

A S.E.I.R. MATHEMATICAL MODEL OF SAR-COV-2

by

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## ABSTRACT OF THESIS

### A S.E.I.R MATHEMATICAL MODEL

Coronaviruses are named for the crown-like spikes on their surface. Human coronaviruses were first identified in the mid-1960s. The well-known coronaviruses that can infect people are: MERS-CoV (Middle East Respiratory Syndrome, or MERS), SARS-CoV (severe acute respiratory syndrome, or SARS), and the topic of this paper SARS-CoV-2 (the novel coronavirus that causes coronavirus disease 2019, or COVID-19). COVID-19 is the disease caused by the new coronavirus that emerged in China in December 2019. Most common symptoms of COVID-19 include cough, fever or chills, shortness of breath or difficulty breathing, muscle or body aches, sore throat, new loss of taste or smell, diarrhea, headache, new fatigue, nausea or vomiting and congestion or runny nose. A compartmental model was developed to describe the interactions among at-risk individuals, infected individuals, and those who are in treatment or recovered. Because of the demographics of the groups affected by this epidemic, the model also considered social factor that might alleviate the spread of the disease. The basic reproduction number was determined and revealed the condition for the stability of the Coronavirus free equilibrium. Stability analysis and numerical simulations were carried out to study the impact of the social factors to the epidemic[1].

## DEDICATION

I would like to dedicate this thesis to my family that has been with me from the beginning and has helped me along the way. Without them I do not know where I would be in life.

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# 1 Introduction

Human coronaviruses were first identified in 1965. Researchers found a group of similar human and animal viruses and named them after their crown-like appearance later that decade. There are four main sub-groupings of coronaviruses and they include alpha, beta, gamma, and delta. The most well-known infectious coronaviruses are: MERS-CoV (the beta coronavirus that causes Middle East Respiratory Syndrome, or MERS), SARS-CoV (the beta coronavirus that causes severe acute respiratory syndrome, or SARS), and the topic of this paper, SARS-CoV-2 (the novel coronavirus that causes coronavirus disease 2019, or COVID-19)[1]. Initially, it was the belief of scientists that the virus that caused SARS (SARS-CoV) was similar to the one that causes COVID-19. However, researchers have recently discovered an important difference that may explain why the new coronavirus is so hard to stop: SARS-CoV-2 (the virus that causes COVID-19) binds 10 to 20 times more tightly to human cells than SARS-CoV (the virus responsible for SARS)[3].

Sometimes coronaviruses that infect animals can evolve and make people sick and become a new human coronavirus. Three recent examples of this are MERS-CoV, SARS-CoV, and SARS-CoV-2. COVID-19 is the disease caused by the new coronavirus that emerged in China in December 2019. Most common symptoms of COVID-19 include cough, fever or chills, shortness of breath or difficulty breathing, muscle or body aches, sore throat, new loss



Coronavirus Symptoms		
Most Common Symptoms	Less Common Symptoms	Serious Symptoms
fever dry cough tiredness	aches and pains sore throat diarrhea conjunctivitis headache loss of taste or smell a rash on skin, fingers or toes	difficulty breathing chest pain loss or speech/movement

Table 1: Table 1.1 Symptoms for COVID-19

of taste or smell, diarrhea, headache, new fatigue, nausea or vomiting and congestion or runny nose. However, as the disease has spread around the world, healthcare providers have noticed a few unusual symptoms, including loss of smell (anosmia) and decreased sense of taste (ageusia)[3]. A chart can be seen in Table 1.1 with symptoms of COVID-19 ranging from most common to serious. COVID-19 can be severe, and some cases have caused death.

Most people infected with the COVID-19 virus will experience mild to moderate respiratory illness and recover without requiring special treatment. Older people, and those with underlying medical problems like cardiovascular disease, diabetes, chronic respiratory disease, and cancer are more likely to develop serious illness. Compared to adults, children appear much less likely to get sick if they contract the novel coronavirus. However, the very young (less than 1 year) appear to be more vulnerable to serious illness than older children. A multisystem inflammatory syndrome (MIS) is affecting some children positive for current or recent SARS-CoV-2 infection. [3].

The COVID-19 virus spreads primarily through droplets of saliva or discharge from the nose when an infected person coughs or sneezes, so it's important that you also practice respiratory etiquette (for example, by coughing into a flexed elbow)[1].

The best way to prevent and slow down transmission is to be well informed about the COVID-19 virus, the complications it causes and how it spreads. However, a study using a decision analytical modeling estimated that more than half of COVID-19 infections were likely transmitted by individuals not presenting with symptoms. Various projections were assessed for time-based transmission from presymptomatic, symptomatic, and asymptomatic individuals. The study assumed a median 5-day incubation period and symptom presentation by day 12 among 95 percent of symptomatic individuals. The investigators estimated that 59 percent of transmissions came from individuals who did not present with symptoms (35 percent presymptomatic; 24 percent asymptomatic) [4].

Protect yourself and others from infection by washing your hands or using an alcohol based rubs frequently and do not touch your face. Table 1.2 shows ways of prevention the contraction and spreading COVID-19 [1]

As of now, there is not a specific treatment for the virus. People who become sick from COVID-19 should be treated with supportive measures that relieve symptoms. For severe cases, there may be additional options for treatment, including research drugs and therapeutics[2].

<b>Coronavirus Prevention</b>
<b>To prevent infection and to slow transmission of COVID-19</b>
Wash your hands regularly with soap and water/clean with alcohol-based hand rub. Maintain at least 1 feet distance between you and people coughing/sneezing. Avoid touching your face Cover your mouth and nose when coughing or sneezing Stay home if you feel unwell Refrain from smoking and other activities that weaken the lungs. Practice physical distancing by avoiding large groups of people.

Table 2: Table 1.2 Symptoms and Preventive Measure for COVID-19

## 2 Method

### 2.1 Approach

The goal of epidemiological studies is to observe a relationship between risk factor and a particular illness. In this paper we use a modified version of the SIR model, with the E incorporated [5]. In the diagram the (S) represents the susceptible class. These are the individuals prone to the coronavirus infection. In this model the individuals will be from the Hampton Roads area from the time frame of April 2020 to February of 2021. The (E) represents the exposed class, is the part the population who are infected and have not been detected by testing. The (I) is for the infectious class, this is the class that has been test and confirmed to be affected by this novel disease. The (R) is for recovery, this is the individuals that have totally recovered from the disease. Clearly this model involves certain assumptions. These

assumption consist of the following:

$$N = S + E + I + R$$

This assumption is that the population is constant. To prove the population is constant we use the characteristic equation and equal then to  $\frac{dN}{dt}$

Proof:

$$\begin{aligned} \frac{dN}{dt} &= \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \\ &= \mu N - \frac{\beta\sigma SI}{N} - \mu S + \frac{\beta\sigma SI}{N} - \tau E - \alpha E - \mu E + \alpha E - \gamma I - \mu I + \gamma I + \tau E - \mu R \\ &= \mu(N - S - E - I - R) \\ &= \mu(N - N) \\ &= 0 \end{aligned}$$

In order to obtain our differential equation for the S class we use the arrows to indicate the rates going in and out the compartments. When an arrow is entering the compartment the rate is positive. When the rate is exiting of the compartment the rate is negative. The S represents the susceptible class those whose are susceptible to the disease. The E represents the exposure class. This is the class that is exposed to the virus. The I represent the infectious class. This is the class that has the infection. The R

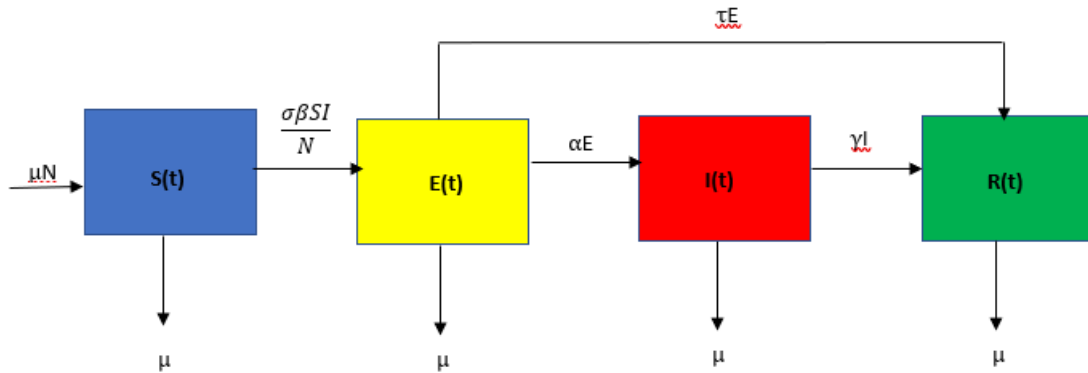


Figure 1: Flowchart of the proposed SEIR model of COVID-19

represents the recovery class. This is the class that has totally recovered or died from the infection. The path from S to E is the transition of becoming transmitted with COVID-19. Individual in the exposed class become infected and move to the infected class because of risk taking behavior. Individuals in the exposed class may or may not become infected with COVID-19. If they do not then individuals that were in the exposed class are transition to the recovered class after fourteen days of quarantine. As there is no treatment for COVID-19, individuals that move to the I compartment when they seek recovery from the disease. The path from I to R is when the individual has not totally recovered from treatment. Then from the R compartment they move back into susceptible class because they are now vulnerable to the infection and it becomes easier for the individual to come in contact with it.

The model can be represented by these differential equations.

$$\begin{aligned}
\frac{dS}{dt} &= \mu N - \frac{\beta\sigma SI}{N} - \mu S \\
\frac{dE}{dt} &= \frac{\beta\sigma SI}{N} - \tau E - \alpha E - \mu E \\
\frac{dI}{dt} &= \alpha E - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma I + \tau E - \mu R
\end{aligned}$$

The previous equations were re-scaled to simplify the analysis, the following equations were obtained where  $x = \frac{S}{N}$ ,  $y = \frac{E}{N}$ ,  $z = \frac{I}{N}$ ,  $w = \frac{R}{N}$ :

$$x' = \mu - x(\beta\sigma z + \mu) \tag{1}$$

$$y' = \beta\sigma xz - y(\alpha + \mu + \tau) \tag{2}$$

$$z' = \alpha y - z(\gamma + \mu) \tag{3}$$

$$w' = \gamma z + \tau y - \mu w \tag{4}$$

where  $x + y + z + w = 1$

Parameters for Graph on COVID-19 Infections		
Parameters	Definition	Values
$\beta$	transmission rate	.05
$\gamma$	rate of recovery	.005
$\alpha$	exposure rate of the infected	.112
$\tau$	rate of exposed individuals that could possibly be infected	.11
$\sigma$	the social factors of becoming infected with COVID-19	$0 < \sigma < 1$
$\mu$	rate of individuals that leave the compartment	.009
$S$	the susceptible class	
$E$	the exposed class	
$I$	the infected class	
$R$	the recovery class	

*Potential Individuals Susceptible to Covid-19:  $S(t)$*

This is the class of individuals that do not have COVID-19, are at risk of at the rate of  $\mu N$ . Members of this class become exposed with COVID-19 via contact with the E class at the rate of  $\beta$ . Members of this class are at a removal rate  $\mu$  is represented by the individuals that leave the class. So the rate of change of individuals susceptible to Covid-19 is given by

$$\frac{dS}{dt} = \mu N - \frac{\beta \sigma SI}{N} - \mu S$$

*Individuals that have COVID-19:  $E(t)$*

This is the class of individual have been exposed to COVID-19. This class increases when the susceptible class let social factors with the transmission rate increase due to not effectively socially distancing (being more than six feet apart)  $(\beta\sigma)$ [6]. A decreasing factor is the exposed rate  $(\tau)$  of persons that could have possibly came in contact with the virus. A decreasing factor is the exposed rate  $(\alpha)$  of those infected with COVID-19. Finally a decreasing factor is the individuals that leave this compartment  $(\mu)$ . So the rate of change of individuals that are infected is given by

$$\frac{dE}{dt} = \frac{\beta\sigma SI}{N} - \tau E - \alpha E - \mu E$$

*Individuals that are Infected to COVID-19 :  $I(t)$*

This is the class of individuals that are infected to COVID-19. This class increases when the exposed rate of the infected increases  $(\alpha)$ . This class decreases when exposed rate of the individuals that could could possibly be infected increase  $(\tau)$ , when recovery rate from quarantining decreases  $(\gamma)$ ,



and when individuals leave this compartment( $\mu$ ). The rate of change for individuals that are treated is given by

$$\frac{dI}{dt} = \alpha E - \gamma I - \mu I$$

*Individuals that Recover or dead from COVID-19:R(t)*

This is the class of individuals that recover from COVID-19. This class increases when the recovery rate from the quarantining increase ( $\gamma$ ). This class decreases when individuals exposed to COVID-19 could possibly be infected( $\tau$ ) and the rate of individuals leaving the compartment ( $\mu$ ). The rate of change for the individuals that recover from COVID-19 is given by

$$\frac{dR}{dt} = \gamma I + \tau E - \mu R$$

## 2.2 Assumptions

- Population is constant
- Infection is affected by the social distancing factor  $\sigma$
- People recovering can't get reinfected
- $\mu$  is natural death

## 3 Results

### 3.1 Explanation of $R_0$

As commonly used in epidemiological models, the calculation of the basic reproductive number,  $R_0$ , gives insight to the dynamic of the disease. In general, the basic reproductive number  $R_0$ , represents the number of secondary infections generated by an infected individual when introduced to a completely susceptible population. In this model it represents the number of young adults that are participating in at risk behaviors. When  $R_0 < 1$ , an epidemic of COVID-19 will not occur. When  $R_0 = 1$ , one individual from the infectious class infects one individual from the susceptible class. When  $R_0 > 1$  every member from the infectious class will infect at least one individual from the susceptible class.  $R_0$  will help in determining the equilibrium of the system and will be used in the stability analysis for the system [9].

### 3.2 Interpretation of $R_0$

The calculation of  $R_0$  is essential to determine the average number of newly infected people caused by one already infected person. It is calculated by observing the cases of new infections as compared with other changes in population of the model. The basic reproduction number is the product of social factors,  $\sigma$ , and transmission,  $\beta$ , and the exposure rate,  $\alpha$ , on an individual becoming infected with COVID-19 divided by the sum of the proportion of individuals who recover from the virus in addition to the rate of

the individual leaving the compartment,  $(\gamma + \mu)$ , multiplied by the sum of individuals leaving the compartment, the rate of exposed individuals that could possibly be infected, and the and the rate of the infected which is defined as,  $(\mu + \alpha + \tau)$ . When the rate of having COVID-19 (the numerator in  $R_0$ ) is greater than the sum of cessations rate (in the  $R_0$  denominator), prevalence, the accumulated population number, of infected individuals will rise.

To find the value for  $R_0$ , the disease free equilibrium (DFE). This is the state in which COVID-19 population is non-existent. The DFE of the equations,(1-4) is obtained by setting the right hand sides of each equation equal to zero. The values of the variables at this state are

$$(x_0, y_0, z_0, w_0) = (1, 0, 0, 0) \text{ with } N = x_0 + y_0 + z_0 + w_0 = 1$$

Following the Next Generation Operator method first introduced by Diekmann, et al, Let  $\mathcal{F}$  represent the rate of new infections caused by transition from the susceptible class to the infected class or the infected class to the recovered class.  $\mathcal{V}$  will symbolize the rate of transfer of individuals into or out of the infected and treatment classes by other means. Following this method we obtain,

$$\mathcal{F} = \begin{bmatrix} \sigma\beta xz \\ 0 \end{bmatrix} \text{ and } \mathcal{V} = \begin{bmatrix} y(\mu + \alpha + \tau) \\ -\alpha y + z(\mu + \gamma) \end{bmatrix}.$$

Then the partial derivatives of each matrix will be taken in respect the variable representing the infectious classes,  $y$  and  $z$  both matrices will be evaluated at the 3.2 resulting in,

$$F = \begin{bmatrix} \frac{\partial \mathcal{F}_1}{\partial y} & \frac{\partial \mathcal{F}_1}{\partial z} \\ \frac{\partial \mathcal{F}_2}{\partial y} & \frac{\partial \mathcal{F}_2}{\partial z} \end{bmatrix} = \begin{bmatrix} 0 & \beta\sigma \\ 0 & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \frac{\partial \mathcal{V}_1}{\partial y} & \frac{\partial \mathcal{V}_1}{\partial z} \\ \frac{\partial \mathcal{V}_2}{\partial y} & \frac{\partial \mathcal{V}_2}{\partial z} \end{bmatrix} = \begin{bmatrix} (\alpha + \mu + \tau) & 0 \\ -\alpha & (\gamma + \mu) \end{bmatrix} \text{ and}$$

$$V^{-1} = \frac{1}{(\alpha + \mu + \tau)(\gamma + \mu)} \begin{bmatrix} (\gamma + \mu) & 0 \\ \alpha & (\alpha + \mu + \tau) \end{bmatrix} \text{ and}$$

$$FV^{-1} = \frac{1}{(\alpha + \mu + \tau)(\gamma + \mu)} \begin{bmatrix} \alpha\beta\sigma & \sigma\beta(\alpha + \mu + \tau) \\ 0 & 0 \end{bmatrix}$$

In order to calculate the value of  $R_0$ , the spectral radius (maximum eigenvalue) of  $FV^{-1}$  must be determined. Here,  $FV^{-1}$  have eigen value 0 and the basic reproductive number

$$R_0 = \frac{\alpha\beta\sigma}{(\alpha + \mu + \tau)(\gamma + \mu)}.$$

### 3.3 Local Stability of Disease Free Equilibrium

When  $R_0 < 1$  in epidemiology models, the disease free equilibrium (DFE) is locally asymptotically stable. This statement is true the eigenvalues of the Jacobian matrix of the model have real negative parts. Here we analyze the stability of the disease free equilibrium point,

$$(x_0, y_0, z_0, w_0) = (1, 0, 0, 0). \quad (5)$$

The Jacobian of the system (1)-(4) is

$$J(x, y, z, w) = \begin{pmatrix} -(\sigma\beta z + \mu) & 0 & -x\sigma\beta & 0 \\ \beta\sigma z & -(\alpha + \mu + \tau) & \beta\sigma x & 0 \\ 0 & \alpha & -(\gamma + \mu) & 0 \\ 0 & \tau & \gamma & -\mu \end{pmatrix}.$$

After evaluating the Jacobian at the DFE, the Jacobian becomes

$$J_0 = J(1, 0, 0, 0) = \begin{pmatrix} -\mu & 0 & -\beta\sigma & 0 \\ 0 & -\epsilon_1 & \beta\sigma & 0 \\ 0 & \alpha & -\epsilon_2 & 0 \\ 0 & \tau & \gamma & -\mu \end{pmatrix}.$$

where  $\epsilon_1 = \alpha + \mu + \tau$  and  $\epsilon_2 = \gamma + \mu$ . The characteristic polynomial is  $|J_0 - \lambda I|$ . Solving this polynomial, the eigenvalues are give by The eigenvalues of the

Jacobian matrix are,

$$J_0 - \lambda I_4 = \begin{pmatrix} -\mu - \lambda & 0 & -\beta\sigma & 0 \\ 0 & -\epsilon_1 - \lambda & \beta\sigma & 0 \\ 0 & \alpha & -\epsilon_2 - \lambda & 0 \\ 0 & \tau & \gamma & -\mu - \lambda \end{pmatrix}.$$

$$\lambda_1 = -\mu,$$

$$\lambda_2 = -\mu,$$

It is clear that  $\lambda_1$ , and  $\lambda_2$  are real values. The characteristic equation lets us easily identify two of the eigenvalues. The last two eigenvalues come from the 2x2 sub-matrix  $A - \lambda I_2$  of  $J_0 - \lambda I_4$ :

$$A - \lambda I = \begin{pmatrix} -\epsilon_1 - \lambda & \beta\sigma \\ \alpha & -\epsilon_2 - \lambda \end{pmatrix}$$

The two eigenvalues are solutions of characteristic polynomial  $|A - \lambda I| = 0$ .

i.e.,

$$(\epsilon_1 + \lambda)(\epsilon_2 + \lambda) - \beta\sigma\alpha = \lambda^2 + (\epsilon_1 + \epsilon_2)\lambda + \epsilon_1\epsilon_2 - \beta\sigma\alpha = 0$$

The roots of the above equation take the following forms:

$$\lambda_3 = -\frac{1}{2} \left[ \epsilon_1 + \epsilon_2 - \sqrt{(\epsilon_1 + \epsilon_2)^2 + 4\beta\sigma\alpha - 4\epsilon_1\epsilon_2} \right]$$
$$\lambda_4 = -\frac{1}{2} \left[ \epsilon_1 + \epsilon_2 + \sqrt{(\epsilon_1 + \epsilon_2)^2 + 4\beta\sigma\alpha - 4\epsilon_1\epsilon_2} \right]$$

Observe that,

$$R_0 = \frac{\alpha\beta\sigma}{(\alpha + \mu + \tau)(\gamma + \mu)} = \frac{\alpha\beta\sigma}{\epsilon_1\epsilon_2}$$

After inserting  $\alpha\beta\sigma = R_0\epsilon_1\epsilon_2$  the eigenvalues take the following form:

$$\lambda_3 = -\frac{1}{2} \left[ \epsilon_1 + \epsilon_2 - \sqrt{(\epsilon_1 - \epsilon_2)^2 + 4R_0\epsilon_1\epsilon_2} \right]$$
$$\lambda_4 = -\frac{1}{2} \left[ \epsilon_1 + \epsilon_2 + \sqrt{(\epsilon_1 - \epsilon_2)^2 + 4R_0\epsilon_1\epsilon_2} \right]$$



Now, we have the following situations:

$$R_0 > 1 \longrightarrow \lambda_3 > 0, \lambda_4 < 0$$

$$R_0 = 1 \longrightarrow \lambda_3 = 0, \lambda_4 < 0$$

$$R_0 < 1 \longrightarrow \lambda_3 < 0, \lambda_4 < 0$$

Hence, we have the following theorem:

**Theorem 1.** *The disease free equilibrium is locally stable if  $R_0 \leq 1$ , whereas it is unstable if  $R_0 > 1$ .*

### 3.4 Disease Endemic Equilibrium

The novel coronavirus pandemic is the perfect model for understanding what exactly a pandemic is and how it impacts life on a global scale. Since the emergence of COVID-19 in 2020, the public has been bombarded with new language to understand the virus and the subsequent global public health response. The CDC (Centers for Disease Control and Prevention) describes an epidemic as an unexpected increase in the number of disease cases in a specific geographical area. Notably, an epidemic disease doesn't necessarily have to be contagious. For example, West Nile fever and the rapid increase in obesity rates are also considered epidemics. The World Health Organization (WHO) declares a pandemic when a disease's growth is exponential. This means growth rate skyrockets, and each day cases grow more than the day prior. In being declared a pandemic, the virus has nothing to do with virology, population immunity, or disease severity. It means a virus covers a wide area, affecting several countries and populations. An endemic is a disease outbreak that is consistently present but limited to a particular region. This makes the disease spread and rates predictable [12].

Now let us take the re-scaled equations to find the Endemic Equilibrium.

There are basically two types of equilibria in disease epidemics, described as follows:

- Disease free equilibrium,  $J_0(1, 0, 0, 0)$  always exist. In this state, there is no any human is infected. Therefore population is free from virus.

- Disease endemic equilibrium,  $J_1(S^*, E^*, I^*, R^*)$  is the equilibrium with all positive components. ie  $(S, E, I, R) \neq (0, 0, 0, 0)$ [5]

$$\mu - \beta\sigma xz - \mu x = 0 \quad (6)$$

$$\beta\sigma xz - y\epsilon_1 = 0 \quad (7)$$

$$\alpha y - z\epsilon_2 = 0 \quad (8)$$

$$\gamma z + \tau y - \mu w = 0 \quad (9)$$

Now from equation (8) we can get  $y^*$  in terms of  $z^*$ :

$$y^* = \frac{z^* \epsilon_2}{\alpha} \quad (10)$$

Now substituting  $y^*$  in equation (7) from equation (10) we can get  $x^*$  :

$$\beta\sigma x^* z^* - z^* \frac{\epsilon_1 \epsilon_2}{\alpha} = 0 \implies x^* = \frac{\epsilon_1 \epsilon_2}{\alpha \beta \sigma} = \frac{1}{R_0} \quad (11)$$

Now using equation (6) and the equation (11) we will obtain  $z^*$

$$\mu - \beta\sigma \frac{1}{R_0} - \mu \frac{1}{R_0} = 0 \implies \mu - \frac{\mu}{R_0} = \frac{\beta\sigma}{R_0} z^* \implies z^* = \frac{\mu}{\beta\sigma} (R_0 - 1) \quad (12)$$

Now using (10) and (12) we can get  $y^*$

$$y^* = \frac{\mu \epsilon_2 (R_0 - 1)}{\alpha \beta \sigma} \quad (13)$$

Substituting (12) and (13) in (9) we have  $w^*$ ,

$$w^* = \frac{(R_0 - 1)(\alpha\gamma + \tau\epsilon_2)}{\alpha\beta\sigma} \quad (14)$$

$R_0$  represents the average number of secondary infections caused by each infective over the course of the infection. Thus, it is intuitively clear that if  $R_0 < 1$ , the infection should die out, while if  $R_0 > 1$ , the infection should establish itself. The basic reproduction number as the number of secondary infections caused by an average infective over the course of the disease. In the SEIR epidemic model the basic reproduction number determines whether there will be an epidemic[13].

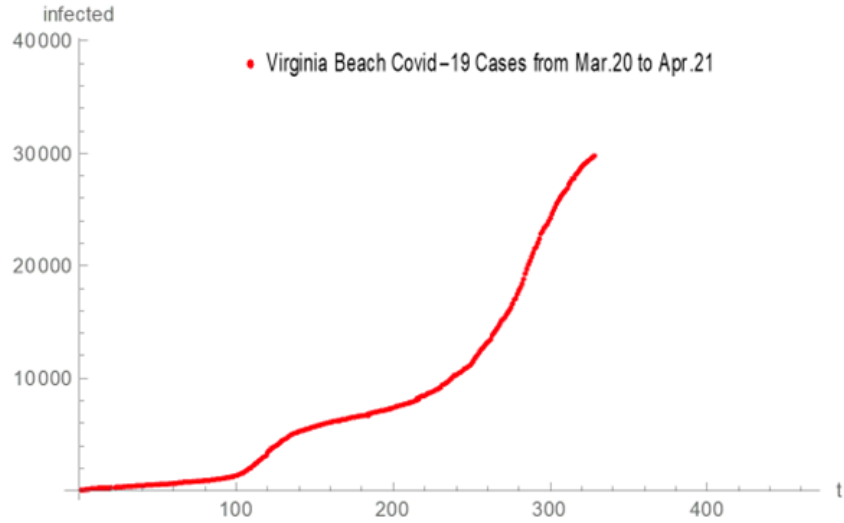


Figure 2: Cases of COVID-19

## 4 Estimation of Parameters

The values of the parameters in this model are estimated to help educated predictions. Due to COVID-19 steady spread and variations during this paper, we used the Center for Disease Control (Virginia Beach) to make our approximations. Our model focuses on the city of Virginia Beach as shown in figure 2 and is measured in days.

Table contains a list of estimated parameter values and an explanation of how each parameter value was determined is described by the paragraphs following. In order to find  $R_0 > 1$  we manipulated the values of alpha and sigma to understand how the factors of changing these parameters change

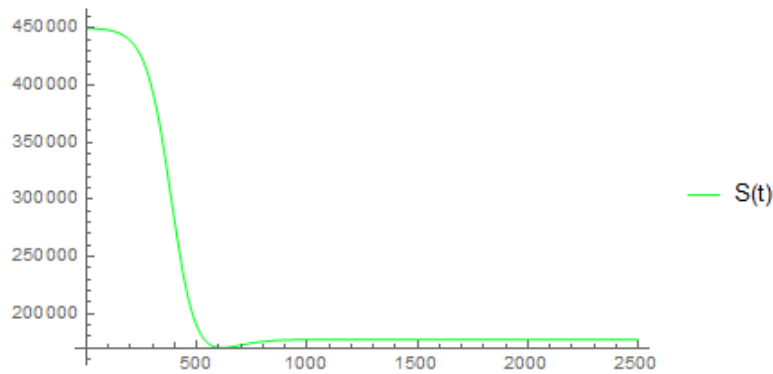


Figure 3: Susceptibility of COVID-19

our population.

#### 4.1 Estimation of $\beta$

$\beta \approx .0588$  according to the New York time 1 out of 17 people in the United States have been infected with COVID-19[14].

#### 4.2 Estimation of $\gamma$

$\gamma \approx .005$  was calculated by using Virginia Department of Health statistic to realize that it takes fourteen to forty- two ,in severe cases, to recover from COVID-19 . Older people are more likely to be affected by this disease.Using this information we took one day divided by the days treatment 14 by 12 months.

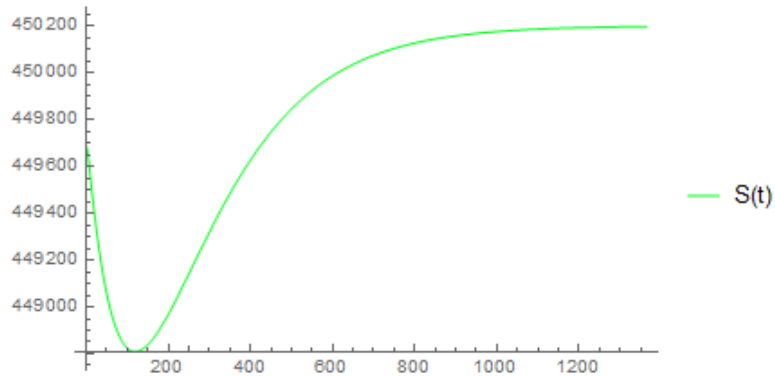


Figure 4: Susceptibility of COVID-19 with  $R_0 < 1$

### 4.3 Estimation of $\alpha$

$\alpha \approx .112668$  was calculated by using Virginia Department of Health statistics of probable cases in eastern Virginia. They had 135,201 cases per 100,000 and we divided by 12 to get a monthly rate.

### 4.4 Estimation of $\tau$

$\tau \approx 0.11$ . was calculated by using Virginia Department of Health statistics, we used the number of known infected cases in the area subtracted by the probable cases in the are and divided by 100,000. Which was then divided by 12 months.

### 4.5 Estimation of $\sigma$

$\sigma$  is an estimation between 1 and 0. It is recommended by the Center for Disease Control to stay out of close contact with individuals with COVID-19

excluding people who have had COVID-19 within the past 3 months or who are fully vaccinated. Close contact counts as if you were within 6 feet of someone who has COVID-19 for a total of 15 minutes or more. In Figure 5 we see just how much of an impact social issues make a difference in the spread of COVID-19.

<b>Parameters for Endemic Equilibrium</b>	
<b>Parameters</b>	<b>Values</b>
the susceptible class	338,293
the exposed class	3,922
the infected class	11,681
the recovery class	89,530
$R_0$	1.4

#### **4.6 Estimation of $\mu$**

$\mu \approx .009$  is calculated by using the Center of Disease Control and Prevention statistics for natural deaths in the United States(2,854,838) divided by the population of the United States (328.2 million). This quotient gave us our natural death rate.

## **5 Discussion**

The ideal situation is to keep infection of COVID-19 to a minimum and in order to do that we must start implementing the following protocols.



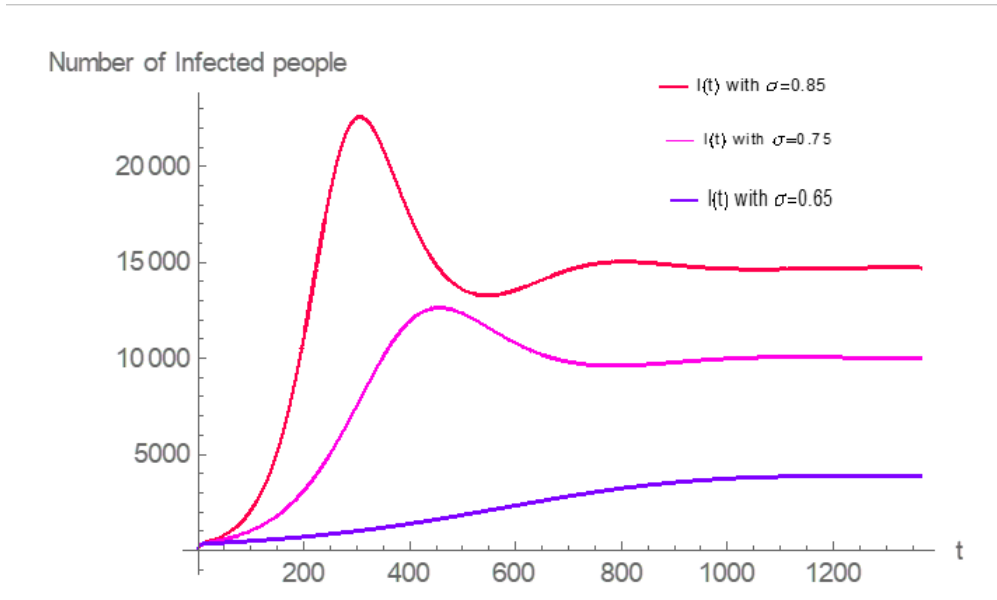


Figure 5: How Social Aspects Can Impact the Spread of COVID-19

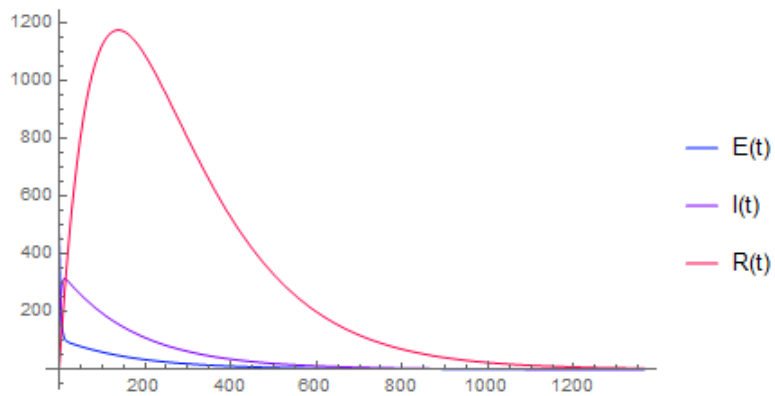


Figure 6: Exposed Infected Recovery of COVID-19 with  $R_0 < 1$

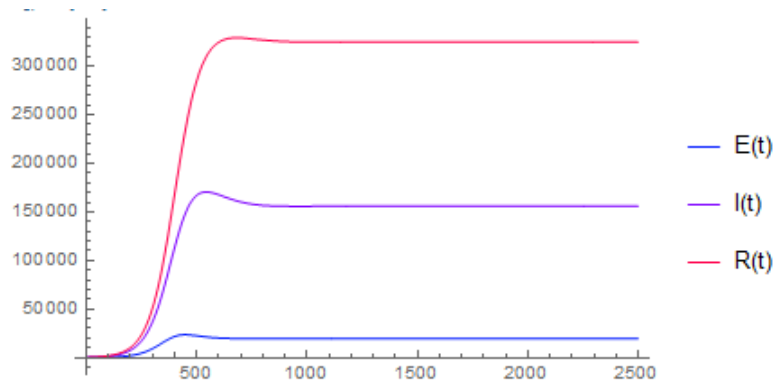
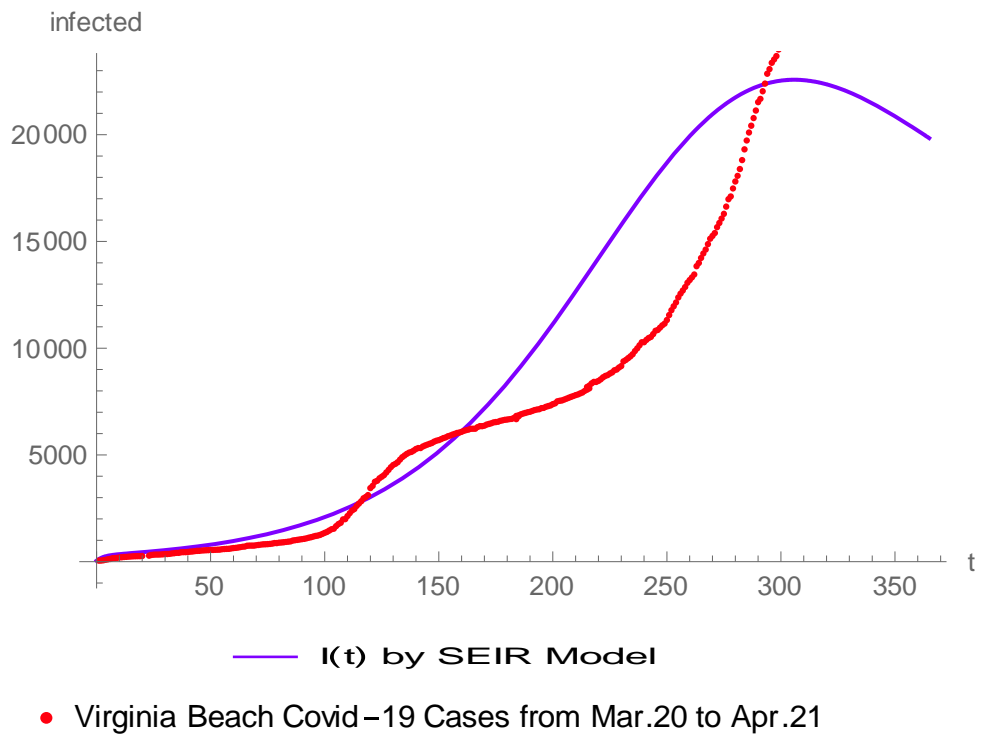


Figure 7: Exposed Infected Recovery of COVID-19 with  $R_0 > 1$

- Decrease the transmission rate ( $\beta < .05$ ) from the susceptible population to the population of that is exposed
- Decrease the transmission rate of exposed population ( $\alpha < .112$ ) of the susceptible population. This can be achieved by ensuring that the infected population stays away for an extended time from other populations and stays in secure zones.
- Decrease the exposure to COVID-19 from the susceptible population through social factors ( $\sigma$ )
- Increase resource of testing COVID-19 to probable ( $\tau$ ) infectives to decrease exposure rate of unknown contact with COVID-19
- Increase transmission rate of recovery ( $\gamma$ ) This strategy involves proper protocols and visits to medical professional for proper diagnosis.



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Figure 8: Comparison between model vs Real data

## 6 Conclusion

We constructed a modified SEIR model for the outbreak of COVID-19. This model is a modified approach for evaluation and management of the COVID-19 pandemic. The real data of COVID-19 spread in Hampton Roads, Virginia were used to verify the results of our modified SEIR model. We demonstrated that the modified SEIR model could be employed to assess the spread of epidemics such as COVID-19 in other states. Valuable insight has been obtained through the analysis of key factors such as the basic reproductive number,  $R_0$ , which indicates under what circumstances an outbreak of infection will occur in the population at risk. Our analysis of  $R_0$  illustrates that the key to reducing infection is through the parameters  $\sigma$ , which are the rate of being social in a population. Reducing the value of these parameters will reduce the number of COVID-19 infections in the Hampton Roads area. When  $R_0 < 1$ , the model is locally asymptotically stable; this is referred to as the disease free equilibrium state. Another important observation is that  $\sigma$  is an important factor that determines whether or not the  $R_0$  is less than or greater than 1. So this means that  $R_0$  is dependent upon the social factors. If the rate of the social factors are high and the treatments are low, this makes the numerator high and the denominator low, and that means that infections will be higher and the time within each compartment will be lower. Our model can be developed to understand the main social factors of COVID-19 infection and to understand the difference between different types of treatment to understand

the most effective treatment.

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