MODELING AND ANALYSIS OF THE SPREAD OF COVID-19 WITH A SIMULTANEOUS VARIANT OF CONCERN

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Abstract. With COVID-19 and its variants still of concern globally [CDC21a], researchers continue to develop mathematical models to capture the dynamics of the spread of the infection. Many of these models utilize a compartmental framework of sub-populations. The typical categories include, but are not limited to, susceptible, exposed, infected, and recovered populations. These SEIR compartmental models are used widely to model infectious diseases such as Zika, Dengue, and COVID-19. These models typically vary in the types of compartments utilized as well as a plethora of parameters. While current research suggests that COVID-19 spreads through the interactions of multiple populations with one another, several of these models may not fully account for such interactions. For instance, there is evidence that multiple variants of the COVID-19 virus impact these sub-populations differently. In this paper, we introduce a new multi-variant COVID-19 model that will help provide insight into the dynamics of the spread of infections. Specifically, the dynamics of the sub-populations are modeled through a coupled system of ordinary differential equations. The basic reproduction number for this model is derived that can potentially inform policy makers to make data-driven decisions. We also perform simulations to study the influence of various parameters employed in the model.

1. Introduction

SARS-CoV-2, also known as COVID-19, has had a historic impact across the globe since its first designation as a pandemic in March 2020 by the World Health Organization (WHO) [WHO20]. The virus has been so widespread that it has become difficult to find a family or person who's life hasn't been affected by COVID-19. Since its first reported cases in December 2019 [WHO20] researchers have been working to understand the dynamics of this disease. In particular, many mathematical models have been developed to better understand the spread of COVID-19 as well as predict possible impacts of the disease such as expected number of deaths due to the disease and number of possible hospitalizations over time. Through these models researchers were able to make informed suggestions as to lessen the impact of the virus.

The primary methods to model the spread of infectious diseases are the Susceptible-Infected-Recovered (SIR) and Susceptible-Exposed-Infected-Recovered (SEIR) compartmental models. These models utilize a coupled system of ordinary differential equations (ODEs) that describe the flow of populations from one state such as susceptible or infected to the next state such as exposed or recovered. These models are not limited to the aforementioned categories as other models use compartments

2020 *Mathematics Subject Classification.* 92-10, 92-D30, 34-Axx .

for social behaviors such as face-mask usage and quarantining [OKS20]. Models such as these aim to illustrate the impact of such behavioral changes on the spread of a disease which in turn are used to guide policy-maker's decisions on how to deal with the disease at hand.

While models presented by Ohajunwa et al. [OKS20] and Prem et al. [PLR$^+$20] focus on social behaviors and dynamics, a new consideration must be made: COVID-19 variants. In particular we seek to model the impact of variants of concern as defined by the Centers for Disease Control and Prevention (CDC) [CDC21b] with the possibility of being infected by the given variant after recovering from COVID-19 and vice-versa. With variants such as B.1.1.7, first discovered in the UK, and B.1.427, first discovered in California, having higher transmission rates it is important to study the disease dynamics of these new threats. This consideration is main focus of this work.

Note that these variants do not happen separately from the ongoing COVID-19 pandemic as they are spreading simultaneously. Therefore this paper works to establish a model that captures the dynamics of such a situation focusing on two simultaneous viruses while also taking into consideration some social behaviors such quarantining and hospitalization. This model will take the classical SEIR model and utilize a few social behaviors as presented in [OKS20] and build upon them. The assumptions and choices of social behaviors of this model is such that the model will be effectively represent the complex set of circumstances of two viruses but simple enough to begin to understand the implications of such a situation.

This paper be outlined as follows. In section 2, we present important definitions as well as the mathematical underpinnings of our model. Here we present the flow diagram of the model as well as the governing system of ODEs that are the computational basis of this model. In section 3 we state and prove the basic reproduction number, $\mathcal{R}_0$, for the model. Section 4 will update the baseline model given in section 2 to include the possibility of those exposed to the virus as being able to also transmit the virus. Section 5 will present numerical experiments and their corresponding graphs and implications of model we have presented. Finally, section 6 will be dedicated to conclusions and future work.

2. Mathematical Model and Governing Equations

2.1. **Model and Sub-populations.** In this work, an extended SEIR compartmental model is given that incorporates a simultaneous variant of the COVID-19 virus, as well as quarantine, recovered, hospitalized and dead sub-populations. For simplicity this model does not include vital dynamics such as birthrate and natural death rates. This model is organized around the flow diagram (see Figure 1). The model includes the following sub-populations:

- Susceptible (S): Individuals who have not been infected with COVID-19 or the considered variant
- Exposed (E_i): Individuals who are in the incubation period of disease progression of virus i
- Second Exposure ($E_{i,j}$): Individuals who have recovered from virus i and currently in the incubation period of disease progression of virus j

- Infected (I_i): Individuals who have been infected with virus i
- Second Infection ($I_{i,j}$): Individuals who have recovered from virus i, and currently infected with virus j
- Quarantine (Q_i): Individuals that are quarantined after being infected with virus i
- Second Quarantine ($Q_{i,j}$): Individuals that have recovered from virus i, and currently being quarantined after being infected with virus j
- Hospitalized (H_i): Individuals who have been hospitalized by virus i
- Second Hospitalization ($H_{i,j}$): Individuals who have recovered from virus i and currently hospitalized for virus j
- Recovered (R_i): Individuals who have recovered from virus i
- Fully Recovered (R): Individuals who have recovered from virus i and j
- Dead (D): Individuals who did not survive either virus

Here we assume that the states $Q_i, Q_{i,j}, H_i, H_{i,j}$ no longer spread COVID-19 or its variants but those who have recovered from one virus can be infected at the same rate as someone who has not contracted either virus.

The dynamics of the spread described is shown in the following flow diagram Figure 1. The various rates in the diagram are defined in table 1.

Table 1. Symbols and definitions of parameters

Parameter	Definition
β_i	Transmission rate of virus i per person per day
σ_i	Rate at which individuals exposed to virus i are infected per day
λ_i	Rate at which individuals infected with variant i are Quarantined per day
γ_i	Rate at which individuals quarantined with virus i become hospitalized or recovered per day
μ_i^{-1}	Duration at which hospitalized individuals infected with virus i recover or die per day
q_i	Fraction of quarantined individuals infected with virus i recover per infection
p_i	Fraction of hospitalized individuals infected with virus i recover per infection

In a population of N individuals where N is the sum of all sub-populations, susceptible individuals S move to the either exposed state E_1 or E_2 after interacting with individuals infected with COVID-19 or its variant respectively. This transmission is represented by a proportion of the respective infected classes, I_1

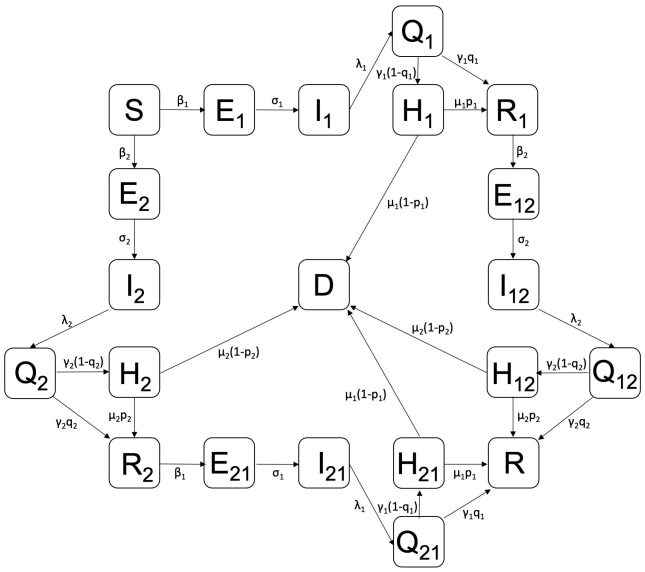

Figure 1. Flow diagram for the two variant COVID-19 model

and I_2 involved in the transmission and an infection rate that is proportional to the infected individuals. This transmission rates are given by the constants β_1 and β_2. While an individual is in either exposed state, E_1 or E_2, the virus has an incubation period, σ_1^{-1} and σ_2^{-1} such that by the end of this period, individuals move to their respective infected state I_1 or I_2. At this point, individuals that are mostly symptomatic, go into the appropriate quarantine state, Q_1 and Q_2 at a certain rate denoted by λ_1 and λ_2. Quarantined individuals then enter either the recovered states, R_1 and R_2 or the Hospitalized states H_1 and H_2 respective to the virus contracted at a proportion, q_1 and q_2 of the recovery rate γ_1 and γ_2 respectively. While in the hospitalization state individuals can either move to the respective recovered state R_1 or R_2 or into the death state D at a proportion p_1 and p_2 of the recovery rate μ_1 and μ_2. This model then allows for individuals to be be infected with a second virus after recovering from the first. The change of states follow the same process as outlined above. Here we denote these states by E_{12} which represents an individual who has recovered from virus 1 and is in the exposed state for virus 2. For this work we assume that the rates that induce state changes are the same whether or not an individual is infected for the first time or the second time. For example, an individual in the E_{12} will change states to I_{12} with the same incubation period of σ_2^{-1}. This leads to the following governing equations.

2.2. **Governing Equations.** The flow diagram in figure 1 is described with the following equations:

$$\frac{dS}{dt} = -\frac{\beta_1 S I_1}{N} - \frac{\beta_2 S I_2}{N} \tag{2.1}$$
$$\frac{dE_1}{dt} = \frac{\beta_1 S I_1}{N} - \sigma_1 E_1 \tag{2.2}$$
$$\frac{dE_2}{dt} = \frac{\beta_2 S I_2}{N} - \sigma_2 E_2 \tag{2.3}$$
$$\frac{dI_1}{dt} = \sigma_1 E_1 - \lambda_1 I_1 \tag{2.4}$$
$$\frac{dI_2}{dt} = \sigma_2 E_2 - \lambda_2 I_2 \tag{2.5}$$
$$\frac{dQ_1}{dt} = \lambda_1 I_1 - \gamma_1 Q_1 \tag{2.6}$$
$$\frac{dQ_2}{dt} = \lambda_2 I_2 - \gamma_2 Q_2 \tag{2.7}$$
$$\frac{dH_1}{dt} = (1-q_1)\gamma_1 Q_1 - \mu_1 H_1 \tag{2.8}$$
$$\frac{dH_2}{dt} = (1-q_2)\gamma_2 Q_2 - \mu_2 H_2 \tag{2.9}$$
$$\frac{dR_1}{dt} = q_1\gamma_1 Q_1 + p_1\mu_1 H_1 - \frac{\beta_2 R_1 I_{1,2}}{N} \tag{2.10}$$
$$\frac{dR_2}{dt} = q_2\gamma_2 Q_2 + p_2\mu_2 H_2 - \frac{\beta_1 R_2 I_{2,1}}{N} \tag{2.11}$$
$$\frac{dE_{1,2}}{dt} = \frac{\beta_2 R_1 I_{1,2}}{N} - \sigma_2 E_{1,2} \tag{2.12}$$
$$\frac{dE_{2,1}}{dt} = \frac{\beta_1 R_2 I_{2,1}}{N} - \sigma_1 E_{2,1} \tag{2.13}$$
$$\frac{dI_{1,2}}{dt} = \sigma_2 E_{1,2} - \lambda_2 I_{1,2} \tag{2.14}$$
$$\frac{dI_{2,1}}{dt} = \sigma_1 E_{2,1} - \lambda_1 I_{2,1} \tag{2.15}$$
$$\frac{dQ_{1,2}}{dt} = \lambda_2 I_{1,2} - \gamma_2 Q_{1,2} \tag{2.16}$$
$$\frac{dQ_{2,1}}{dt} = \lambda_1 I_{2,1} - \gamma_1 Q_{2,1} \tag{2.17}$$
$$\frac{dH_{1,2}}{dt} = (1-q_2)\gamma_2 Q_{1,2} - \mu_2 H_{1,2} \tag{2.18}$$
$$\frac{dH_{2,1}}{dt} = (1-q_1)\gamma_1 Q_{2,1} - \mu_1 H_{2,1} \tag{2.19}$$
$$\frac{dR}{dt} = q_1\gamma_1 Q_{2,1} + q_2\gamma_2 Q_{1,2} + p_1\mu_1 H_{2,1} + p_2\mu_2 H_{1,2} \tag{2.20}$$
$$\frac{dD}{dt} = (1-p_1)\mu_1(H_1 + H_{2,1}) + (1-p_2)\mu_2(H_2 + H_{1,2}) \tag{2.21}$$

Remark 2.1. Note that adding equations (2.1)-(2.21) yields the right hand side to be zero justifying a constant population.

3. Basic Reproduction Number

In this section we will derive the basic reproduction number, $\mathcal{R}_0$ for this model. This number can be used to quantify the transmission potential of two different variants of COVID-19 as modeled by the system(1)-(21). $\mathcal{R}_0$ is the average number of secondary infections produced by a typical case of an infection in a population where everyone is susceptible. We will use the *Next Generation Matrix* utilized in [BCC01] to solve for $\mathcal{R}_0$.

Theorem 3.1. *The basic reproduction number $\mathcal{R}_0$ is given by*

$$\mathcal{R}_0 = max\left\{\frac{\beta_1}{\lambda_1}, \frac{\beta_2}{\lambda_2}\right\} \tag{3.1}$$

Proof. Given infections states $E_1, E_2, I_1, I_2, E_{12}, E_{21}, I_{1,2}, I_{2,1}$ in equations (2.2)-(2.5) and (2.12)-(2.15) we create vector $\mathcal{F}$ representing the inflow of new infections into the aforementioned infectious states. Here we consider that $S \approx N$

$$\mathcal{F} = \left\{\beta_1 I_1, \beta_2 I_2, 0, 0, \frac{\beta_2 R_1 I_{1,2}}{N}, \frac{\beta_1 R_2 I_{2,1}}{N}, 0, 0\right\} \tag{3.2}$$

Similarly we define vector $\mathcal{V}$ by the outflow of equations (2.2)-(2.5) and (2.12)-(2.15) respectively.

$$\mathcal{V} = \{\sigma_1 E_1, \sigma_2 E_2, -\sigma_1 E_1 + \lambda_1 I_1, -\sigma_2 E_2 + \lambda_2 I_2, \sigma_2 E_{1,2}, \sigma_1 E_{2,1}, -\sigma_2 E_{1,2} + \lambda_2 I_{1,2}, -\sigma_1 E_{2,1} + \lambda_1 I_{2,1}\}$$

We now compute the Jacobian matrix F from vector $\mathcal{F}$ and Jacobian matrix V from vector $\mathcal{V}$

$$F = \begin{bmatrix} 0 & 0 & \beta_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_2 R_1}{N} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_1 R_2}{N} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \sigma_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \sigma_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\sigma_1 & 0 & \lambda_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\sigma_2 & 0 & \lambda_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \sigma_2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_1 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\sigma_2 & 0 & \lambda_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\sigma_1 & 0 & \lambda_1 \end{bmatrix}$$

We then find the inverse of V:

$$V^{-1} = \begin{bmatrix} \frac{1}{\sigma_1} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{\sigma_2} & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{1}{\lambda_1} & 0 & \frac{1}{\lambda_1} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{\lambda_2} & 0 & \frac{1}{\lambda_2} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\sigma_2} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{1}{\sigma_1} & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\lambda_2} & 0 & \frac{1}{\lambda_2} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda_1} & 0 & \frac{1}{\lambda_1} \end{bmatrix}$$

The Next Generation Matrix is given by FV^{-1} which is calculated as:

$$FV^{-1} = \begin{bmatrix} 0 & 0 & \beta_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_2 R_1}{N} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_1 R_2}{N} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\sigma_1} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{\sigma_2} & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{1}{\lambda_1} & 0 & \frac{1}{\lambda_1} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{\lambda_2} & 0 & \frac{1}{\lambda_2} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\sigma_2} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{1}{\sigma_1} & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\lambda_2} & 0 & \frac{1}{\lambda_2} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda_1} & 0 & \frac{1}{\lambda_1} \end{bmatrix}$$

$$= \begin{bmatrix} \frac{\beta_1}{\lambda_1} & 0 & \frac{\beta_1}{\lambda_1} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_2}{\lambda_2} & 0 & \frac{\beta_2}{\lambda_2} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\beta_2 R_1}{\lambda_2 N} & 0 & \frac{\beta_2 R_1}{\lambda_2 N} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{\beta_1 R_2}{\lambda_1 N} & 0 & \frac{\beta_1 R_2}{\lambda_1 N} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

The basic reproduction number is found as the maximum eigenvalue of FV^{-1}. Hence we take the determinant of $FV^{-1} - \lambda I$ and setting the characteristic polynomial to zero. Note that $\lambda \neq \lambda_1, \lambda_2$ as it represents the eigenvalues of the matrix.

$$\det(FV^{-1} - \lambda I) = \lambda^4 \left(\frac{\beta_1}{\lambda_1} - \lambda\right)\left(\frac{\beta_2}{\lambda_2} - \lambda\right)\left(\frac{\beta_2 R_1}{\lambda_2 N} - \lambda\right)\left(\frac{\beta_1 R_2}{\lambda_1 N} - \lambda\right)$$

Note that $\frac{R_1}{N}, \frac{R_2}{N} < 1$ since we assume that the outflow of state S is partitioned between E_1 and E_2. This implies that the basic reproduction number for this system is given as $\mathcal{R}_0 = \max\left\{\frac{\beta_1}{\lambda_1}, \frac{\beta_2}{\lambda_2}\right\}$ □

The result given by theorem 3.1 implies that the basic reproduction number for the system $(2.1) - (2.21)$ is the largest ratio of the transmission rate to quarantine rate of the two variants of COVID-19.

4. Effect of Exposed population

One may also consider the impact of the interaction of exposed populations to cause new infections. This can be modeled by updating equations (2.1) - (2.3) and (2.10) - (2.13) as follows:

$$\begin{aligned}
\frac{dS}{dt} &= -\frac{\beta_1 S}{N}(E_1 + I_1) - \frac{\beta_2 S}{N}(E_2 + I_2) && (4.1)\\
\frac{dE_1}{dt} &= \frac{\beta_1 S}{N}(E_1 + I_1) - \sigma_1 E_1 && (4.2)\\
\frac{dE_2}{dt} &= \frac{\beta_2 S}{N}(E_2 + I_2) - \sigma_2 E_2 && (4.3)\\
\frac{dR_1}{dt} &= q_1\gamma_1 Q_1 + p_1\mu_1 H_1 - \frac{\beta_2 R_1}{N}(E_{1,2} + I_{1,2}) && (4.4)\\
\frac{dR_2}{dt} &= q_2\gamma_2 Q_2 + p_2\mu_2 H_2 - \frac{\beta_1 R_2}{N}(E_{2,1} + I_{2,1}) && (4.5)\\
\frac{dE_{1,2}}{dt} &= \frac{\beta_2 R_1}{N}(E_{1,2} + I_{1,2}) - \sigma_2 E_{1,2} && (4.6)\\
\frac{dE_{2,1}}{dt} &= \frac{\beta_1 R_2}{N}(E_{2,1} + I_{2,1}) - \sigma_1 E_{2,1} && (4.7)
\end{aligned}$$

A basic reproduction can also be derived for the updated system with the impact of the exposed states, following the steps shown in Theorem 3.1. This gives the following new result.

Theorem 4.1. *The basic reproduction number $\mathcal{R}_0$ is given by*

$$\mathcal{R}_0 = \max\left\{\frac{\beta_1(\sigma_1+\lambda_1)}{\sigma_1\lambda_1}, \frac{\beta_2(\sigma_2+\lambda_2)}{\sigma_2\lambda_2}\right\} \tag{4.8}$$

Proof. We follow the same process as shown in the proof for theorem3.1

$$\mathcal{F} = \left\{\beta_1(I_1+E_1), \beta_2(I_2+E_2), 0, 0, \frac{\beta_2 R_1(E_{1,2}+I_{1,2})}{N}, \frac{\beta_1 R_2(E_{2,1}+I_{2,1})}{N}, 0, 0\right\}$$

$$\mathcal{V} = \{\sigma_1 E_1, \sigma_2 E_2, -\sigma_1 E_1 + \lambda_1 I_1, -\sigma_2 E_2 + \lambda_2 I_2, \sigma_2 E_{1,2}, \sigma_1 E_{2,1}, -\sigma_2 E_{1,2} + \lambda_2 I_{1,2}, -\sigma_1 E_{2,1} + \lambda_1 I_{2,1}\}$$

$$F = \begin{bmatrix}
\beta_1(I_1+1) & 0 & \beta_1(E_1+1) & 0 & 0 & 0 & 0 & 0 \\
0 & \beta_2(I_2+1) & 0 & \beta_2(1+E_2) & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \frac{\beta_2 R_1(I_{1,2}+1)}{N} & 0 & \frac{\beta_2 R_1(E_{1,2}+1)}{N} & 0 \\
0 & 0 & 0 & 0 & 0 & \frac{\beta_2 R_1(I_{2,1}+1)}{N} & 0 & \frac{\beta_1 R_2(E_{2,1}+1)}{N} \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{bmatrix}$$

$$V = \begin{bmatrix} \sigma_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \sigma_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\sigma_1 & 0 & \lambda_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\sigma_2 & 0 & \lambda_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \sigma_2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_1 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\sigma_2 & 0 & \lambda_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\sigma_1 & 0 & \lambda_1 \end{bmatrix}$$

$$V^{-1} = \begin{bmatrix} \frac{1}{\sigma_1} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{\sigma_2} & 0 & 0 & 0 & 0 & 0 & 0 \\ \frac{1}{\lambda_1} & 0 & \frac{1}{\lambda_1} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{\lambda_2} & 0 & \frac{1}{\lambda_2} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\sigma_2} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{1}{\sigma_1} & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{1}{\lambda_2} & 0 & \frac{1}{\lambda_2} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{1}{\lambda_1} & 0 & \frac{1}{\lambda_1} \end{bmatrix}$$

Let $\omega_1 = E_1 + 1, \omega_2 = I_1 + 1, \omega_3 = E_2 + 1, \omega_4 = I_2 + 1$ and $\xi_1 = E_{1,2} + 1, \xi_2 = I_{1,2} + 1, \xi_3 = E_{2,1} + 1, \xi_4 = I_{2,1} + 1$

$$FV^{-1} = \begin{bmatrix} \frac{\beta_1[\lambda_1\omega_2+\sigma_1\omega_1]}{\sigma_1\lambda_1} & 0 & \frac{\beta_1\omega_1}{\lambda_1} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_2[\sigma_2\omega_3+\lambda_2\omega_4]}{\sigma_2\lambda_2} & 0 & \frac{\beta_2\omega_3}{\lambda_2} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\beta_2 R_1[\lambda_2\xi_2+\sigma_2\xi_1]}{\sigma_2\lambda_2 N} & 0 & \frac{\beta_2 R_1\xi_1}{\lambda_2 N} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{\beta_1 R_2[\sigma_1\xi_3+\lambda_1\xi_4]}{\sigma_1\lambda_1 N} & 0 & \frac{\beta_1 R_2\xi_3}{\lambda_1 N} \end{bmatrix}$$

$$\det(FV^{-1} - \lambda I) = \lambda^4 \left(\frac{\beta_1(\lambda_1\omega_2 + \sigma_1\omega_1)}{\sigma_1\lambda_1} - \lambda \right) \left(\frac{\beta_2(\sigma_2\omega_3 + \lambda_2\omega_4)}{\sigma_2\lambda_2} - \lambda \right) \cdots$$

$$\cdots \left(\frac{\beta_2 R_1(\lambda_2\xi_2 + \sigma_2\xi_1)}{\sigma_2\lambda_2 N} - \lambda \right) \left(\frac{\beta_1 R_2(\sigma_1\xi_3 + \lambda_1\xi_4)}{\sigma_1\lambda_1 N} - \lambda \right)$$

The basic reproduction number for this system is the maximum of the four eigenvalues above.

Note that in the derivation of the basic reproduction number, we assume that $S \approx N$. Recall that N is the sum of all sub-populations and hence we have that $E_1, E_2, I_1, I_2, E_{12}, E_{21}, I_{12}, I_{21}$ are all approximately equal to 0. Therefore the basic reproduction number can be expressed as:

$$\mathcal{R}_0 = \max \left\{ \frac{\beta_1(\sigma_1 + \lambda_1)}{\sigma_1\lambda_1}, \frac{\beta_2(\sigma_2 + \lambda_2)}{\sigma_2\lambda_2} \right\}$$

□

5. **Computational Experiments**

5.1. **Initial Conditions and Parameter Values.** In this section we will give values of the parameters being used in the model and the resource that justifies them. We will also employ the model given in this work and perform numerical simulations.

The parameters for COVID-19 are listed in table 2 while parameters for variants B.1.1.7 and B.1.427 are given in table 3 and 4. For the parameters not listed in table 3 or 4, we assume that they are equal to their corresponding parameters of table 2. For our numerical computations we will assume that $\beta_1 = .5$. Since the CDC estimates that $\mathcal{R}_0 = 2.5$ [CDC20] for COVID-19 we can then use the result of theorem 3.1 to estimate λ_1. Assuming the $\mathcal{R}_0$ estimation is referring only to the original virus we have that $\beta_2 = 0$. Thus we have $\mathcal{R}_0 = \max\left\{\frac{\beta_1}{\lambda_1}, 0\right\}$ which implies that $2.5 = \frac{.5}{\lambda_1}$ and hence $\lambda_1 = .2$.

Table 2. SARS-CoV-2 parameters

Parameter	Value	Reference(s)
β_1	.5	
σ_1^{-1}	6 days	[CDC20]
λ_1	.2	
γ_1^{-1}	5 days	[OKS20]
μ_1^{-1}	14 days	[CDC20]
q_1	.81	[OKS20]
p_1	.93	[CDC20]

Table 3. Variant B.1.1.7

Parameter	Value	Reference(s)
β_2	.75	[CDC21b]
q_2	.81	[NER21]
p_2	.91	[NER21]

Table 4. Variant B.1.427

Parameter	Value	Reference(s)
β_2	.6	[DGKK]

Remark 5.1. Note that as scientific research continues to evolve, these parameters are subject to change.

With these initial conditions and parameters we can calculate the basic reproduction for various scenarios (See table 5 and table 6.) Note that because it is assumed that the quarantine rate λ_i and infection rate σ_i are equal across the viruses, $\mathcal{R}_0$ is determined by whichever virus has the larger transmission rate β_i. To put these values into perspective, figure 7 gives $\mathcal{R}_0$ values of past infectious diseases.

To put these values into perspective, figure 7 gives $\mathcal{R}_0$ values of past infectious diseases.

Table 5. Model with equations (2.1)-(2.21)

Virus 1	Virus 2	$\mathcal{R}_0$
SARS-CoV-2	B.1.1.7	3.75
SARS-CoV-2	B.1.427	3
B.1.1.7	B.1.427	3.75

Table 6. Model with equations (4.1)-(4.7)

Virus 1	Virus 2	$\mathcal{R}_0$
SARS-CoV-2	B.1.1.7	8.24
SARS-CoV-2	B.1.427	6.59
B.1.1.7	B.1.427	8.24

Table 7. Basic Reproduction Numbers for well-known diseases

Disease	$\mathcal{R}_0$	**Reference**
Measels	12-18	[GBL$^+$]
Chickenpox	10-12	[IRE20]
Pertussis	5.5	[KTP10]
Smallpox	3.5-6	[GL01]
COVID-19	2.4-3.4	[BMK20]
HIV/Aids	2-5	[HIV20]
Common Cold	2-3	[Fre14]
Influenza	1.3	[CMV07]

5.2. **Numerical Computations.** To implement our model, we used a higher-order Runge-Kutta method in MATLAB to solve our system of ODEs (2.1) - (2.21). For initial conditions we use $N = 8,500,000$ which is approximately the state of Virginia. We then assume that for every ten infected individuals, we have one that is infected with virus 2. By setting the initial number of infected individuals to 100 we have that $I_1(0) = 90$ and $I_2(0) = 10$. We similarly set the initial conditions of individuals infected with a 2nd virus and hence $I_{12} = 10$ and $I_{21} = 90$. This means that we have $S(0) = 8,499,800$ with all other initial conditions being set to zero.

Remark 5.2. For the following figures and tables, assume that they are results of simulating the model governed by equations (2.1)-(2.21) unless otherwise stated.

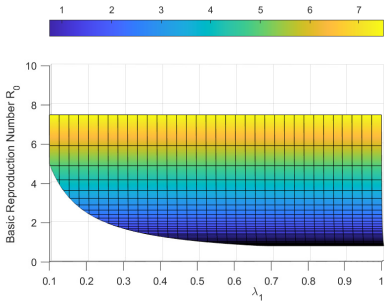

Figure 2. Effect of λ_1 on R_0

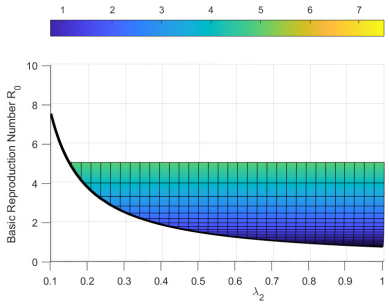

Figure 3. Effect of λ_2 on R_0

In figures 2 and 3 we present the effect of quarantine rates λ_1 and λ_2 on the basic reproduction number $\mathcal{R}_0$ given a fixed transmission rate for β_1 and β_2. Here we are

comparing the SARS-CoV-2 virus with the B.1.1.7 variant. Our graph in figure 2 shows that change in quarantine rate for the first virus, having a lower transmission rate compared to the second virus, does not change the basic reproduction number. It also shows how the quantity β_1/λ_1 changes as the bottom of the surface. In figure 3 we see that $\mathcal{R}_0$ is effected by a change in λ_2 up to the point where λ_2 is approaching a value of 0.2. Simply put, this implies that to lower the basic reproduction number, the quarantine rate for the virus that has a higher transmission rate must increase. On the other hand, increasing efforts to raise the quarantine rate for a single virus is not sufficient. Figure 4 shows the impact of changing both quarantine rates.

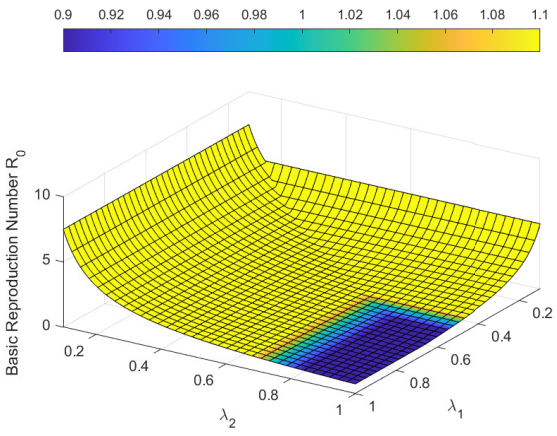

Figure 4. $\mathcal{R}_0$ in response to changes in λ_1 and λ_2

Typically the goal of fighting a pandemic is to achieve a state of endemic equilibrium which would translate to having $\mathcal{R}_0 < 1$. In figure 4, we see that to reach this target it must either be the case that the individual quarantine rates must be greater than their respective transmission rates or the quarantine rate over both viruses is greater than the larger than the rate for the virus with the higher transmissibility.

In comparison, figure 5 and figure 6 show how parameters σ and λ influence $\mathcal{R}_0$ for the updated models. In the case of figure 5 we see that to achieve endemic equilibrium we would require $\sigma_1 > 1$ since $\lambda_1 \not> 1$. This effectively means that to get the desired effect, we must move individuals from the exposed state to the infected state as quickly as possible. For figure 6 to reach endemic equilibrium we must have that $\sigma_2 > 3$. Thus for the whole model to have $\mathcal{R}_0 < 1$ we must have both conditions as outlined above.

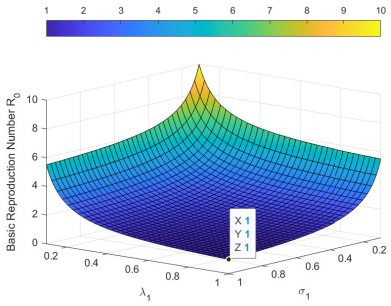

Figure 5. Effect of λ_1 and σ_1 on R_0

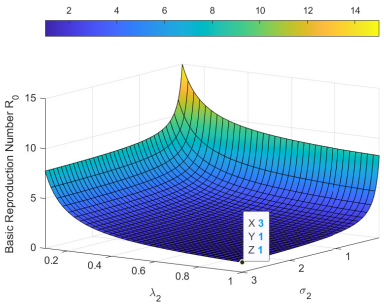

Figure 6. Effect of λ_2 and σ_1 on R_0

In figure 7 we plot the states in equations (2.1)-(2.11) to examine the disease dynamics for individuals exposed or infected with their first virus. Here we let virus 1 be SARS-CoV-2 and virus 2 be the B.1.1.7. variant. We observe from figure 7 that the B.1.1.7 variant causes the largest impact on the population compared to the original COVID-19 virus by a large margin despite the disparity of initial infections.

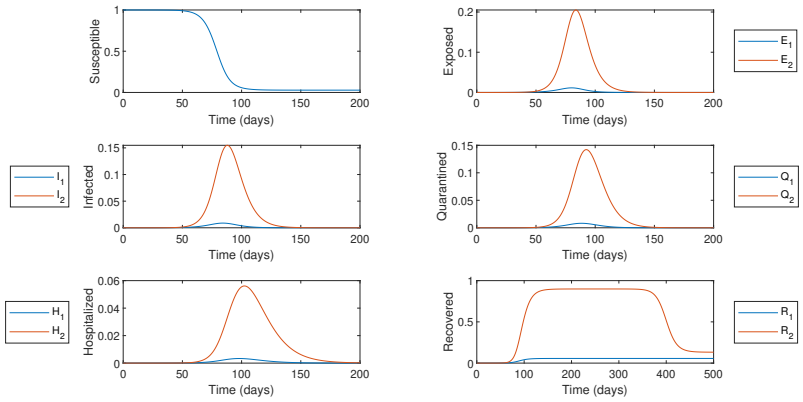

Figure 7. Dynamics of the sub-population proportions for individuals infected with their first virus

One observation to note is in the graph of the recovered state, R_2 specifically. We see that the number of recovered individuals peaks at about 150 days which is when the infected and quarantined states approach 0. Then we see that near day 400, the number begins to decrease as those individuals are then infected with COVID-19. On the other hand, figure 8 shows that R_1 hits a peak between 100 and 150 days and stays constant.

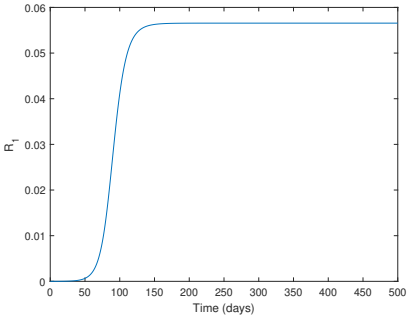

Figure 8. Population proportion of individuals recovered from COVID-19

In comparison, figure 9 shows the disease dynamics of the updated model that allows for the exposed sub-population to cause new infections. Some key differences of note involve the speed and severity of the spread. In the baseline model we see that the initial infections start around day 50 and ends around day 150 whereas the updated model shows the spread begins before day 20 and ends around day 60. This shows a significant increase in the speed of the spread when infections from exposed individuals are considered. We can also see a difference in the height of the peak of infections. For instance, we see a peak of the proportion of infections of the baseline model for the variant B.1.1.7 is about .15. A likewise comparison to the updated model sees a peak proportion of .3 for variant B.1.1.7. We should notice here that the infected curve for the baseline model is roughly symmetric whereas the curve for the updated model is clearly skewed right. Hence, by allowing for infections to be spread from the exposed population, we see that the corresponding infected population reaches its peak from the onset of infections much faster than the baseline counterpart. In addition, the rate at which individuals leave the infected state is slower than that of the baseline model. The same can be said of the exposed, quarantined, and hospitalized states as well.

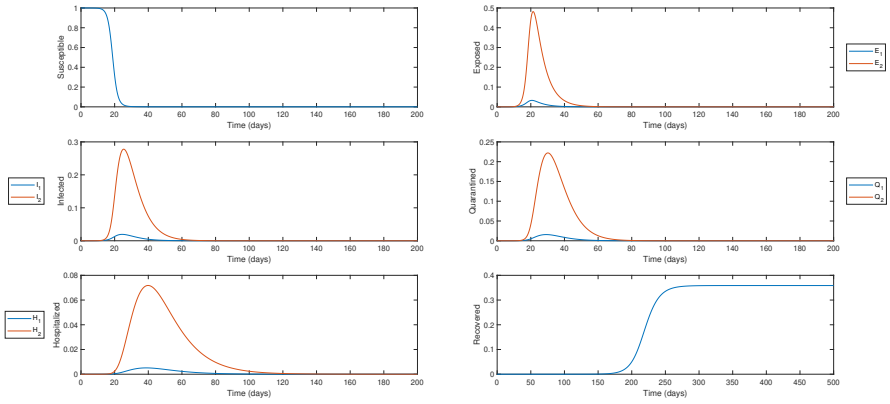

Figure 9. Dynamics of the sub-population proportions of individuals infected with their first virus for the model with equations (4.1)-(4.7)

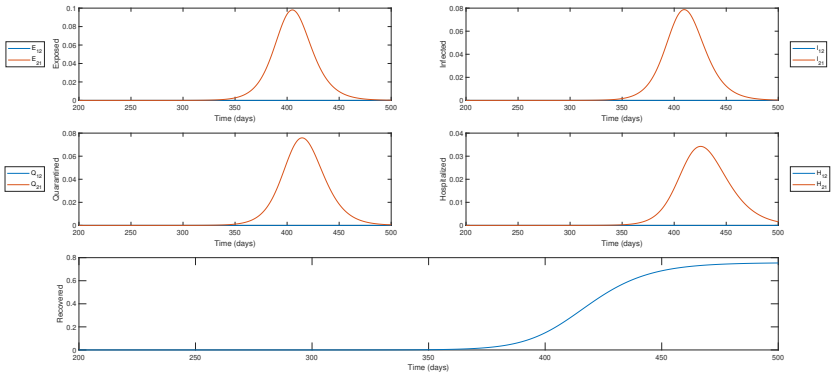

Figure 10. Dynamics of the sub-population proportions for individuals infected with their second virus

In figure 10 we plot the states corresponding to individuals being infected with a second virus. The second infections and exposures begin around day 350. From these graphs we observe that states that represent individuals who have recovered from Coronavirus and are now infected with variant B.1.1.7 are uniformly zero. This suggests that individuals that have recovered from SARS-CoV-2 will not be infected by variant B.1.1.7. This phenomenon is shown in figures 11 and 12 where we see that R_1 begins to decrease as the exposed and infected states begin to populate. In particular, figure 13 shows that I_{12} will be nonzero for $\beta_1 > .62$ and figure 14 shows that I_{12} will be nonzero for $\lambda_1 < .14$.

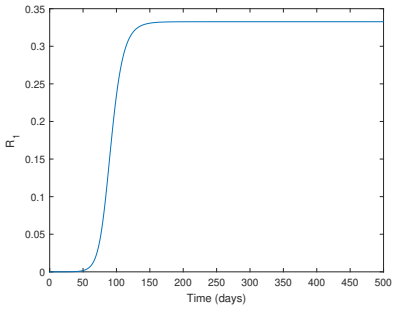

Figure 11. R_1 with $\beta_1 = .6$

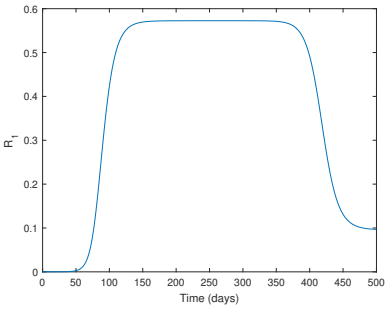

Figure 12. R_1 with $\beta_1 = .65$

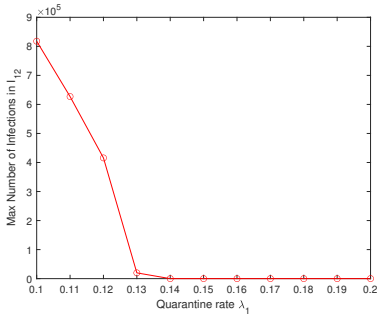

Figure 13. Influence of λ_1 on I_{12}

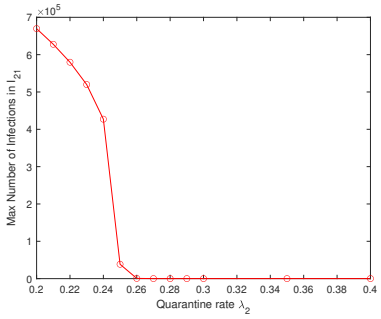

Figure 14. Influence of λ_2 on I_{21}

Further analysis shows that for I_{12} population to grow, λ_1 must be less than 0.14. Figure 13 illustrates that to stop a second infection after COVID-19 within 500 days, we must have a quarantine rate of 0.14 or greater for individuals that are infected with COVID-19. Figure 14 shows that having a quarantine rate of 0.26 for individuals infected with B.1.1.7 susceptible individuals won't contract both viruses in a 500 day period.

As shown in figure 15 we have graphed the total amount of infections across all infected states. We observe that for our initial parameter assumptions we see an initial buildup of infections around day 50 followed by a new wave of infections approximately day 300. For figure 16 we set $\lambda_2 = .26$ and see that susceptible individuals should not expect to be infected twice within 500 days.

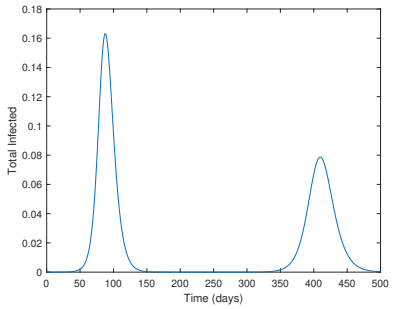

Figure 15. Total infections across all Infected categories

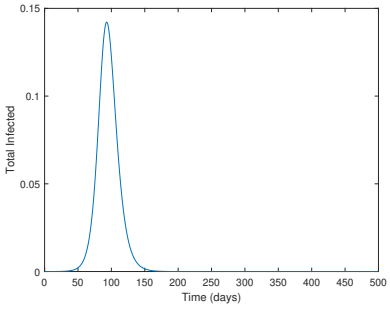

Figure 16. Total infections across all infected categories with $\mathcal{R}_0 \approx 3.1$

6. **Conclusions and Future Work**

In this work we have created a COVID-19 model that incorporates a simultaneous variant as well as the possibility to recover from one virus and be infected with the other. We then derived a basic reproduction number for this model. Next we formed an updated model by allowing for infections to be spread by individuals who have been exposed to the virus and derived a basic reproduction number for this updated system. Finally, through simulations of these models we analyzed the role of multiple parameters and their effects on different sub-populations.

In the future, we plan on adding more compartments to simulate social behaviors. In addition, we will split the infected state to asymptomatic and symptomatic which will have their own infection and quarantine rates. We will also look to modify the updated model by splitting the exposed state into carriers and non-carriers. We may also look into adding a third virus to the model. We hope to study the impact of certain social behaviors such as face mask usage and lock-downs on the number of infections and deaths. By adding a third virus, we may look to further understand interactions between these viruses and the effectiveness of safety measures such as quarantining.

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