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Modeling and Analysis of the Spread of COVID-19 with simultaneous Variants of Concern

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***Abstract*— With COVID-19 and its variants still of concern globally, 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.**

Keywords*—*COVID, Epidemiology, Compartmental models, Reproduction Number, Variants

I. 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). The virus has been

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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 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 [1]. 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 for social behaviors such as face-mask usage and quarantining [2]. 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.

Along with focus focusing on social behaviors and dynamics [2, 3], a new consideration must be made: COVID-19 variants of interest. In particular we seek to model the impact of variants of concern as defined by the Centers for Disease Control and Prevention (CDC) and who with the possibility of being infected by the given variant after recovering from COVID-19 and vice-versa. With variants such as Alpha for B.1.1.7 (U.K. variant), Beta for B.1.351 (South Africa), Gamma for P.1 (Brazil), Delta for B.1.617.2 (India), Omicron for B.1.1.529 (South Africa), 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 [2] 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 II, 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 III we state and prove the basic reproduction number, $\mathcal{R}_0$, for the model. Section IV 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 V will present numerical experiments and their corresponding graphs and implications of model we have presented. Finally, section VI will be dedicated to conclusions and future work.

II. Mathematical Model and Governing Equations

A. 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.

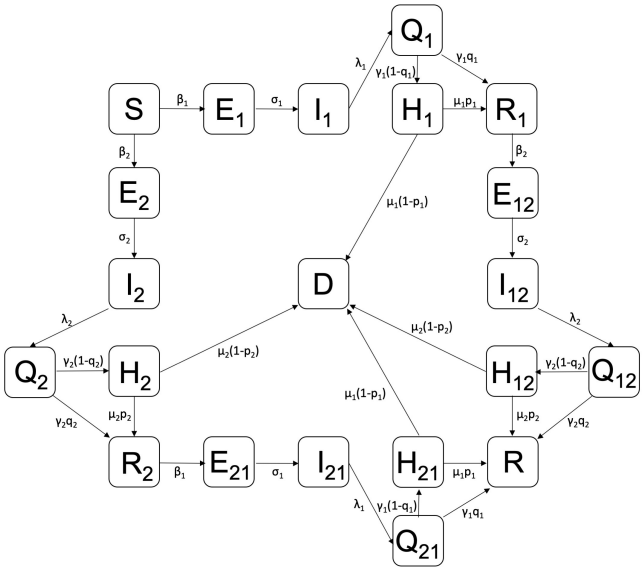

Fig. 1. Flow diagram for the two variant COVID-19 model

The dynamics of the spread described is shown in the following flow diagram Figure 1.

B. Governing Differential Equations

The flow diagram in figure 1 is described with the following equations:

$$\frac{dS}{dt} = -\sum_{i=1}^{2} \frac{\beta_i S I_i}{N} \tag{1}$$

$$\frac{dE_1}{dt} = \frac{\beta_1 S I_1}{N} - \sigma_1 E_1 \tag{2}$$

$$\frac{dE_2}{dt} = \frac{\beta_2 S I_2}{N} - \sigma_2 E_2 \tag{3}$$

$$\frac{dI_1}{dt} = \sigma_1 E_1 - \lambda_1 I_1 \tag{4}$$

$$\frac{dI_2}{dt} = \sigma_2 E_2 - \lambda_2 I_2 \tag{5}$$

$$\frac{dQ_1}{dt} = \lambda_1 I_1 - \gamma_1 Q_1 \tag{6}$$

$$\frac{dQ_2}{dt} = \lambda_2 I_2 - \gamma_2 Q_2 \tag{7}$$

$$\frac{dH_1}{dt} = (1-q_1)\gamma_1 Q_1 - \mu_1 H_1 \tag{8}$$

$$\frac{dH_2}{dt} = (1-q_2)\gamma_2 Q_2 - \mu_2 H_2 \tag{9}$$

$$\frac{dR_1}{dt} = q_1\gamma_1 Q_1 + p_1\mu_1 H_1 - \frac{\beta_2 R_1 I_{1,2}}{N} \tag{10}$$

$$\frac{dR_2}{dt} = q_2\gamma_2 Q_2 + p_2\mu_2 H_2 - \frac{\beta_1 R_2 I_{2,1}}{N} \tag{11}$$

$$\frac{dE_{1,2}}{dt} = \frac{\beta_2 R_1 I_{1,2}}{N} - \sigma_2 E_{1,2} \tag{12}$$

$$\frac{dE_{2,1}}{dt} = \frac{\beta_1 R_2 I_{2,1}}{N} - \sigma_1 E_{2,1} \tag{13}$$

$$\frac{dI_{1,2}}{dt} = \sigma_2 E_{1,2} - \lambda_2 I_{1,2} \tag{14}$$

$$\frac{dI_{2,1}}{dt} = \sigma_1 E_{2,1} - \lambda_1 I_{2,1} \tag{15}$$

$$\frac{dQ_{1,2}}{dt} = \lambda_2 I_{1,2} - \gamma_2 Q_{1,2} \tag{16}$$

$$\frac{dQ_{2,1}}{dt} = \lambda_1 I_{2,1} - \gamma_1 Q_{2,1} \tag{17}$$

$$\frac{dH_{1,2}}{dt} = (1-q_2)\gamma_2 Q_{1,2} - \mu_2 H_{1,2} \tag{18}$$

$$\frac{dH_{2,1}}{dt} = (1-q_1)\gamma_1 Q_{2,1} - \mu_1 H_{2,1} \tag{19}$$

$$\frac{dR}{dt} = q_1\gamma_1 Q_{2,1} + q_2\gamma_2 Q_{1,2} + p_1\mu_1 H_{2,1} + p_2\mu_2 H_{1,2} \tag{20}$$

$$\frac{dD}{dt} = (1-p_1)\mu_1(H_1 + H_{2,1}) + (1-p_2)\mu_2(H_2 + H_{1,2}) \tag{21}$$

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 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}. The various rates in the diagram and equations are summarized in table I.

Table I. 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/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

III. 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* described in [4] to solve for $\mathcal{R}_0$.

Theorem 1. *The basic reproduction number $\mathcal{R}_0$ is given by*

$$\mathcal{R}_0 = \max\left\{\frac{\beta_1}{\lambda_1}, \frac{\beta_2}{\lambda_2}\right\} \tag{22}$$

Proof. Given infections states $E_1, E_2, I_1, I_2, E_{1,2}, E_{2,1}, I_{1,2}, I_{2,1}$ in equations (2)-(5) and (12)-(15) we create vector $\mathcal{F}$ representing the inflow of new infections into the aforementioned infectious states. Given $S \approx N$ in the beginning,

$$\mathcal{F} = \left\{ \beta_1 I_1, \beta_2 I_2, 0, 0, \frac{\beta_2 R_1 I_{1,2}}{N}, \frac{\beta_1 R_2 I_{2,1}}{N}, 0, 0 \right\} \tag{23}$$

Similarly we define vector $\mathcal{V}$ by the outflow of equations (2)-(5) and (12)-(15) respectively.

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

Next, we now compute the Jacobian matrix F from vector $\mathcal{F}$ and Jacobian matrix V from vector $\mathcal{V}$

$$F = \begin{bmatrix} 0 & 0 & \beta_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_2 R_1}{N} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_1 R_2}{N} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad V = \begin{bmatrix} \sigma_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \sigma_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\sigma_1 & 0 & \lambda_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\sigma_2 & 0 & \lambda_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \sigma_2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_1 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\sigma_2 & 0 & \lambda_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\sigma_1 & 0 & \lambda_1 \end{bmatrix}$$

The Next Generation Matrix given by FV^{-1} can be calculated as:

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

The basic reproduction number is the maximum eigenvalue of FV^{-1}. For this we take the determinant of $FV^{-1} - \lambda I$ and solve for the roots of the characteristic polynomial. 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

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

□

Remark 1. *The result given by theorem 1 implies that the basic reproduction number for the system (1) – (21) is the largest ratio of the transmission rate to quarantine rate of the two variants of COVID-19.*

IV. 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 (1) - (3) and (10) - (13) as follows:

$$\frac{dS}{dt} = -\frac{\beta_1 S}{N}(E_1 + I_1) - \frac{\beta_2 S}{N}(E_2 + I_2) \tag{24}$$

$$\frac{dE_1}{dt} = \frac{\beta_1 S}{N}(E_1 + I_1) - \sigma_1 E_1 \tag{25}$$

$$\frac{dE_2}{dt} = \frac{\beta_2 S}{N}(E_2 + I_2) - \sigma_2 E_2 \tag{26}$$

$$\frac{dR_1}{dt} = q_1\gamma_1 Q_1 + p_1\mu_1 H_1 - \frac{\beta_2 R_1}{N}(E_{1,2} + I_{1,2}) \tag{27}$$

$$\frac{dR_2}{dt} = q_2\gamma_2 Q_2 + p_2\mu_2 H_2 - \frac{\beta_1 R_2}{N}(E_{2,1} + I_{2,1}) \tag{28}$$

$$\frac{dE_{1,2}}{dt} = \frac{\beta_2 R_1}{N}(E_{1,2} + I_{1,2}) - \sigma_2 E_{1,2} \tag{29}$$

$$\frac{dE_{2,1}}{dt} = \frac{\beta_1 R_2}{N}(E_{2,1} + I_{2,1}) - \sigma_1 E_{2,1} \tag{30}$$

A basic reproduction can also be derived for the updated system with the impact of the exposed states, following the steps shown in Theorem 1. This gives the following new result.

Theorem 2. *The basic reproduction number $\mathcal{R}_0$ is given by*

$$\mathcal{R}_0 = \max\left\{\frac{\beta_1}{\sigma_1} + \frac{\beta_1}{\lambda_1}, \quad \frac{\beta_2}{\sigma_2} + \frac{\beta_2}{\lambda_2}\right\} \tag{31}$$

Proof. We follow the same process as shown in the proof for theorem **??** to calculate,

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

and

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

Then the respective Jacobians can be calculated as:

$$F = \begin{bmatrix} \beta_1 & 0 & \beta_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & \beta_2 & 0 & \beta_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\beta_2 R_1}{N} & 0 & \frac{\beta_2 R_1}{N} & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{\beta_1 R_2}{N} & 0 & \frac{\beta_1 R_2}{N} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad V = \begin{bmatrix} \sigma_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \sigma_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\sigma_1 & 0 & \lambda_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\sigma_2 & 0 & \lambda_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \sigma_2 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_1 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\sigma_2 & 0 & \lambda_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\sigma_1 & 0 & \lambda_1 \end{bmatrix}$$

The next generation matrix can then be computed as:

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

Next, we compute the characteristic equation as before with $\det(FV^{-1} - \lambda I) = 0$ which yields,

$$\lambda^4 \left[\lambda - \left(\frac{\beta_1}{\sigma_1}+\frac{\beta_1}{\lambda_1}\right)\right]\left[\lambda - \left(\frac{\beta_2}{\sigma_2}+\frac{\beta_2}{\lambda_2}\right)\right]\left[\lambda - \left(\frac{\beta_2 R_1}{\sigma_2 N}+\frac{\beta_2 R_1}{\lambda_2 N}\right)\right]\left[\lambda - \left(\frac{\beta_1 R_2}{\sigma_1 N}+\frac{\beta_1 R_2}{\lambda_1 N}\right)\right] = 0$$

Since $R_i < N$ for $i = 1, 2$, the basic reproduction numberis given by

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

□

Remark 2. *The result given by theorem 2 implies that $\mathcal{R}_0$ for the updated system with (24) - (30) is impacted by the rate of exposed people becoming infected along with the transmission rate and quarantine rate of the two variants of COVID-19.*

V. Computational Experiments

In this section, we study the dynamics of the system proposed in this work to understand the impact of variants of concern.

A. Initial Conditions and Parameter Values.

The parameters for COVID-19 we employ are listed in table II while parameters for variants B.1.1.7 and B.1.427 are given in table III and IV. Note that these are only chosen for simplicity to demonstrate the importance of studying variants and one may expand this work to new variants such as Omicron B.1.1.529 also once we have more reliable data.

Table II. SARS-CoV-2 parameters

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

For the parameters not listed in table III or IV, we assume that they are equal to their corresponding parameters of table II. For our numerical computations we will assume that $\beta_1 = .5$. Since the CDC estimates that $\mathcal{R}_0 = 2.5$ [5] for COVID-19 we can then use the result of theorem 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 III. Variant B.1.1.7

Parameter	Value	Reference(s)
β_2	.75	[6]
q_2	.81	[7]
p_2	.91	[7]

Table IV. Variant B.1.427

Parameter	Value	Reference(s)
β_2	.6	[8]

Remark 3. *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 V and table VI.) 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, table VII gives $\mathcal{R}_0$ values of past infectious diseases.

Table V. Model (1)-(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 VI. Updated Model with equations (24)-(30)

Virus 1	Virus 2	$\mathcal{R}_0$
SARS-CoV-2	B.1.1.7	8.25
SARS-CoV-2	B.1.427	6.5
B.1.1.7	B.1.427	8.25

Table VII. Basic Reproduction Numbers for well-known diseases

Disease	$\mathcal{R}_0$	**Reference**
Measles	12-18	[9]
Chickenpox	10-12	[10]
Pertussis	5.5	[11]
Smallpox	3.5-6	[12]
COVID-19	2.4-3.4	[13]
HIV/Aids	2-5	[14]
Common Cold	2-3	[15]
Influenza	1.3	[16]

B. Understanding the dynamics

To study the dynamics of the disease modeled by the system of ODEs (1) - (21), we employ a higher-order Runge-Kutta method in MATLAB. For our simulation we used the population of Virginia, USA as $N = 8,570,400$ which was around the population in April 2020. We assumed in this, the initial population of the various groups in the system of equations were given to be the following: $S^0 = 7000000, E_1^0 = 1000000, E_2^0 = 7000, I_1^0 = 490000, I_2^0 = 7000, E_{12}^0 = 1000, E_{21}^0 = 01000, I_{12}^0 = 700, I_{21}^0 = 700$. The rest of the initial conditions for quarantined, hospitalized, recovered and dead were taken to be zero.

Figure 2 shows the impact of increasing the quarantine rate. Clearly as more people quarantine the basic reproduction number $\mathcal{R}_0$ decreases. The figure suggests that one can get epidemic to vanish with $\mathcal{R}_0 < 1$ if we are able to quarantine more than 90% of the population. While this maybe unreasonable, it may be noted that by getting over 30% quarantines, we can get $\mathcal{R}_0 < 2$ which is very reasonable.

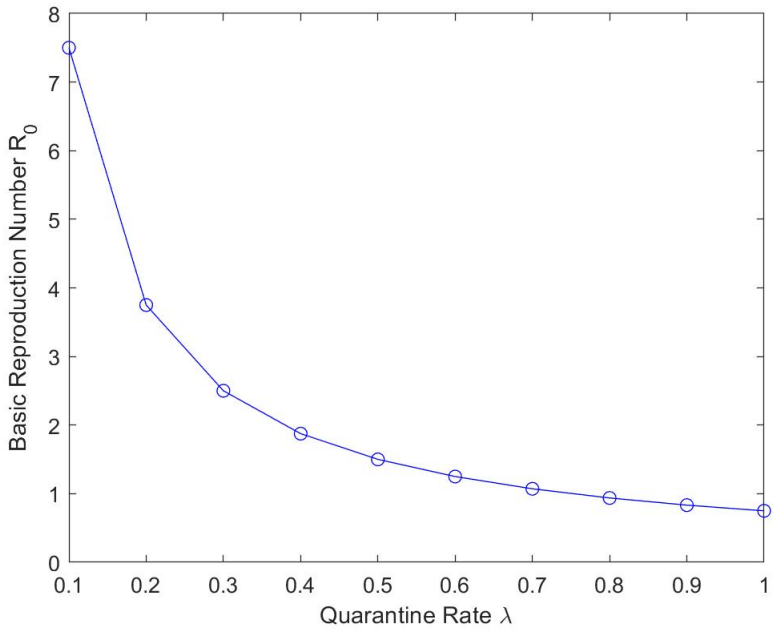

Fig. 2. $\mathcal{R}_0$ in response to increased quarantine

Next we plot the various susceptible, exposed, infected and recovered population fractions for those that were infected once (Figure 3) and those that were reinfected by another variant (Figure 4). As expected the peaks shift as people move from the first recovered states to being reinfected as they are exposed to new variants.

We also plot the population fractions for all the infected populations including those that were infected by one of the variants and then were reinfected by another in Figure 5. We also plot the two recovered states for people who were infected by one virus and also plot the fully recovered state after they were reinfected again in Figure 6. These graphs exhibit expected behaviors which can be used to inform policy.

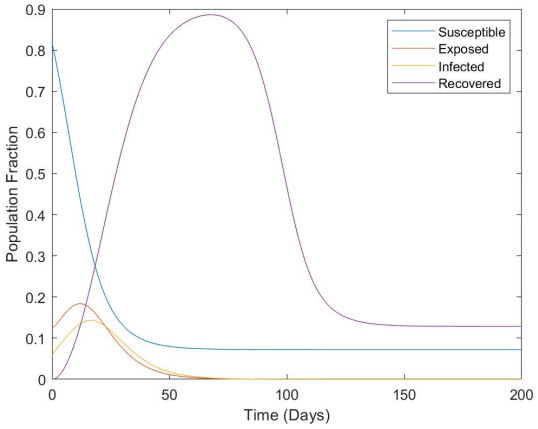

Fig. 3. The dynamics of those with a single infection

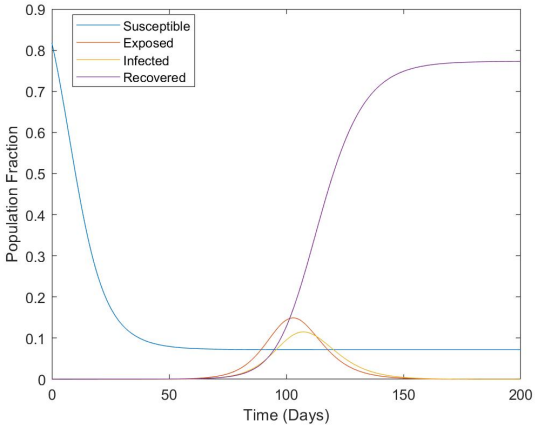

Fig. 4. The dynamics of those infected once being reinfected

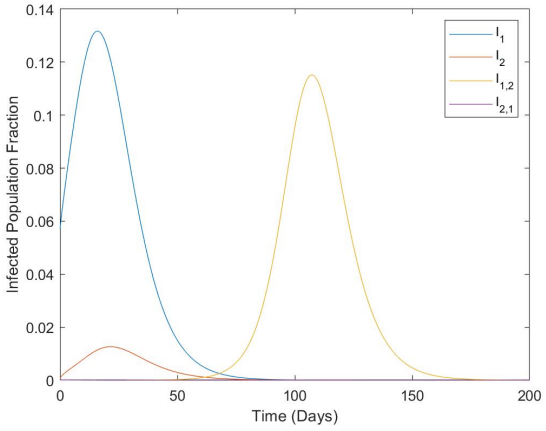

Fig. 5. The dynamics of those with a single infection

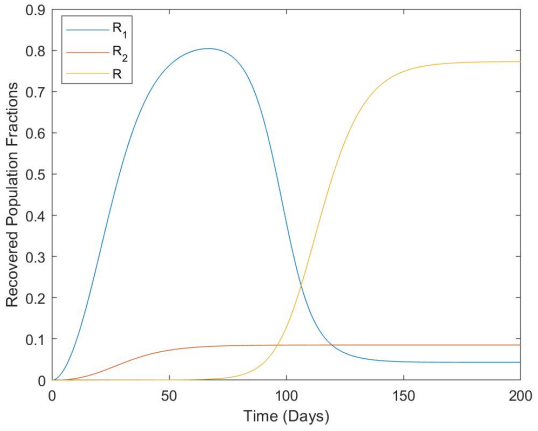

Fig. 6. The dynamics of those infected once being reinfected

VI. 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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