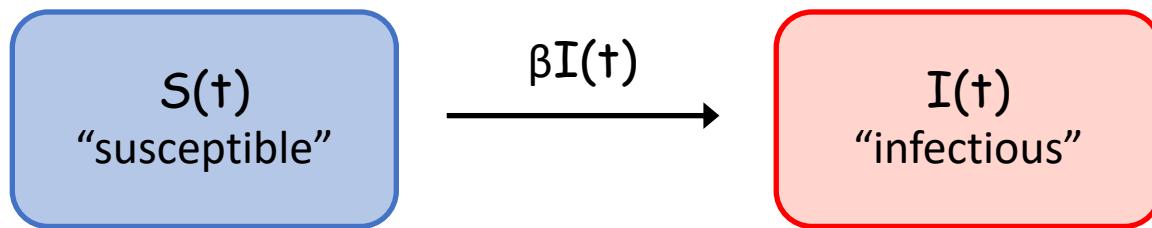
- The simplest model for an epidemic should involve at least **3 stages**:
 - $S(t)$ = “**susceptible population**” (still can get the disease)
 - $I(t)$ = “**infectious population**” (spreading the disease)
 - $R(t)$ = “**removed population**” (no longer spreading the disease)
- The block diagram for the “**SIR Model**” can be expressed by showing the transition from $S(t)$ to $I(t)$ and then to $R(t)$.



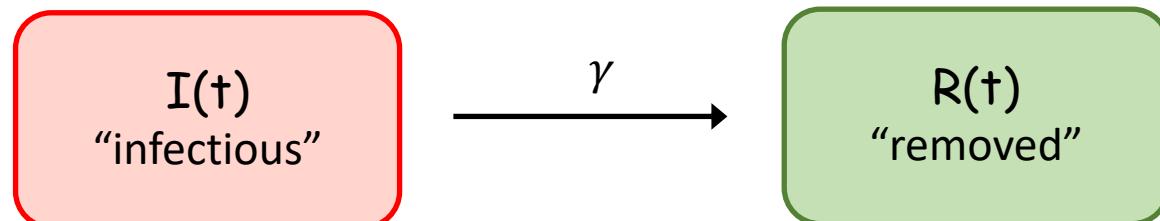
- ❖ Of course, many other stages and transitions could be added, such as an exposed/latent stage (E), a stage for infants with maternally-derived immunities (M), or a relapse transition, but a lot can still be understood from the simple **SIR Model**.

SIR Model

- To complete the model, we must provide “transition rates” between each stage (or compartment).
- The transition rate between $I(t)$ and $S(t)$ is $\beta I(t)$, where β is the average number of contacts per person times the probability of disease transmission.



- The transition rate between $I(t)$ and $R(t)$ is simply γ , where $1/\gamma$ is the time duration of the infection.



SIR Model

- Now that we know the rates, we can combine these relations between each stage to make a *system of differential equations*.

The “**susceptible population**” only has an output to the “infectious population”, so the ODE has one term:

$$\frac{dS}{dt} = -[\text{output rate}] \times S = -\beta IS$$

SIR Model

- Now that we know the rates, we can combine these relations between each stage to make a *system of differential equations*.

The “**infectious population**” has both an input from the “susceptible population” and an output to the “recovered population”, so the ODE has two terms:

$$\begin{aligned}\frac{dI}{dt} &= [\text{input rate}] \times S - [\text{output rate}] \times I \\ &= \beta IS - \gamma I\end{aligned}$$

SIR Model

- Now that we know the rates, we can combine these relations between each stage to make a *system of differential equations*.

The “**removed population**” only has an input from the “infectious population”, so the ODE has one term:

$$\frac{dR}{dt} = [\text{input rate}] \times I = \gamma I$$

SIR Model

- Now that we know the rates, we can combine these relations between each stage to make a *system of differential equations*.
- Combining all three ODEs, we have the standard SIR Model:

$$\frac{dS}{dt} = -\beta IS, \quad \frac{dI}{dt} = \beta IS - \gamma I, \quad \frac{dR}{dt} = \gamma I$$

- ❖ Again, this is a **simplified model**. More realistic models include important factors such as variations in population density and air travel, which can also be treated as separate stages. We are only trying to *qualitatively* understand the dynamics of epidemics here.

Basic Reproduction Ratio

- With any mathematical model, it is important to have as few parameters as possible. This model has two parameters (β, γ), but we can reduce it to one with the following substitution: $\tau = \gamma t$.

$$y(t) \rightarrow y(\tau) \implies \frac{dy}{dt}(\tau) = \frac{d\tau}{dt} \frac{dy}{d\tau}(\tau) = \gamma \frac{dy}{d\tau}(\tau)$$

- The SIR model in terms of this new time scale will become:

$$\frac{dS}{d\tau} = -\frac{\beta}{\gamma} IS, \quad \frac{dI}{d\tau} = \frac{\beta}{\gamma} IS - I, \quad \frac{dR}{d\tau} = I$$

- Note: there is a common ratio throughout the problem.

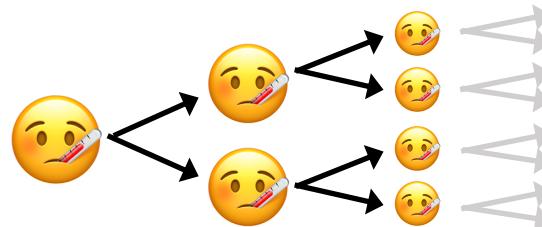
Basic Reproduction Ratio

- We can introduce the following parameter: $R_0 = \beta/\gamma$, which is known as the **basic reproduction ratio** and pronounced “R naught” or “R zero”.
- The entire SIR model can now be written in terms of this *single parameter*, which makes it easier to study.

$$\frac{dS}{d\tau} = -R_0 IS, \quad \frac{dI}{d\tau} = R_0 IS - I, \quad \frac{dR}{d\tau} = I$$

- R_0 can be interpreted as the number of new infections coming from a single infected person.

Example $R_0 = 2$:



How do we solve these equations?

- Nonlinear systems of ODEs are difficult to deal with, and it is usually impossible to obtain a “closed form solution” by hand.
- Instead, numerical algorithms can be used to determine the solutions with a *high degree of accuracy* (e.g., the Forward-Euler method discussed earlier this semester).
- Any given simulation will require knowing both the initial conditions and the value of R_0 .

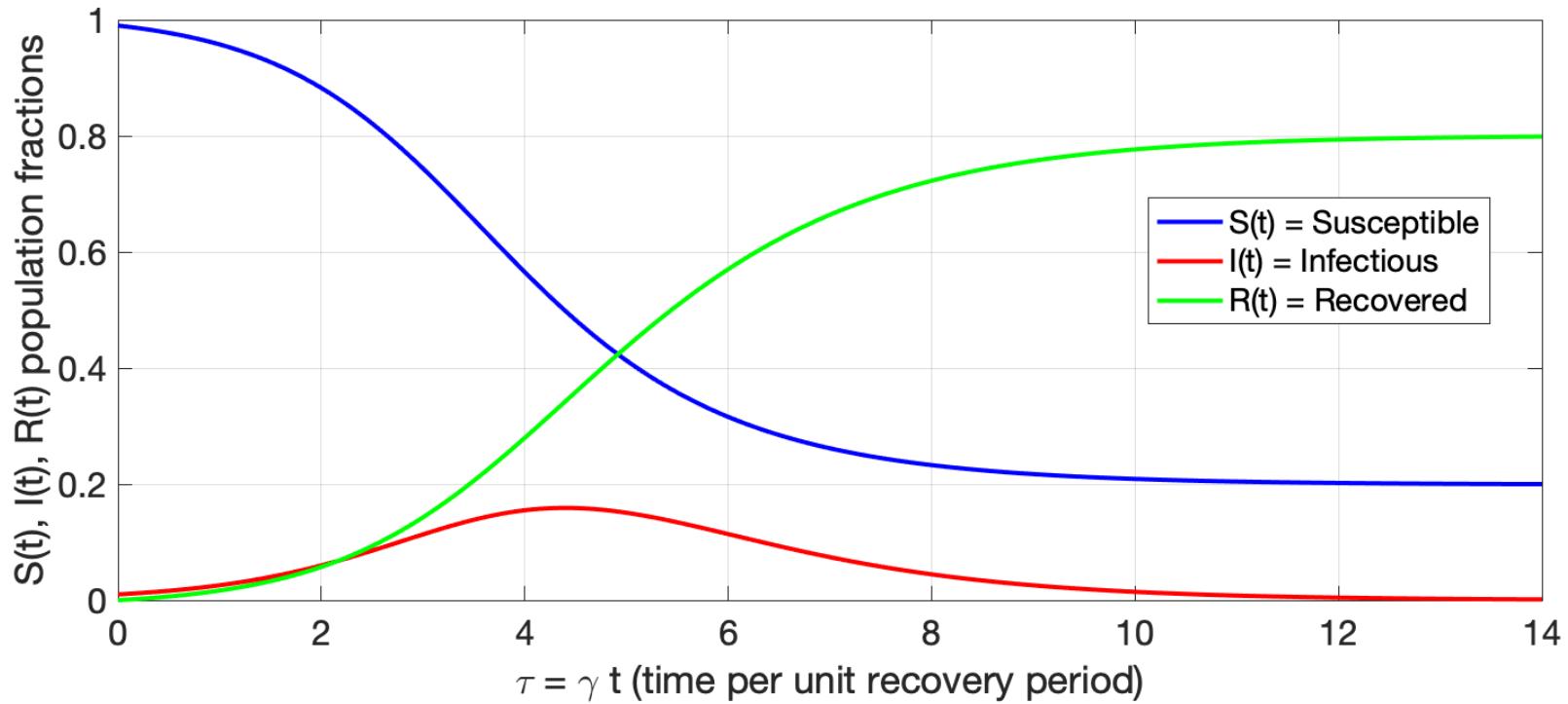
Example 1: Initial infection of 1% of the population with $R_0 = 2$.

$$R_0 = 2, \quad S(0) = 0.99, \quad I(0) = 0.01, \quad R(0) = 0$$

Simulation of the SIR Model

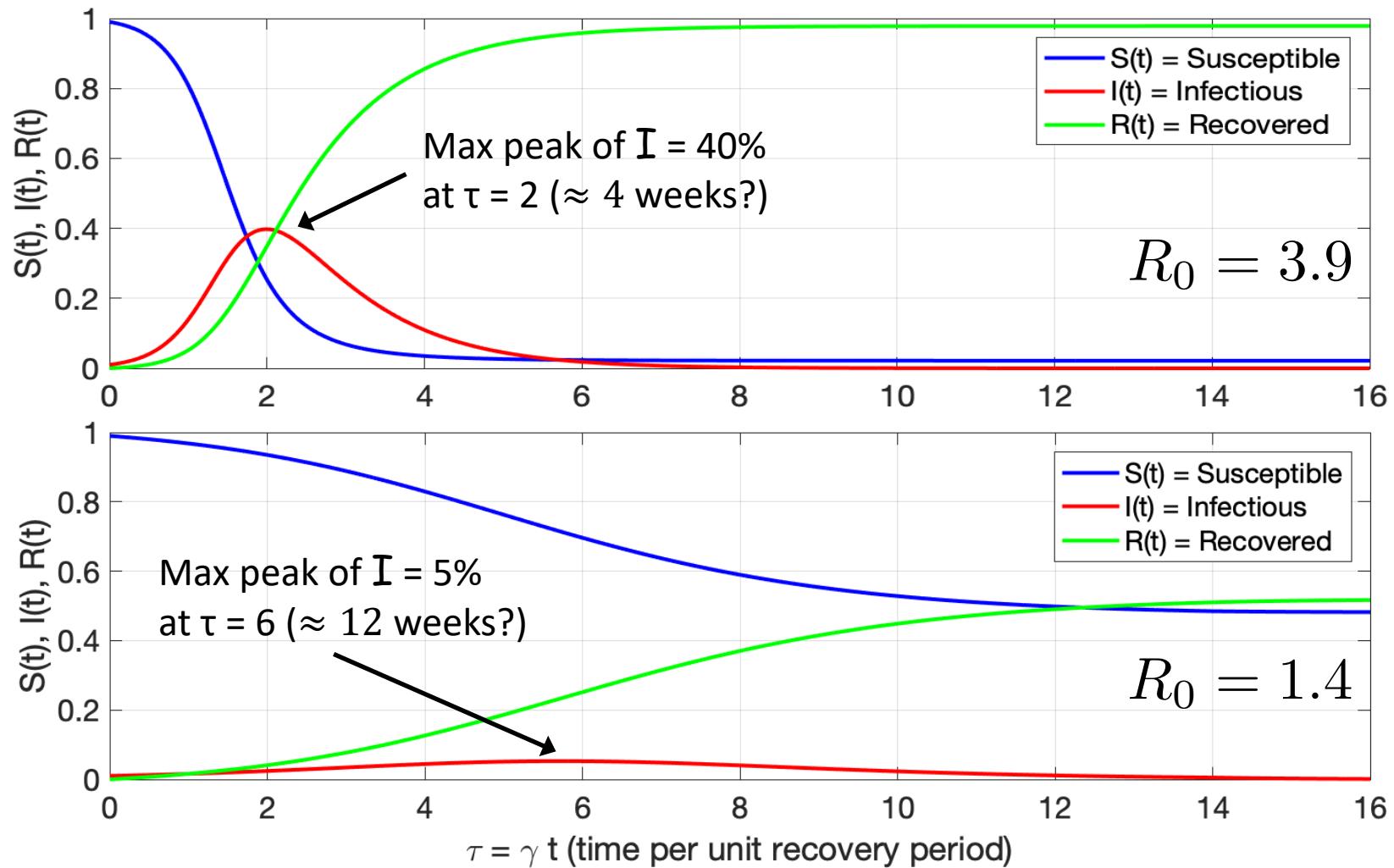
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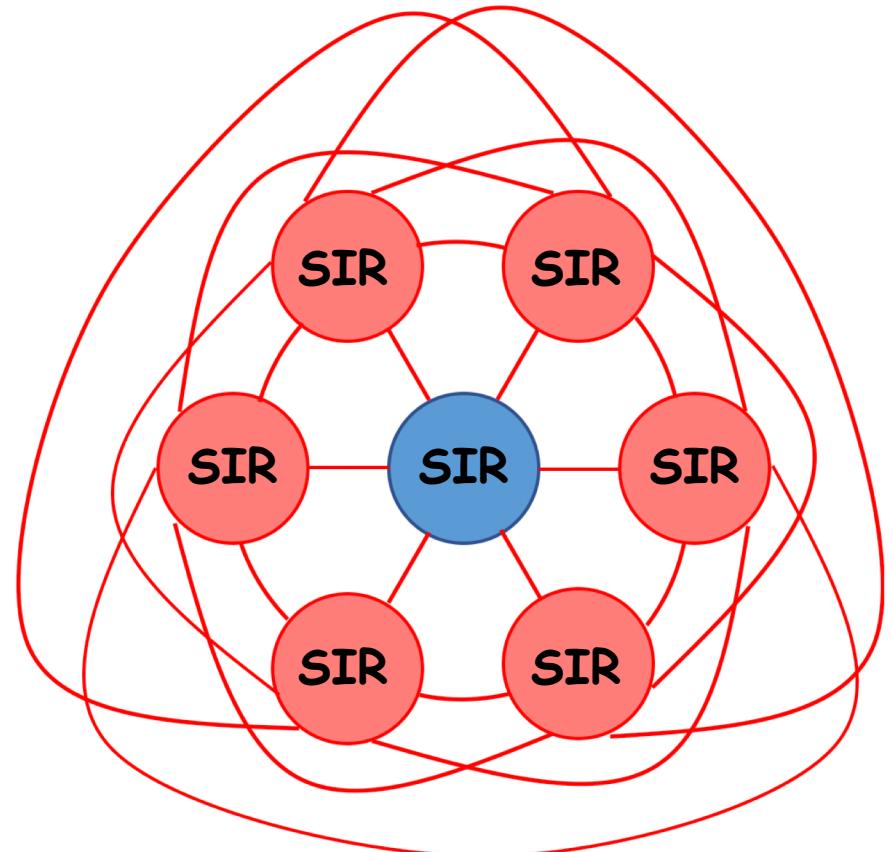
Example 2: The current range of R_0 for COVID-19 is $1.4 < R_0 < 3.9$, so how do these values compare?



PAUSE

Wait, if the “worst case scenario” is 3 months, then why are we still in frickin’ quarantine???

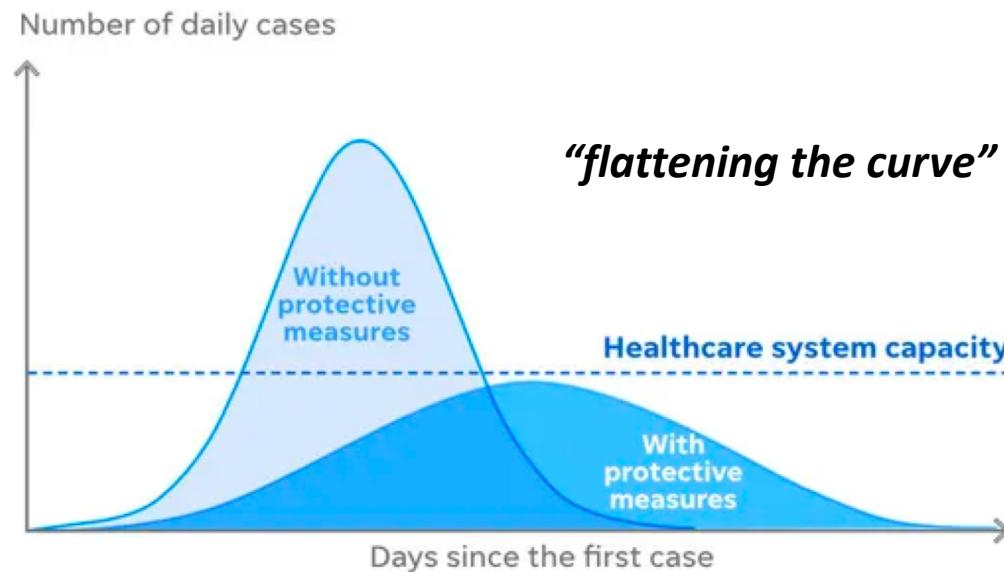
- Adding the “exposed” compartment will lengthen the simulations
- More importantly: San Jose is not an *isolated* population. A more realistic simulation would include an SIR-type model for all connected populations (“metapopulations”)
- As the disease travels from urban to rural areas and back, the epidemic can be prolonged greatly.



Ok, Back to the SIR Model

Summary: What happens when R_0 drops from 3.9 to 1.4?

- Maximum infection rate drops from 40% to 5%
- Infection peak is delayed three times longer
- Total infections over course of epidemic drops from 98% to 52%

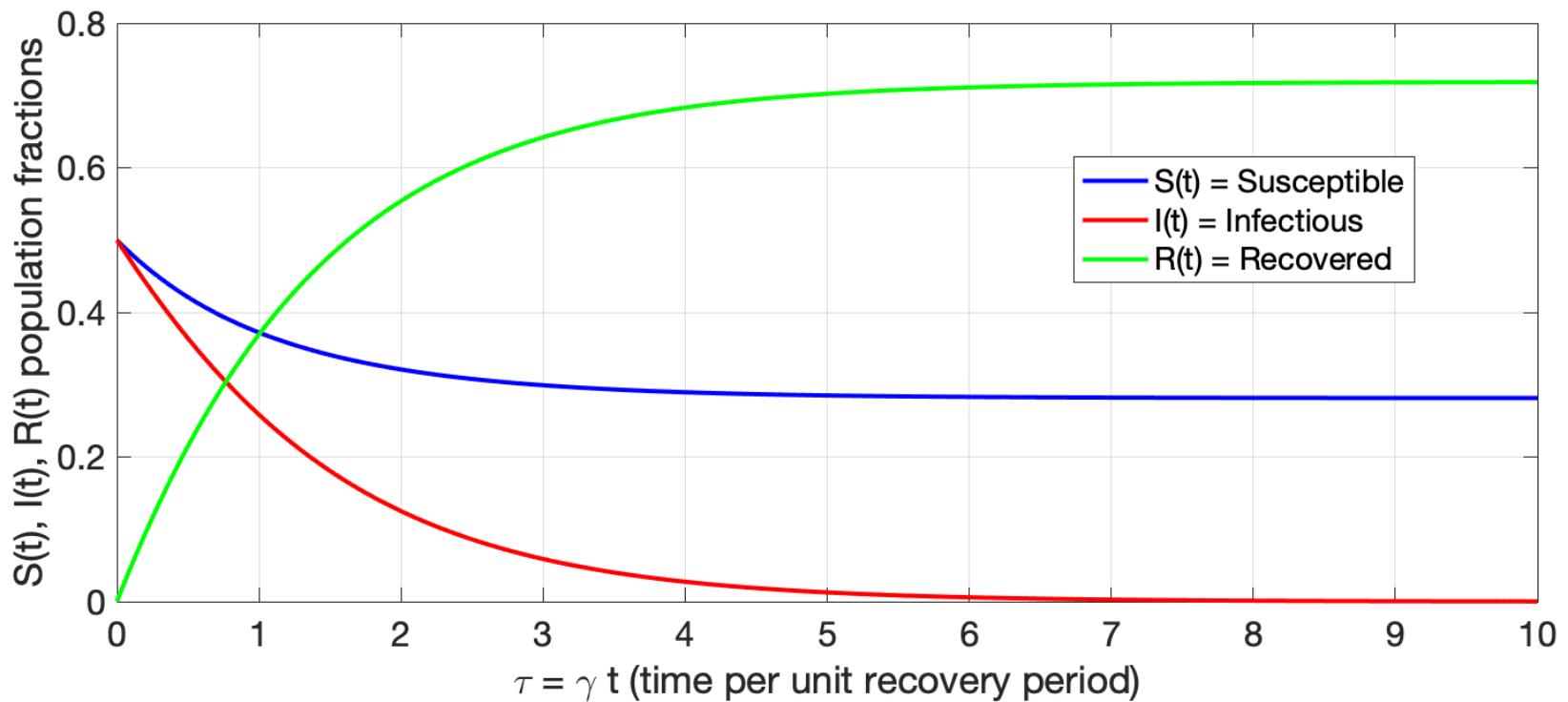


SOURCE: CDC

Simulation of the SIR Model

Example 3: Initial infection of 50% of the population with $R_0 = 0.8$.

$$R_0 = 0.8, \quad S(0) = 0.5, \quad I(0) = 0.5, \quad R(0) = 0$$



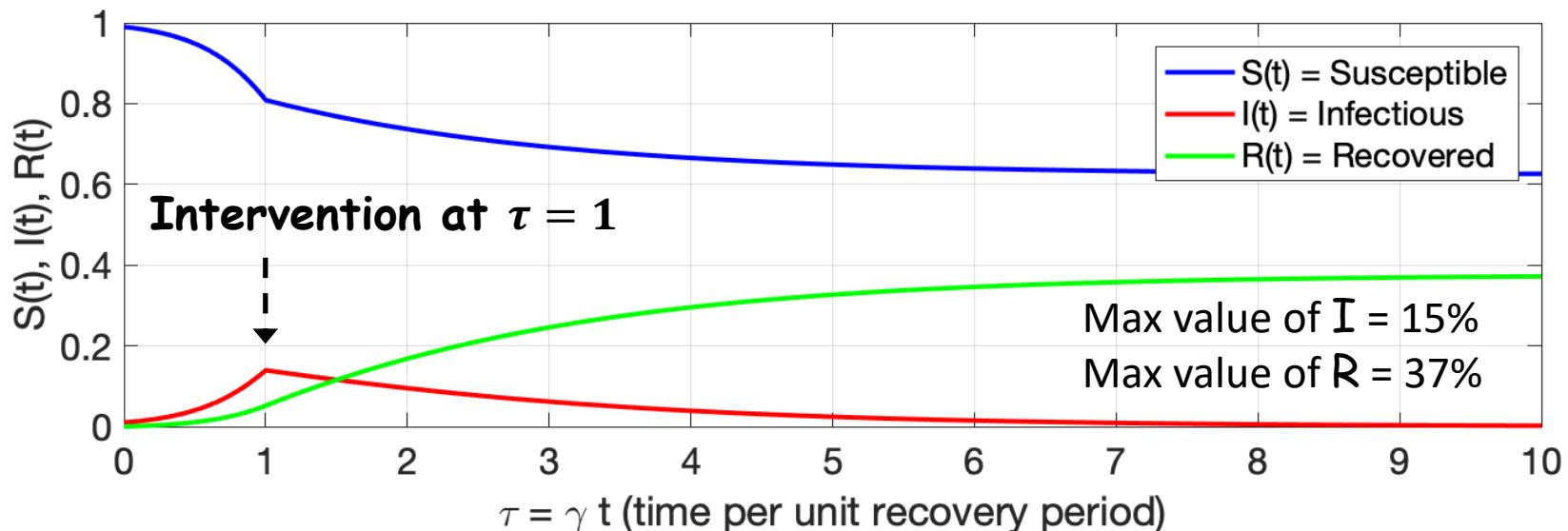
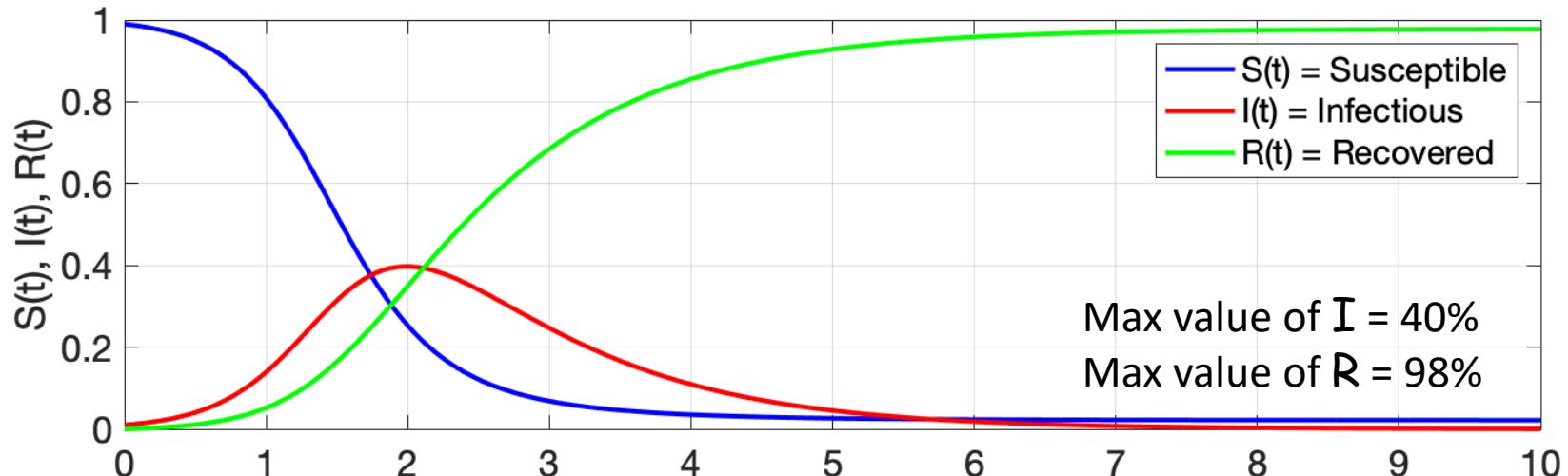
When $R_0 < 1$, infections will automatically drop!!!

What can we do with this information?

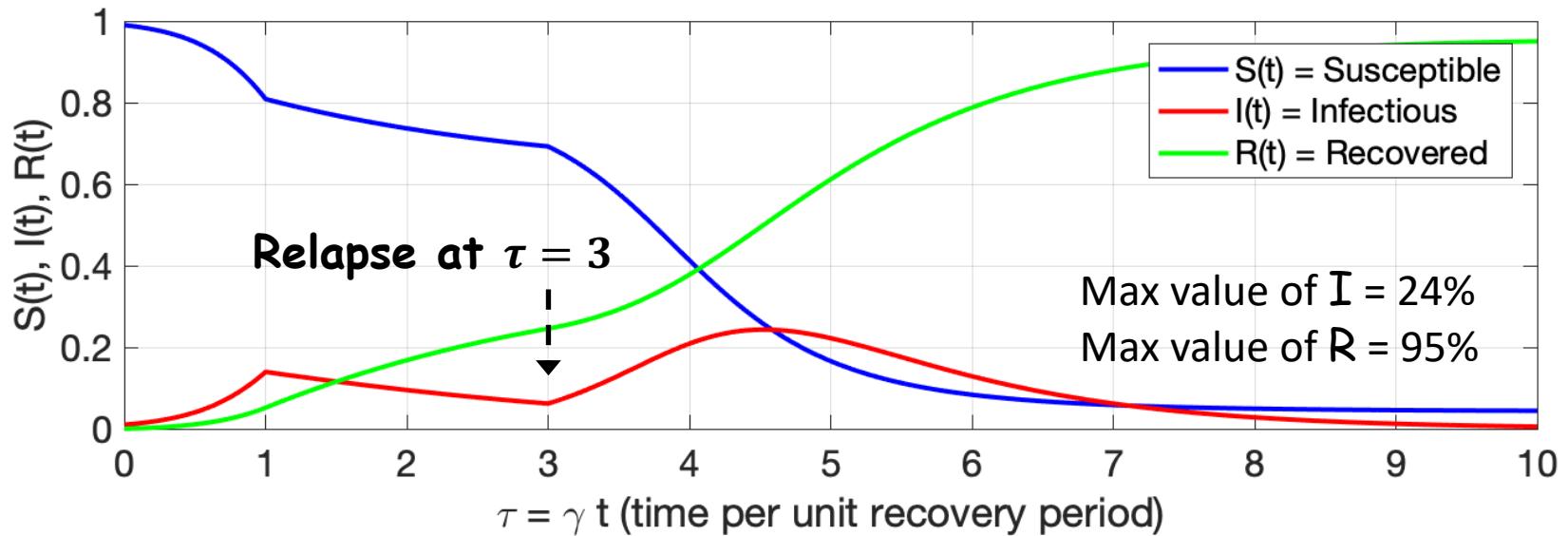
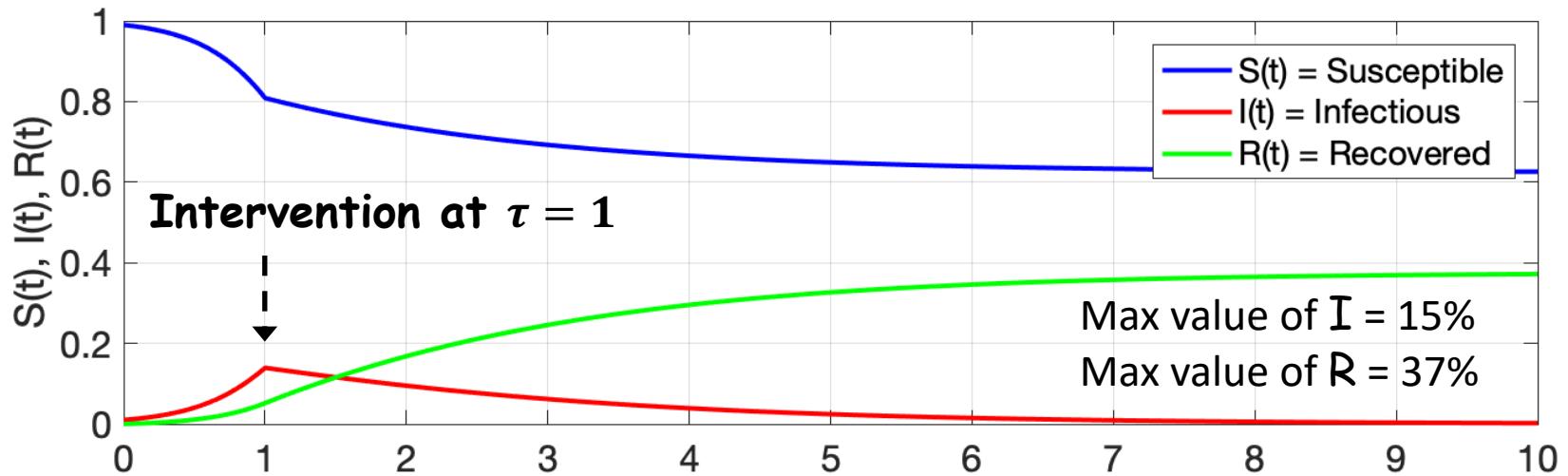
- Recall the definition: $R_0 = \frac{\beta}{\gamma} = \frac{\text{recovery time}}{\text{time between contacts}}$
- Without vaccine or treatment options, we can still intervene and reduce R_0 by *maximizing* the time between contacts.
- ***That is, we have the ability to change R_0 !***

Example 4: Initial infection of 1% of the population with $R_0 = 3.9$, but we intervene at $\tau = 1$ and drop to $R_0 = 0.8$.

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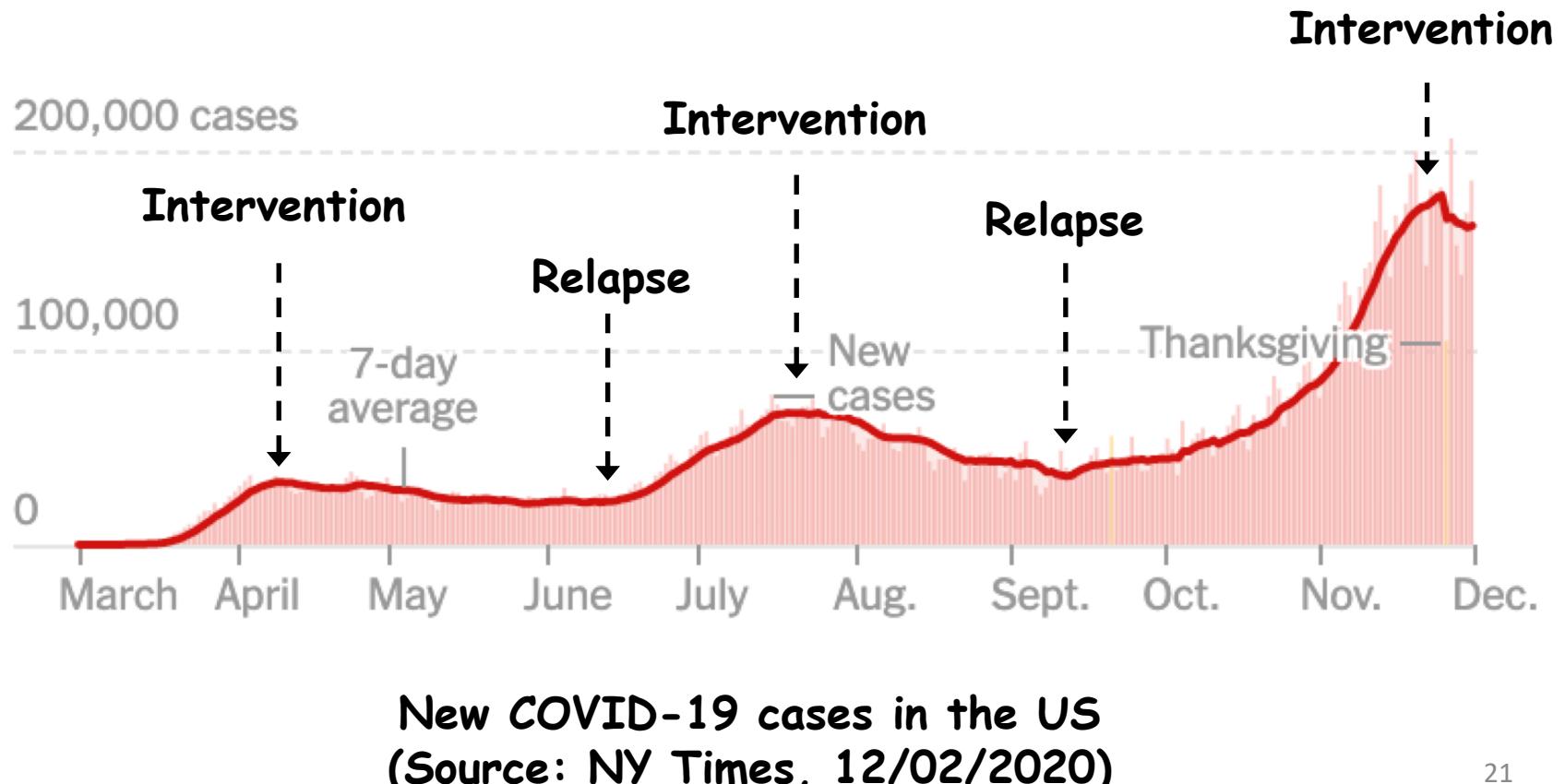


Example 5: Initial infection of 1% of the population with $R_0 = 3.9$, but we intervene at $\tau = 1$ and drop to $R_0 = 0.8$, BUT we then stop the intervention at $\tau = 3$.



COVID-19 in the United States

While this model is an over-simplification, the phenomenon of quarantine policies that are both dynamic (changing in time) and heterogeneous (different for each state/county) can be observed in the data.



So, what's the takeaway here for the current COVID-19 pandemic?

- ❖ We can use mathematical models to better understand the qualitative (and sometimes quantitative) features of epidemics.
- ❖ In the simple SIR Model, the infection rates *strongly* depend on the parameter R_0 , which is the “basic reproduction ratio”.
- ❖ By reducing R_0 below 1 as a society, we can dramatically reduce infection rates and the stress on our healthcare system!
- ❖ Wear your mask, wash your hands often and avoid close contact with others, especially if you are feeling sick.

(<https://www.cdc.gov/coronavirus/2019-ncov/prepare/prevention.html>)