Rahul Naik
COE 322
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<u>Infectious Disease Simulation Report</u>

Project Overview:

Several experiments were conducted throughout the course of this project to examine the relationship of different factors such as infection transmission risk, vaccination rates, disease duration, and herd immunity and ultimately how these change the progression of an infectious disease through a society. After collecting the data of several of these experiments, MATLAB was used to create graphical representations in hopes of better visualizing and understanding phenomena. To set up the basis of the project, a library with class and method definitions, "disease.h", was created that is used across the various other programs. A class "Person" and another class "Population", that is made up of Persons, were created to serve as the people the disease would infect. Each "Person" is classified as being either healthy, currently sick, recovered or vaccinated. Initially a person is randomly chosen to be infected and other members of the population can get sick only by interacting with someone next to them. As complexity was added to the model, the interactions were randomized and increased in quantity to better emulate society.

Initial Tests:

In order to ensure that the method functions as well as the class definitions were correctly functioning, a disease simulation was conducted on a singular "Person", named Joe, who had a 50% chance of contracting the disease and once contracted would be sick for five days. This disease time frame of five days was kept consistent throughout the entire project. Next, a small population of five people was created and a simulation ran to examine the disease progression was occurring correctly. The outputs are included below.

```
On day 0 Joe is Healthy
On day 1 Joe is Currently Sick
On day 2 Joe is Currently Sick
On day 3 Joe is Currently Sick
On day 4 Joe is Currently Sick
On day 5 Joe is Currently Sick
On day 6 Joe is Recovered

Process finished with exit code 0
```

```
In step1  #sick:  1: Currently Sick,Healthy,Healthy,Healthy,Healthy,
In step2  #sick:  3: Currently Sick,Currently Sick,Currently Sick,Healthy,Healthy,
In step3  #sick:  3: Currently Sick,Currently Sick,Currently Sick,Healthy,Healthy,
In step4  #sick:  5: Currently Sick,Currently Sick,Currently Sick,Currently Sick,Currently Sick,
In step5  #sick:  5: Currently Sick,Currently Sick,Currently Sick,Currently Sick,Currently Sick,
In step6  #sick:  2: Recovered,Recovered,Recovered,Currently Sick,Currently Sick,
In step7  #sick:  2: Recovered,Recovered,Recovered,Currently Sick,Currently Sick,
Disease ran its course everyone is recovered

Process finished with exit code 0
```
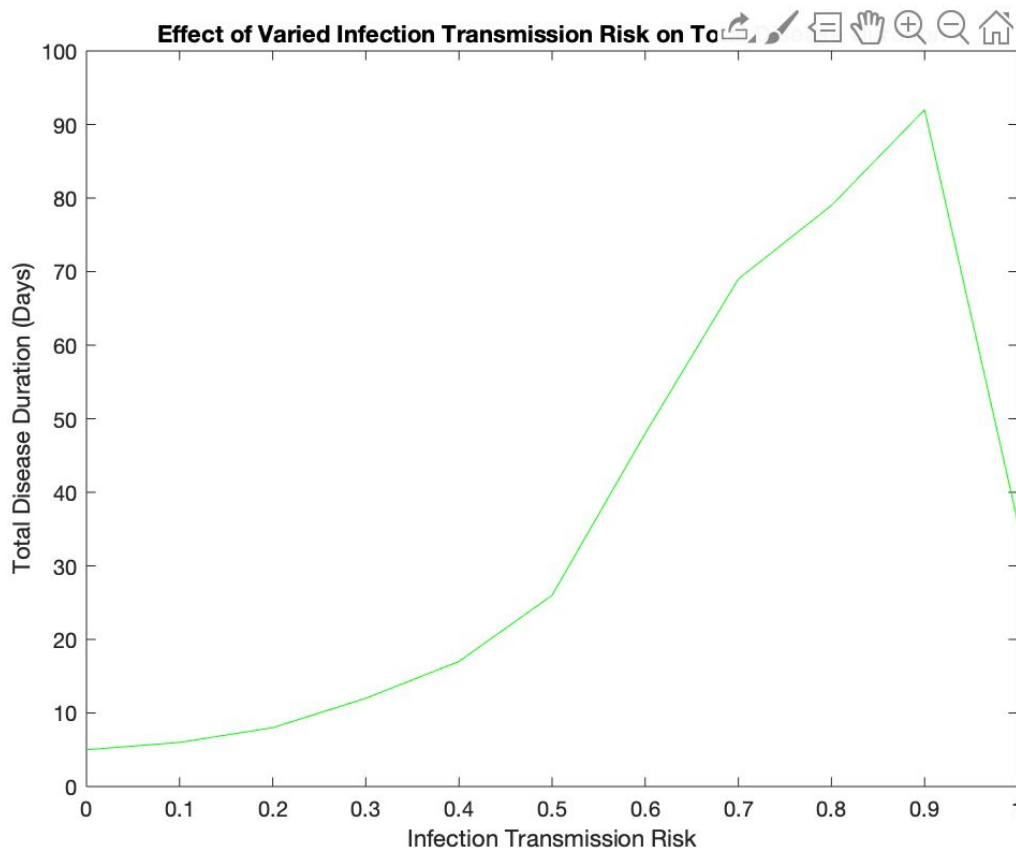
Experiment One:

In this experiment, the effect of varied infection risks on the total disease duration, the days it took for the disease to go through the whole population, was examined. Infection risk was varied from 0 to 1 at intervals of 0.1. It was concluded that increasing the infection transmission risk tended to increase the total disease durations. The maximum number of days occurred at an infection risk of 0.9 with a duration of 92 days. Interestingly enough after the maximum point there was a steep drop in disease duration until the limit of 1. This is perhaps because at that point the chance of getting sick is so high that there is not much time for disease progression as almost the entire population is infected in the span of a couple days. The population size used was 10,000 people and 100 trials were conducted to ensure the veracity of the data.

Graph showing this relationship:

Experiment Two:

  To add a degree of complexity to the simulations, a method for vaccinating a proportion of the population was created. Those who were vaccinated were chosen at random and rendered unable to contract the disease. Once more, the infection transmission risk was varied and the data on disease duration was collected. At this point in the model the vaccination rate was held constant at 20%. The population size, number of trials, and variance of infection risk were kept the same as in Experiment One. It was found that by introducing vaccination the disease was consistently eradicated in under ten days. While there was still some positive correlation between infection transmission risk and total disease duration was found, this was a rather inconclusive experiment. An upward trend of disease duration was noticed which occurred between .4 and .6 infection risks with the total disease duration being 10 days. After this maximum the days declined slightly likely because so much of the population was vaccinated. This experiment was likely hampered by the relatively simple model wherein people do not have random interactions across the entire populace and were vaccinated at the start only.

  Graph:
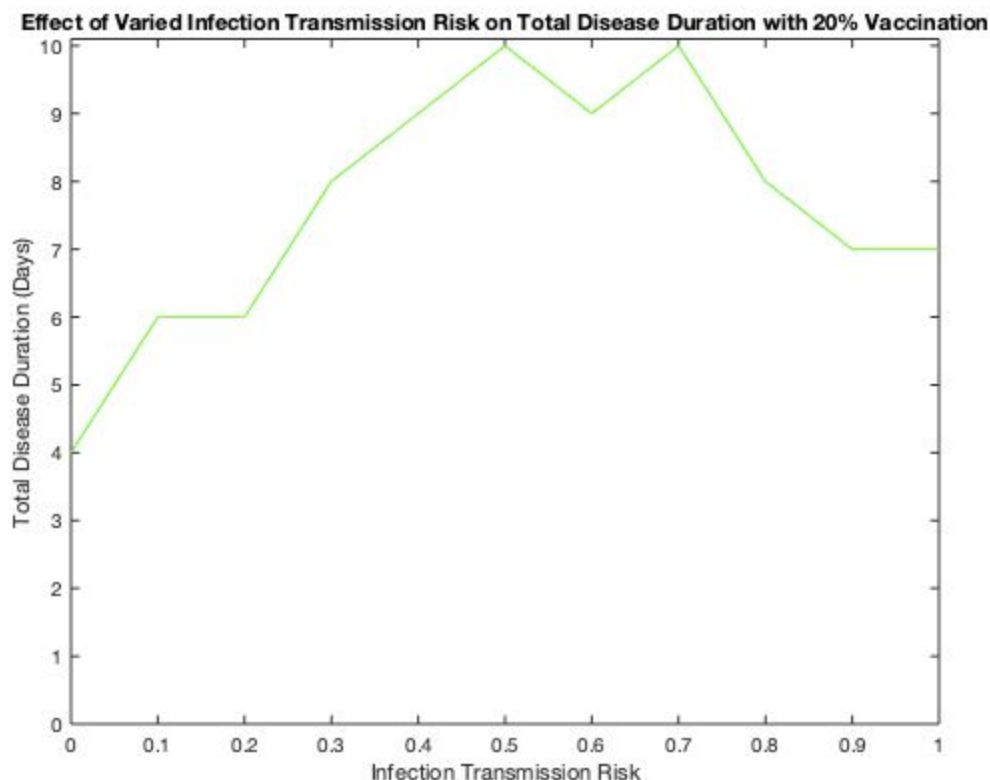
Experiment Three:

  This experiment explored the relationship of changing vaccination rates on disease duration. For this experiment the population size was increased to 1,000,000 people in order to simulate the population of Austin, TX. In addition, each person in the population now interacted

with six other people at random daily. This serves to add another level of complexity and make the model more realistic. The infection transmission risk was kept constant at 0.2 and the number of interactions was kept at six. The vaccination rates were varied from 0 to 100% at intervals of 5%. To ensure the accuracy of data, 100 trials were conducted at each vaccination rate. It was concluded that there is a strong positive correlation between vaccination rates and disease duration. By vaccinating more people, the spread of the virus is slowed and this in turn would limit the strain on medical resources needed to treat the ill. However, this trend experienced a steep drop around the 80% vaccination rate. After 80% the disease duration dropped sharply perhaps due to having so many people vaccinated that the disease's effects are not really felt at all on a societal level.

   Graph:
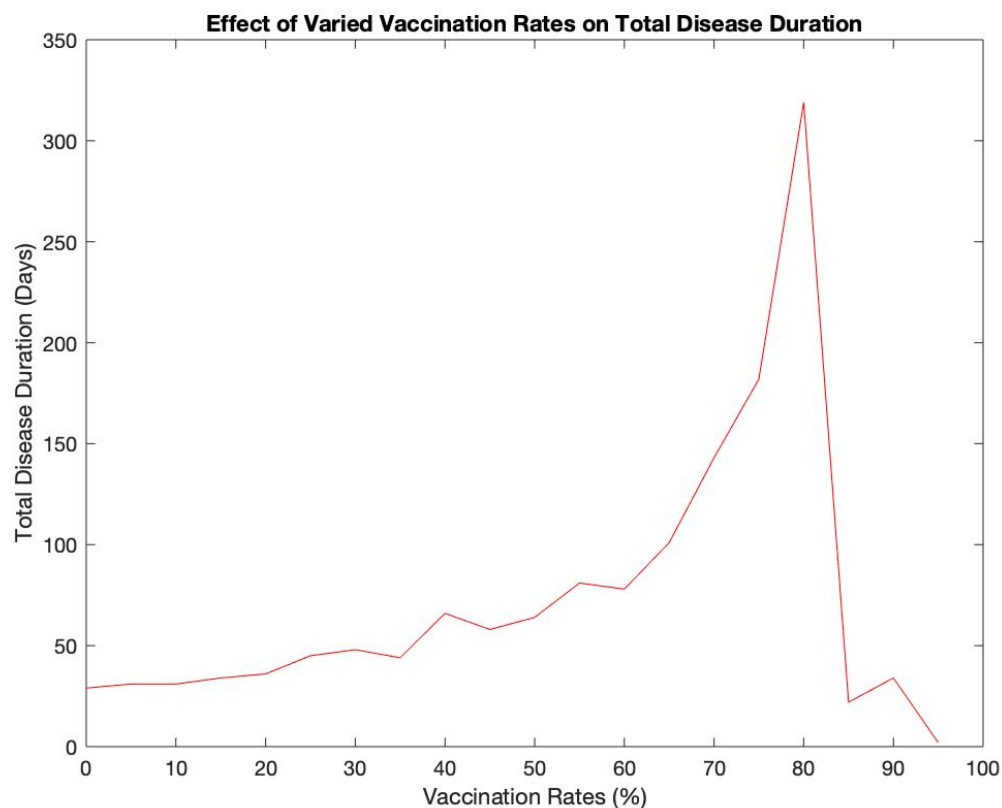
Experiment Four:

   This experiment served to build off of the previous experiment. As in the previous experiment the vaccination rates are varied from 0 to 100% at an interval of 5%. The number of trials, population size, number of interactions, and infection transmission risk were all kept constant as in Experiment Three. The goal for this experiment was to see how changing vaccination rates would impact herd immunity. For the purposes of this experiment, herd immunity was calculated as the percent of people who were left untouched by the disease out of the amount of people who were not vaccinated. Those left untouched benefit from the herd immunity as they were never vaccinated nor infected by the disease. As herd immunity grows

stronger, the effect of the disease lessens to the point where it does not debilitate the society. In this experiment, the goal herd immunity was deemed to be 95%. The resulting data was graphed and the relationship appears to be sigmoidal. All the way to 70% vaccination the herd immunity percentage is rather low and grows slowly. From 70% to 80% vaccination a sharp rise in herd immunity is seen going from 36.26% to 95.59% respectively. The goal herd immunity is found to be at approximately 79.89%. These are key findings as one is able to gauge the probation of a population that must be vaccinated to see significant herd immunity.

Graph:
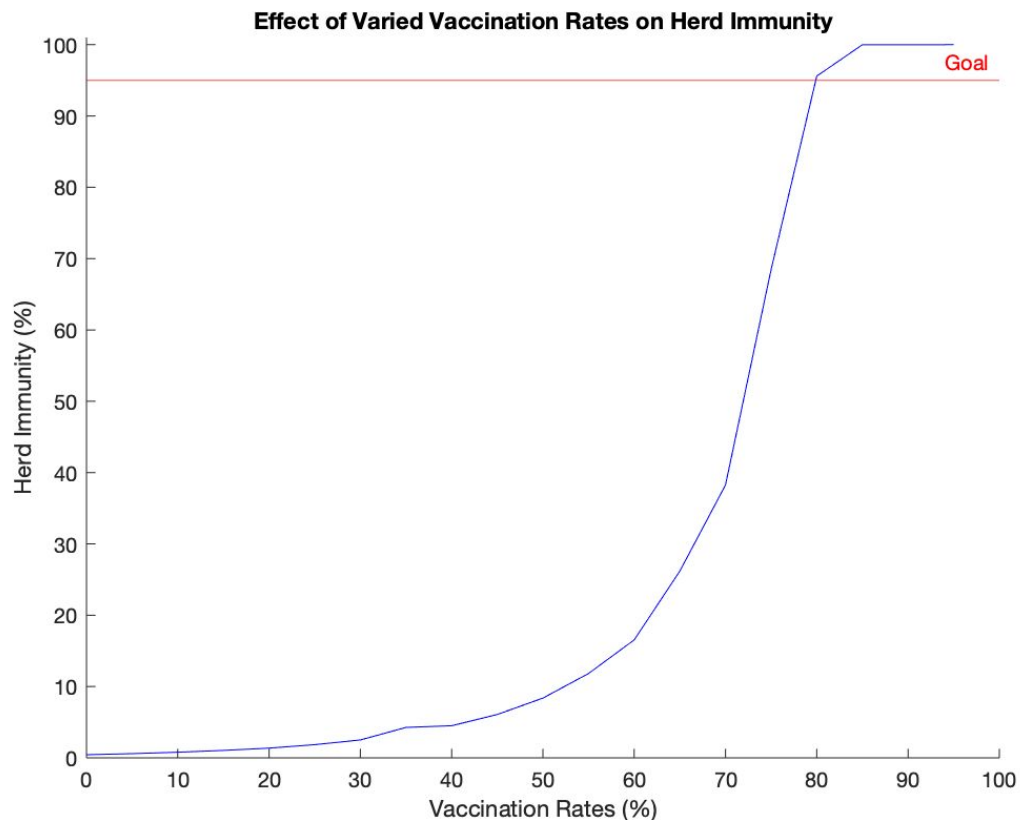
Conclusion:

This project was very interesting and served to demonstrate important relationships in the spread of disease. In the context of COVID-19 being on the cusp of a vaccine deployment, it is essential to understand how vaccines affect disease spread and the massive amount of people that must be vaccinated in order to keep the virus at bay through herd immunity. For a COVID-19 vaccine projected to be 95% effective, if Austin wants to reach 95% herd immunity they will have to vaccinate around 840,947 people. (Calculated by doing (100/95)*.7989*1,000,000) While this model is relatively simple, it is clear to see that achieving a useful level of herd immunity in Austin and worldwide will require a Herculean effort. This model is limited due to the special circumstances with COVID-19 as many people are staying home, interacting in social

bubbles, and wearing masks. For future studies, it would be interesting to analyze how the aforementioned factors would alter the model.