Dynamical Networks and Control

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In essence, the primary goal of our project is to build a strategy to predict, control, and write policies based on the dynamical network in order to maximize the benefits considering the interventions of vaccine and/or treatments. First, we implemented the SIRD model to apply and describe how COVID-19 evolves within the population regions of St. Louis, Kansas City, and the rest of Missouri. Then, using fmincon, we tried to achieve "parameter optimization" which helps us to find the rate-constants and initial conditions in order to minimize the cost. We upgraded our model in order to construct a stronger and larger dynamical network that updates the model while considering the flow of population within- and across- regions. We applied this model to paradigm A in order to analyze the difference in viral propagation dynamics and paradigm B to discover intervals of time stamps that model different phases of propagation. By taking a careful look at our final model, we created certain algorithms that can predict, control, and design policies regarding the progression of the disease that optimizes the relative benefits of the population given the intervention strategies. In conclusion, we implicated that while our intervened data resulted in less cumulative cases and slightly less death cases, the predicted trend showed a linear growth of cumulative cases and death cases which isn't the optimal idea that we desired.

I. INTRODUCTION

This project leads the students to employ the concepts taught in the textbook and lecture in order to not only express them theoretically, but also practically by applying the concepts to real life situations. Specifically, the project challenges the students to utilize the concept of dynamical networks taught during class and pod videos which builds up to the ultimate goal to create an algorithm that determines the trend of COVID19 disease progression.

II. METHODS

The goal of this project is to use the SRI models to build a policy design that describes how to effectively use the vaccines and/or treatment to maximize the relative benefits compared to the cost.

In order to achieve this goal, first we had to successfully accomplish SIR Modeling. We initialized a matrix with the first row representing susceptible, second row representing the infected, third row representing the recovered, and the fourth row representing the deceased. Then, we used a for loop that iterated through

$$D_i = A * D_{(i-1)}$$

(1)

D_i: Data of day i

A: Matrix that contains constants

D_{i-1}: Data of day i-1

After plotting the new matrix D, we would get our SIR model of that situation.

Then, since we found how to plot the base model of SRI, we continued to work on to find the model rate constants (infection rate, fatality rate, recover rate) and initial conditions (initial values of susceptible, infected, recovered and deceased fraction).

For Paradigm A, we set our values for initial settings described in the code in Matlab, then using siroutput(), we are able to calculate the cost given,

$$C = ||c_p\text{-}c_a|| + ||d_p\text{-}d_a||$$

(2)

C: Cost

c_p: predicted number of cumulative cases

c_a: actual number of cumulative cases

d_p: predicted number of death cases

d_a: actual number of death cases

Then we can use the fmincon() function in order to minimize the given cost from the siroutput() function. Using this, we can use siruput_full() function which calculates the values needed for the SIRD model of ST. Louis City, Kansas City, and other Missouri areas. Finally, we plotted the final SIRD model.

For Paradigm B, we used our intuition (our eyes) to choose the time-points that seem to model different phases of propagation. Our interval was day 1 to 120, day 121 to 150, and day 151 to 229. In order to model this data, we would first split the data of cumulative cases and death percentage into our three intervals. Then we would use fmincon() for each of the intervals independently in order to calculate the SIRD model. Applying the methods independently is an important step since we need to initialize new lower and upper boundaries for the next intervals.

To build a larger network we created new interaction parameters. To do so, we utilized the interaction_siroutput() which calculated the cost of the interaction model. In this

function, we set up three SIRD within-population transmission matrices, and then concatenated them into a single and larger matrix. In addition, using interaction_siroutput_full(), it is possible to simulate the larger SIRD model for t (a given time scalar) times. After extracting the data from April 1st to November 1st, we can set t as 215 days and by using fmincon() and interaction_siroutput_full(), we can analyze best set of 27 parameters, and use them to calculate the large SIRD model for the three given regions.

In order to successfully plot prediction of the cases past 229 days, we loaded the data that contained number of cumulative cases and death percentage in St. Louis City for 365 days. Then, by setting the fmincon() with the new time length, we plotted the new SIRD model that drew predicted cases and death past 229 days.

$$J_{benefit} = 10*(||\Delta I||)+10*(||\Delta D||)$$

(3)

$$J_{cost} = 800*(1-\gamma)(||\Delta I||)^2 + 800*(1-\beta)(||\Delta D||)^2$$

(4)

$$J_{relative} = J_{benefit} - J_{cost}$$

(5)

To find how our model changed due to the intervention, we completed the jrelative(). In this function, we set up one SIRD model affected by our policy and another not affected by our policy. Then, we were able to find delta D which is the norm of the difference of deaths between both models and delta I which is the norm of the difference between the number of cumulative cases. Gamma is defined k_infections2/k_infections which is the ratio of the transmission parameter of infection after intervention over current transmission parameter of infection respectively. Beta is defined k_fatality2/k_fatality, which is the ratio of the transmission parameter of fatality after intervention over current transmission parameter of fatality respectively.

Then using the J_relative, we applied the fmincon() function on this value and new initial settings. Our next step involved us to create a new SIRD matrix for the policy parameters in order to generate a new SIRD model using sproutput_full() method. Using the new SIRD model, we plotted the measured number of cumulative cases, measured number of deaths, predicted number of cumulative cases, predicted number of deaths, intervened number of cumulative cases, and intervened number of deaths.
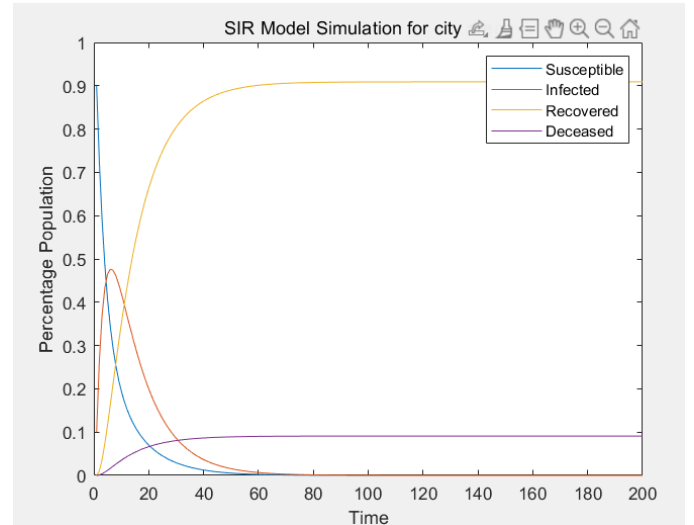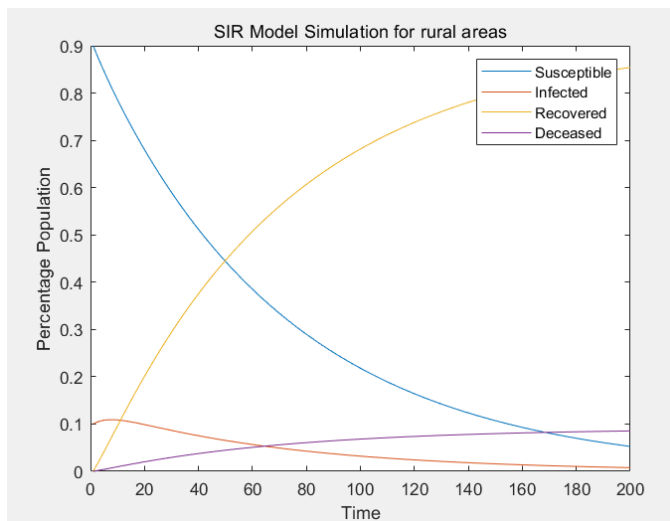
III.   RESULTS AND DISCUSSION
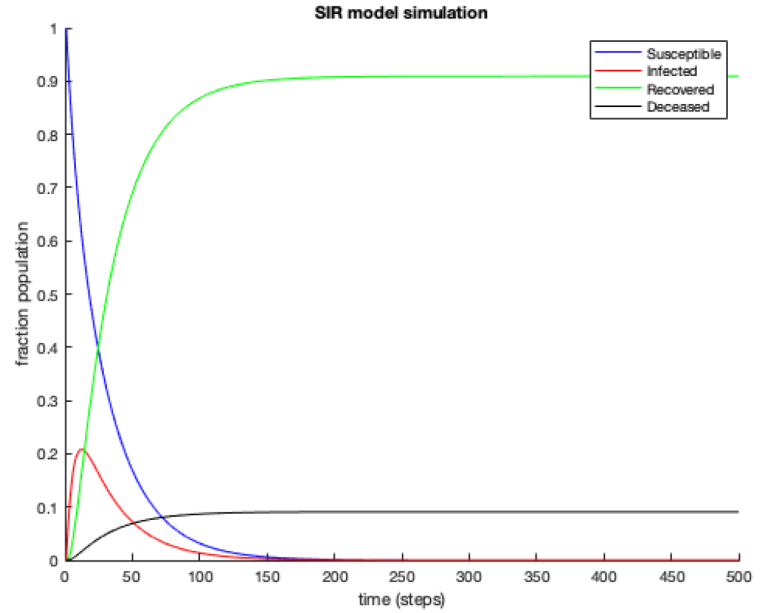
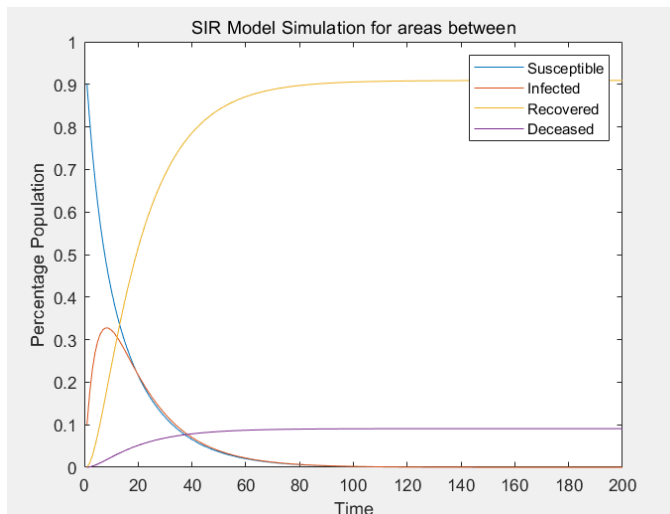1.   x- axis: Time (steps)

2.   y-axis: Fraction Population

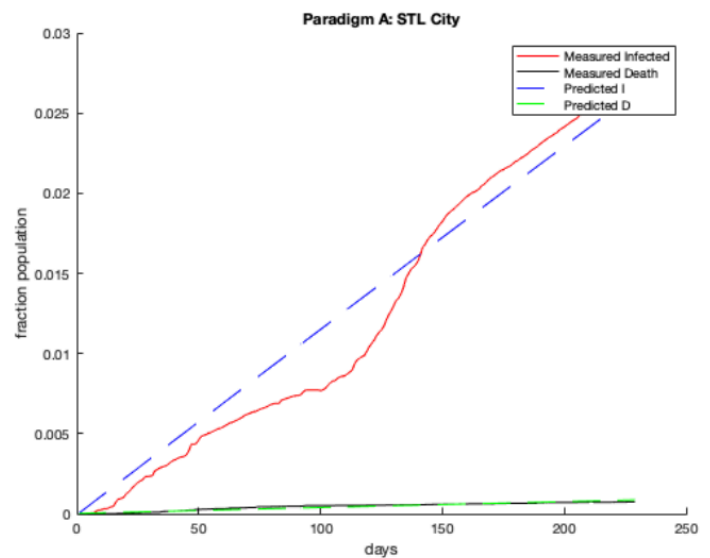
1. x- axis: Time (steps)

2.   y-axis: Fraction Population

SIR Model Simulation for rural areas

1. x- axis: Time (steps)

2. y-axis: Fraction Population

Paradigm A: STL City

1. x-axis: days

2. y-axis: Fraction Population
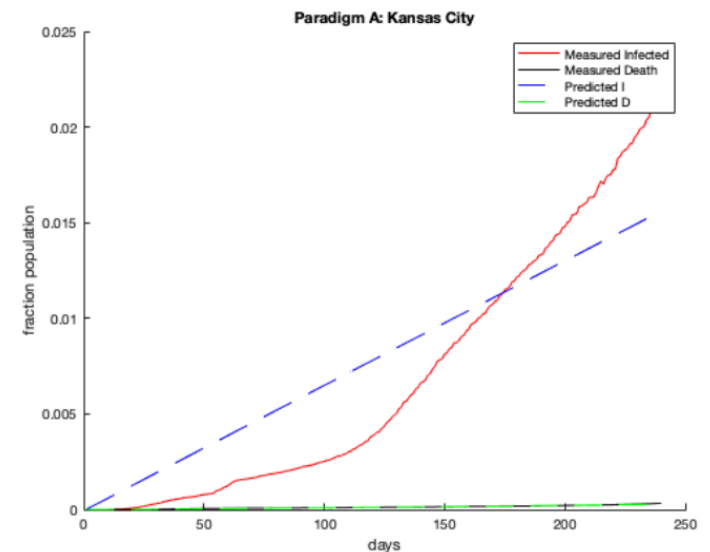

SIR Model Simulation for areas between

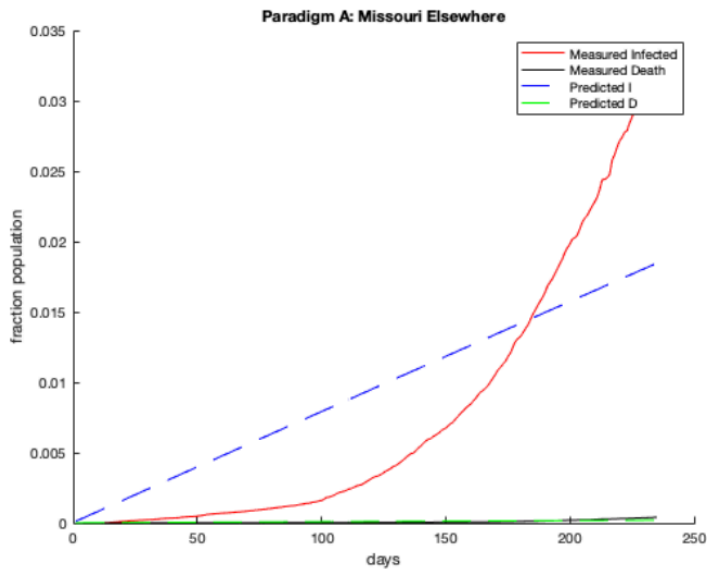1. x- axis: Time (steps)

2. y-axis: Fraction Population

The plots above show the SIR model from the textbook section 9.3, from higher population density, from lower population density, and middle population density respectively. From the simulated model of the graphs, we see higher population density means more people will be infected in one day. Higher population density areas have greater maximum infected population and reach that maximum rapidly. The rural areas have much fewer people infected than in city areas. It takes relatively shorter period of time for dense population area to reach an equilibrium than low population density area.

Paradigm A: Kansas City

1. x-axis: days

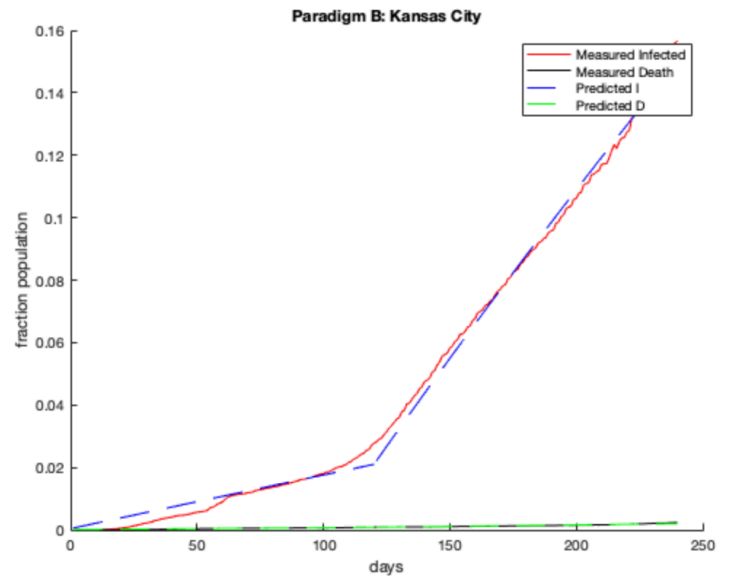2. y-axis: Fraction Population

Paradigm A: Missouri Elsewhere

1. x-axis: days
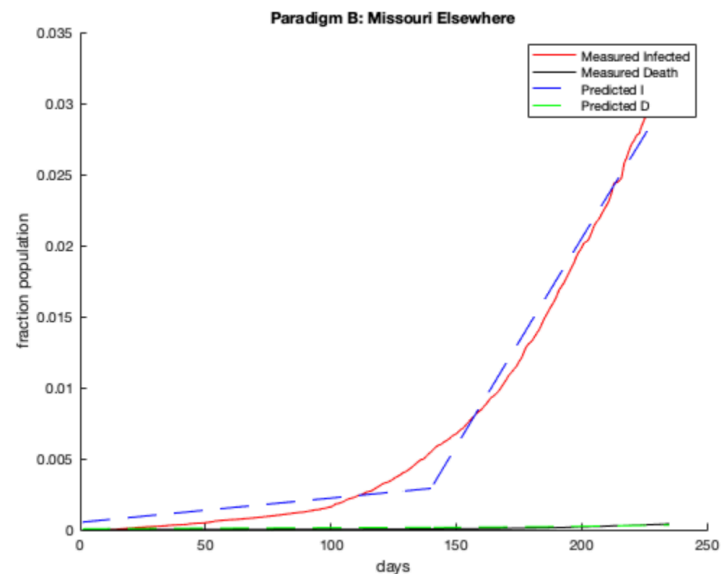
2. y-axis: Fraction Population

In the three plots above given from paradigm A, the model fits do speak to differences in viral propagation dynamics in each regions. This is due to the different data of cumulative cases and death percentage for each area resulting in various rate-constants when calculated through fmincon() and the cost from siroutput().

Paradigm B: STL City
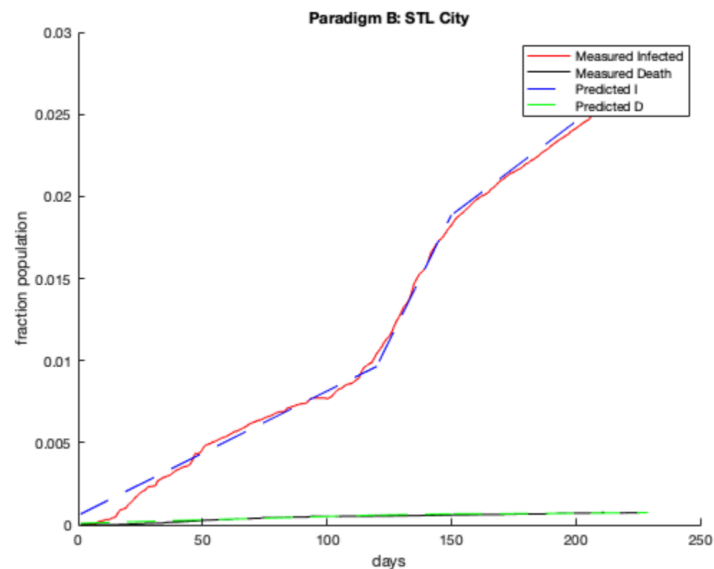
1. x-axis: day

2. y-axis: Fraction Population

Paradigm B: Kansas City

1. x-axis: days

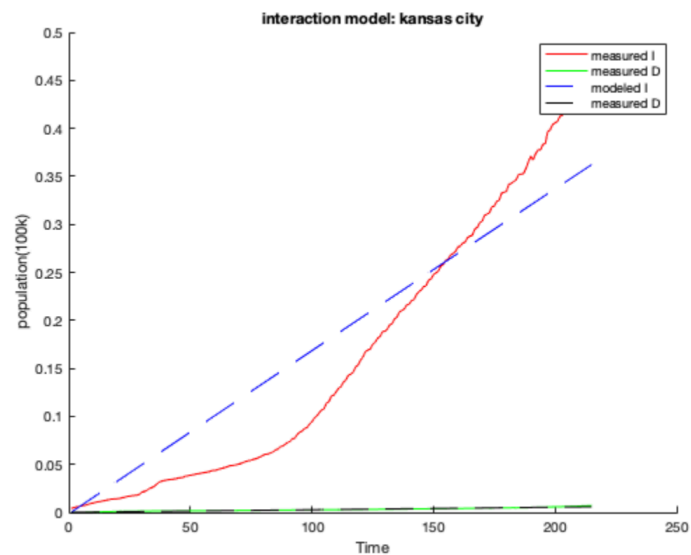2. y-axis: Fraction Population

Paradigm B: Missouri Elsewhere

1.x-axis: days

2.y-axis: Fraction Population

By choosing the time interval of day 1 to 120, day 121 to 150, and day 151 to 229, we are able to find out that the model fits do speak to differences in viral propagation dynamics between these phases. We chose these intervals based on the fact that there is a curve on measured infected around those days. However, the plot isn't perfect because the interval is chosen solely depending on our intuition and eyeing out. Thus, the time phases that we chose might not be the best/ optimized time intervals at which the propagation dynamics appear to change. In other words, there might exist another
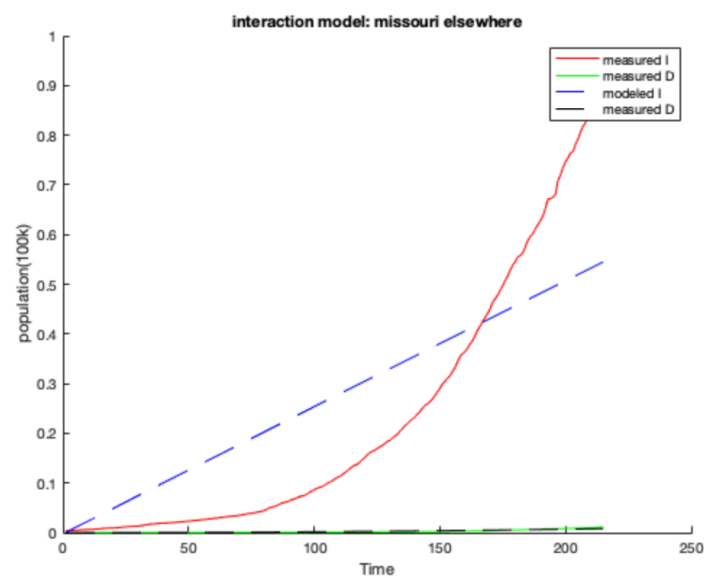
time points in which the propagation dynamics appear to change in a clearer manner.
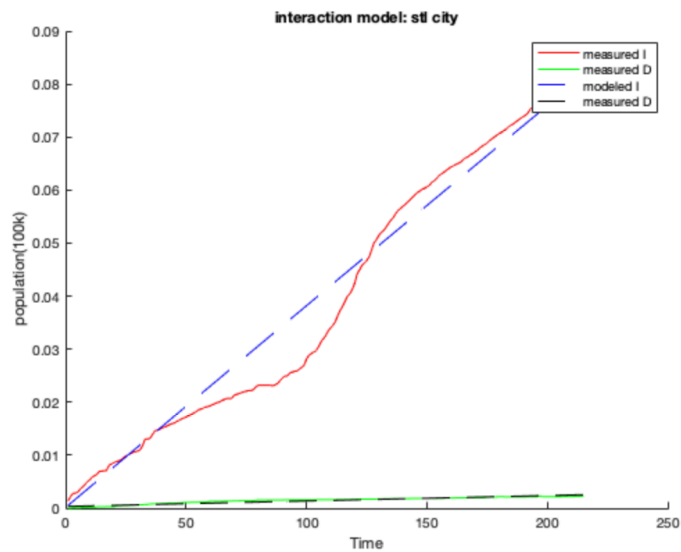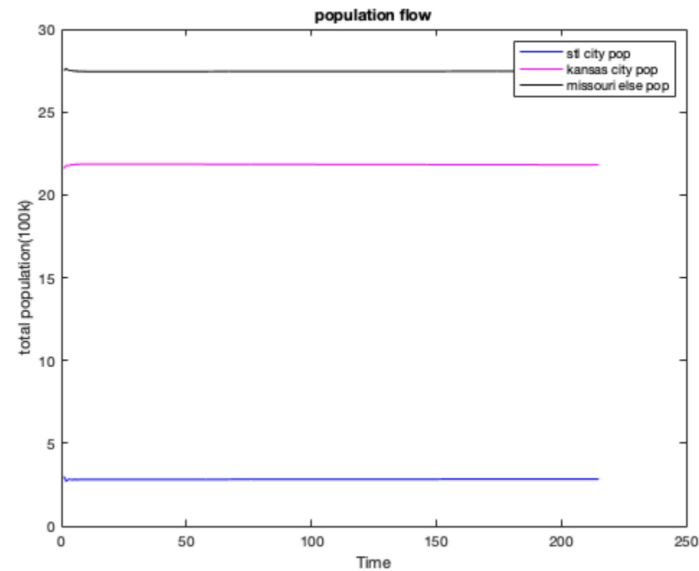
interaction model: stl city

1. x-axis: Time (days)

2. y-axis: Population (100k)

interaction model: kansas city

1. x-axis: Time (days)

2. y-axis: Population (100k)
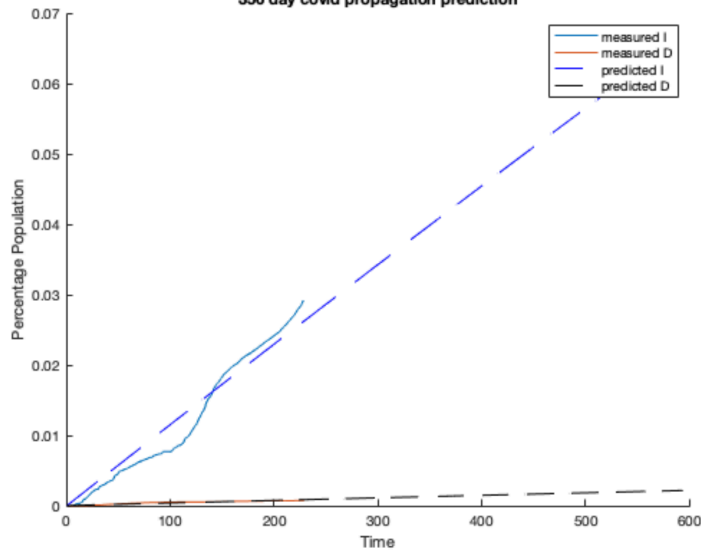
interaction model: missouri elsewhere

1. x-axis: Time (days)

2. y-axis: Population (100k)

population flow

1. x-axis: Time (days)

2. y-axis: Population (100k)

The above plots draw the interaction models based on the new parameters. Taking internal transmission rate, initial conditions, interaction rate which describes the population traveling outside to other regions into considerations, we are able to use interaction_siroutput_full() to calculate the large SIRD model for each regions.

356 day covid propagation prediction

The result of this graph interprets the predicted number of cumulative cases and deaths in 365 days. This means we simulated how the disease would evolve in the future based on past data. Our prediction doesn't take into account of 'herd immunity' as the predicted cumulative cases seem to linearly grow as where if 'herd immunity' was applied then over time, more people should have become immune to the disease leading to shortening of cases. This, however, also elucidates a limitation in our prediction in which it fails to take an external factor into account. In other words, since the prediction is based on past trends, even if there are any severe outbreaks (festival seasons) or beginning of 'herd immunity' in the future, the model fails to take those into account.

policy design
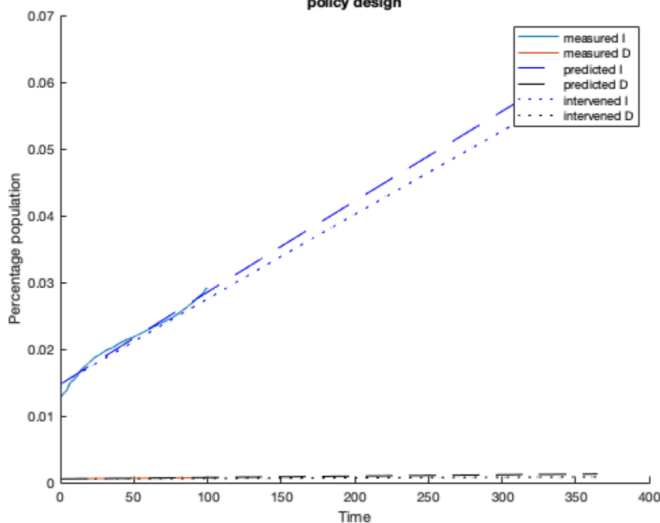
1.x-axis: Time (days)

2.y-axis: Percentage Population

The graph above plots the predicted cumulative cases and deaths based on the intervention of a new vaccine and/or treatment which are applied to calculate Jrelative. By generating 2 parameters intervened_I and intervened_D which have the highest relative cost, we can then derive find the optimized parameters using fmincon(). Then, we can generate the SIRD model that can be used to plot the simulation. While, the intervened number of cases decreased compared to the predicted number of cases, certain limitations exist in which the intervened D doesn't necessarily show a huge difference. In addition, the policy design doesn't prevent the trend to linearly grow meaning that the policy could not optimize the number of cases and deaths by curving them down.

IV.   CONCLUSION

In summary, our final model regarding policy did show positive results in terms of down regulating infection rate and reducing fatality rate. However, there were also clear shortcomings in which our prediction was strictly linear meaning that it fails to take into account 'herd immunity' or potential external factors. Thus, our model isn't totally accurate since it doesn't take into account for some realistic factors that might affect the data in the future; however, it does show how the interventions affect the infection and fatality rate meaning some validity is shown. There could be situations in which some countries might find our policy framework against their ethical standards. For instance, if our transmission rate was close to 0%, then that means most people would be locked up at home which could not be ethically tolerated in certain areas. However, our policy framework would be valid for those countries that accept the transmission rate given from our algorithm. Key findings such as applying fmincon() to utilize parameters optimization, using siroutput() to generate the value of cost, and plotting out accurate SIRD models did help us reach the desired result to certain extent.

REFERENCES

1.   B. Stephen, and V. Lieven "Introduction to Linear Algebra," Clays. Cambridge Unverisyt Press.London, 168, 2018.