Comparison of Historical Epidemics

Evaluating the similarities and differences between the Measles, COVID-19, and SARS pandemics using a modified SEIR model

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1 Introduction

Mathematical models are commonly used in biological sciences. The idea is to use existing research, data, and concepts to develop a model that will estimate the quantitative behavior of a dynamical system. Modeling can also be especially helpful in urgent situations, like epidemiology. Modeling viral patterns rather than running empirical studies can produce predictions at a faster pace.

Mathematicians and biologists must collaborate in order to develop models that are not only accurate but also simple enough to use the available data. Disease modeling generates opportunities to identify various parameters and mechanisms that affect infectious disease spread. Some of these parameters can be of the form of environmental factors, mitigation factors or biological factors.

This report focuses on comparing three different pandemics - SARS, Measles, and COVID-19, in order to identify effective mitigation efforts to reduce infectious rates in the future, specifically the effects of quarantining. Pandemics have significant social and political impacts, including increased social and political tension, and demographic shifts. Understanding the effects that mitigation efforts such as quarantining and vaccinations have on transmission and death rates can help future generations effectively minimize social and political impacts. While many studies have mathematically modeled and compared various diseases, few have considered both asymptomatic and quarantine classes when building their models. See for instance the Heterogeneous Model of COVID-19 Dynamics published by the Frontiers in Public Health (Gerasimov, 2021) and the references therein. In their report, they failed to take into account the effects of asymptomatic individuals when it comes to infection rates. They did however consider the effects of a quarantine period. Considering the effects of various mitigation factors when comparing various pandemics will help us to make predictions about the effects that quarantine and vaccination have on

different populations. Therefore, this report develops a modeling framework which enhances an SEIR model to include an asymptomatic, quarantine, and hospitalization class. Such a model will introduce a new perspective to understanding how pandemics are transmitted and eventually eliminated. We hypothesize quarantining will have a positive effect on eliminating diseases. In other words, higher rates of quarantine will lead to a decrease in infection, hospitalization and death.

This section provides an overview of the biological and mathematical backgrounds of SARS, measles, and COVID-19. During 1989 and 1990 reported measles cases in the United States increased 6 to 9 fold over the annual mean of 3000 cases in the previous 5 years, officially becoming a pandemic. Mitigation factors for measles included both quarantine and a two dose vaccination period. It's important to note that children were particularly affected by measles. In 2002, another virus called Severe Acute Respiratory Syndrome (SARS) emerged in Hong Kong. With over 8,000 reported cases in over 30 countries worldwide, SARS was defined as the first pandemic in the twenty-first century. Quarantine was used as a mitigation factor much like the measles outbreak in the US. However, unlike measles, there was no available vaccination to combat against the virus. Towards the end of 2020 and the beginning of 2021 the Delta variant of COVID-19 emerged worldwide. Unlike previous strains of COVID-19, the Delta variant proved to be much more contagious. This viral outbreak caused worldwide quarantines, mask mandates, and vaccinations in order to combat the enormous number of infected persons. COVID-19 belongs to the same Betacoronavirus genus as the coronaviruses responsible for SARS but seems to be associated with milder symptoms. When comparing the two viruses, COVID-19 possesses a lower fatality rate, milder symptoms and a two dose vaccination. Commonalities between the three outbreaks include a quarantine period and highly infectious virus. In comparison to measles, both COVID-19 and SARS have higher infectious rates.

Many mathematical models have been used to explore the commonalities and differences between various worldwide epidemics in order to understand and generate better mitigation tactics. See for instance, an article by Gail Dutton and others published by Biospace comparing the SARS and COVID-19 pandemics (Dutton, 2020). They found differences between transmission patterns and infectious rates. These results can help researchers in the future when it comes to mandating various mitigation controls in a population, such as mask mandates or quarantine periods. This report begins by presenting a thorough review of previous modeling and comparisons of SARS, COVID-19, and measles, identifying various mitigation trends and current knowledge gaps. The main body of this report introduces an enhanced SEIR model used to accurately compare all three epidemics in order to analyze commonalities and differences. This modeling framework takes into account an asymptomatic stage, quarantine stage, and hospitalization stage with the aim of analyzing the effectiveness of mitigation factors, specifically quarantining, against various diseases. These predictions were simulated using MATLAB to give a comprehensible representation of the model predictions. Additionally, the models identify areas of possible future research.

2 Previous Work

Many studies have modeled and compared pandemics throughout history. This section presents a review of previous mathematical models of SARS, COVID-19, and measles. Reviewing these studies is imperative to understanding the procedures developed up to this point as well as identifying current knowledge gaps.

The National Library of Medicine published a report on the SARS outbreak in Hong Kong and the role of diagnosis and isolation as a control mechanism. (Chowell, Fenimore, Castillo-Garsow, & Castillo-Chavez, 2003).

They found that extreme isolation measured in conjunction with rapid diagnosis had a strong impact on local dynamics. Intuitively, quarantining individuals who have been in close contact with positively diagnosed people will reduce the total number of cases. They also found SARS to have an R_0 between 1.1 and 1.2 for the provinces of Ontario, Hong Kong, and Singapore.

Frontiers in Public Health published a Heterogeneous Model of COVID-19 Dynamics (Gerasimov, 2021). The model predicts that anti-epidemic measures, like the ones undertaken throughout the world, decrease the basic reproductive number but do not result in the development of sufficient collective immunity, which poses a risk of a second wave. In other words, the epidemic has a high likelihood to restart after the quarantine measures are lifted (Gerasimov, 2021). This study failed to take into account the effect of asymptomatic individuals when it comes to the rate of infection.

In 2020, BioSpace published an article by Gail Dutton comparing the 2003 SARS pandemic to the 2020 COVID-19 pandemic (Dutton, 2020). According to Dutton, COVID-19 is more virulent and more deadly than SARS. Both viruses can induce a high fever, shortness of breath and diarrhea, while COVID-19 includes loss of taste or smell, fatigue, muscle aches, headaches, congestion, nausea, and sore throat. Initially, SARS and COVID-19 both originated in animals before being transmitted to humans. Once SARS jumped to humans, it was transmitted from person to person and most virulent during the second week of infection when the virus was excreted through the mucus and stool peak. COVID-19 on the other hand spreads from person to person via droplets that are expelled when a person sneezes or coughs and then is inhaled by a nearby person (Dutton, 2020). Different transmission patterns cause COVID-19 to have higher infection rates. SARS and COVID-19 also differed in pandemic duration. SARS endured for an eight month period before the crisis ended in July 2003. In contrast, COVID-19 may be around for many years.

The National Library of Medicine published a comparative overview of COVID-19, MERS, and SARS (International Journal of Surgery (London, 2020). The review analyzes the epidemiology, etiology, clinical characteristics, treatment and consequences of SARS, MERS, and COVID-19 to help provide direction for further studies trying to understand COVID-19. For background, MERS or the Middle East Respiratory Syndrome is a viral respiratory illness originating in the twenty-first century. MERS exhibits symptoms similar to COVID-19 and SARS such as fever, cough, and shortness of breath. The study found that all three viruses were primarily transmitted by individuals who had contact with clinics, hospitals, health care, and nursing homes. The study was done during the early stages of COVID-19, so transmission of the disease evolved after the conclusion of the study. They also found that all three diseases originated from animal to human contact. After extensive research, the R_0 among fully susceptible people for SARS was about 3, for COVID-19 about 2.2, and for MERS about 0.7. When it comes to peak viral load, SARS appeared on the 10^{th} day, MERS during the second week, and COVID-19 during the first week. The clinical characteristics of the three viruses proved interesting. Age and chronic hepatitis B virus infection were shown to be important independent risk factors for the progression of SARS to ARDS. Acute Respiratory Disease Syndrome (ARDS) is a life threatening disease that allows fluid to leak into the lungs. Severe cases of COVID-19 and SARS can transform into ARDS. Advanced age was a predictor of adverse outcomes for both SARS and COVID-19. Besides age, organ and coagulation dysfunctions were also found to be associated with the progression of COVID-19 to ARDS and possibly even to death. In terms of recovery, the study found patients who have recovered from SARS and MERS had observable damage to the lungs. This study was published shortly after the onset of the COVID-19 pandemic and it is important to note the low R_0 values associated with COVID-19 and SARS found in the study. That being said, future research will be needed to observe the long term effects of the virus.

3 Methods

The proposed model accounts for asymptomatic individuals, quarantine, and hospitalization rates. These features are imperative to analyzing how mitigation efforts like quarantine affect the overall rate of fatalities and hospitalizations. Understanding the effects of mitigation efforts can also help policy makers reduce fatalities of diseases and pandemics in the future.

3.1 A Model for Measles, SARS, and COVID-19

In order to compare the three diseases to each other with efficiency, one model was needed. The SEIR model was used as a basis for this model. A SEIR model doesn't include important classes such as asymptomatic, quarantine, hospitalizations, and death. Part of what is being compared is how well mitigation efforts worked in each disease's case, as well as how severe the disease was in terms of deaths and hospitalizations. To account for these factors, more stages needed to be added to the SEIR model. Taking inspiration from Dr. Ledder's SEAIHRD COVID-19 model (Ledder & Homp, 2022), we developed the SEAIQHRD epidemic model. In the SEIR model, the infectious class I is the only class capable of transmitting the disease, whereas the SEAIHRD model has different categories of infectives with different levels of infectivity, which contribute to the effective infectivity and mitigation in different ways. The SEAIHRD COVID-19 model provided a lot of the components that we found essential in our project, but we wanted incorporate an additional mitigation class to answer our research question. Adjusting the SEAIHRD COVID-19 model we developed the SEAIQHRD epidemic model. A flow chart of the final model used is shown below with its corresponding differential equations in Section 3.3.

The SEAIHRD COVID-19 model and the SEAIQHRD epidemic model share many similarities and characteristics. Between the two models, the only

difference seen between the two is one class. Unlike to the SEAIHRD COVID-19 model, our SEAIQHRD epidemic model takes into account quarantine. With the addition of a quarantine class to the SEAIHRD model, there was a need to adjust the model and its parameters accordingly. While the SEAIHRD's effective infectivity count X is specifically catered towards COVID-19, the effective infectivity of SEAIQHRD model needed to be changed in order to model multiple diseases over time. The effective infectivity count X needed to be simplified into a count that would best suit our model and our diseases. In order to avoid a significant number of additional assumptions, we we simplified the effective infectivity from $\mathrm{X} = \delta f_a(1 - p_{ca})A + \delta(1 - p_c)I + f_c(p_c I + p_{ca} A) + f_h H)$ to $\mathrm{X} = I + f_a A$. With this adjustment, the SEAIQHRD model aims to represent the demographics of developed countries and homogeneous mixed populations throughout the measles, SARS, and COVID-19 epidemics.

After deciding on our final model, we needed to find values for each of the parameters in the model. To obtain parameters, data for each of the diseases was analyzed. For SARS, we looked at a specific outbreak in Hong Kong. (Anderson et al., 2004) The outbreak lasted over the years 2002-2003. For measles, we looked at the number of infections in the US over the first 26 weeks of the year 1990. One part of our model that wasn't needed for measles was the asymptomatic class. Measles isn't a disease that has a high number of asymptomatic individuals, so it didn't make sense to include this class. To get around this, we simply defined the fraction of individuals who are asymptomatic as 0. For COVID, we were only interested in the delta variant. This data was taken from populations in the United States, China, and the United Kingdom.

Once a set of parameters was properly defined, we could implement them into our model. To run a simulation of each of the diseases, we used Matlab to write a program to model the differential equations we defined. The code takes an input of each of our parameters and then implements them into the differential equations we defined from our model. The code runs a simulation of

the solution to these equations over a set amount of time for a given population. The results of the simulation are then plotted.

3.2 Model Development

Figure 1 displays the flow chart that represents our epidemic model. The diagram is based on a set of assumptions about the processes that move individuals among the classes.

1. Susceptible individuals are exposed at a total rate $\beta S(I+f_a A)$. Susceptible individuals become exposed at a rate β and an effective infectivity of $I + f_a A$, where f_a is the mitigation factor.

2. Exposed individuals become infectious at rate ηE; a fraction ρ_a of these become asymptomatic, while the remainder become symptomatic.

3. Asymptomatic individuals recover at rate $\gamma_a A$.

4. Some symptomatic infectives recover at a total rate $\gamma_i I c_h$; while other become hospitalized with total rate $\sigma\gamma_i I(1 - c_h)$. A fraction c_h of these infective individuals become hospitalized, while the remainder become recovered.

5. Quarantined individuals recover at a total rate $\gamma_q Q c_h$; a fraction c_h of these quarantined individuals become hospitalized, while the remainder become recovered.

6. Hospitalized individuals recover or die of the disease, with total rates $(1 - \mu)\gamma_h H$ and $\mu\gamma_h H$, respectively.

7. Recovered individuals are immune for long enough that we can ignore possible loss of immunity.

8. Birth and deaths from unrelated causes are sufficiently small over the course of the epidemic that they can be ignored.

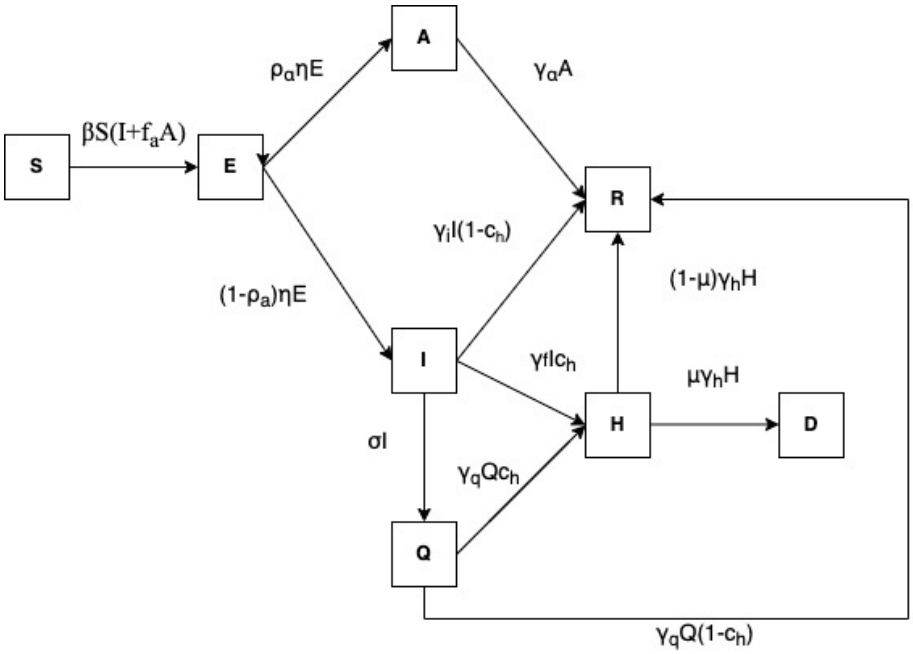

Figure 1: SEAIQHRD Epidemic Model

These assumptions lead to the differential equations;

$$\frac{dS}{dt} = -\beta S(I + f_a A) \tag{1}$$

$$\frac{dE}{dt} = \beta S(I + f_a A) - \eta E \tag{2}$$

$$\frac{dA}{dt} = \rho_a \eta E - \gamma_a A \tag{3}$$

$$\frac{dI}{dt} = (1 - \rho_a)\eta E - \gamma_i I(1 - c_h) - \gamma_f I c_h - \sigma I \tag{4}$$

$$\frac{dQ}{dt} = \sigma I - \gamma_q Q \tag{5}$$

$$\frac{dH}{dt} = \gamma_f I c_h + \gamma_q Q c_h - \gamma_h H \tag{6}$$

$$\frac{dR}{dt} = \gamma_a A + \gamma_i I(1 - c_h) + (1 - \mu)\gamma_h H + \gamma_q Q(1 - c_h) \tag{7}$$

$$\frac{dD}{dt} = \mu \gamma_h H \tag{8}$$

3.3 Model Parameters

The parameters were taken from a variety of sources. For SARS, we took data from Hong Kong in 2003. For measles, data came from The United States in the 1990s. Lastly, for the delta variant of COVID-19, we took data from the United States, Hong Kong, and the United Kingdom in 2021. The data allowed us to find variables like β and R_0, as well as the latent period, incubation periods, and hospitalization rates for COVID-19, SARS, and measles. From this information, we were able to cross reference differences in variable estimates to minimize error. All of the parameters listed in the table below were collected from published literature about each of the epidemics considered.

Parameters	Meaning	SARS	Measles	COVID-19
β	Transmission Rate	0.25	0.16667	0.1724
β_a	Transmission Rate of A	0	0	0.1293
f_a	Transmission Reduction Due to A	0	0	0.75
η	Latent Rate	0.1570	0.0714	0.25
γ_a	Transition Rate of A	0.0352	0	0.7155
γ_i	Transition Rate of I	0.0426	0.125	0.2145
γ_q	Transition Rate of Q	0.0536	0.25	0.0714
γ_h	Transition Rate of H	0.04	0.0625	0.1111
γ_f	Transition Rate to H	0.4	0.25	0.2222
σ	Incubation Rate	0.2062	0.0833	0.1724
μ	Hospital Death Probability	0.0279	0.003	0.0089
$1-\mu$	Hospitalization Recovery Probability	0.9721	0.997	0.9911
c_h	Hospitalization Probability	1	0.211	0.023
$1-c_h$	Non-Hospitalization Recovery Probability	0	0.789	0.977
ρ_a	Asymptomatic Probability	0.13	0	0.325
$1-\rho_a$	Non-Asymptomatic Probability	0.87	1	0.675

Once we had made an appropriate model and found values for our parameters, we needed to actually run a simulation. To do this, we used MATLAB to solve the differential equations and plot the results. We utilized the code written by our teaching assistant, Stephen Becklin. It allowed us to insert our own differential equations and assign parameter values in the beginning of the code.

All of the parameters listed in our table above were used in each run of the simulation. The only parameter that we wanted to change was σ, the fraction of infected people who will quarantine. Our research was focused on comparing how different amounts of quarantine could have changed how the diseases ran their course. Our model was designed to run for short amounts of

time with small populations. For each run of the simulation, we started with a population of 1000 susceptible individuals and 1 infected. The simulation was run for 365 days and the differential equations were calculated with a dt of 0.01. For each disease, we ran three simulations with our different values of the quarantine rate, σ. The values reflect three different possibilities: no one quarantines, everyone quarantines, or people quarantine at a rate of $\sigma = 0.2174$. This rate was taken from the rate at which people entered the quarantine class during the current COVID-19 pandemic. The idea was to examine how SARS and measles would have been affected if similar quarantine efforts were enforced for the diseases. There was a heavy emphasis on quarantining during the COVID-19 pandemic, and we wanted to see what would happen if people quarantined at a similar rate for measles and SARS. For everyone quarantines and no one quarantines we used the values 1 and 0 respectively.

4 Results

We ran a simulation of each disease three times, each time changing our quarantine parameter σ. Our quarantine parameter can take on values of 0, 1, or 0.2174. Here 0 is when no one in the population the no quarantines, 1 is when everyone in the population quarantines, and 0.2174 is the rate at which people quarantine during COVID-19. Each value was substituted into the MATLAB code, giving us a total of nine simulations. The results are plotted and all shown in the following sections for COVID-19, SARS, and measles.

4.1 No Quarantine Simulation

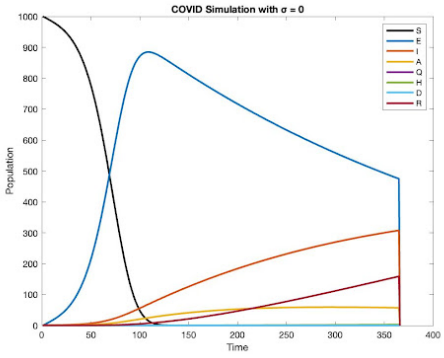

Figure 2: COVID-19

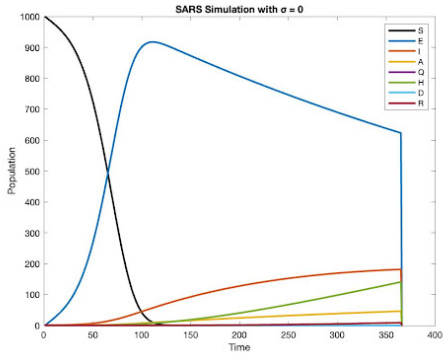

Figure 3: SARS

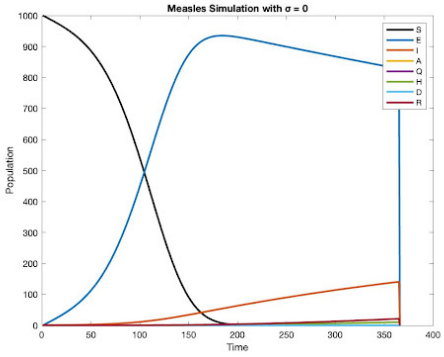

Figure 4: Measles

The graphs above depict the three pandemics when no quarantine mitigation efforts are put in place. Based on the graphs, COVID-19 is shown to be the most infectious, then SARS, then measles. The susceptible individuals for COVID-19 have the largest slope, causing the exposed individuals to increase at a faster rate. The orange line depicts the infectious class and is largest for COVID-19. The death rate for all three diseases is shown to remain at or slightly above zero during the entirety of the time period. This contradicts the data and research we discovered in the literature review. It is likely that the small population size

of 1001 people, and the small parameter we used for the death rate caused this deviation from expectation and reality. The parameter we used for the death rate also only took into account the people who are hospitalized that die of the disease which could have also caused the above results.

4.2 Complete Quarantine Simulation

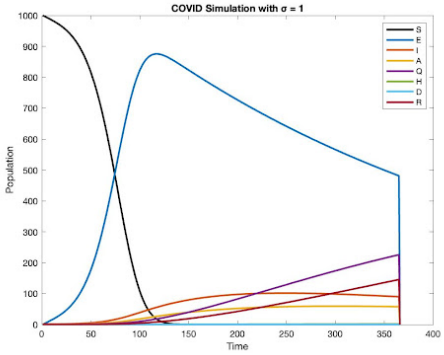

Figure 5: COVID-19

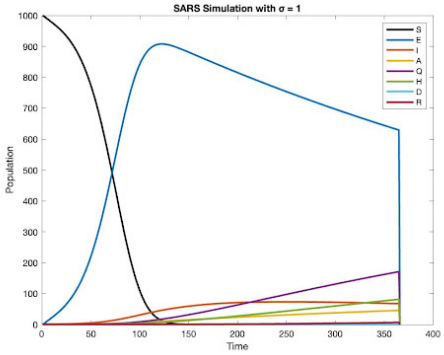

Figure 6: SARS

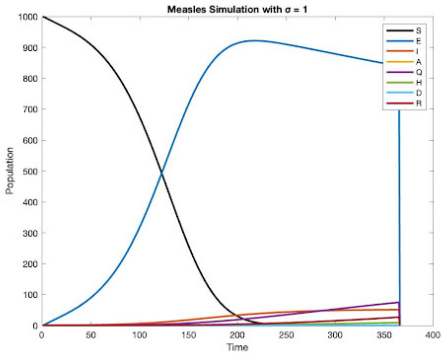

Figure 7: Measles

The graphs above depict the three pandemics when complete quarantine measures are put in place. Similar to no quarantine measures, the graphs show COVID-19

to be the most infectious pandemic. COVID-19 has the highest rate of infectious individuals as well as the largest slope of exposed and susceptible individuals. As for quarantine, all three of the pandemics show enforcing quarantine measures at the fullest causes the disease to completely die out.

4.3 COVID-19 Quarantine Measures Simulation

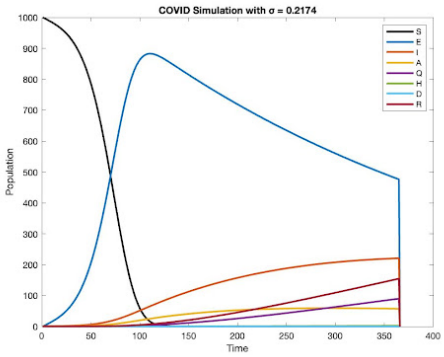

Figure 8: COVID-19

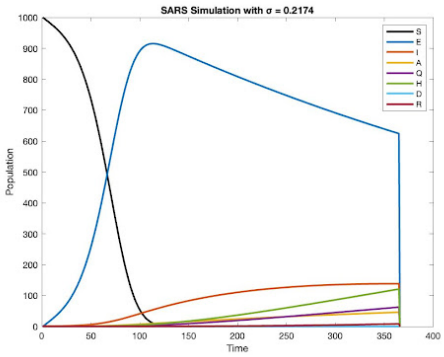

Figure 9: SARS

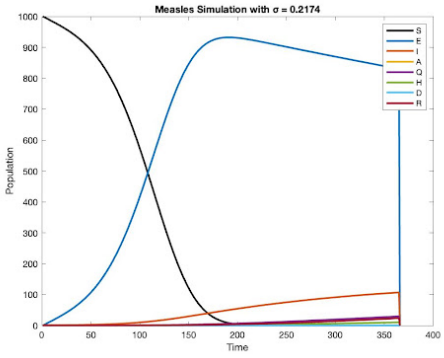

Figure 10: Measles

The graphs above depict the three pandemics if they were present at current day and COVID-19 quarantine measures were put in place. Similar to the

previous graphs, COVID-19 remains the most infectious disease. When COVID-19 quarantine measures are used for both SARS and Measles, a decrease in infectious persons and an increase in recovered persons over time is present. From these results we are able to conclude quarantine mitigation efforts led to a decrease in the presence of the disease over time.

5 Conclusions

Based on the above results, we came to a few conclusions when comparing the three pandemics. For all three diseases, increasing quarantine led to a decrease in hospitalizations and infected individuals ultimately confirming our hypothesis. It's important to note, there are more susceptible and infected individuals during the 6 month time period of the COVID-19 pandemic in 2021 than SARS in 2003 or Measles in the 1990s. This led to more asymptomatic and recovered individuals for COVID-19. Based on the graphs above, during the COVID-19 pandemic, people recovered quicker and had less hospitalizations than SARS. Measles had a slow recovery time in comparison to COVID-19 and SARS. Measles also varied from the other two pandemics because there were no asymptomatic individuals. Overall, the results show quarantine is an effective mitigation effort for different diseases. Quarantine led to a decrease in infected individuals and hospitalizations for all three diseases.

6 Discussion

An important note to consider is that our model only accounts for quarantine as the only form of mitigation in the population. Since, we were comparing historical disease epidemics, we had to choose a mitigation that was common among all of our chosen diseases of interest. In reality, there are multiple mitigation efforts put in place in a population to reduce the spread of diseases.

Besides quarantine, other mitigation efforts such as masking, social distancing, vaccination would make a great impact towards containing COVID-19, SARS, and measles. As seen in our results, quarantine did help in minimizing the affects of the diseases but it still isn't enough. So utilizing multiple mitigation efforts would need to be implemented to further contain these diseases. Although the SEAIQHRD served it's purpose in comparing these epidemics, if we had more time it would be interesting to see results if we could account for more mitigation efforts in our model. Another thing to take into consideration is that our parameters were taken from multiple different regions, with SARS from Hong Kong, measles from the United States, and the Delta Variant of COVID-19 from a combination of China, the United States, and the United Kingdom. If we could have found parameters from one common specific region, our results and conclusion could've further been improved. Lastly, due to the nature of our model, our MATLAB code was restricted to a total population of only 1001 individuals. The results and conclusions of our project would have greatly benefited if we were able to adjusted our total population to better represents our selected regions.

7 Bibliography

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(LMIC, n.d.)

(*nc*, n.d.-b)

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8 MATLAB Code

The MATLAB code used to run all nine simulations for COVID-19, SARS, and measles are provided below.

Note:

1. Must run each parameter values of SARS, COVID-19, and measles individually for each simulation.
2. Must change title after each simulation.
3. Must change σ value or the eighth value in parameters = [] to 0, 1, 0.2174 to see all nine different quarantine simulations for COVID-19, SARS, and measles.

Code:

function simulated_stages=general_covid19_sim(initial_values, parameters, max_time_units, dt)

SARS:
parameters = [0.25, 0, 0.03521126761, 0.04255319149, 0.04, 0.05361930295, 0.1569858713, 0, 0.0279, 0.9721, 0.13, 0.87, 1, 0, 0.4];

COVID:
parameters = [0.1652892562, 0.75, 0.71548, 0.1072425, 0.1111111111, 0.07142857143, 0.25, 0, 0.0089, 0.9911, 0.3, 0.7, 0.023, 0.977, 0.222222];

```
        Measles:
parameters = [0.1666666667, 0, 0, 0.125, 0.0625, 0.25, 0.07143, 0, 0.003, 0.997,
0, 1, 0.211, 0.789, 0.25];


        initial_values = [1000, 0, 1, 0, 0, 0, 0, 0];
dt = 0.01;
max_time_units = 3.65/dt;


        if  ismatrix(initial_values)
disp('Initial values input is not in the form of a Matlab matrix.');
return;
end


        if size(initial_values, 1)  = 1
disp('Initial values input is not a 1-by-n matrix.');
return;
end


        if  ismatrix(parameters)
disp('Parameters input is not in the form of a Matlab matrix.');
return;
end


        if size(parameters, 1)  = 1
disp('Parameters input is not a 1-by- matrix.');
return;
end
```

```
        if  isnumeric(max_time_units) — mod(max_time_units,1)  = 0
disp('Max time units input is not an integer.');
return;
end


        if size(max_time_units, 1)  = 1 —— size(max_time_units, 2)  = 1
disp('Max time units input must be a single numeric input and not a matrix.');
return;
end


        if  isnumeric(dt)
disp('dt input is not a number.');
return;
end


        if size(dt, 1)  = 1 —— size(dt, 2)  = 1
disp('dt input must be a single numeric input and not a matrix.');
return;
end


        simulated_stages = zeros(max_time_units + 1, size(initial_values, 2));


        simulated_stages(1, :) = initial_values;


        Y = initial_values;
y = transpose(Y);
for t = 1:max_time_units
```

```
y = rk4(dt,y,parameters);
Y = transpose(y);
simulated_stages(t+1, :) = Y;
end


        function y=rk4(dt,y0,parameters)
k1 = yprime(y0,parameters);
k2 = yprime(y0+0.5*dt*k1,parameters);
k3 = yprime(y0+0.5*dt*k2,parameters);
k4 = yprime(y0+dt*k3,parameters);
y = y0+dt*(k1+2*k2+2*k3+k4)/6;
end


        function yp = yprime(y,parameters)
yp = sqrt(-1)*ones([size(y, 1) 1]);
yp(1) = -1*parameters(1)*y(1)*y(3)-parameters(1)*y(1)*parameters(2)*y(4);
yp(2) = 1*parameters(1)*y(1)*y(3)+parameters(1)*y(1)*parameters(2)*y(4) -
parameters(7)*y(2);
yp(3) = parameters(12)*parameters(7)*y(2)-parameters(4)*y(3)*parameters(14)-
parameters(15)*y(3)*parameters(13)-parameters(8)*y(3);
yp(4) = parameters(11)*parameters(7)*y(2)-parameters(3)*y(4);
yp(5) = parameters(8)*y(3)-parameters(6)*y(5);
yp(6) = parameters(6)*y(5)*parameters(13)+parameters(15)*y(3)*parameters(13)-
parameters(5)*y(6);
yp(7) = parameters(9)*parameters(5)*y(6);
yp(8) = parameters(4)*y(3)*parameters(14)+parameters(3)*y(4)+parameters(10)*parameters(5)*y(6)+param
```

```
        S = simulated_stages(:,1);
E = simulated_stages(:,2);
I = simulated_stages(:,3);
A = simulated_stages(:,4);
Q = simulated_stages(:,5);
H = simulated_stages(:,6);
D = simulated_stages(:,7);
R = simulated_stages(:,8);


        time = 0:dt:maxsimulated_stages time simulated_stagesunits*dt;
newcolors = [ 0 0 0
0 0.4470 0.7410
0.8500 0.3250 0.0980
0.9290 0.6940 0.1250
0.4940 0.1840 0.5560
0.4660 0.6740 0.1880
0.3010 0.7450 0.9330
0.6350 0.0780 0.1840];
colororder(newcolors);
plot(S, '-', 'LineWidth',2);
hold on
plot(E, '-', 'LineWidth',2);
plot(I, '-', 'LineWidth',2);
plot(A, '-', 'LineWidth',2);
plot(Q, '-', 'LineWidth',2);
plot(H, '-', 'LineWidth',2);
plot(D, '-', 'LineWidth',2);
plot(R, '-', 'LineWidth',2);
hold off
legend('S', 'E', 'I', 'A', 'Q', 'H', 'D', 'R')
```

```
title('COVID Simulation with $\sigma$= 0')
xlabel('Time')
ylabel('Population')
end
end
```