Age Structured SIR Models with Quarantining and Vaccination

by

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Abstract

In a time dominated by the effects of the COVID-19 global pandemic, disease models become an invaluable tool to model the behavior and progression of infectious diseases. This thesis will investigate a simple SIR disease model stratified by age to see how the adjustment of variables affects the peak infected population. The thesis will further analyze the impacts of quarantining and vaccination on peak hospitalization rates. The thesis will also analyze contact matrices and how various contact patterns affect the overall pattern of an outbreak. The model will further investigate how the differences in hospitalization rates among age groups affects the overall peak hospitalization rates. The results of the model simulations suggest that the most effective treatment is to the group that interacts the most proportionally compared to other groups. The results also show a large relative effect in lowering the peak hospitalization rate when vaccination treatment is applied to the more at-risk groups.

Contents

1 Introduction

In a time dominated by the effects of the COVID-19 global pandemic, it becomes a necessity to investigate the behavior of infectious diseases with models. A simple way to depict such behavior is through disease modelling. This thesis will investigate a simple SIR disease model stratified by age to see how the adjustment of variables affects the peak infected and hospitalized population. The thesis will further analyze the impacts of quarantining and vaccination on peak hospitalization rates.

2 Background

In this section, we will go over the necessary background information for this thesis. The main topic will be the disease model and the basics of COVID-19. We will also discuss age structuring a disease model.

2.1 SIR Models

A SIR model is a type of Markov model where every component observation of the model is part of a compartment. A SIR model assumes that the population can be divided into 3 categories: "S", "I", and "R". The "S", or susceptible, compartment represents the section of the population who lack immunity to the disease and are thus susceptible to infection. The "I", or infected, compartment represents the section of the population who are currently infected or actively spreading the disease. The "R" compartment is the section of the population who have recovered or are otherwise resistant to the disease.

The SIR model makes some crucial assumptions that must be noted. An SIR model assumes that the population, denoted N, is constant and normalized to be equal to 1 so all population states will be a percentage of the whole. The total sub populations will be denoted as Y for young, M for middle-aged, and O for elderly. The notation in the model will be of the form S_{yt} which in this case denotes the susceptible population in the "young" subgroup at time t. It is assumed that the R category consists of people who are vaccinated [12], have been infected and recovered, as well as those who have died from the disease. SIR models assume that reinfection is impossible or improbable for the given time period. It is assumed that the model is deterministic, which works for a normal outbreak, but is not as accurate

when the number of infected is low and those periods a more stochastic approach would be necessary. It is also assumed that the spread of disease is caused by uniform, random contact between a susceptible individual and an infected individual.

It may be useful to define the parameters the SIR model utilizes. The parameter γ represents the recovery rate in which infected individuals move into the recovered category. β is the parameter that represents the transmission rate of the disease. This dictates the rate that infected individuals spread the disease and cause new infections.

It may be valuable to consider that due to the nature of infectious diseases we can make some further assumptions. In a virus like COVID-19, the recovery rate γ is something that should be assumed constant and as something that people are not able to control. [1]

The initial conditions of the model assume that the percentage of S is a large proportion. There is also a small percentage of I to represent the starting number of infected individuals. The R population is considered to be very small or zero given few people should be resistant at the start of an outbreak without vaccinations. The most critical factor measured in SIR Models is the peak percentage infected at any given time as too high of a percentage will cause medical and health services to be overloaded. We note that it is possible to simulate vaccinations by simply considering that population as part of the "recovered" if we assume that they will not become infected or spread the disease in any way.

The basic formulation of a discrete SIR Model is:

$$S_{t+1} = S_t - \beta I_t S_t$$
$$I_{t+1} = I_t + \beta I_t S_t - \gamma I_t$$
$$R_{t+1} = R_t + \gamma I_t$$

These formulas show the population for each of the compartments in the next period given the values of the compartments in the current period.

As seen in the figure, the susceptible population follows a decreasing s-curve and the recovered

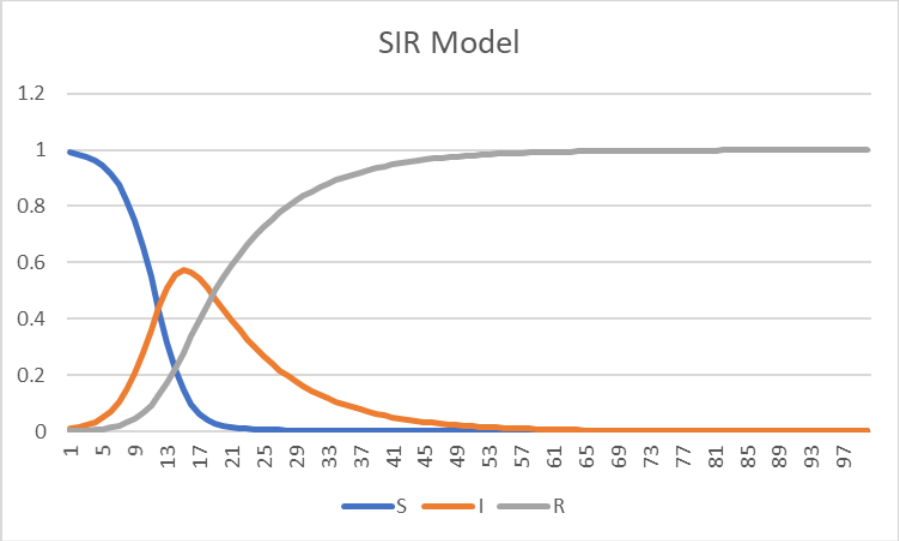

Figure 1: A Basic SIR Model

population follows an increasing s-curve. The R population is offset to the S population by a few time units and is predominantly impacted by the recovery rate. The I population appears as a skewed bell curve. It increases in proportion to the transmission rate and the percentage of the population in the S compartment. As β increases, the peak total infected population increases and the time to peak decreases. A higher β in effect causes shorter and more severe outfits. If γ is larger than β, the infection will quickly end as the I population will decrease faster than the S population can be infected.

2.2 The Basic Reproductive Number

The Basic Reproductive Number, or R_0, is a critical parameter of an infectious disease. The R_0 of a disease represents the average number of new infections caused by a single infected individual. [11] For a disease to perpetuate and cause a pandemic we must have $R_0 > 1$. If $R_0 < 1$, the disease will die out and end the pandemic.[6] The R_0 of a disease modeled by a SIR approach equals the ratio between the transmission rate and the recovery rate β_t/γ.

2.3 Age Structuring an SIR Model

The normalization of the population into percentages has the advantage that the population can be split into subsections. Each of these subsections can then be made into their own separate SIR model. The

value of this approach is that there may be differences in the subsections that have a significant impact on the results of the model.[10] Each of the subsections intermix and therefore are not completely independent of each other. In order to account for this, it becomes necessary to add interaction terms for each of the separate SIR models.

In order to create the interaction terms for cross infections among the subsections, a contact matrix must be created.[7] The contact matrix will be the number of individuals that interact with members of another subsection. For the sake of simplicity, we will divide the population into 3 broad categories of "young", "middle-aged", and "old".

The contact matrix will be of the form:

	C_y	C_m	C_o
C_y	C_{yy}	C_{ym}	C_{yo}
C_m	C_{my}	C_{mm}	C_{mo}
C_o	C_{oy}	C_{om}	C_{oo}

The symbols in the contact matrix represent contact between different age groups. The symbol C_{ym} represents the interaction young people have with middle-aged individuals. We will assume that there is no symmetry or reciprocity in the values of the contact matrix. The interaction young people have with middle-aged individuals is not the same as the interaction middle-aged people have with young people, i.e. $C_{ym} \neq C_{my}$.

With the contact matrix defined, we can define the discrete formulation of an SIR model with 3 categories.

$$S_{y_{t+1}} = S_{y_t} - \beta(I_{y_t}C_{yy} + I_{mt}C_{ym} + I_{ot}C_{yo})S_{y_t}$$
$$S_{mt+1} = S_{mt} - \beta(I_{y_t}C_{my} + I_{mt}C_{mm} + I_{ot}C_{mo})S_{mt}$$
$$S_{ot+1} = S_{ot} - \beta(I_{y_t}C_{oy} + I_{mt}C_{om} + I_{ot}C_{oo})S_{ot}$$
$$I_{y_{t+1}} = I_{y_t} + \beta(I_{y_t}C_{yy} + I_{mt}C_{ym} + I_{ot}C_{yo})S_{y_t} - \gamma_y I_{y_t}$$

$$I_{mt+1} = I_{mt} + \beta(I_{y_t}C_{yy} + I_{mt}C_{ym} + I_{ot}C_{yo})S_{mt} - \gamma_m I_{mt}$$
$$I_{ot+1} = I_{ot} + \beta(I_{y_t}C_{yy} + I_{mt}C_{ym} + I_{ot}C_{yo})S_{ot} - \gamma_o I_{ot}$$
$$R_{y_{t+1}} = R_{y_t} + \gamma_y I_{y_t}$$
$$R_{mt+1} = R_{mt} + \gamma_m I_{mt}$$
$$R_{ot+1} = R_{ot} + \gamma_o I_{ot}$$

The S equations can be described as the population of the susceptible percentage for a group subtracted by the interaction of those susceptible individuals by all infected individuals scaled by interaction weights. The I equations are the previous I percentage plus the new infected individuals due to interactions between susceptible and infected individuals minus the infected who recovered between periods. The R equations are simply the previous R percentage plus the newly recovered individuals for a given age group. The primary difference these formulas have with the standard SIR formula is the I term. The I terms are replaced by a weighted average of the infected populations with the weights given by the contact matrix. The other S and R terms are the values for each subgroup.

I have included terms such as γ_o as it may be possible for different age groups to have slightly different recovery rates. I have not given this treatment to β to preserve simplicity and quarantining among age groups may be a better control. I will also assume that all of the γ terms are equivalent for the simulations as it is not a variable that people could control for in a realistic scenario.

The contact matrix allows for a mathematical representation of quarantining to be included. Further, the effects of quarantining on specific age groups can be analyzed. This can be performed by multiplying an age group by a factor in the contact matrix to simulate the change in contact between individuals among that age category.

Within an age-structured SIR model, R_0 is represented by the ratio of the transmission rate and the recovery rate multiplied by the dominant eigenvalue of the contact matrix, or λ_c. The other eigenvalues relate to the other groups within the simulation and can be used to analyze individual population behavior to an extent.[8]

$$R_0 = \lambda_c \frac{\beta}{\gamma}$$

2.4 COVID-19

The disease that this paper will strive to analyze and model is the COVID-19 pandemic. The Coronavirus Disease 2019, or COVID-19, was first reported in Wuhan, China in February of 2020. The virus was initially given multiple names such as 2019-nCov and was later given the official identifier, SARS-CoV-2. Following the initial outbreak in Wuhan, the disease quickly spread around the world and was declared a pandemic by the World Health Organization on March 11, 2020.[5]

COVID-19 is primarily transmitted by droplets from the respiratory systems of two individuals. The Airborne nature of the virus makes it especially virulent and exacerbated the pandemic. This property also indicates that social distancing, quarantining, and mask mandates to have significant effects on the spread of the disease. Though the disease is extremely infectious, the majority of the cases are shown to be asymptomatic. The asymptomatic individuals are also shown to still be capable of transmitting the virus. Common symptoms of COVID-19 are fever, coughs, shortness of breath, fatigue, headaches, loss of taste or smell, nausea, vomiting, diarrhea, congestion or runny nose, and muscle or body aches. The severity of the disease has also been shown to be directly correlated to conditions of the host such as age, sex, and health.

Most cases of COVID-19 tend to involve the lungs. The most severe cases of the illness tend to be found among elderly as well as very young individuals. Among hospitalized patients, complications such as pneumonia, sepsis, respiratory failure, and acute respiratory distress syndrome.

It is useful to assess COVID in terms of age groups as different age groups as the disease impacts different age groups with varying degrees of severity. The Hospitalization rate for elderly individuals is 5 to 10 times larger than the rate for individuals in the 18–29 age group. The death rate is also significantly higher with rates 65 to 370 times that of the 18–29 year group. Using CDC cumulative hospitalization rates[4], the elderly population has a hospitalization rate of approximately 2%. Taking

the average of the normalized rates for other age groups, we get an approximate hospitalization rate for the young group of 0.15% and a rate of 0.64% for the middle-aged population. The rates were calculated by taking the simple average of each of the cumulative hospitalizations per 100,000 people for each of the age groups that make up each of the models three age categories.

2.5 Vaccines

In the United States, there are three main vaccines to prevent COVID-19. These are the Pfizer-BioNTech, Moderna, and Johnson and Johnson vaccines.[2]

The Pfizer vaccine is recommended for people aged 5 and older while the Moderna and Johnson and Johnson vaccines are only intended for individuals 18 and older. The Pfizer and Moderna vaccines both require two doses for full immunity with each does administered 3 and 4 weeks apart respectively. The Johnson and Johnson vaccine only requires one dose to be considered fully vaccinated. Individuals can be considered fully vaccinated two weeks after their final dose.

The vaccines work by preparing the body for pathogens by increasing familiarity with the pathogen so that the immune response is much faster and more efficient. There are two main types of vaccines currently being administered for COVID-19. The first type are mRNA vaccines such as the Pfizer and Moderna vaccines. The second type are Viral Vector Vaccines such as the Johnson and Johnson vaccine. The mRNA vaccines enter the body and mimic the COVID-19 virus' proteins and cause a similar immune response. The subsequent response effectively trains the body how to fight the disease and the body can produce an immune response to an actual infection effectively. Viral Vector Vaccines work by injecting a harmless virus into the body to create proteins similar to that of COVID-19. This causes a similar immune response as seen in the mRNA vaccines and prepare the body for an actual COVID-19 infection.

As of November 2021, the CDC state that some 73.4% of the population above the age of 5 has had at least one dose of a vaccine administered.[3] It is estimated that 86.2% of the population older than 65 are fully vaccinated. Further, 70.8% of the population older than 18 and 59% of the total population

are fully vaccinated. The vaccines are allocated primarily to the older section of the population. The vaccines were than distributed to younger individuals who worked in occupations where the risk of infection was much greater. The vaccine was then distributed among the younger subsections of the population.

3 Model Analysis

In this section we will analyze the initial conditions and scenarios for the model. We will go into further detail on the contact patterns of the model.

3.1 Model Parameters

With the information laid out, a model can be created and tested. The model was created in Microsoft Excel and calculated by following the discrete variables over 100 periods. The initial conditions of the model will be set to $\gamma = 0.1$, $\beta = 0.6$, and thus a $R_0 = 6$. We will assume that contact matrix is uniform with all values set to 0.33. We will also assume that $\gamma = \gamma_y = \gamma_m = \gamma_o$.

According to US Census data from 2019[9], 31.7% of the population is less than 24 years old and will be categorized as "young". Another 52% of the population is between the age of 25 and 64 and will be categorized as "middle-aged". The final 16.3% of the population will be categorized as "old". Of these populations, we will assume $1/300$ of the total population will be infected in each age group. The other initial values are determined by the formulas $S_0 = (1 - V) * P - 1/300$ and $R_0 = V * P$ where V is the percentage of the population vaccinated and P is the population of that group. In a scenario with each of the age categories with 50% vaccination we will have the initial values:

The main value we will be measuring is the peak infected population and the time until this peak. This is as if the peak population is too large, hospitals will be overwhelmed and cannot treat all individuals with serious cases. Therefore this is an important value to control for when searching for effective responses and controls to the pandemic. We will also analyze vaccination effects by adding population to the recovered compartment at the onset of the model.

S_y	15.52%
S_m	25.67%
S_o	7.82%
I_y	0.33%
I_m	0.33%
I_o	0.33%
R_y	15.85%
R_m	26.00%
R_o	8.15%

From peak infected population we can approximate the peak hospitalization rate given the hospitalization rates of each age group we approximated from CDC data. This can be found by simply multiplying the peak infected population of each age group by their respective rate. This will return the percentage of the total population that is expected to be hospitalized at the highest possible point. If we calculate without respect to time, we will get an overestimate of the actual rate as the peaks for each age group do not necessarily occur at the same time. The formula will be $H = Max(y)h_y + Max(m)h_m + Max(o)h_o$.

Another aspect we will analyze is how different subgroups interact with one another. These interactions will be determined by the contact matrix. The values in this matrix will allow us to model the behavior of each population such as quarantining or lack thereof. The rows of each contact matrix will not sum to be more than 1. Decreasing the values of each row in the contact matrix is tantamount to lowering β for each age group.

The parameter values used in the model will be:

β	0.6
γ	0.1
q_y	1
q_m	1
q_o	1
v_y	0
v_m	0
v_o	0
h_y	0.0015
h_m	0.0064
h_o	0.02
p_y	0.317
p_m	0.52
p_o	0.163

3.2 No Contact

An important fact to consider before analyzing the effects of the contact matrix is to analyze a model with no contact between age groups. This effectively creates 3 separate SIR models that are completely independent of each other. The contact matrix for this scenario is just an identity matrix.

	C_y	C_m	C_o
C_y	1	0	0
C_m	0	1	0
C_o	0	0	1

We get peak infected populations and times at 4.60% at time 48, 17.15% at time 30, and a peak of 0.33%, the initial condition time 1 for young, middle-aged, and elderly populations respectively. The max infected is 20.33% at time 31. The max hospitalizations are 0.12%.

This scenario shows that in a case with a lack of interaction each model is independent of each other and the effects of the other parameters is scaled to the new population proportions. The size of the elderly population also caused β to become smaller than γ and thus the infection quickly died out among that age group.

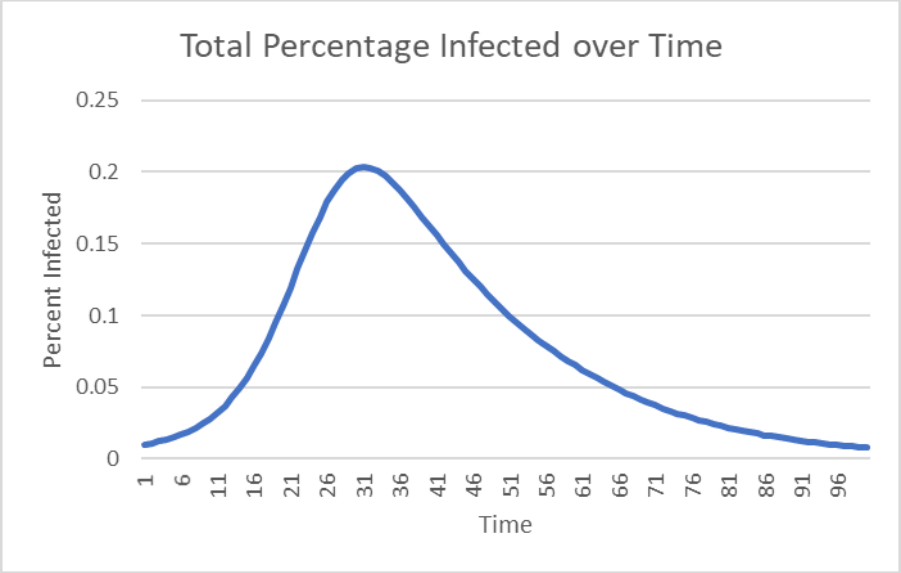

Figure 2: No Contact Model: Total Infected Population

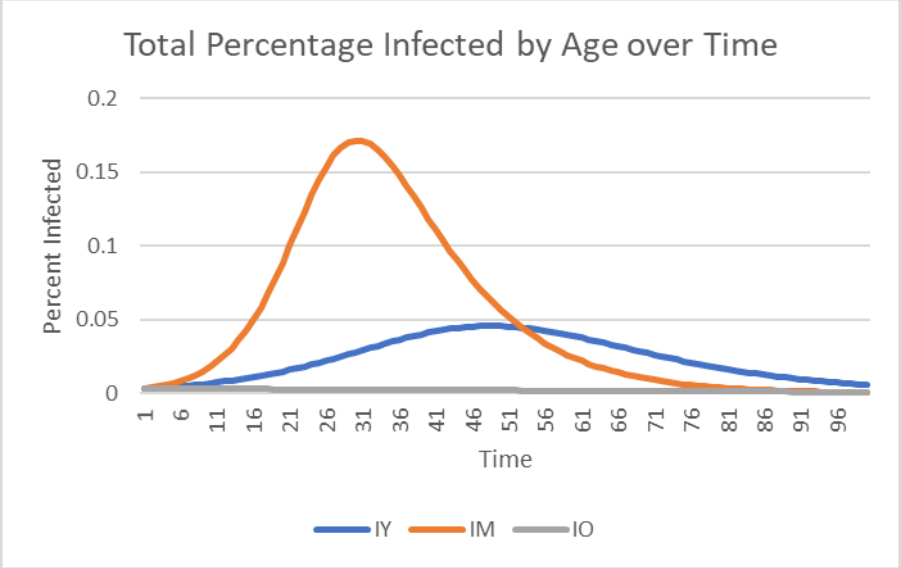

Figure 3: No Contact Model: Total Infected Population by Age Category

This scenario in the overall infection curve heavily resembles a basic SIR model. The lack of contact effectively acts as a quarantine that directly scales down β as the subgroups not interacting heavily stifles the spread of the disease. In a sense, each of the individual subgroups is its own SIR model, though the scaling down of the population for each group has a large impact on each of the curves.

3.3 Uniform Contact

The initial distribution of the population will assume that there are no recovered or immunized individuals and that 0.33% of the total population will be infected for each age category at the start of the simulation. The remaining majority of the population will be placed in the susceptible compartment.

	C_y	C_m	C_o
C_y	0.33	0.33	0.33
C_m	0.33	0.33	0.33
C_o	0.33	0.33	0.33

With the base parameters set, we can find a control model to compare the other results to.

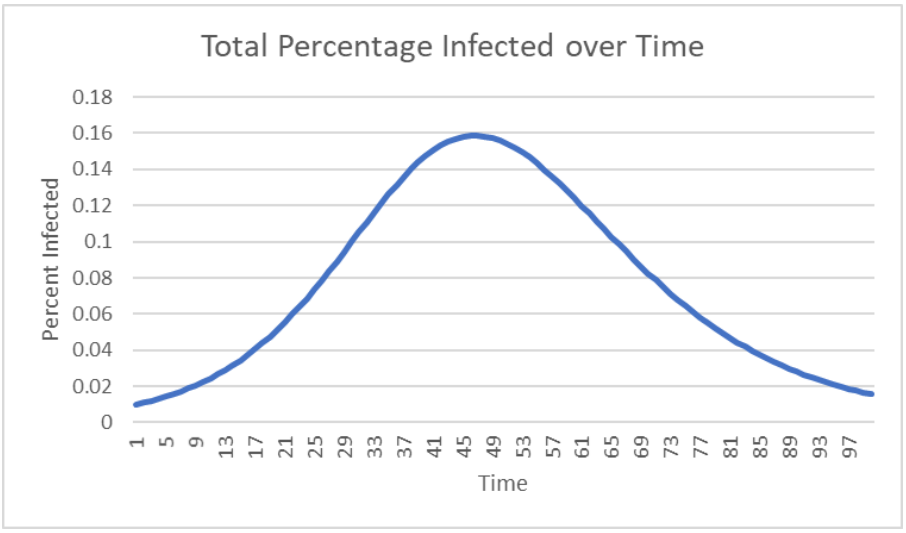

Figure 4: Uniform Contact Model: Total Infected Population

The control model returns a total max infected population of 15.87% and a time to reach peak of 47. The peak infected population for the subgroups was 5.03%, 8.03%, and 2.56% for the young, middle-aged, and old age groups respectively. The max hospitalizations were 0.11%

The time to peak remained constant for each subgroup. These values will serve as baseline to consider the effects of adjustments to different variables.

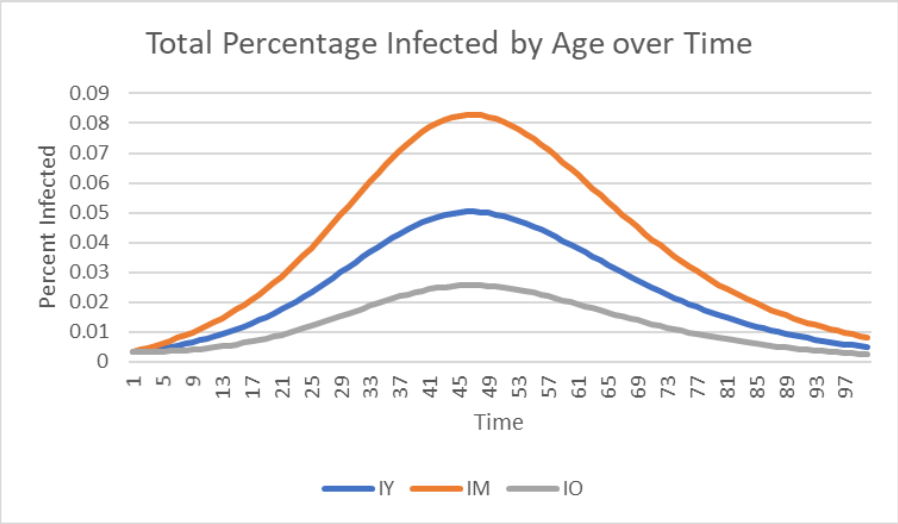

Figure 5: Uniform Contact Model: Total Infected Population by Age Category

An interesting point about the uniform contact is that all of the infection curves have the same center and move at proportional rates to each other without any controls applied to them.

3.4 Group Preference Contact

We will first analyze the effects of changing the contact matrix to encourage a preference towards the same subgroup by adding a value of 0.66 to individuals within the same group and a value of 0.17 to those outside the subgroup.

	C_y	C_m	C_o
C_y	0.66	0.17	0.17
C_m	0.17	0.66	0.17
C_o	0.17	0.17	0.66

The in-group preference led to larger peaks overall as well as a faster progression of the infection. The peak infected population was 19.76% with a time to peak of 40. The peaks for young, middle-aged,

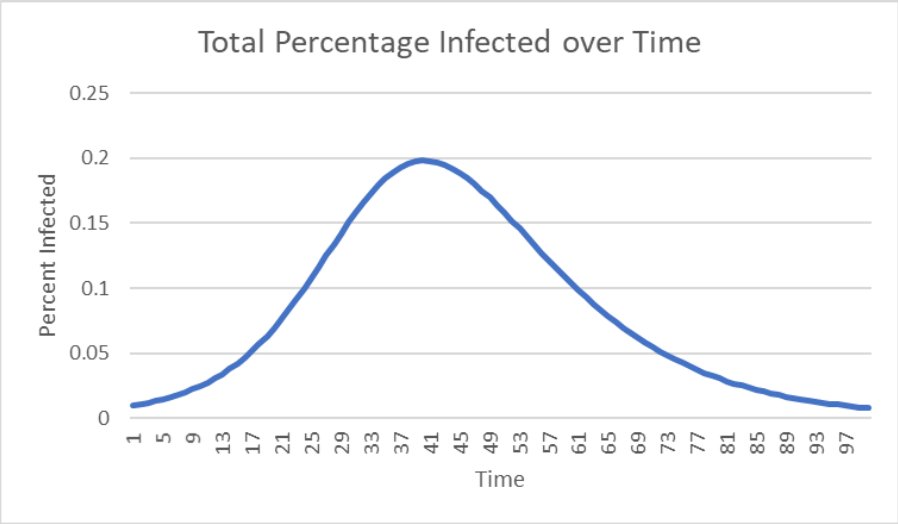

Figure 6: Control Model: Total Infected Population

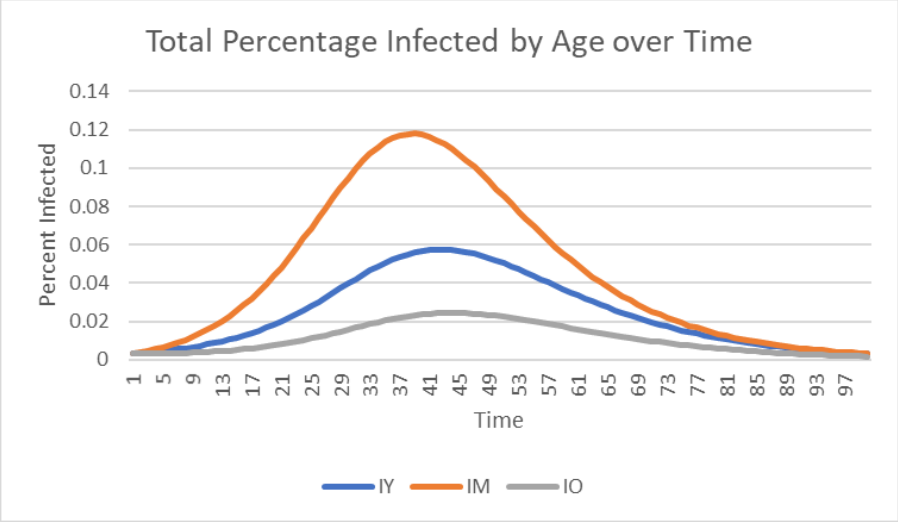

Figure 7: Control Model: Total Infected Population by Age

and old respectively are 5.76%, 11.79%, and 2.44% with times of 43, 39, and 44. The max hospitalizations are 0.13%.

The preference towards in-groups led to the infection to progress relatively faster in the larger subgroups than in the smaller subgroups. While the peaks for the young and old groups increased, the smaller elderly group's peak infection decreased as the groups small size lessened contact acted effectively as quarantining.

This scenario is a bit of a blend in-between the no contact and uniform contact scenarios. Each curve tends to follow the same near symmetric pattern of the uniform contact scenario with a slight right skew. The time to peak is also offset with the larger subgroups peaking faster than the smaller subgroups.

It will now be useful to lay out the control scenario response values in a table to easily compare the values. These will be useful for comparing variations due to different quarantine and vaccination scenarios.

	$Max(I)$	$Max(I_y)$	$Max(I_m)$	$Max(I_o)$	H
No Contact	20.33%	4.60%	17.15%	0.33%	0.12%
Uniform Contact	15.87%	5.03%	8.03%	2.56%	0.11%
Preferential Contact	19.76%	5.76%	11.79%	2.44%	0.13%

4 Quarantining

In this section we will apply a quarantine treatment to our model. We will run simulations on each of the contact patterns and analyze their effects.

4.1 Scenario Introduction

To model the effectiveness of quarantining, we will scale down individual rows of the contact matrix by a factor to get a lower value. If universally applied it would simply scale down the entire model. We will also assume a lack of reciprocity in the contact matrix in quarantining. The logic behind this is that one age group may be taking active measures to avoid contact but individuals from the other group may not avoid contact at the same rate. In some of the following simulations, we will assume a total lack of reciprocity for the sake of testing and others will account for some reciprocity.

We will assume the population is quarantining to varying levels of efficiency based on age group. We will product the quarantine effect by applying a scalar of $1 - \textit{efficiency}$ to the contact matrix of each group. These values will be labelled as q_y, q_m, and q_o.

The values of the contact matrices will be modified as follows:

	C_y	C_m	C_o
C_y	$q_y C_{yy}$	$q_y C_{ym}$	$q_y C_{yo}$
C_m	$q_m C_{my}$	$q_m C_{mm}$	$q_m C_{mo}$
C_o	$q_o C_{oy}$	$q_o C_{om}$	$q_o C_{oo}$

4.2 No Contact Scenario

The trivial "No Contact" scenario is not all that interesting. As the different age groups do not interact with one another, the curves for each age group is simply scaled down by a factor. Something to note is that the initial infected population for each age category is 0.33% and if that is the maximum then the infection simply decayed from its initial value. The following simulations will be variations of the no contact control simulation where the quarantine efficiency for each age group will be set to 0.5 and then a final simulation where all of the efficiencies will be set to 0.5. The values of the simulations are as follows:

	$Max(I)$	$Max(I_y)$	$Max(I_m)$	$Max(I_o)$	H
No Contact Control	20.33%	4.60%	17.15%	0.33%	0.123%
$.5q_y$	17.70%	0.33%	17.15%	0.33%	0.117%
$.5q_m$	7.94%	4.60%	4.12%	0.33%	0.040%
$.5q_o$	20.13%	4.60%	17.15%	0.33%	0.123%
All .5	4.31%	0.33%	4.12%	0.33%	0.034%

Across these simulations, the most notable scenarios were when all groups were quarantining and middle-aged people quarantined. This effect is due to the effect of group size on the model in the no contact scenario, where larger groups tended to have more severe outbreaks than smaller groups. This effect also caused the quarantine to have no noticeable effect on the elderly population as the isolation due to the contact matrix was already effectively quarantining the population.

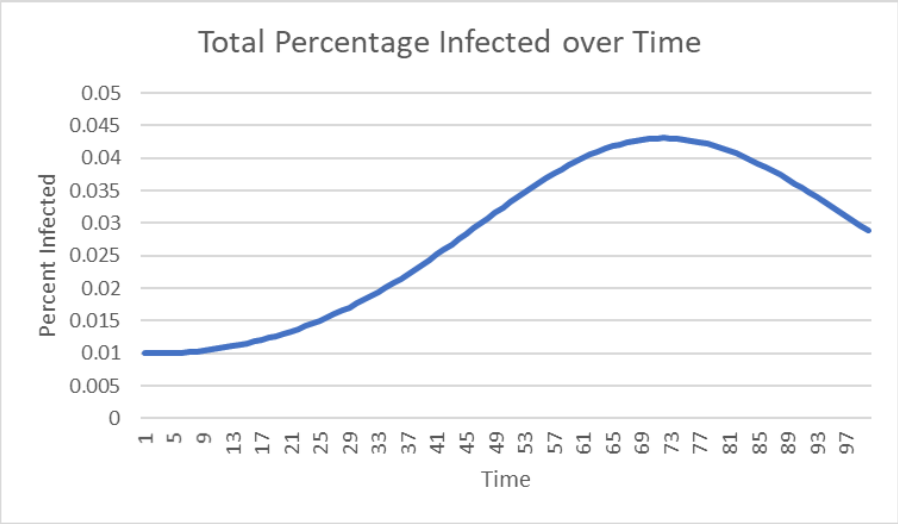

Figure 8: All 0.5 Model: Total Infected Population

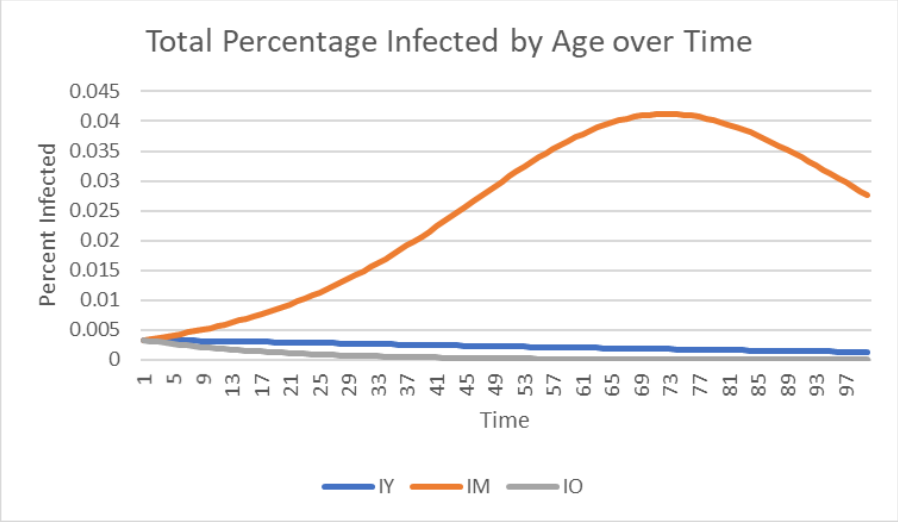

Figure 9: All 0.5: Total Infected Population by Age

4.3 Uniform Contact

While the no contact scenario gave useful insight into the behavior of the model, it is not realistic for there to be zero contact between different age groups. Furthermore we shall investigate the other extreme, where every group interacts equally with one another to see the impacts to our parameters. We will run simulations on the Uniform Contact Control Model and apply an efficiency of 0.5 for each of the age groups and then a combined model where all groups are given a quarantine efficiency of 0.5.

	$Max(I)$	$Max(I_y)$	$Max(I_m)$	$Max(I_o)$	H
Uniform Contact Control	15.87%	5.02%	8.28%	2.56%	0.112%
$.5q_y$	9.54%	2.15%	5.68%	1.75%	0.075%
$.5q_m$	5.91%	2.38%	2.35%	1.21%	0.043%
$.5q_o$	12.56%	4.24%	6.98%	1.37%	0.078%
All .5	1.00%	0.33%	0.47%	0.33%	0.010%

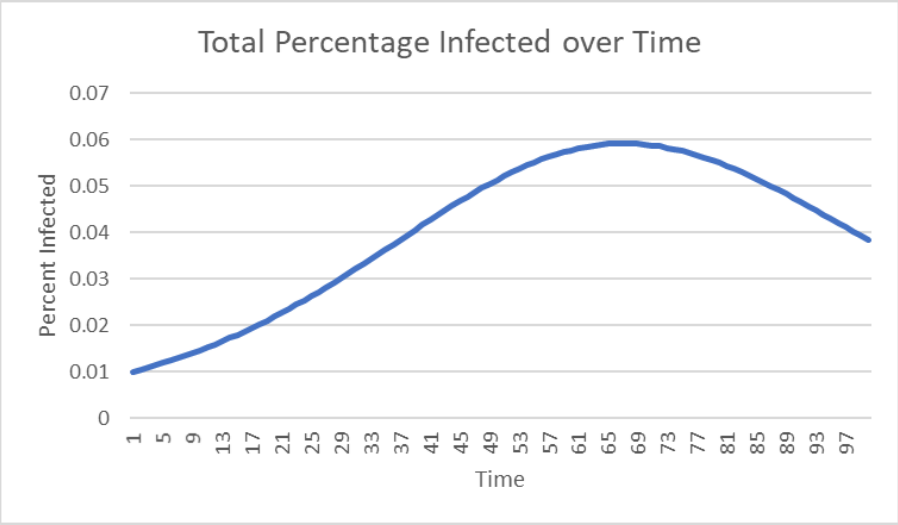

Figure 10: $q_m = 0.5$ Model: Total Infected Population

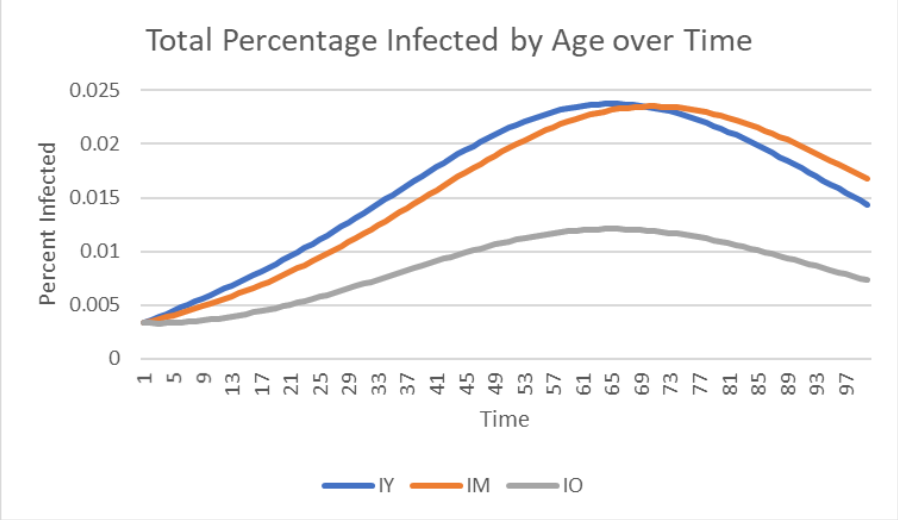

Figure 11: $q_m = 0.5$ Model: Total Infected Population by Age

There are some interesting results from these simulations. The max infected for the elderly population was lower in the scenario where middle-aged people quarantined than in the scenario where the elderly quarantined. This shows an effect where the larger the proportion of the population is quaran-

tining, the severity of the outbreak is smaller.

4.4 Group Preference Scenario

It is also very unlikely that people from different age groups interact equally. Therefore, it may be productive to analyze a scenario with reduced contact among out groups with a preference for people of the same age. The contact matrix will be the uniform matrix with in-groups multiplied by a factor of 2 and out-groups multiplied by a factor of 0.5. Much like earlier simulations, we will apply a quarantine efficiency of 0.5 to each and then to all of the age groups contacts. We will also than include another scenario where we assume the more at risk groups quarantine with greater efficiency than other groups. We will assume for this simulation that $q_y = 0.7$, $q_m = 0.5$, and $q_o = 0.2$.

	$Max(I)$	$Max(I_y)$	$Max(I_m)$	$Max(I_o)$	H
Group Preference Control	19.80%	5.76%	11.79%	2.45%	0.133%
$.5q_y$	14.67%	2.46%	10.57%	2.01%	0.112%
$.5q_m$	7.17%	3.05%	3.06%	1.16%	0.047%
$.5q_o$	17.83%	5.46%	11.35%	1.25%	0.106%
All .5	1.56%	0.38%	1.02%	0.33%	0.014%
Varying Efficiency	2.23%	0.87%	1.34%	0.33%	0.017%

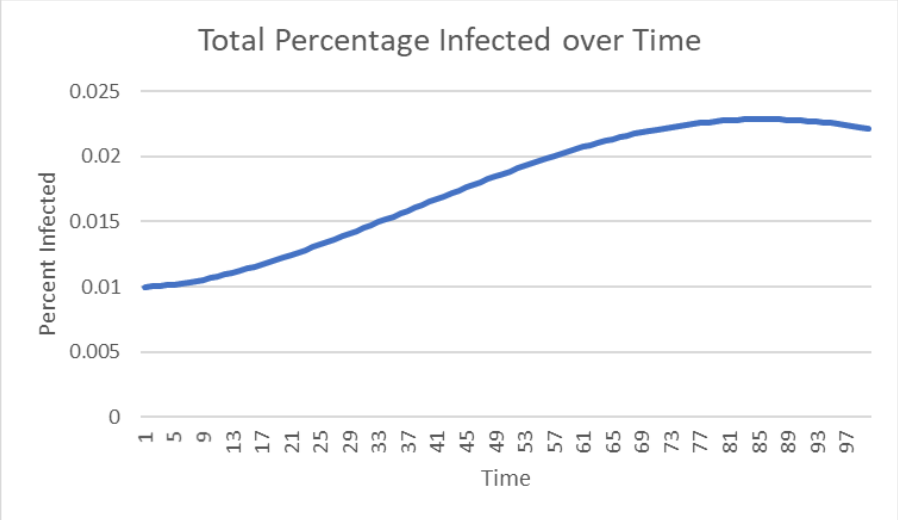

Figure 12: Combined Model: Total Infected Population

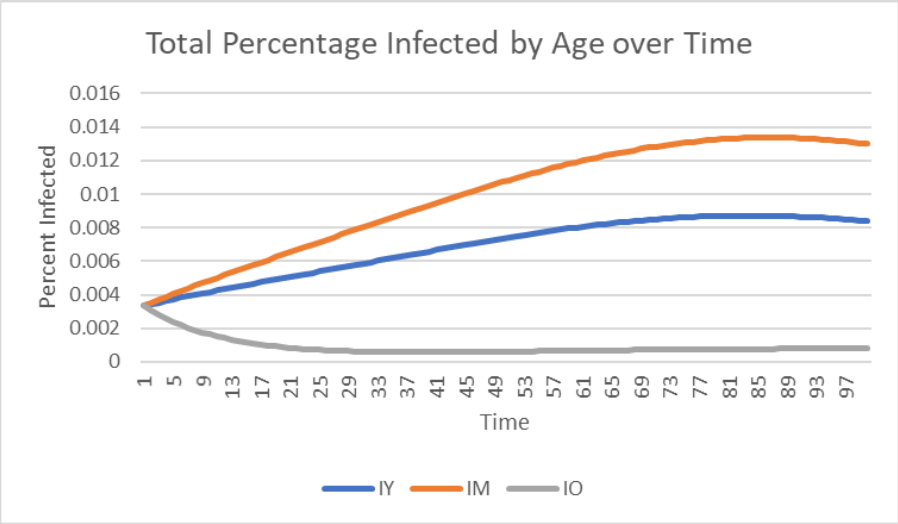

Figure 13: Combined Model: Total Infected Population by Age

These simulations grant additional insights to those seen in the uniform contact simulations. While the effect from population size was not as pronounced, it still provided significant impact on the spread of the disease. With these insights it is possible to state that larger proportions of the population quarantining have a larger effect than individual groups quarantining more efficiently. It is reasonable to conclude that it is more effective for the entire population to quarantine rather than a single at risk group quarantine.

5 Vaccinations

In this section we will apply a vaccination treatment to each of the models and analyze its effect. We will do this for each of the contact patterns.

5.1 Model Conditions

The main modification to the age structured SIR Model we have been using that we will use to account for vaccinations is to assume the vaccinated populated are completely immune and are already in the R compartment at the beginning of the simulation. We will effect the vaccination across one of each of the age groups and then all of them in subsequent simulations for each of the three contact types we have discussed. The initial values of each category will be determined by the formulas such as: $I_0 = 1/300$,

$S_0 = Population * (1 - V) - 1/300$, and $R_0 = Population * V$.

5.2 No Contact

The No Contact model where it is effectively three separate SIR models was earlier shown as a good way to assess how the parameter effects the output in isolation. This scenario also has the benefit of showing the effects of population size relative to other groups has on the outcome.

	$Max(I)$	$Max(I_y)$	$Max(I_m)$	$Max(I_o)$	H
No Contact Control	20.33%	4.60%	17.15%	0.33%	0.123%
$.5v_y$	17.68%	0.33%	17.15%	0.33%	0.117%
$.5v_m$	6.87%	4.60%	2.17%	0.33%	0.027%
$.5v_o$	20.12%	4.60%	17.15%	0.33%	0.123%
All .5	2.36%	0.33%	2.17%	0.33%	0.021%

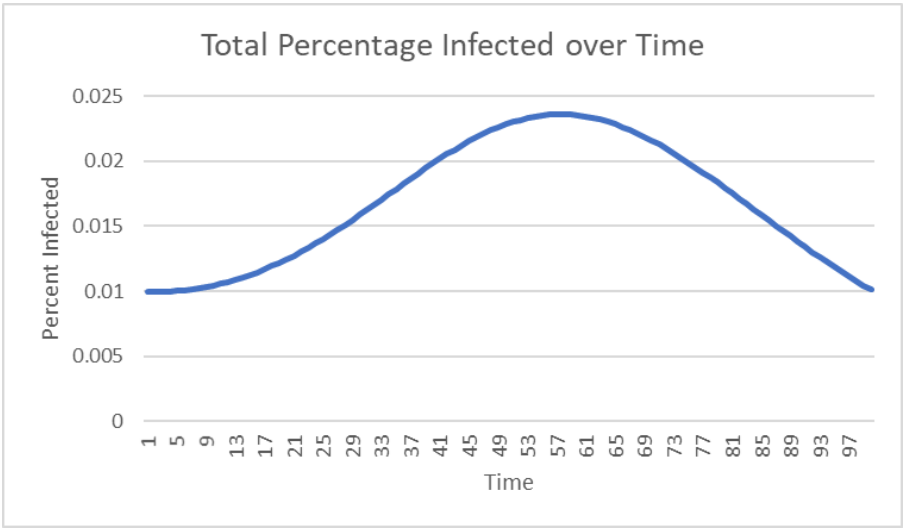

Figure 14: .5 V All Model: Total Infected Population

The results are very similar to those of the no contact quarantine simulations. The vaccination scenario does show greater efficacy overall to the quarantine scenario as the total infected was slightly less than or equal to the values under the quarantine scenario with the hospitalization values also be less than or equal to the quarantine results. Likewise, the results also show the same effect that treatment to larger population groups results in lower overall infections and hospitalizations.

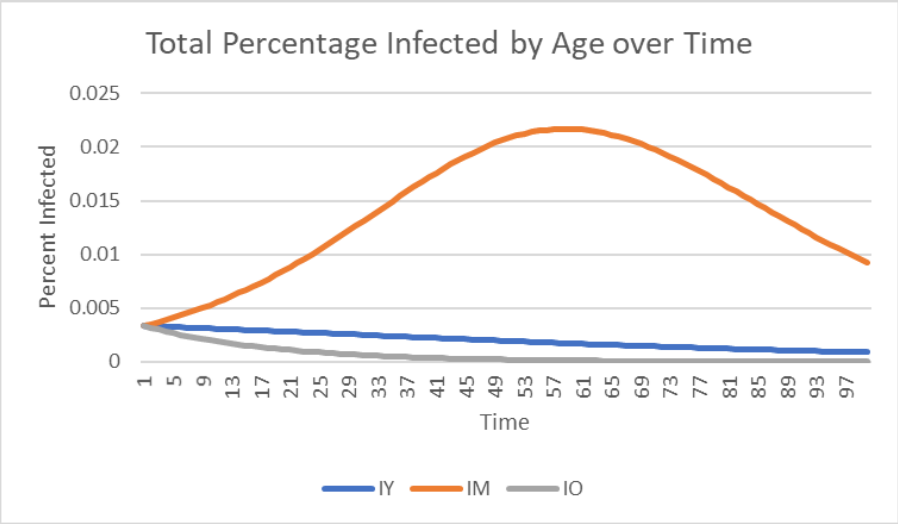

Figure 15: .5 V All Model: Total Infected Population by Age

5.3 Uniform Contact

For the same reasons stated in the quarantine section, we will proceed to run the same simulations on a uniform contact model.

	$Max(I)$	$Max(I_y)$	$Max(I_m)$	$Max(I_o)$	H
Uniform Contact Control	15.87%	5.02%	8.28%	2.56%	0.112%
$.5v_y$	8.62%	1.61%	5.35%	1.66%	0.070%
$.5v_m$	4.96%	2.13%	1.74%	1.08%	0.036%
$.5v_o$	11.94%	4.12%	6.79%	1.03%	0.070%
All .5	1.00%	0.33%	0.45%	0.33%	0.010%

The results look very similar to that of the quarantine results. A key difference is that the middle-aged infection curve is effectively scaled down instead of flattened like it was in the quarantine scenario. The resulting graphs show a trend where the control graphs curves are scaled down to the point where they cause the local R_0 to be less than 1 and the infection dies off. The effects of vaccinations appear to be more pronounced than those of quarantining though the values used are arbitrary and might not be the ideal for comparing the two treatments.

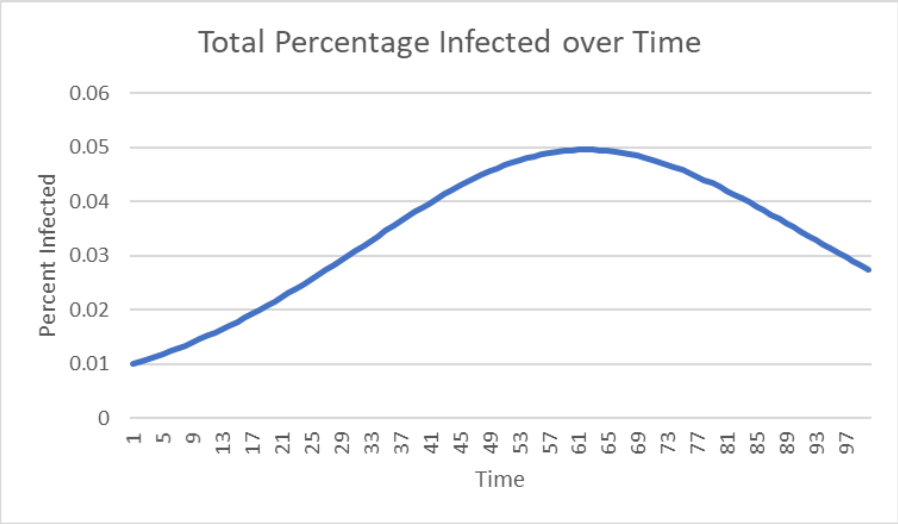

Figure 16: $v_m = 0.5$ Model: Total Infected Population

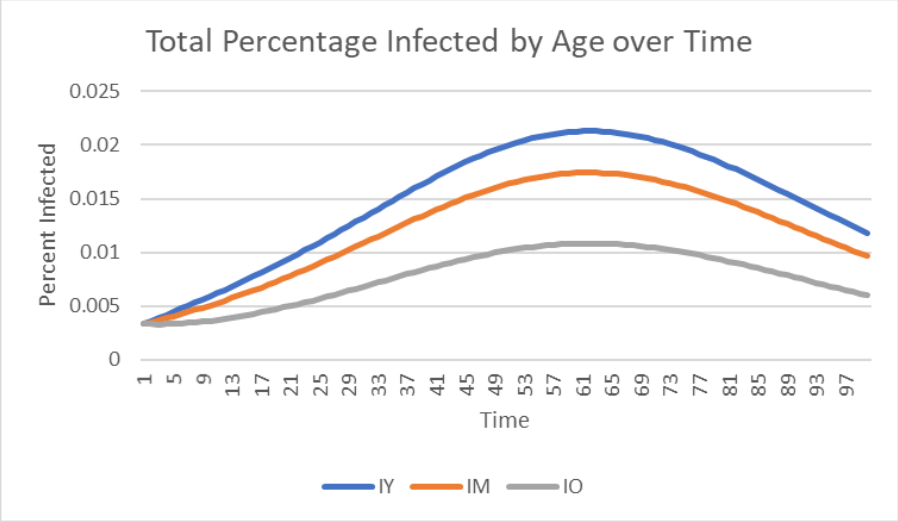

Figure 17: $v_m = 0.5$ Model: Total Infected Population by Age

5.4 Preferential Contact

We will again move to the preferential contact model as our control as we assess the effects of vaccination as we adjust contact. We will run the four simulations where we adjust one of each variables to be equal to 0.5 and then all of the vaccination variables to be 0.5. For a pointlessly complex simulation we will add an additional simulation to show varying vaccination rates and analyze the effects therein. For this we will use the values $v_y = 0.3$, $v_m = 0.5$, and $v_o = 0.8$.

	$Max(I)$	$Max(I_y)$	$Max(I_m)$	$Max(I_o)$	H
Group Preference Control	19.80%	5.76%	11.79%	2.45%	0.133%
$.5v_y$	14.19%	1.91%	10.51%	1.98%	0.110%
$.5v_m$	5.96%	2.87%	2.06%	1.04%	0.038%
$.5v_o$	17.59%	5.43%	11.32%	1.00%	0.101%
All .5	1.14%	0.33%	0.74%	0.33%	0.012%
Varying Efficiency	1.59%	0.64%	0.89%	0.33%	0.013%

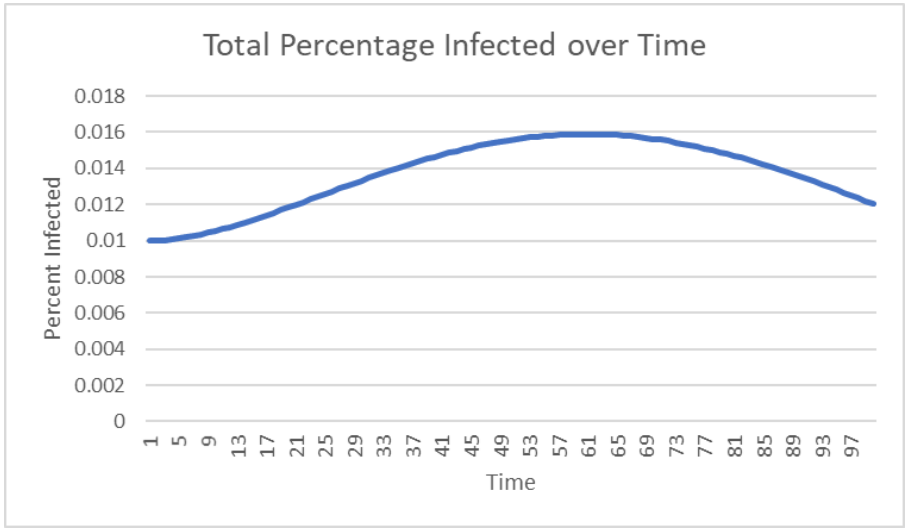

Figure 18: Preferential Contact with varying Vaccinations: Total Infected Population

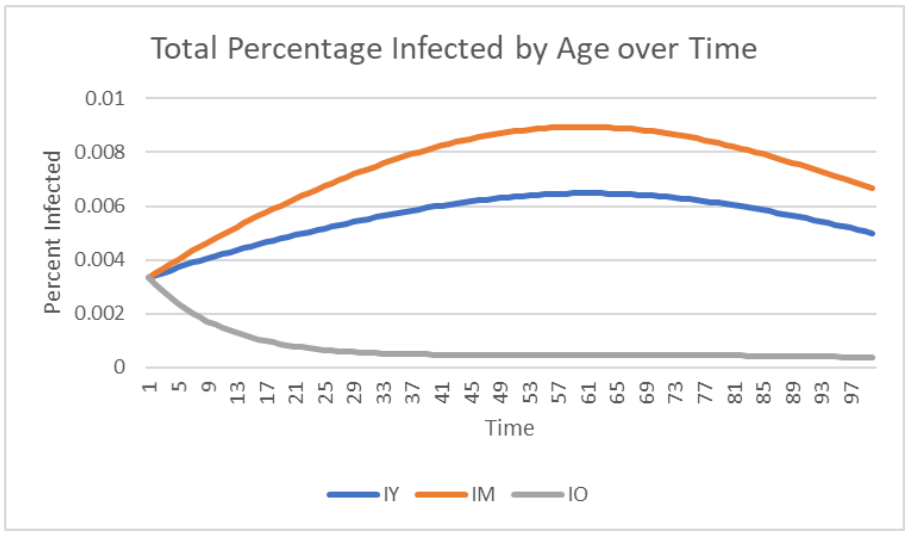

Figure 19: Preferential Contact with varying Vaccinations: Total Infected Population by Age

These results reinforce the results and conclusions seen in the quarantine results. The results are very similar to that of the uniform contact simulations. The overall efficacy of the vaccine treatment on

a single group is not as large as it was in the uniform contact simulations.

6 Conclusions

In this section we will go over a broad analysis of the results of the simulations. Further we will investigate the issues which arose during the creation of this thesis as well. Finally we will look into the interesting potential future research that can be done on this topic.

6.1 General Conclusions

	$Max(I)$	H
No Contact Control	20.33%	0.123%
$.5q_o$	20.13%	0.123%
$.5v_o$	20.12%	0.123%
$.5q_y$	17.70%	0.117%
$.5v_y$	17.68%	0.117%
$.5q_m$	7.94%	0.040%
All $q = .5$	4.31%	0.034%
$.5v_m$	6.87%	0.027%
All $v = .5$	2.36%	0.021%

	$Max(I)$	H
Uniform Contact Control	15.87%	0.112%
$.5q_o$	12.56%	0.078%
$.5q_y$	9.54%	0.075%
$.5v_o$	11.94%	0.070%
$.5v_y$	8.62%	0.070%
$.5q_m$	5.91%	0.043%
$.5v_m$	4.96%	0.036%
All $q = .5$	1.00%	0.010%
All $v = .5$	1.00%	0.010%

The results of the simulations give us insight in how to best address an infectious disease such as COVID-19. The key takeaway is that as interaction becomes more equalized across the subgroups of the population, quarantining needs to be practiced by all members of the population and all groups should

	$Max(I)$	H
Group Preference Control	19.80%	0.133%
$.5q_y$	14.67%	0.112%
$.5v_y$	14.19%	0.110%
$.5q_o$	17.83%	0.106%
$.5v_o$	17.59%	0.101%
$.5q_m$	7.17%	0.047%
$.5v_m$	5.96%	0.038%
All $q = .5$	1.56%	0.014%
All $v = .5$	1.14%	0.012%

be vaccinated. The models show that large groups of people interacting with at risk people have a large effect on at risk groups even if they are getting vaccinated and quarantining.

The less people interact with each other overall results in quicker, less severe outbreaks. By separating the population into separate groups, we can effectively lower the β and thus the R_0 value to the point that the outbreak will be contained through quarantining. There also exists a threshold where when each of the groups exceeds their local threshold, the disease will decay and the disease will not spread.

The groups to focus treatments on can be summarized as those who are at highest risk of hospitalization as well as those who have the highest interactions total relative to their proportion of the population. In the scenarios where we assume contact was uniform, the effective contact values are not uniform as they are all scaled by the relative sizes of each of the age categories. The middle-aged category having a population percentage of 52% meant that any treatment applied to the entire group had a much larger effect than to the other groups.

6.2 Issues and Future Work

The structure of this model is versatile and can be extrapolated to other subgroups of the population. It is possible to create separate subgroups for variables such as race, general health, occupation, or any combination of variables. The ensuing model could provide further insight on how to allocate resources to more at risk groups or mitigate the spread of diseases among “Super Spreaders”.

A key failing of this model is its simplicity. SIR Models make a lot of large assumptions that do not always hold true. SIR Models do not take into account the possibility of reinfection nor intermediary states of disease progression. It is possible to create models with Exposed, Hospitalized, or Vaccinated compartments. The model also ignores births, deaths, and migration which can cause the population within the system to change. Another failing is the deterministic approach to the spread of disease when a more stochastic approach may be appropriate.

This thesis was unable to cover other factors do to either a lack of time or data. A question I continually asked myself during the creation of this thesis is how the local R_0 would be calculated and what kind of function it would be. I also would have liked to have better data for the model itself to use rather than the generalizations of the overall US population and rough approximations of other parameters.

I would have like to go into a deeper analysis of eigenvalues and their impact on the results. My research suggested that the non-dominant eigenvalues could be used to predict the behavior of the subgroups. It would give valuable insights to further investigate these in the future as it could lead to a solution for the formulation of the local R_0 values.

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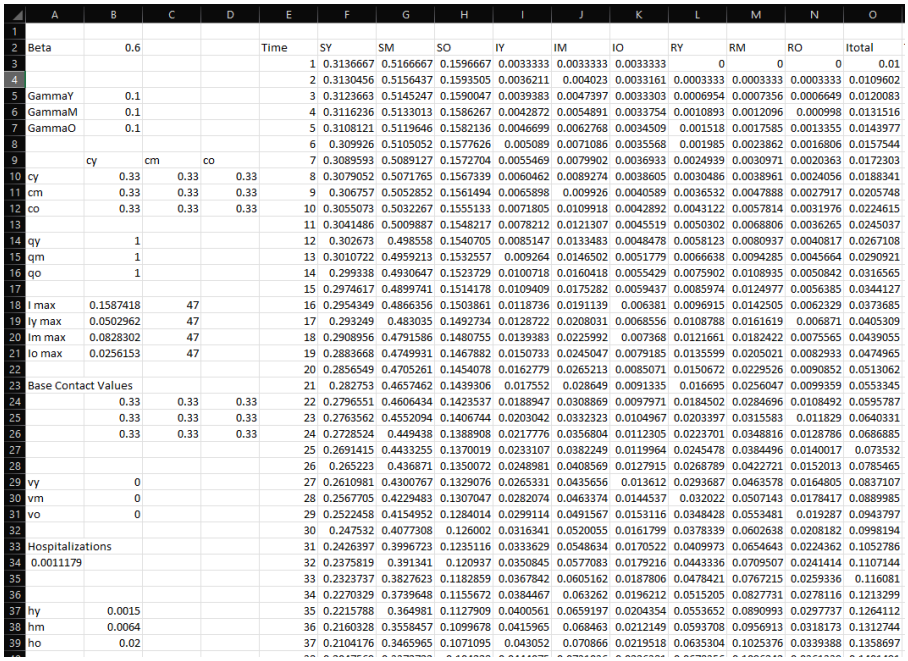
7 Appendix

For the sake of replication, I will give my model.



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1															
2	Beta	0.6			Time	SY	SM	SO	IY	IM	IO	RY	RM	RO	Itotal
3					1	0.3136667	0.5166667	0.1596667	0.0033333	0.0033333	0.0033333	0	0	0	0.01
4					2	0.3130456	0.5156437	0.1593505	0.0036211	0.004023	0.0033161	0.0003333	0.0003333	0.0003333	0.0109602
5	GammaY	0.1			3	0.3123663	0.5145247	0.1590047	0.0039383	0.0047397	0.0033303	0.0006954	0.0007356	0.0006649	0.0120083
6	GammaM	0.1			4	0.3116236	0.5133013	0.1586267	0.0042872	0.0054891	0.0033754	0.0010893	0.0012096	0.000998	0.0131516
7	GammaO	0.1			5	0.3108121	0.5119646	0.1582136	0.0046699	0.0062768	0.0034509	0.001518	0.0017585	0.0013355	0.0143977
8					6	0.309926	0.5105052	0.1577626	0.005089	0.0071086	0.0035568	0.001985	0.0023862	0.0016806	0.0157544
9		cy	cm	co	7	0.3089593	0.5089127	0.1572704	0.0055469	0.0079902	0.0036933	0.0024939	0.0030971	0.0020363	0.0172303
10	cy	0.33	0.33	0.33	8	0.3079052	0.5071765	0.1567339	0.0060462	0.0089274	0.0038605	0.0030486	0.0038961	0.0024056	0.0188341
11	cm	0.33	0.33	0.33	9	0.306757	0.5052852	0.1561494	0.0065898	0.009926	0.0040589	0.0036532	0.0047888	0.0027917	0.0205748
12	co	0.33	0.33	0.33	10	0.3055073	0.5032267	0.1555133	0.0071805	0.0109918	0.0042892	0.0043122	0.0057814	0.0031976	0.0224615
13					11	0.3041486	0.5009887	0.1548217	0.0078212	0.0121307	0.0045519	0.0050302	0.0068806	0.0036265	0.0245037
14	qy	1			12	0.302673	0.498558	0.1540705	0.0085147	0.0133483	0.0048478	0.0058123	0.0080937	0.0040817	0.0267108
15	qm	1			13	0.3010722	0.4959213	0.1532557	0.009264	0.0146502	0.0051779	0.0066638	0.0094285	0.0045664	0.0290921
16	qo	1			14	0.299338	0.4930647	0.1523729	0.0100718	0.0160418	0.0055429	0.0075902	0.0108935	0.0050842	0.0316565
17					15	0.2974617	0.4899741	0.1514178	0.0109409	0.0175282	0.0059437	0.0085974	0.0124977	0.0056385	0.0344127
18	I max	0.1587418	47		16	0.2954349	0.4866356	0.1503861	0.0118736	0.0191139	0.006381	0.0096915	0.0142505	0.0062329	0.0373685
19	Iy max	0.0502962	47		17	0.293249	0.483035	0.1492734	0.0128722	0.0208031	0.0068556	0.0108788	0.0161619	0.006871	0.0405309
20	Im max	0.0828302	47		18	0.2908956	0.4791586	0.1480755	0.0139383	0.0225992	0.007368	0.0121661	0.0182422	0.0075565	0.0439055
21	Io max	0.0256153	47		19	0.2883668	0.4749931	0.1467882	0.0150733	0.0245047	0.0079185	0.0135599	0.0205021	0.0082933	0.0474965
22					20	0.2856549	0.4705261	0.1454078	0.0162779	0.0265213	0.0085071	0.0150672	0.0229526	0.0090852	0.0513062
23	Base Contact Values				21	0.282753	0.4657462	0.1439306	0.017552	0.028649	0.0091335	0.016695	0.0256047	0.0099359	0.0553345
24		0.33	0.33	0.33	22	0.2796551	0.4606434	0.1423537	0.0188947	0.0308869	0.0097971	0.0184502	0.0284696	0.0108492	0.0595787
25		0.33	0.33	0.33	23	0.2763562	0.4552094	0.1406744	0.0203042	0.0332323	0.0104967	0.0203397	0.0315583	0.011829	0.0640331
26		0.33	0.33	0.33	24	0.2728524	0.449438	0.1388908	0.0217776	0.0356804	0.0112305	0.0223701	0.0348816	0.0128786	0.0686885
27					25	0.2691415	0.4433255	0.1370019	0.0233107	0.0382249	0.0119964	0.0245478	0.0384496	0.0140017	0.073532
28					26	0.265223	0.436871	0.1350072	0.0248981	0.0408569	0.0127915	0.0268789	0.0422721	0.0152013	0.0785465
29	vy	0			27	0.2610981	0.4300767	0.1329076	0.0265331	0.0435656	0.013612	0.0293687	0.0463578	0.0164805	0.0837107
30	vm	0			28	0.2567705	0.4229483	0.1307047	0.0282074	0.0463374	0.0144537	0.032022	0.0507143	0.0178417	0.0889985
31	vo	0			29	0.2522458	0.4154952	0.1284014	0.0299114	0.0491567	0.0153116	0.0348428	0.0553481	0.019287	0.0943797
32					30	0.247532	0.4077308	0.126002	0.0316341	0.0520055	0.0161799	0.0378339	0.0602638	0.0208182	0.0998194
33	Hospitalizations				31	0.2426397	0.3996723	0.1235116	0.0333629	0.0548634	0.0170522	0.0409973	0.0654643	0.0224362	0.1052786
34	0.0011179				32	0.2375819	0.391341	0.120937	0.0350845	0.0577083	0.0179216	0.0443336	0.0709507	0.0241414	0.1107144
35					33	0.2323737	0.3827623	0.1182859	0.0367842	0.0605162	0.0187806	0.0478421	0.0767215	0.0259336	0.116081
36					34	0.2270329	0.3739648	0.1155672	0.0384467	0.063262	0.0196212	0.0515205	0.0827731	0.0278116	0.1213299
37	hy	0.0015			35	0.2215788	0.364981	0.1127909	0.0400561	0.0659197	0.0204354	0.0553652	0.0890993	0.0297737	0.1264112
38	hm	0.0064			36	0.2160328	0.3558457	0.1099678	0.0415965	0.068463	0.0212149	0.0593708	0.0956913	0.0318173	0.1312744
39	ho	0.02			37	0.2104176	0.3465965	0.1071095	0.043052	0.070866	0.0219518	0.0635304	0.1025376	0.0339388	0.1358697

Figure 20: SIR model Excel sheet

- The initial values for Sm are ”=0.52*(1-B30)-J3”.
- The initial values for So are ”=0.163*(1-B31)-K3”.
- The initial values for Iy, Im, and Io are ”=0.01/3”.
- The initial values for Ry are ”=0.317*B29”.
- The initial values for Rm are ”=0.52*B30”.
- The initial values for Ro are ”=0.163*B31”.
- Itotal is just the sum of the I columns ”=SUM(I3:K3)”.

The first iteration (time 2) has the following formulas that are iterated over time.

- The formula for Sy is ”=F3-F3*($I3*$B$10+$J3*$C$10+$K3*$D$10)*$B$2”.

- The formula for Sm is ”=G3-G3*($I3*$B$11+$J3*$C$11+$K3*$D$11)*$B$2”.
- The formula for So is ”=H3-H3*($I3*$B$12+$J3*$C$12+$K3*$D$12)*$B$2”.
- The formula for Iy is ”=I3+($I3*$B$10+$J3*$C$10+$K3*$D$10)*$B$2*F3-I3*$B$5”.
- The formula for Im is ”=J3+($I3*$B$11+$J3*$C$11+$K3*$D$11)*$B$2*G3-J3*$B$6”.
- The formula for Io is ”=K3+($I3*$B$12+$J3*$C$12+$K3*$D$12)*$B$2*H3-K3*$B$7”.
- The formula for Ry is ”=L3+$B$5*I3”.
- The formula for Rm is ”=M3+$B$6*J3”.
- The formula for Ro is ”=N3+$B$7*K3”.