Mathematical Modeling, Analysis and Simulation of a Two-Variant Model for Understanding the Spread of COVID- 19

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Motivation

- New variants of SARS-CoV-2 (the virus that causes COVID-19) are emerging worldwide, with potential for increased transmissibility.

- Variant B.1.1.7 was first detected in the United Kingdom, and has since spread throughout the globe, reaching Virginia in late January 2021

- We are interested in capturing the dynamics of the spread of multiple variants of this disease
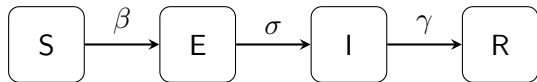
Motivation
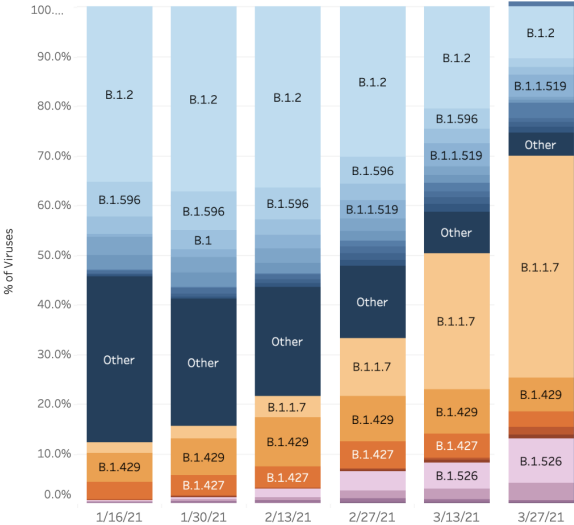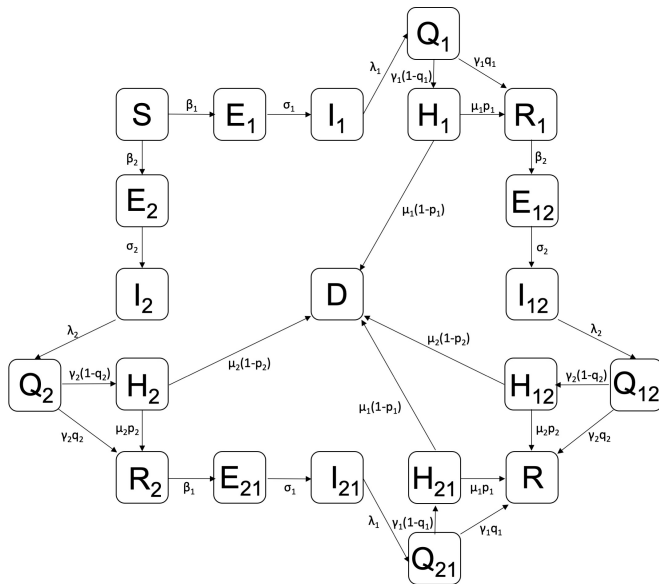

Collection date, two weeks ending

Definitions

- **Compartmental Model** - A mathematical model that utilizes different compartments to simulate interactions between populations.

- **Variant of Concern** - A variant which poses risk of increased disease severity, has an increased ability to spread, or potentially has an impact on testing, treatment, or vaccination.

- **SARS-CoV-2** - The virus that causes the disease COVID-19.

- **B.1.1.7**- A SARS-CoV-2 variant of concern first observed in the UK.

$$\begin{cases} \dfrac{dS}{dt} = -\beta \dfrac{SI}{N} \\[2ex] \dfrac{dE}{dt} = \beta \dfrac{SI}{N} - \sigma E \\[2ex] \dfrac{dI}{dt} = \sigma E - \gamma I \\[2ex] \dfrac{dR}{dt} = \gamma I \end{cases} \tag{1}$$

Our Model

- Susceptible (S): Individuals who have not been infected

- 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 are currently infected with virus j

- Quarantine (Q_i): Individuals that are quarantined after being infected with virus i

Our Model

- Second Quarantine ($Q_{i,j}$): Individuals that have recovered from virus i and are 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 died from either virus

Our Model

Parameter	Definition
β_i	Transmission rate of virus i
σ_i	Infection rate of virus i
λ_i	Quarentine rate of virus i
γ_i	Hospitalization rate of virus i
μ_i	Death rate of virus i
q_i	Proportion of quarantined individuals who recover from virus i
p_i	Proportion of hospitalized individuals who recover from virus i

Our Model

$$\frac{dS}{dt} = -\frac{\beta_1 S I_1}{N} - \frac{\beta_2 S I_2}{N} \tag{1}$$

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Our Model

The Basic Reproduction Number is the average number of secondary infections produced by a typical case of an infection in a population where everyone is susceptible. We used the Next Generation Matrix approach to solve for $\mathcal{R}_0$.

Theorem:

The Basic Reproduction Number $\mathcal{R}_0$ for the system described by equations (1)-(21) is given by
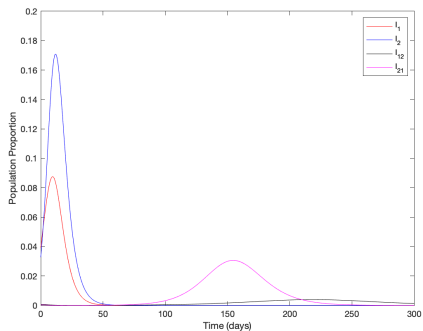
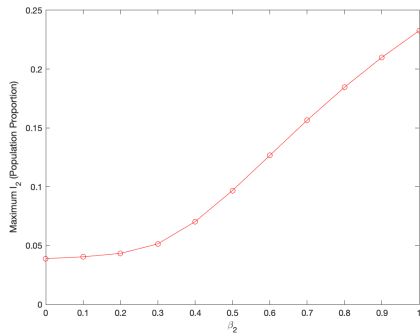$$\mathcal{R}_0 = \max\left\{\frac{\beta_1}{\lambda_1}, \frac{\beta_2}{\lambda_2}\right\}$$
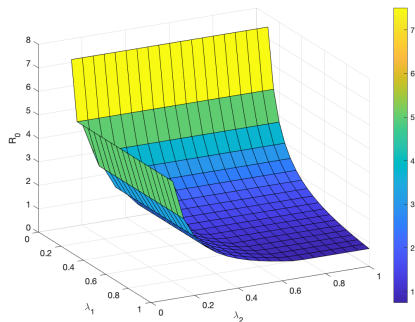
This figure shows $\mathcal{R}_0$ as a function of λ_1 and λ_2, for fixed values of β_1 and β_2.

This figure shows infected individuals for variants 1 and 2, as well as re-infected individuals, as a function of time.

This figure shows the max number of variant 2 infections as a function of the transmission rate.

- It is important to contain the spread of the B.1.1.7 variant and other variants of concern because they can spread more rapidly, leading to increased infections.

- Future work could involve modifying the model to better simulate social behaviour (such as the use of face masks), analyzing more variants, and incorporating vaccinations into the model.

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