Big Question:

How do the factors of vaccination and death effect disease?

We are asking this question to gain a better understanding of the SIRVD model. We arent looking for a specific numerical answer, instead our aim is to interpret broad trends in our simulations. Seeing the direct effects of these variables can be used to inform disease response. In order to build our models we'll have to understand the math behind the SIRVD and SIRS models.

Research Matrix

Sources -> Themes | v	Modeling the Spread of COVID-19 Using Nonautonomous Dynamical System with Simplex Algorithm-Based Optimization for Time-Varying Parameters *Kevin Yotongyos, Somchai Sriyab*	Mathematics of Epidemics: On the General Solution of SIRVD, SIRV, SIRD, and SIR Compartment Models *Reinhard Schlickeiser, Martin Kröger*	Deep learning infused SIRVD model for COVID-19 prediction: XGBoost-SIRVD-LSTM approach *Hisham Alkhalefah, D. Preethi, Neelu Khare, Mustfa Haider Abidi*
Overall focus	Using the SIRVD model to represent COVID-19	Math behind the SIR models	Tuning variable rates using DL
Modeling	- The flow parameters for R and D should add to 1 - p is probability of death - sigma is vaccination rate	- The model rates can be described as the ratios: gamma(recovery)/sigma and gamma(death)/beta	-Variable rate models are able to achieve R^2 values of 0.99 when compared to validation data
Synergies	Establishes the rate parameters used by the other papers.	Builds on the Yotogyos and Sriyab paper by describing the relationship between the rate parameters.	This paper is similar to the Yotongyos and Sriyab paper in that they are varying the parameters with respect to time

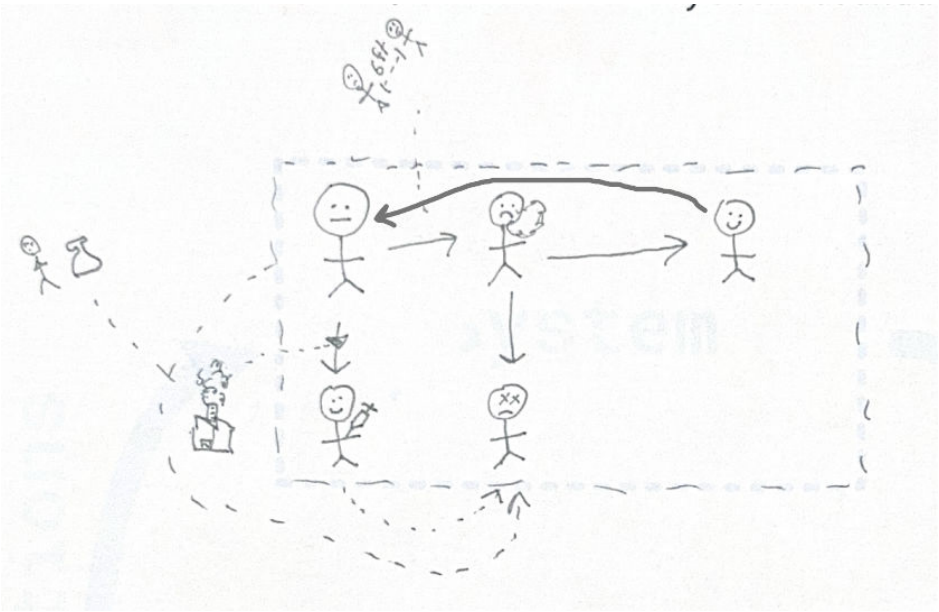
Methodology:

The plan is as follows:

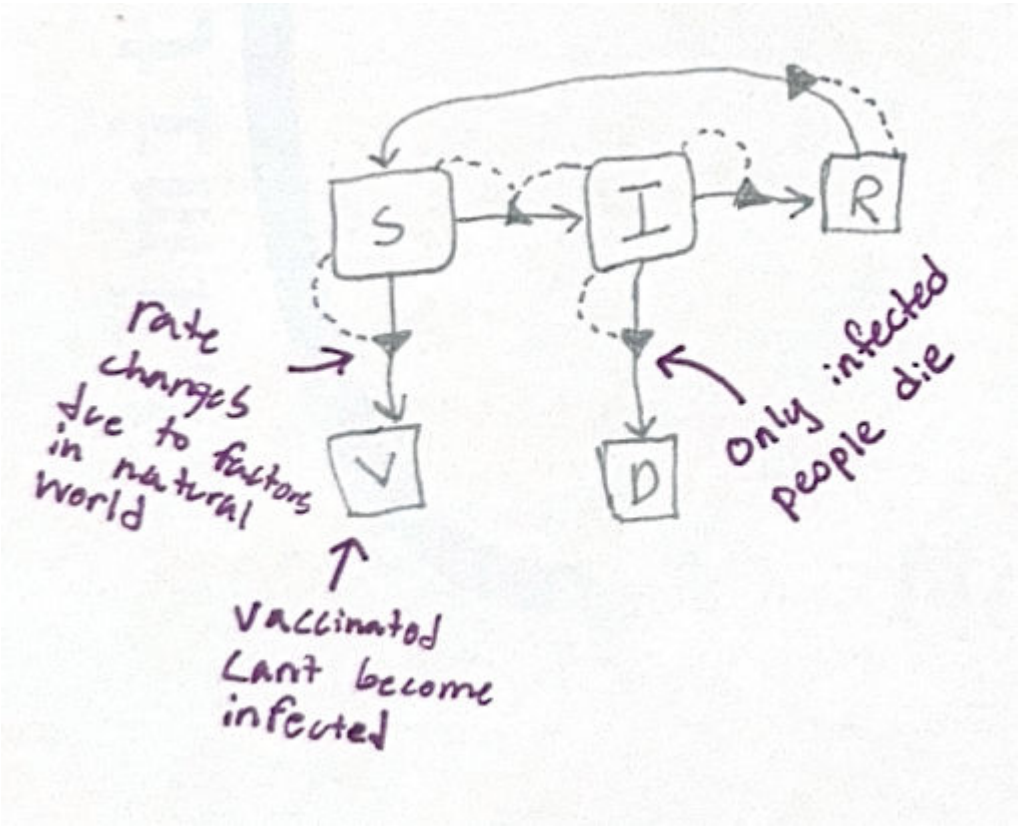
1. Implement the SIRS model and the SIRVD model
2. Perform parameter sweeps over all variables for both model
3. Compare and interpret thedata to see the effects of vaccination and death

Model:

We will implement the SIRVD model and adapt it as the SIRS model. We have drawn a tenchi diagram that shows the boundry od the natural world:



For a clearer view of whats going on we have a stock and flow model:



- S = Susceptible
- I = Infected
- R = Recovered

- V = Vaccinated
- D = Dead

As noted in the diagram, our model is subject to certain limitations:

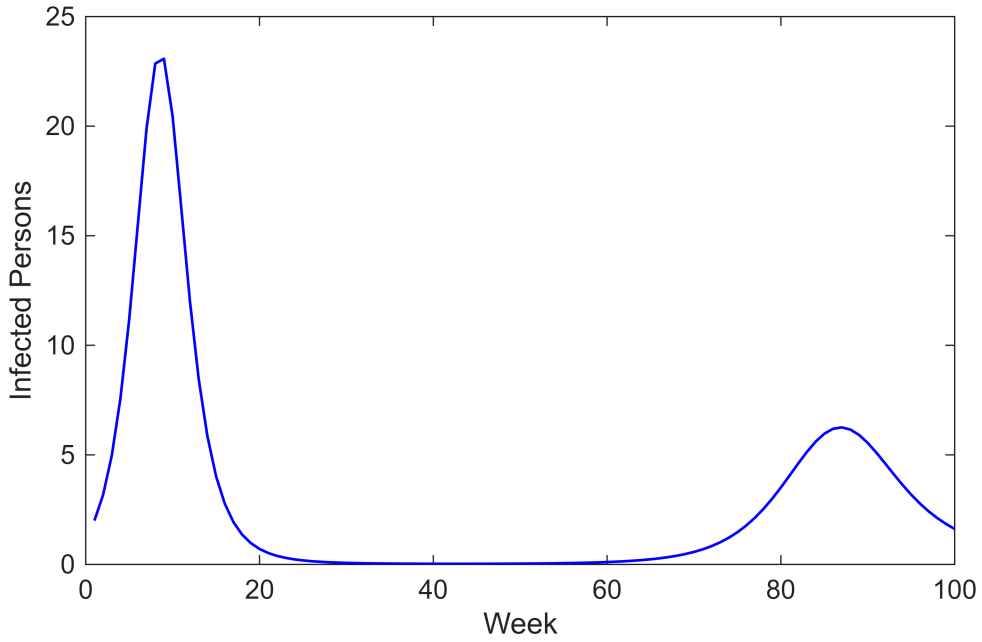
- Only infected people die. In the real world all groups have an additional miniscule chance of dying at all times. The parameters typically used for this chance are extremely small (<2x10^-5) and given this parameter will not be a factor in either the SIRVD or SIRS model it can safely be disregarded
- Vaccinated people can't become infected. In reality vaccine effectiveness can differ between people and wear off. While this may make our models less useful for looking at raw number statistics, the effect that vacines have will remain the same in principle
- Vaccine rate only changes based on the number of susceptible people. There are many external factors in the real world that can contribute to vaccination rates. These include funding for programs, development time, and manufacturability. While this could be useful information, it's not necessary to see the effects of vaccination in general.

Implementation:

First lets take a look at the SIRS model. This is a model primarily used for modeling infectious diseases. The name SIRS comes from the stocks that are used in the model. These being people that are **S**usceptible, **I**nfectious, **R**ecovered, and **S**usceptible (again). The reason susceptible appears twice is to take into account recovered indivicuals becoming re-susceptible.

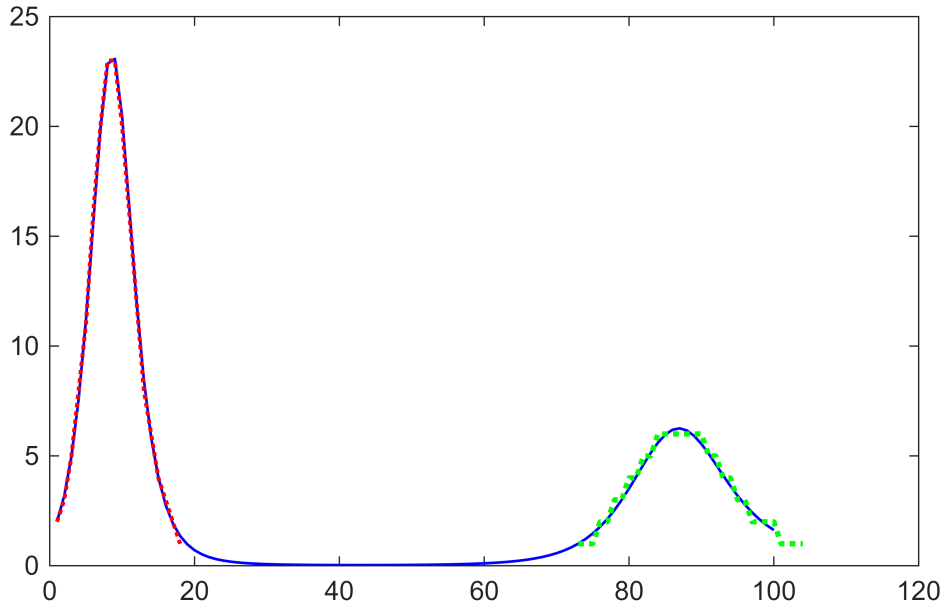
Here is a simple implementation of the SIRS model:

```
% Configure the simulation
beta = 1 / 90;                    % Infection rate
gamma = 1 / 2;                   % Recovery rate
alpha = 1/60;                     % Resuseptible Rate
week_end = 100;                % Weeks to simulate
i_1 = 2;                              % Initial count of infected persons
s_1 = 100 - i_1;                 % Initial count of susceptible persons
r_1 = 0;                              % Initial count of recovered persons

% Run simulation
[S_long, I_long, R_long, W_long] = simulate_sirs(s_1, i_1, r_1, beta, gamma, alpha,
week_end);

% Plot the fitted simulation
figure()
plot(W_long, I_long, 'b-', 'LineWidth', 1, 'DisplayName', 'Simulated'); hold on
xlabel("Week")
ylabel("Infected Persons")
hold off
```



This model can be overlaid with a dataset to anecdotally show its accuracy:

```
% Load the training + validation data
tab_data_validate = readtable("wave1.csv", "Delimiter", ",");
tab_data_wave2 = readtable("wave2.csv", "Delimiter", ",");

% Plot the model + data
plot(W_long, I_long, 'b-', 'LineWidth', 1, 'DisplayName', 'Simulated'); hold on
plot(tab_data_validate.Week, tab_data_validate.InfectedCount, 'r:', 'LineWidth',
1.5, 'DisplayName', 'Wave 1')
plot(tab_data_wave2.Week, tab_data_wave2.InfectedCount, 'g:', 'LineWidth', 2.0,
'DisplayName', 'Wave 2')
```



Noteably this model can show a second wave of infections due to recovered individuals becoming re-susceptible.

The step function for the SIRS model is shown below:

```
% -- Compute new infections and recoveries --
% infected = beta * i * s;
% recovered = gamma * i;
% resuseptible = alpha * r;
%

% -- Stocks cannot decrease by more than their current value --
% infected = min(infected, s);
% recovered = min(recovered, i);
% resuseptible = min(resuseptible, r);
%
% -- Update state --
% s_n = s - infected + resuseptible;
% i_n = i + infected - recovered;
% r_n = r + recovered - resuseptible;
```

Now for the SIRVD model. Similar to the SIRS model the SIRVD model takes into account people becoming re-susceptible. The main difference is the additional variables for **V**accinations and **D**eaths. By adding these stocks in we are able to see more complex behavior.

This is the code for one step of the SIRVD model:

```
% -- Compute new infections and recoveries --
% infected = beta * i * s;
% resuseptible = alpha * r;
% vaccinated = sigma * s;
% recovered = (1-p) * gamma * i;
% dead = p * gamma * i;
%
% -- Stocks cannot decrease by more than their current value --
% infected = min(infected, s);
% recovered = min(recovered, i);
% resuseptible = min(resuseptible, r);
%
% -- Update state --
% s_n = s - infected + resuseptible - vaccinated;
% i_n = i + infected - recovered - dead;
% r_n = r + recovered - resuseptible;
% v_n = v + vaccinated;
% d_n = d + dead;
```

In order to verify our model works we run a few tests using arbitrary data

1. Does the population ever go up?

```
% -- Add all of the stocks to check the total number of people --
% T_sirvd = S_sirvd + I_sirvd + R_sirvd + V_sirvd + D_sirvd;
%
% -- Assert that the total never exceeds 100 peeople --
% assert(all(T_sirs-100 < 1e-10))
```

2. Do the number of vaccinations ever go down?

```

```

3. Do vaccinations and deaths ever go down?

With the model implemented and verified we needed to decide on parameters such as infection rate, recovery rate, etc. and starting conditions. Since we dont have to do validation, we can use the values from previous models. With our parameters set we can run all the models, performing parameter sweeps on vaccination rate and mortality rate

```
%run simulations but dont graph them
```

Results:

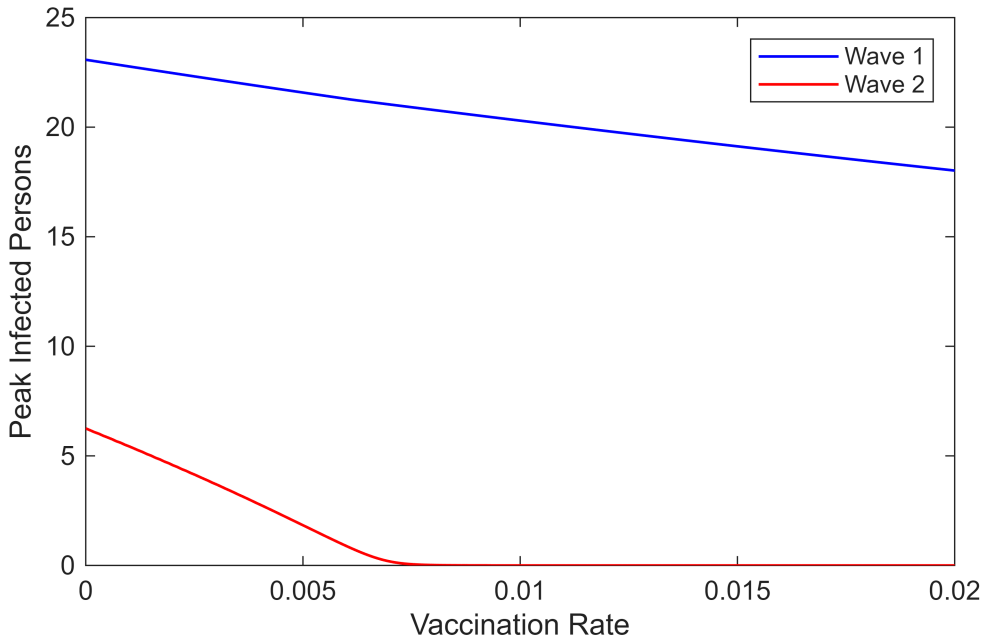
The parameters we will be sweeping are vaccination rate and mnortality rate. The metric thqat will be used to judge these are infections.

```
% Vaccination rates to sweep over
sigma_all = linspace(0, 1/50, 200);

% Mortality rates to sweep over
p_all = linspace(0, 0.5, 200);

% Metrics
wave1_maxes_v = zeros(1, length(sigma_all));
wave2_maxes_v = zeros(1, length(sigma_all));

wave1_maxes_d = zeros(1, length(p_all));
wave2_maxes_d = zeros(1, length(p_all));

% Configure the simulation
beta = 1 / 90; % Infection rate (New / Susceptible / Infected / day)
gamma = 1 / 2; % Recovery rate (1 / day)
alpha = 1/60; % Resuseptible Rate
sigma = 0;
p = 0; % Mortality Rate
week_end = 300;
i_1 = 2;       % Initial count of infected persons
s_1 = 100 - i_1;
r_1 = 0;
v_1 = 0;
d_1 = 0;

function [I_max_wave1, I_max_wave2] = wave_maxes(I_sirvd, W_sirvd)
    % Isolate the two maxima
    idx = islocalmax(I_sirvd);

    W_max = zeros(1, 2);
    I_max = zeros(1, 2);

    W_max = W_sirvd(idx);
    I_max = I_sirvd(idx);

    I_max_wave1 = I_max(1);

    if numel(I_max) >= 2
        I_max_wave2 = I_max(2);
    else
        I_max_wave2 = 0;
    end
end
```

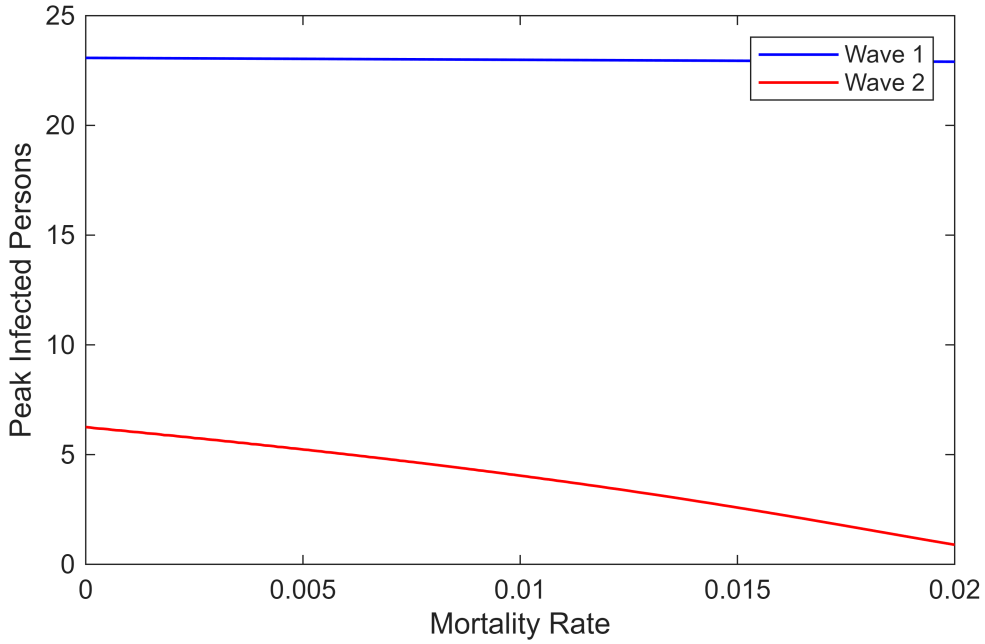
```
for i = 1:length(sigma_all)
    sigma_temp = sigma_all(i);
    [S_sirvd, I_sirvd, R_sirvd, V_sirvd, D_sirvd, W_sirvd] = simulate_sirvd(s_1,
i_1, r_1, v_1, d_1, beta, gamma, alpha, sigma_temp, p, week_end);
    [wave1_maxes_v(i), wave2_maxes_v(i)] = wave_maxes(I_sirvd, W_sirvd);
end

for i = 1:length(p_all)
    p_temp = p_all(i);
    [S_sirvd, I_sirvd, R_sirvd, V_sirvd, D_sirvd, W_sirvd] = simulate_sirvd(s_1,
i_1, r_1, v_1, d_1, beta, gamma, alpha, sigma, p_temp, week_end);
    [wave1_maxes_d(i), wave2_maxes_d(i)] = wave_maxes(I_sirvd, W_sirvd);
end
```

Result Graphs

```
figure()
title("Vaccination")
plot(sigma_all, wave1_maxes_v, 'b-', 'LineWidth', 1, 'DisplayName', 'Wave 1'); hold
on
plot(sigma_all, wave2_maxes_v, 'r-', 'LineWidth', 1, 'DisplayName', 'Wave 2');
legend()

yl = ylim;
ylim([0, yl(2)])

xlabel("Vaccination Rate")
ylabel("Peak Infected Persons")
```



```
figure()
title("Death")
plot(sigma_all, wave1_maxes_d, 'b-', 'LineWidth', 1, 'DisplayName', 'Wave 1'); hold
on
plot(sigma_all, wave2_maxes_d, 'r-', 'LineWidth', 1, 'DisplayName', 'Wave 2');
legend()

yl = ylim;
ylim([0, yl(2)])

xlabel("Mortality Rate")
ylabel("Peak Infected Persons")
```



Analysis

- What are the most important trends in your parameter sweep(s)?
- How do your results relate to your modeling question?

Vaccination

The trend in the first wave infected people was that even a large increase in vaccination could not produce a large decrease in peak infected people. However, even a tiny change in vaccination (0.007) was able to entirely remove the second wave and prevent further sickness.

Todo: Expand

Mortality

An increasing mortality rate had no effect on wave 1 peak infections. This is because deaths only decrease the number of infections by preventing people from going from recovered back to suseptible. Therefore, the only way death could have an effect on the first peak is if it happened over a very large period of time. However, death *did* have a large impact on the second wave. While it didn't shrink the peak infections significantly, it shifted the second wave back enormously. Even a relatively small death rate of 0.013 shifted the second wave beyond week 150. As such, we had to exand the time frame of the simulation to accomodate for the late-acting second wave.

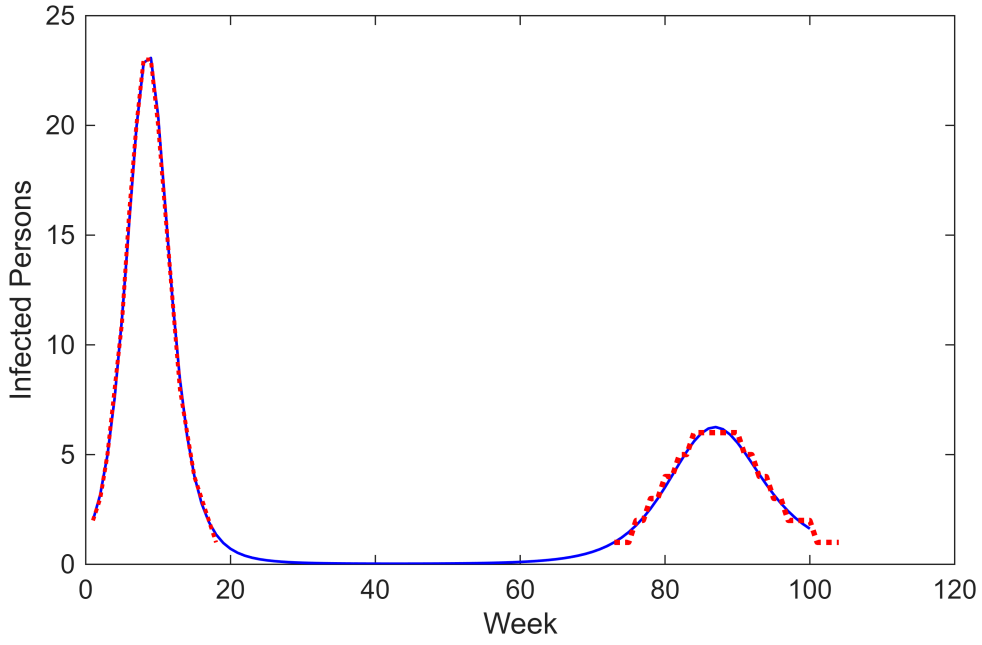
Interpretation (todo):

- ***Therefore***
- How do the results answer the question?
- ***Limitations and Future Work***
- What are some questions we might like to to answer, but the current limitations prevent us from answering?
- How could you modify the model to overcome those limitations?

```
% Load the training + validation data
tab_data = readtable("infected.csv", "Delimiter", ",");
W_data = tab_data.Week;
I_data = tab_data.InfectedCount;
tab_data_validate = readtable("wave1.csv", "Delimiter", ",");
tab_data_wave2 = readtable("wave2.csv", "Delimiter", ",");
```

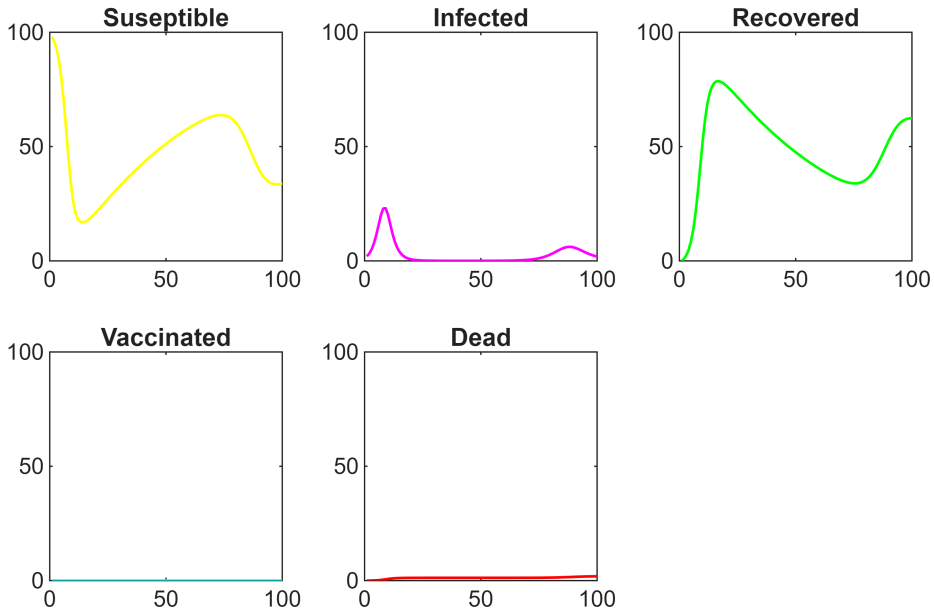
```
% Configure the simulation
beta = 1 / 90; % Infection rate (New / Susceptible / Infected / day)
gamma = 1 / 2; % Recovery rate (1 / day)
alpha = 1/60; % Resuseptible Rate
% week_end = 100;
week_end = 100;
i_1 = 2;       % Initial count of infected persons
s_1 = 100 - i_1;
r_1 = 0;

% Run simulation
[S_sirs, I_sirs, R_sirs, W_sirs] = simulate_sirs(s_1, i_1, r_1, beta, gamma, alpha,
week_end);
```

```
% Plot the fitted simulation
figure()
plot(W_sirs, I_sirs, 'b-', 'LineWidth', 1, 'DisplayName', 'Simulated SIRS'); hold on
plot(tab_data_validate.Week, tab_data_validate.InfectedCount, 'r:', 'LineWidth',
1.5, 'DisplayName', 'Wave 1')
plot(tab_data_wave2.Week, tab_data_wave2.InfectedCount, 'r:', 'LineWidth', 2.0,
'DisplayName', 'Wave 2')
xlabel("Week")
ylabel("Infected Persons")
```




```
v_1 = 0;
d_1 = 0;

beta = 1/90;
gamma = 1/2;
alpha = 1/60;
sigma = 0;
p = 0.013;

[S_sirvd, I_sirvd, R_sirvd, V_sirvd, D_sirvd, W_sirvd] = simulate_sirvd(s_1, i_1,
r_1, v_1, d_1, beta, gamma, alpha, sigma, p, week_end);

T_sirvd = S_sirvd + I_sirvd + R_sirvd + V_sirvd + D_sirvd;
assert(all(T_sirvd-100 < 1e-10))

assert(all(diff(V_sirvd) >= 0))

figure()
```

```
subplot(2, 3, 1)
plot(W_sirvd, S_sirvd, 'y-', 'LineWidth', 1, 'DisplayName', 'Simulated SIRVD');
hold on
ylim([0 100])
title('Suseptible')

subplot(2, 3, 2)
plot(W_sirvd, I_sirvd, 'm-', 'LineWidth', 1, 'DisplayName', 'Simulated SIRVD');
hold on
ylim([0 100])
title('Infected')

subplot(2, 3, 3)
plot(W_sirvd, R_sirvd, 'g-', 'LineWidth', 1, 'DisplayName', 'Simulated SIRVD');
hold on
ylim([0 100])
title('Recovered')

subplot(2, 3, 4)
plot(W_sirvd, V_sirvd, 'c-', 'LineWidth', 1, 'DisplayName', 'Simulated SIRVD');
hold on
ylim([0 100])
title('Vaccinated')


subplot(2, 3, 5)
plot(W_sirvd, D_sirvd, 'r-', 'LineWidth', 1, 'DisplayName', 'Simulated SIRVD');
hold on
ylim([0 100])
title('Dead')
```



```
figure()
hold on
plot(W_sirvd, S_sirvd, 'y-', 'LineWidth', 1, 'DisplayName', 'Suseptible');
plot(W_sirvd, R_sirvd, 'g-', 'LineWidth', 1, 'DisplayName', 'Recovered');
plot(W_sirvd, V_sirvd, 'c-', 'LineWidth', 1, 'DisplayName', 'Vaccinated');
plot(W_sirvd, D_sirvd, 'r-', 'LineWidth', 1, 'DisplayName', 'Dead');
plot(W_sirvd, I_sirvd, 'm-', 'LineWidth', 1, 'DisplayName', 'Infected');
legend()
```