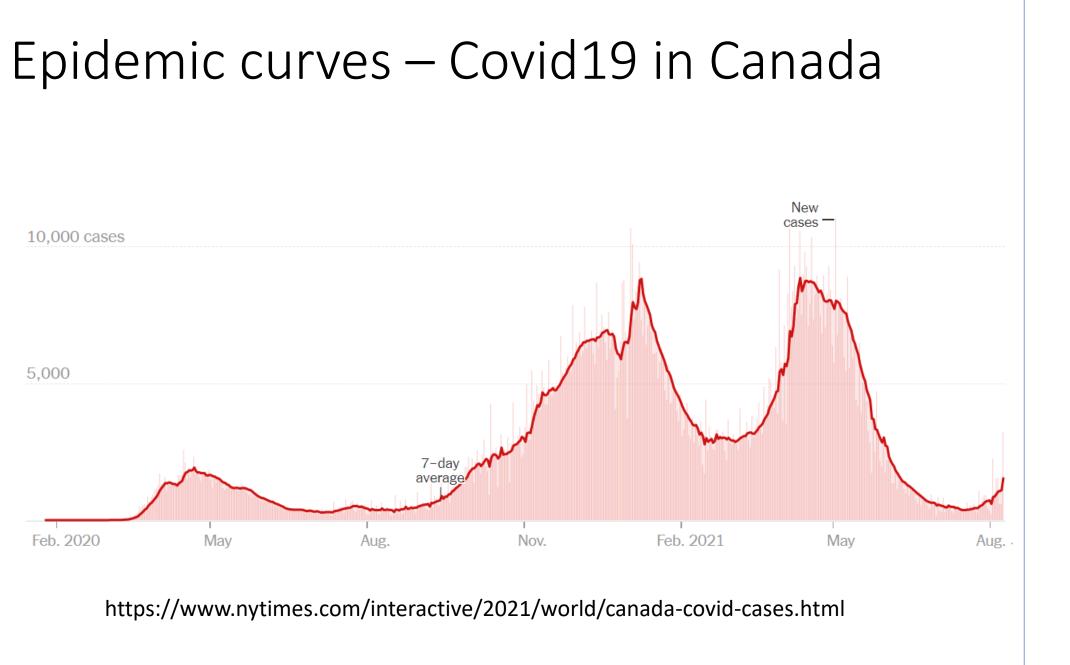
Epidemic modelling (SIR models) Lecture 12b: 2021-08-11

> MAT A35 – Summer 2021 – UTSC Prof. Yun William Yu

Image credit: https://commons.wikimedia.org/wiki/File:Coronavirus\_SARS-CoV-2.jpg



## SIS Model

- Modified assumption 1: The infection rate is proportional to the average number of times an infected individual encounters a susceptible individual in the population, assuming random encounters.
- Assumption 2: there is a total fixed population size N = I(t) + S(t), where S is the number of Susceptible individuals.
- Assumption 3: Individuals recover at rate  $\gamma$ , and become susceptible to re-infection.

#### SIS Model Properties

- In the SIS model, we call the ratio  $R_0 = \frac{\beta}{\gamma}$  the *basic reproduction number* of the system because it is the number of secondary infections  $\beta$  caused during the infectious period  $\frac{1}{\gamma}$ .
- If  $R_0 > 1$ , the disease persists and we are at the endemic disease equilibrium.

#### 1D systems and complex behavior

• Autonomous 1D ODE systems  $\dot{x} = f(x)$  can't have cycles or any doubling back because you'd have to cross a point going the other direction.

## Modelling waves

• How can ODE models capture the infection waves that we see in real epidemics?

A: Add more variablesB: Make them nonautonomousC: Add in births/deathsD: All of the aboveE: None of the above

• Let's try out a couple of options numerically.

## SIR Model

- Modified assumption 3: Individuals recover at rate  $\gamma$ , and become *Removed* R(t) from the population.
- Modified assumption 2: There is a total fixed population size N = I(t) + S(t) + R(t).

#### Reduce SIR model to two variables

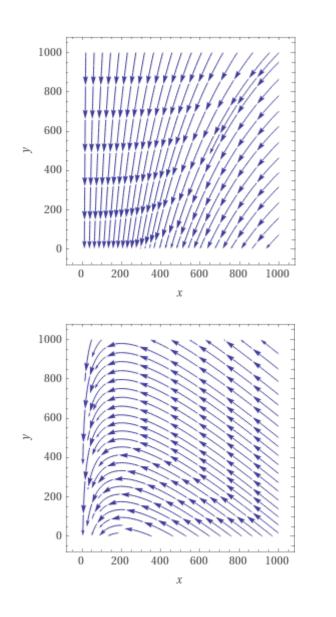
• 
$$\begin{cases} \dot{S} = -\frac{\beta}{N}SI\\ \dot{I} = \frac{\beta}{N}SI - \gamma I\\ \dot{R} = \gamma I \end{cases}$$

Plots of basic SIR model

• Let 
$$\beta = 0.1, \gamma = 0.2, N = 1000$$
  
•  $\begin{cases} \dot{S} = -\frac{0.1}{1000}SI \\ \dot{I} = \frac{0.1}{1000}SI - 0.2I \end{cases}$ 

• Let 
$$\beta = 0.1, \gamma = 0.02, N = 1000$$
  
•  $\begin{cases} \dot{S} = -\frac{0.1}{1000}SI \\ \dot{I} = \frac{0.1}{1000}SI - 0.02I \end{cases}$ 

WolframAlpha: streamplot {-1/10000 \* x \* y, x\*y/10000 - 0.2\*y}, x=0..1000, y=0..1000



## Basic SIR model gives a single wave

- Again,  $R_0 = \frac{\beta}{\gamma}$ .
- If  $R_0 < 0$ , then no epidemic happens because infected individuals never increase.
- If  $R_0 > 1$ , then an epidemic with a single wave happens.
- Then higher the  $R_0$ , the higher the peak. We can "flatten the curve" by reducing  $\beta$ , the transmission rate.
- <u>https://www.geogebra.org/m/p5ucts</u>
   <u>38</u> by Ivan De Winne

#### Nonautonomous Epidemic model

- What if  $\beta$  is sometimes high, and sometimes low, as a function of
- Then  $\begin{cases} \dot{S} = -\frac{\beta(t)}{N}SI \\ \dot{I} = \frac{\beta(t)}{N}SI \gamma I \end{cases}$  is not autonomous.

#### (autonomous) SIRS Epidemic Model

• Assumption 4: Removed individuals lose immunity at rate v.

Phase plane analysis of SIRS model

• 
$$\begin{cases} \dot{S} = -\frac{\beta}{N}SI + \nu(N - I - S) \\ \dot{I} = \frac{\beta}{N}SI - \gamma I \end{cases}$$

#### Qualitative analysis of equilibria

• 
$$\begin{cases} \dot{S} = -\frac{\beta}{N}SI + \nu(N - I - S) \\ \dot{I} = \frac{\beta}{N}SI - \gamma I \end{cases}$$

• Equilibria at  

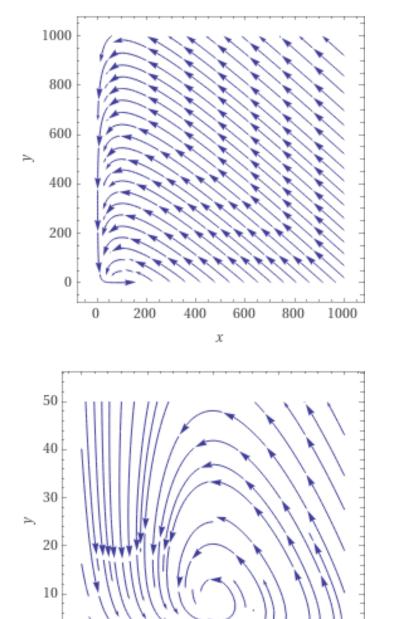
$$\begin{cases}
(S,I) = (N,0) \\
(S,I) = \left(\frac{N\gamma}{\beta}, \frac{\nu N \left(1 - \frac{\gamma}{\beta}\right)}{\gamma + \nu}\right)
\end{cases}$$

## Example with periodic behavior

• 
$$\beta = 0.1, \gamma = 0.01, \nu = 0.0001, N = 1000$$
  
•  $\dot{S} = -\frac{\beta}{N}SI + \nu(N - I - S) = -0.0001SI + 0.0001(1000 - S - I)$   
•  $\dot{I} = \frac{\beta}{N}SI - \gamma I = 0.0001SI - 0.01I$   
• Equilibria:  $(S, I) = (1000, 0) \text{ or } (S, I) \approx (100, 8.91)$   
• Jacobian  $J(S, I) = \begin{bmatrix} -0.0001I - 0.0001 & -0.0001S - 0.0001\\ 0.0001I & 0.0001S - 0.01 \end{bmatrix}$   
•  $J(1000, 0) = \begin{bmatrix} -0.0001 & -0.1001\\ 0 & 0.09 \end{bmatrix}, \lambda_1 = -0.0001, \lambda_2 = 0.09, \text{ saddle pt}$   
•  $J(100, 8.91) = \begin{bmatrix} -0.000991 & -0.0101\\ 0.000891 & 0\\ 0.000891 & 0 \end{bmatrix}, \lambda_{1,2} \approx -0.0004955 \pm 0.00296i$   
so the equilibrium is an attracting spiral

# Visualization

- streamplot {- x \* y/10000 + 0.0001\*(1000-x-y), x\*y/10000 - 0.01\*y}, x=0..1000, y=0..1000
- streamplot {- x \* y/10000 + 0.0001\*(1000-x-y), x\*y/10000 - 0.01\*y}, x=0..400, y=0..50



100

50

150

200

0

#### More sophisticated epidemic models

- Vaccinations
- Birth/Death
- Exposed but not Infectious

# Modelling summary



- We can build models of complex biological phenomenon like epidemics by looking at behavior we care about and adding more assumptions to reproduce that real behavior in our models.
- Sometimes, we can get similar behavior with two different assumptions, so as mathematical biologists we need to decide what fits better.
- For epidemic modelling, these can include additional variables/compartments, as well as new arrows between compartments.