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Cover Page Footnote

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Mathematical Modeling, Analysis, and Simulation of the COVID-19 Pandemic with Behavioral Patterns and Group Mixing

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Abstract

Due to the rise of COVID-19 cases, many mathematical models have been developed to study the disease dynamics of the virus. However, despite its role in the spread of COVID-19, many SEIR models neglect to account for human behavior. In this project, we develop a novel mathematical modeling framework for studying the impact of mixing patterns and social behavior on the spread of COVID-19. Specifically, we consider two groups, one exhibiting normal behavior who do not reduce their contacts and another exhibiting altered behavior who reduce their contacts by practicing non-pharmaceutical interventions such as social distancing and self-isolation. The dynamics of these two groups are modeled through a coupled system of ordinary differential equations that incorporate mixing patterns of individuals from these groups, such that contact rates depend on behavioral patterns adopted across the population. Additionally, we derive the basic reproduction number, perform numerical simulations, and create an interactive dashboard.

Keywords: COVID-19, Compartmental Models, Social Behavior, Mixing Patterns, Non-Pharmaceutical Interventions

1 Introduction

In late 2019, the novel coronavirus disease COVID-19 was traced to Wuhan, China. Since then, the disease has spread such that by March of 2020, the World Health Organization declared it was a pandemic [17, 16]. As a result, much research has been focused on understanding the nature of COVID-19. Mathematical models, in particular, have been used to predict the spread of the disease, or more importantly, estimate the influence of certain interventions on reducing the spread.

In fact, several epidemiological models for infectious diseases are based on classical compartmental models that use an ordinary differential equation system, such as the Susceptible-Exposed-Infected-Recovered (SEIR) structure [1]. In the case of COVID-19, many researchers have adapted the SEIR model to study the effects of public health interventions based on certain assumptions [14, 15]. Some researchers have also accounted for the influence of specific key factors, such as containment strategies [12]; undetected infected people [10]; and mobility patterns [15]. Though they may have been effective in modeling the nature of COVID-19, however, several models do not account for other relevant factors, especially the

influence of social behavior.

Yet, the pandemic has had a strong effect on the way individuals live and interact with each other. For instance, the rapid spread of COVID-19 has prompted government lock-downs and business closures. Furthermore, individuals are encouraged to avoid public gatherings, wear face masks, and practice basic hygiene, such as hand washing. In turn, these measures help protect people from COVID-19 and reduce the disease burden. Some researchers have accounted for the impact of behavior, particularly in relation to lock-down measures and social distancing. For example, an SIR-based model can be developed with a time-dependent transmission rate that accounts for lock-down time and other key behaviors, like riots [19]. The impact of social distancing can also be represented as a time-dependent function that is applied on the transmission rate, as found in [5].

Our previous work focused on studying the effects of human behaviors through three novel SEIR-based models: a baseline model, an explicit intervention model, and an implicit intervention model. The implicit model, in particular, considers two types of behaviors within the susceptible sub-population: normal behavior, indicating they do not limit their contacts, and altered behavior, indicating they practice interventions such as social distancing and confinement. In addition, for this model, the

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overall transmission rate is a function of the proportion of susceptible individuals with normal behavior, which is also modeled as a differential equation [13]. However, it is important to consider that it is not just susceptible individuals who can exhibit these behaviors, but rather the entire population. As seen in the COVID-19 pandemic, the population as a whole generally consists of individuals who have normal or altered behavior. Therefore, the interactions between these two groups must be accounted for to understand how they affect each group and the entire population as a whole.

Ultimately, the main purpose of this paper is to present a novel mathematical framework that accounts for the interactions between individuals who have different behaviors. Our model expands on our previous model as well as earlier SIR/SEIR models that have been developed to include mixing patterns between two groups [13, 2]. Furthermore, we aim to study the effects of mixing patterns and behavior on the disease dynamics of COVID-19.

The paper is outlined as follows. In Section 2, we introduce the mathematical model. We also review three major types of mixing patterns and derive the basic reproduction number using the Next Generation Matrix. In Section 3, we present the results of our numerical computations for our model. Section 4 describes a user-friendly dashboard we created for our model. Finally, in Section 5, we summarize our work and future directions.

2 The Mathematical Model and Governing Equations

2.1 An Implicit Behavior Mixing Model

In this work, we present an extended SEIR mathematical model that considers two groups of individuals within a population: a normal behavior group and an altered behavior group. Normal behavior indicates the individual does not limit their social contacts, whereas altered behavior indicates the individual reduces their contacts through interventions such as social distancing and self-isolation. This model excludes natural birth and death rates for simplicity.

Figure 1 depicts the model, which is organized as follows. Within each behavior group, N_n and N_a , there is a Susceptible (S), Exposed (E), Asymptomatic (I^A), Symptomatic (I^S), and Quarantine (Q) sub-population. In this paper, we denote which group a sub-population belongs to with a subscript n for the normal behavior group and a subscript a for the altered behavior group. The susceptible sub-population consists of individuals who have not contracted COVID-19. Exposed individuals are those who are in the incubation stage of disease progression. Asymptomatic individuals are infec-

tious individuals who are not exhibiting symptoms of COVID-19. Symptomatic individuals are infectious individuals who do exhibit symptoms of COVID-19. In this model, we assume that symptomatic and asymptomatic individuals are equally infectious and have equal periods of infectiousness. Lastly, quarantined individuals are symptomatic individuals who are isolated from the population and no longer spread the disease. Our model also contains Hospitalized (H), Recovered (R), and Dead (D) sub-populations, which are not associated with any particular group. Hospitalized individuals are symptomatic infectious individuals who show severe symptoms of COVID-19 and are in a hospital. The recovered class consists of individuals who survived the disease, whereas the dead class contains hospitalized individuals who did not survive.

Furthermore, we allow susceptible individuals, $S = S_n + S_a$, where S_n and S_a represent susceptible individuals with normal and altered behavior, respectively, to switch behaviors and mix with infected individuals from either group. We also introduce y , which is defined as the proportion of susceptible individuals with normal behavior or $y = S_n / (S_n + S_a)$. Please note that the coupling between S_n and S_a through y is represented as red arrows in Figure 1. We define f_{ij} as the fraction of contacts made by an individual in group i with group j and c_i as the number of contacts made by an individual in group i . Thus, we write the dynamics of the two susceptible groups as follows:

$$\dot{S}_n = -f_{nn}c_n y \frac{SI_n}{N_n} - f_{na}c_n y \frac{SI_a}{N_a}, \quad (1)$$

$$\dot{S}_a = -f_{an}c_a(1-y) \frac{SI_n}{N_n} - f_{aa}c_a(1-y) \frac{SI_a}{N_a}. \quad (2)$$

Note that y changes over time to represent the change in the susceptible with normal behavior and susceptible with altered sub-populations. A decrease in y , for instance, corresponds with an increase in the altered behavior population as more susceptible individuals with normal behavior switch to having altered behavior. Therefore, we can consider four different transmission rates that encapsulate both group mixing and behavioral changes:

$$\begin{aligned} b_{nn}(y) &= f_{nn}c_n y \\ b_{na}(y) &= f_{na}c_n y \\ b_{aa}(y) &= f_{aa}c_a(1-y) \\ b_{an}(y) &= f_{an}c_a(1-y) \end{aligned}$$

Notice that each transmission rate is a function of behavior. Also, note that $f_{nn} + f_{na} = f_{an} + f_{aa} = 1$, so $b_{nn}(y) + b_{na}(y) = c_n y$ and $b_{aa}(y) + b_{an}(y) = c_a(1-y)$. Additionally, y changes based on a natural selection process

and is modeled with the following differential equation:

$$\frac{dy}{dt} = y(1-y) \left[\frac{(b_{an} - b_{nn})I_n}{N_n} + \frac{(b_{aa} - b_{na})I_a}{N_a} \right]. \quad (3)$$

In the first part of equation (3), $y(1-y)$ represents individuals with normal behavior and individuals with altered behavior interacting with each other. The rate at which individuals with normal behavior change to altered behavior is proportional to the difference in the transmission associated with altered behavior and the transmission associated with normal behavior. Within the normal behavior group, this is $(b_{an} - b_{nn})$, since b_{an} indicates the transmission rate from individuals with altered behavior interacting with normal behavior and b_{nn} indicates the transmission rate from individuals with normal behavior interacting with other individuals with normal behavior. Similarly, within the altered behavior group, the difference is $(b_{aa} - b_{na})$.

The overall model is then governed by the following system of differential equations:

$$\begin{aligned} \frac{dS_n}{dt} &= -b_{nn}(y) \frac{SI_n}{N_n} - b_{na}(y) \frac{SI_a}{N_a}, \\ \frac{dE_n}{dt} &= b_{nn}(y) \frac{SI_n}{N_n} + b_{na}(y) \frac{SI_a}{N_a} - \sigma E_n, \\ \frac{dI_n^A}{dt} &= (1-p)\sigma E_n - \omega I_n^A, \\ \frac{dI_n^S}{dt} &= p\sigma E_n + (1-\nu)\omega I_n^A - \xi I_n^S, \\ \frac{dQ_n}{dt} &= \xi I_n^S - \gamma Q_n, \\ \frac{dS_a}{dt} &= -b_{an}(y) \frac{SI_n}{N_n} - b_{aa}(y) \frac{SI_a}{N_a}, \\ \frac{dE_a}{dt} &= b_{an}(y) \frac{SI_n}{N_n} + b_{aa}(y) \frac{SI_a}{N_a} - \sigma E_a, \\ \frac{dI_a^A}{dt} &= (1-p)\sigma E_a - \omega I_a^A, \\ \frac{dI_a^S}{dt} &= p\sigma E_a + (1-\nu)\omega I_a^A - \xi I_a^S, \\ \frac{dQ_a}{dt} &= \xi I_a^S - \gamma Q_a, \\ \frac{dH}{dt} &= q\gamma Q - ((1-x)\alpha^R + x\alpha^D)H, \\ \frac{dR}{dt} &= \nu\omega I^A + (1-q)\gamma Q + (1-x)\alpha^R H, \\ \frac{dD}{dt} &= x\alpha^D H, \\ \frac{dy}{dt} &= y(1-y) \left(\frac{b_n I_n}{N_n} + \frac{b_a I_a}{N_a} \right). \end{aligned} \quad (4)$$

Here $Q = Q_n + Q_a$, $b_n = b_{an} - b_{nn}$ and $b_a = b_{aa} - b_{na}$.

Also, note that

$$\begin{aligned} N_n &= S_n + E_n + I_n^A + I_n^S + Q_n + \delta_n^R R + \delta_n^H H, \\ N_a &= S_a + E_a + I_a^A + I_a^S + Q_a + \delta_a^R R + \delta_a^H H, \end{aligned}$$

where δ_n^R and δ_n^H indicates the fraction of recovered and hospitalized individuals in the normal behavior group and δ_a^R and δ_a^H indicates the fraction of recovered and hospitalized individuals in the altered behavior groups. We exclude the dead (D) compartment from the total population, so $N = N_n + N_a$.

Within both N_n and N_a , susceptible individuals (S) become exposed (E) by interacting with an infected individual at a transmission rate that is modeled with $b_{ij}(y)$. Exposed individuals (E) become either asymptomatic infectious or symptomatic infectious at a rate proportional to the incubation rate, σ , such that a fraction $(1-p)$ of exposed individuals become asymptomatic and a fraction p become symptomatic. Asymptomatic individuals (I^A) either recover or become symptomatic (I^S) infectious at a rate proportional to ω , where a fraction $(1-\nu)$ become symptomatic infectious and a fraction ν become recovered. Symptomatic individuals (I^S) enter the quarantine (Q) sub-population at a rate of ξ . At a rate proportional to γ , a fraction q of quarantined individuals become hospitalized while a fraction $(1-q)$ become recovered. Finally, hospitalized individuals who die and recover leave their sub-population at a rate of x and $(1-x)$, respectively. Hospitalized individuals who die are hospitalized for $1/\alpha^D$ days and hospitalized individuals who recover remain for $1/\alpha^R$. The death rate, x , is a function of time:

$$x(t) = \begin{cases} \hat{x} & \text{if } H(t) \leq B, \\ \frac{\hat{x}B + H(t) - B}{H(t)} & \text{if } H(t) > B, \end{cases} \quad (5)$$

where B represents the number of ICU beds and $\hat{x}$ is the lethality rate associated with severe cases of COVID-19 in the scenario where all hospitalized individuals have access to a bed. When there are enough beds to supply all hospitalized individuals, the death rate, x , is assumed to be equal to $\hat{x}$, which is indicated in the first part of the function. However, the second part of the function represents a shortage of beds in which there are more hospitalized individuals than the number of beds. In Figure 2, we show the relationship between x and H . We summarize all the model parameters in Table 1.

2.2 Mixing Patterns

In this section, we briefly discuss types of mixing patterns, which were outlined by [2]. We describe three types of mixing: proportionate, preferred, and like-with-like.

In proportionate mixing, the fraction of contacts, f_{ij} , is equal to the ratio of the total number of contacts from

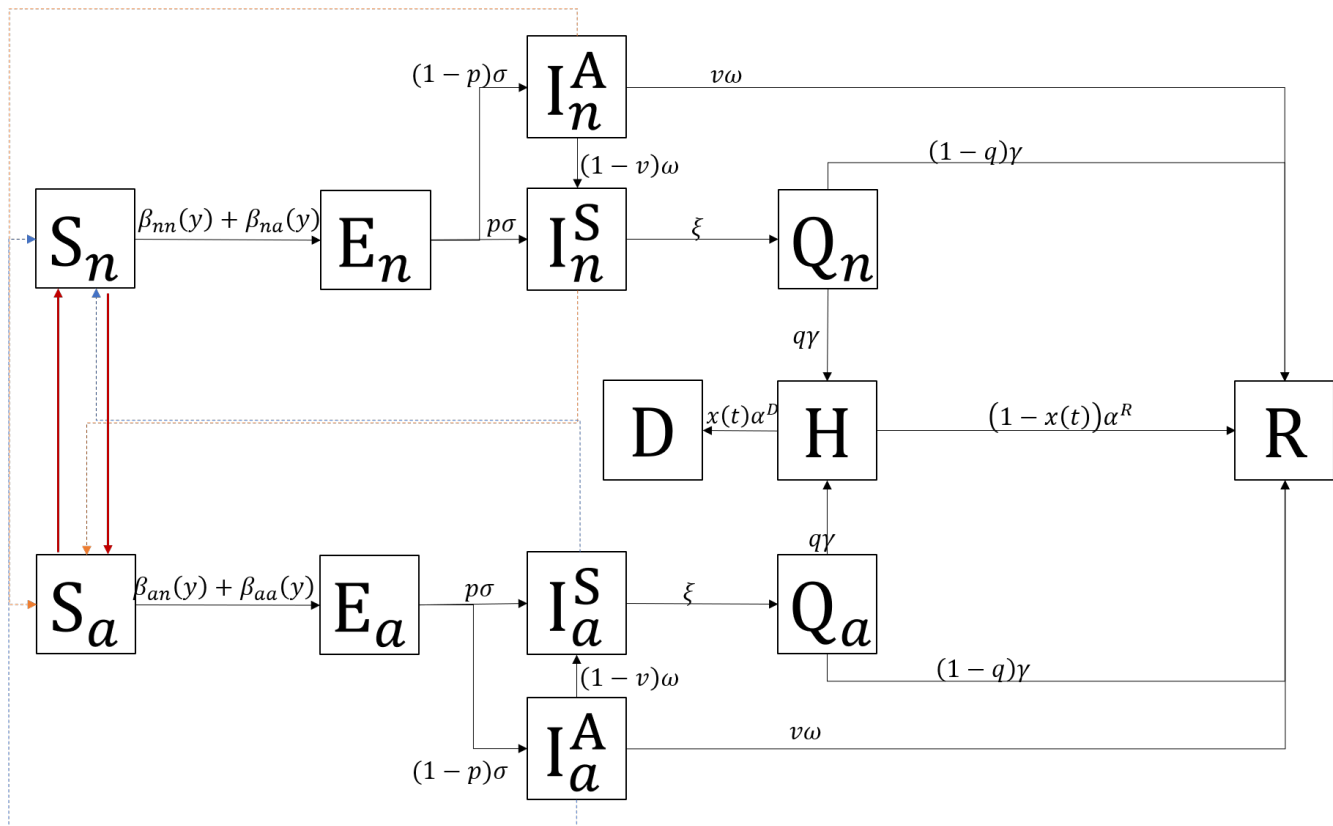


Figure 1: Flow Diagram of the Implicit Behavior Mixing Model.

Table 1: Definition and Value of Parameters in the COVID-19 Model.

Parameter	Definition	Value	References
b_{ij}	Transmission Rate	Function of y	N/A
f_{ij}	The fraction of contacts made by members of group i with group j	Varies	Assumed
c_i	The number of contacts made by members group i	Varies	Assumed
σ	Incubation Rate	1/6	[18]
ω	Rate at which asymptomatic individuals become symptomatic or recovered	1/14	[18]
ξ	Rate at which symptomatic individuals become quarantined	0.5	Assumed
γ	Rate at which quarantined individuals become hospitalized or recovered	1/5	[7]
$1/\alpha^R$	Duration at which hospitalized individuals who recover remain hospitalized	12	[3, 4]
$1/\alpha^D$	Duration at which hospitalized individuals who die remain hospitalized	14	[3, 4]
$x(t)$	Death rate of hospitalized individuals	Function of time	N/A
$\hat{x}$	Lethality rate of hospitalized individuals with access to an ICU bed	0.04	Assumed
p	Fraction of exposed individuals who became symptomatic	0.6	Assumed
q	Fraction of quarantined individuals who become hospitalized	0.19	[3, 4]
ν	Fraction of asymptomatic individuals who recover	0.8	Assumed

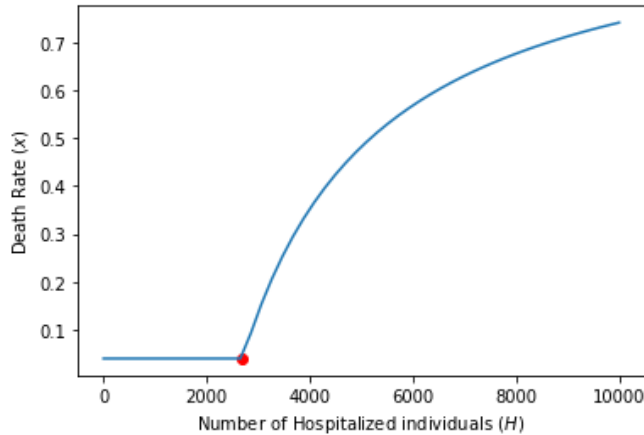


Figure 2: Relationship between the number of hospitalized individuals (H) and the death rate (x). The red dot indicates where $H = B$, or when bed capacity has been reached. Up to this point, $x = \hat{x}$. Beyond this point, the death rate increases above $\hat{x}$ as it approaches 1.

all members of group i to the combined total number of contacts from both groups. In other words,

$$f_{nn} = f_{an} = \frac{c_n N_n}{c_n N_n + c_a N_a},$$

$$f_{na} = f_{aa} = \frac{c_a N_a}{c_n N_n + c_a N_a}.$$

In preferred mixing, a portion of individuals, π_i , mixes only with others that share their behavior while the remaining $(1 - \pi_i)$ performs proportionate mixing. Thus, let

$$f_i = \frac{(1 - \pi_i)c_i N_i}{(1 - \pi_n)c_n N_n + (1 - \pi_a)c_a N_a}, i = n, a.$$

f_i can be thought of as the ratio of the total number of contacts from just members of group i who mix proportionately to the total number of contacts from members of both groups who mix proportionately. Note that proportionate mixing occurs when $\pi_n = \pi_a = 0$. For preferred mixing,

$$\begin{aligned} f_{nn} &= \pi_n + (1 - \pi_n)f_n, \\ f_{an} &= (1 - \pi_a)f_n, \\ f_{aa} &= \pi_a + (1 - \pi_a)f_a, \\ f_{na} &= (1 - \pi_n)f_a. \end{aligned}$$

Finally, in like-with-like mixing, all individuals in a group randomly mix exclusively within their own group. Therefore, $\pi_n = \pi_a = 1$, $f_n = f_a = 0$,

$$\begin{aligned} f_{nn} &= f_{aa} = 1, \\ f_{na} &= f_{an} = 0. \end{aligned}$$

2.3 Derivation of the Basic Reproduction Number R_0

In this section, we derive a basic reproduction number $\mathcal{R}_0$ that can be used to measure the transmission potential of COVID-19 as proposed by the system (4). $\mathcal{R}_0$ is the average number of secondary infections produced by a typical case of an infection in a population where everyone is susceptible [6].

Recall that the proposed mathematical model for COVID-19 includes sub-populations with different infectious states. We will employ a general approach called the *Next Generation Matrix* [1] to find the basic reproduction number $\mathcal{R}_0$ which is given by the following theorem.

Theorem 2.1. For $i = n, a$, the basic reproduction number $\mathcal{R}_0$ is given by

$$\mathcal{R}_0^i = R_0^{1,i} + R_0^{2,i} + R_0^{3,i} \quad (6)$$

with

$$R_0^{1,i} = \beta_{ii} \cdot \frac{p}{\xi} \quad (7)$$

$$R_0^{2,i} = \beta_{ii} \cdot \frac{(1-p)}{\omega} \quad (8)$$

$$R_0^{3,i} = \beta_{ii} \cdot \frac{(1-\nu)(1-p)}{\xi} \quad (9)$$

where

$$\beta_{nn} = b_{nn}(y) \frac{N}{N_n}, \quad \beta_{aa} = b_{aa}(y) \frac{N}{N_a}.$$

Proof. Given the infectious states $E_n, I_n^A, I_n^S, E_a, I_a^A, I_a^S$ in the system (4), we create a vector $\mathcal{F}$ that represents the new infections flowing only into the exposed compartments given by

$$\mathcal{F} = \{\beta_{nn}I_n + \beta_{na}I_a, 0, 0, \beta_{an}I_n + \beta_{aa}I_a, 0, 0\}, \quad (10)$$

where $I_n^A + I_n^S = I_n$ and $I_a^A + I_a^S = I_a$. We have also assumed that initially most of the susceptible population (S) is approximately the entire population (N).

Along with $\mathcal{F}$, we will also consider $\mathcal{V}$ which denote the outflow from the infectious compartments in the system (4) which is given by

$$\mathcal{V} = \{A, B, C, D, E, F\}, \quad (11)$$

where

$$\begin{aligned} A &= \sigma E_n, \\ B &= \omega I_n^A - (1-p)\sigma E_n, \\ C &= \xi I_n^S - p\sigma E_n - (1-\nu)\omega I_n^A, \\ D &= \sigma E_a, \\ E &= \omega I_a^A - (1-p)\sigma E_a, \\ F &= \xi I_a^S - p\sigma E_a - (1-\nu)\omega I_a^A. \end{aligned}$$

Next, we compute the Jacobian F from $\mathcal{F}$ given by

$$F = \begin{pmatrix} 0 & \beta_{nn} & \beta_{nn} & 0 & \beta_{na} & \beta_{na} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \beta_{an} & \beta_{an} & 0 & \beta_{aa} & \beta_{aa} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

and the Jacobian V from $\mathcal{V}$ given by

$$V = \begin{pmatrix} \sigma & 0 & 0 & 0 & 0 & 0 \\ G & \omega & 0 & 0 & 0 & 0 \\ H & I & \xi & 0 & 0 & 0 \\ 0 & 0 & 0 & \sigma & 0 & 0 \\ 0 & 0 & 0 & G & \omega & 0 \\ 0 & 0 & 0 & H & I & \xi \end{pmatrix}$$

where

$$G = -(1-p)\sigma, \quad H = -p\sigma, \quad I = -(1-\nu)\omega.$$

We can then compute the inverse of the matrix V to be

$$V^{-1} = \begin{pmatrix} J & 0 & 0 & 0 & 0 & 0 \\ K & L & 0 & 0 & 0 & 0 \\ M & N & O & 0 & 0 & 0 \\ 0 & 0 & 0 & J & 0 & 0 \\ 0 & 0 & 0 & K & L & 0 \\ 0 & 0 & 0 & M & N & O \end{pmatrix}$$

where

$$\begin{aligned} J &= \frac{1}{\sigma}, & M &= \frac{(1-\nu)(1-p)}{\xi} + \frac{p}{\xi}, \\ K &= \frac{1-p}{\omega}, & N &= \frac{1-\nu}{\xi}, \\ L &= \frac{1}{\omega}, & O &= \frac{1}{\xi}. \end{aligned}$$

Using matrices F and V one can then compute the Next Generation Matrix FV^{-1} given by

$$FV^{-1} = \begin{pmatrix} \beta_{nn}P & \beta_{nn}Q & \beta_{nn}O & \beta_{na}P & \beta_{na}Q & \beta_{na}O \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ \beta_{an}P & \beta_{an}Q & \beta_{an}O & \beta_{aa}P & \beta_{aa}Q & \beta_{aa}O \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

where

$$P = H + J, \quad Q = I + K.$$

Note that (i, j) entry of the Next Generation Matrix FV^{-1} is the expected number of secondary infections in compartment i produced by individuals initially in compartment j assuming that the environment seen by the

individual remains homogeneous for the duration of its infection. Also, matrix FV^{-1} is non-negative and therefore has a non-negative eigenvalue. The basic reproduction number can then be computed as $\mathcal{R}_0 = \rho(FV^{-1})$ which is the spectral radius of the matrix. This non-negative eigenvalue is associated with a non-negative eigenvector which represents the distribution of infected individuals that produces the greatest number $\mathcal{R}_0$ of secondary infections per generation. The basic reproduction number $\mathcal{R}_0$ corresponds to the dominant eigenvalue and is given by $\mathcal{R}_0 = \max\{\mathcal{R}_0^n, \mathcal{R}_0^a\}$ where for $i = n, a$,

$$\mathcal{R}_0^i = R_0^{1,i} + R_0^{2,i} + R_0^{3,i}$$

Here,

$$\begin{aligned} R_0^{1,i} &= \beta_{ii} \cdot \frac{p}{\xi} \\ R_0^{2,i} &= \beta_{ii} \cdot \frac{(1-p)}{\omega} \\ R_0^{3,i} &= \beta_{ii} \cdot \frac{(1-\nu)(1-p)}{\xi}. \end{aligned}$$

Note that Theorem 2.1 yields a general result for the basic reproduction number $\mathcal{R}_0$ corresponding to the COVID-19 disease transmission model given by the system of equations (4). Note that R_0 denoted with a superscript n or a corresponds to the basic reproduction number within a group, whereas R_0 without a superscript represents the basic reproduction number for the overall population. In addition, the basic reproduction number for a group, R_0^i is written the sum of three expressions, $R_0^{1,i}$, $R_0^{2,i}$, and $R_0^{3,i}$, for simplicity. Each of these expressions are the product of the transmission rate, the probability of entering an infectious state (symptomatic or asymptomatic), and the mean duration of that infectious state respectively. Thus, each expression represents the average number of secondary cases produced by an infectious individual in a certain infectious state during their infectious period.

3 Numerical Computations

In this section, we implement the implicit behavior mixing model and perform numerical simulations. We implement our model in Python using the Runge-Kutta method for solving systems of ODEs.

The set of parameter values we used for our computations are found in Table 1.

First, we consider the basic reproduction number that was derived in Theorem 2.1, and we assume $N_n = N_a = 5,000,000$ and $c_n = c_a = 0.5$.

In Figures 3 and 4 we show the influence of y and π on R_0^n and R_0^a . Both y and π are related to the transmission

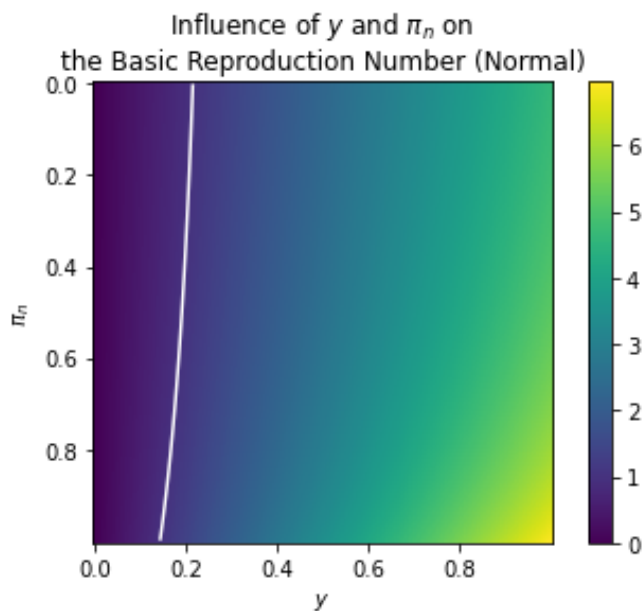


Figure 3: Influence of y and π_n on R_0^n . The colors range from dark blue to yellow to indicate the value of R_0^n . In addition, the white line in the heat plot indicates where $R_0^n = 1$. Note that $R_0^n < 1$ when y is roughly less than 0.2.

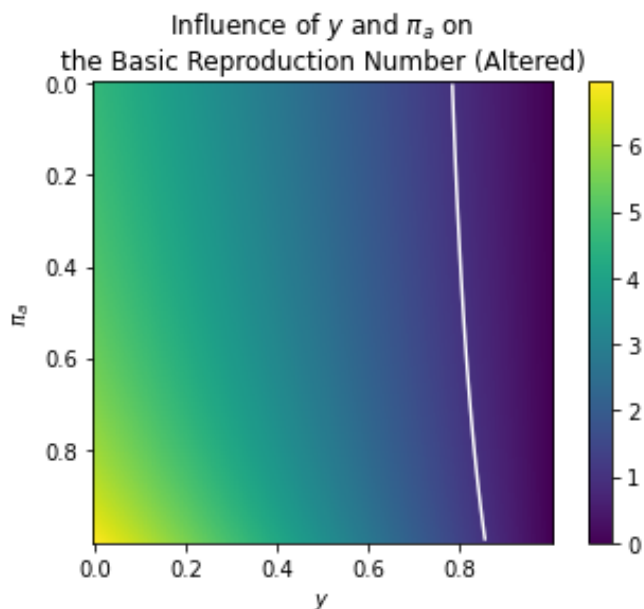


Figure 4: Influence of y and π_a on R_0^a . The colors range from dark blue to yellow to indicate the value of R_0^a . In addition, the white line in the heat plot indicates where $R_0^a = 1$. Note that $R_0^a < 1$ when y is roughly greater than 0.8.

rates, b_{ij} . Varying π and y allows us to see the impact of different mixing patterns and proportion of susceptible individuals with normal behavior on the basic reproduction number, especially since R_0^n and R_0^a are functions of y . Notice that in both figures, π_n values correspond to a greater basic reproduction number for both the normal behavior and the altered behavior group. This is particularly true when $y > 0.2$ for R_0^n and $y < 0.8$ for R_0^a . Recall from Theorem 2.1 that $R_0 = \max\{R_0^n, R_0^a\}$, from which we can assume $R_0 = R_0^n$ for the entire population. Thus, as seen in Figure 3, to keep the overall R_0 below 1, at least roughly 80% of the susceptible subpopulation must have altered behavior, regardless of the amount of mixing. This demonstrates that a higher proportion of susceptible individuals with normal behavior and a higher proportion of inner-group mixing furthers the spread within both groups.

Next, we explore the effects of mixing patterns on the disease dynamics of the two groups by varying π and c . Here, we assume a total initial population, $N(0)$ of 10,000,000. We assume that $S(0) = 9,999,990$, $E(0) = 10$, $y(0) = 0.99$, such that $S_n(0) = S(0) \times y$, $S_a(0) = S(0) \times (1 - y)$, $E_n(0) = 5$, and $E_a(0) = 5$. The remaining compartments are assumed to have an initial population of zero.

In Figure 5, we show the effects of changing π_i on the peak number of infections in the normal behavior and altered behavior group. We let $c_n = 1$ and $c_a = 0.25$. Already, the altered behavior group has a significantly lower peak number of infections (asymptomatic and symptomatic) compared to the normal behavior group, since it has a reduced number of contacts. In fact, at $\pi_n = \pi_a = 0$, the peak number of infected individuals from the normal behavior group consist of roughly 0.22 of the initial total population whereas the peak number of infected individuals from the altered behavior consist of only roughly 0.0016 of the initial total population. Nonetheless, as π_i increases, the peak number of infections decreases for the altered behavior group. At $\pi_a = \pi_n = 1$, the peak number of infections in the altered behavior group is very close to 0% of the total population. Given that members of the altered behavior group have a much lower number of contacts, infected individuals with altered behavior are less likely to spread their disease. Thus, limiting their contacts to just other individuals with altered behavior at $\pi_a = 1$ reduces the chance for susceptible individuals with altered behavior to become infected. On the other hand, susceptible individuals in the normal behavior group are more likely to encounter infected individuals from either group, regardless of their mixing patterns. Hence, increasing π_i has a negligible impact on the peak number of Infected individuals with normal behavior.

We expand on this by also changing c_a in Figures 6,

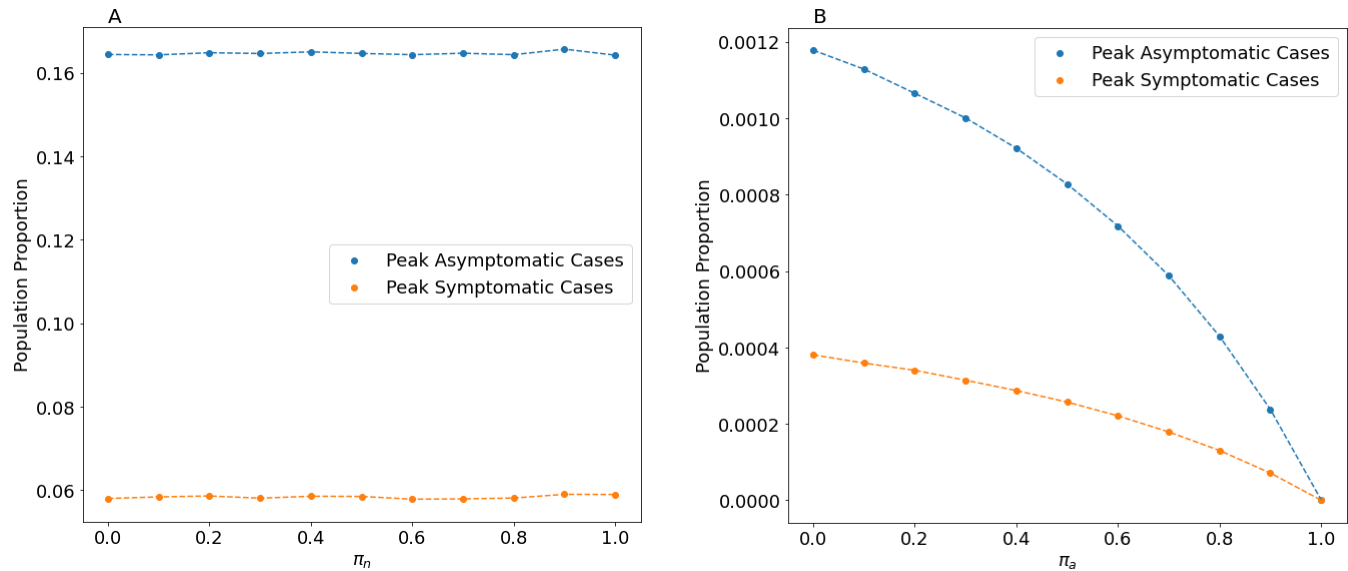


Figure 5: Subplots A and B show the peak proportion of infections with respect to π_i for the normal behavior and altered behavior group, respectively. Asymptomatic cases are represented in blue and symptomatic cases are represented in orange. Note that $c_n = 1$ and $c_a = 0.25$.

7, and 8. As expected, a similar relationship between π_i and the peaks is shown in these figures. In addition, increasing the number of contacts for the altered behavior group also increases the number of infections in that group, especially when $\pi_n = \pi_a = 1$. When $c_a = 0.75$ and $\pi_n = \pi_a = 1$, as seen in Figure 8, the number of peak infections in the altered behavior group is roughly 0.0010 of the total population, which is much higher compared to the number of peak infections for $c_a = 0.25$ and $c_a = 0.5$, as found in Figures 6 and 7. For a higher number of contacts, mixing with other individuals who share the same behavior becomes more riskier. Therefore, this emphasizes the importance of both reducing one's contacts as well as being careful with who one interacts with.

4 Dashboard as a Graphical User Interface

In this section, we show a dashboard we created for our model. For this dashboard, we used a framework for creating web-based applications called Dash, which is made by Plotly. Our dashboard gives users the ability to interact with the model and change various parameter values. This dashboard will not only help share our work, but may also aid in informing public decisions. In Figure 9, we show the topmost portion of our dashboard, which contains three graphs corresponding to the normal behavior group, altered behavior group, and the remaining hospitalized, recovered, and dead sub-populations. Users

may hover over a point on the graph to receive information about the time and value of the plot. In addition, the user can isolate certain plots by clicking in the legend to the right of each graph.

In Figure 10, there is an image of another portion of the dashboard directly below the graphs in Figure 9. Here, users may change the initial conditions by typing in input boxes. They may also drag sliders corresponding to c_n , c_a , π_n , and π_a . As users change these values, the graphs alter immediately to reflect these changes. Similarly, Figure 11 shows the bottom-most portion of the dashboard, where there are more sliders and input boxes for the other parameters values, including the number of days and the number of beds.

The dashboard is currently available here: <https://covid-19-mixing-dashboard.herokuapp.com/>. In the future, this dashboard may be improved to include more features as we continue our work.

5 Conclusions and Future Work

In this work, we considered a novel epidemiological model that includes two groups with different behaviors: normal and altered. We also derived the basic reproduction number using the Next Generation Matrix. Moreover, we performed numerical simulations to study the effects of behavior and mixing patterns. We demonstrated how having a higher proportion of susceptibles with normal behavior and a higher proportion of inner-group mixing increases the basic reproduction number for the total pop-

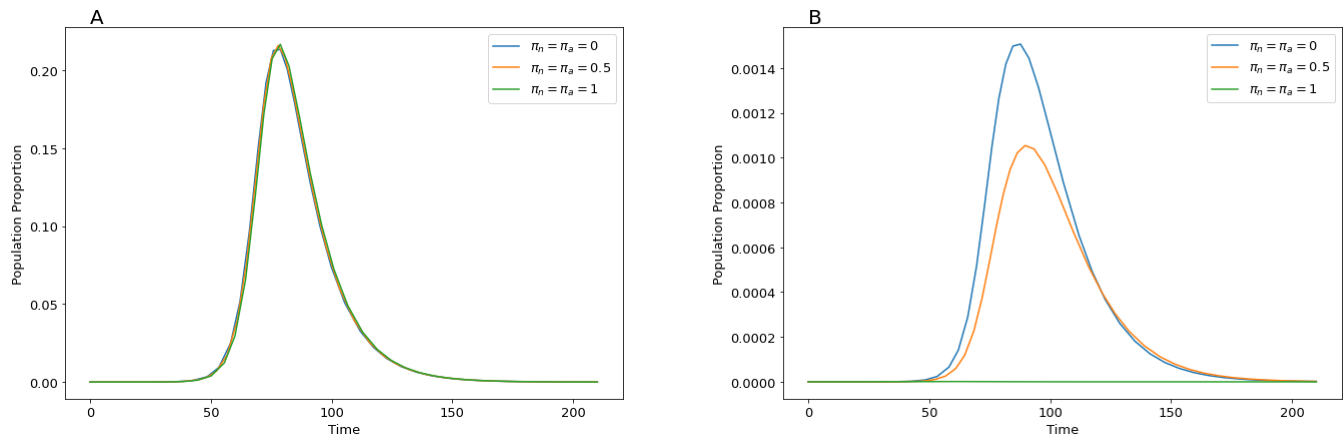


Figure 6: Subplots A and B correspond to the total proportion of infected individuals (asymptomatic and symptomatic) in the normal and altered behavior groups, respectively. The blue curves correspond to $\pi_n = \pi_a = 0$ (proportionate mixing), the orange curves correspond to $\pi_n = \pi_a = 0.5$ (preferred mixing), and the green curves correspond to $\pi_n = \pi_a = 1$ (like-with-like mixing). In this figure, $c_n = 1$ and $c_a = 0.25$. In Subplot A, the peak number of infections are roughly 20% of the total population for all tested π_i values. In Subplot B, the peak number of infections are close to 0.15%, 0.11%, and 0.00% of the population for $\pi_i = 0$, $\pi_i = 0.5$, and $\pi_i = 1$, respectively.

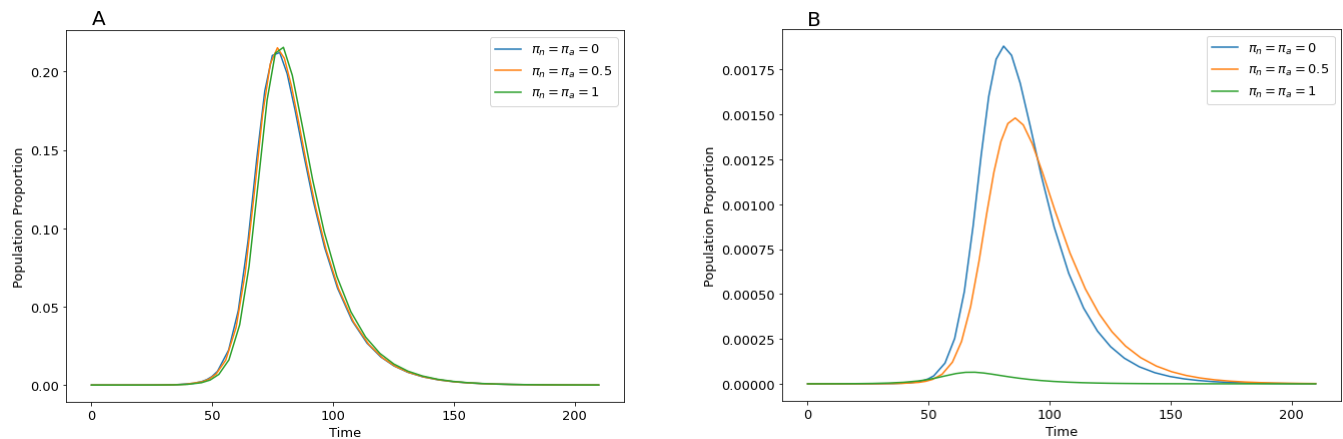


Figure 7: Subplots A and B correspond to the total proportion of infected individuals (asymptomatic and symptomatic) in the normal and altered behavior groups, respectively. The blue curves correspond to $\pi_n = \pi_a = 0$ (proportionate mixing), the orange curves correspond to $\pi_n = \pi_a = 0.5$ (preferred mixing), and the green curves correspond to $\pi_n = \pi_a = 1$ (like-with-like mixing). In this figure, $c_n = 1$ and $c_a = 0.5$. In Subplot A, the peak number of infections are roughly 20% of the total population for all tested π_i values. In Subplot B, the peak number of infections are close to 0.18%, 0.15%, and 0.00% of the population for $\pi_i = 0$, $\pi_i = 0.5$, and $\pi_i = 1$, respectively.

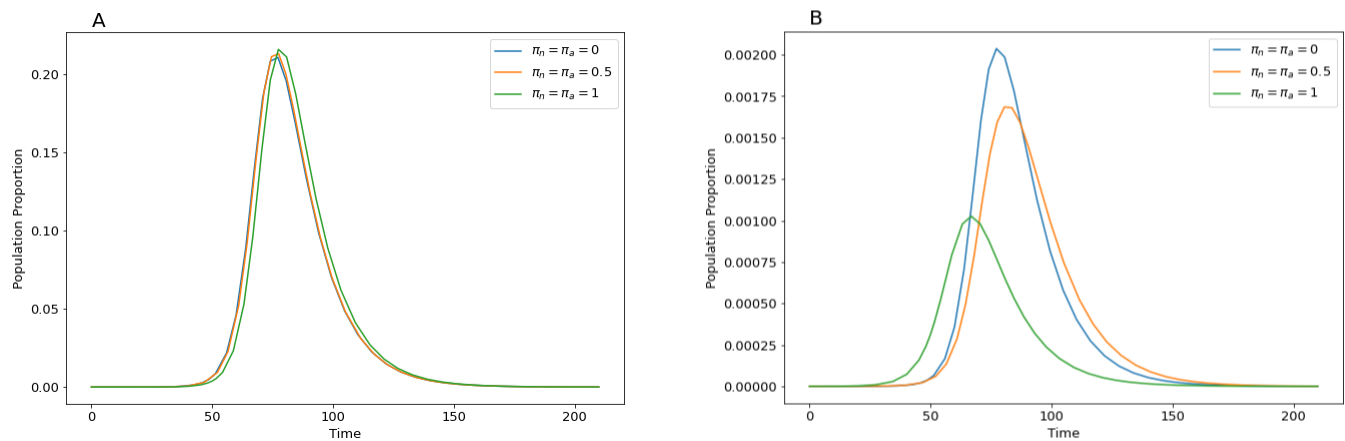


Figure 8: Subplots A and B correspond to the total proportion of Infected individuals (asymptomatic and symptomatic) in the normal and altered behavior groups, respectively. The blue curves correspond to $\pi_n = \pi_a = 0$ (proportionate mixing), the orange curves correspond to $\pi_n = \pi_a = 0.5$ (preferred mixing), and the green curves correspond to $\pi_n = \pi_a = 1$ (like-with-like mixing). In this figure, $c_n = 1$ and $c_a = 0.75$. In Subplot A, the peak number of infections are roughly 20% of the total population for all tested π_i values. In Subplot B, the peak number of infections are close to 0.20%, 0.17%, and 0.10% of the population for $\pi_i = 0$, $\pi_i = 0.5$, and $\pi_i = 1$, respectively.

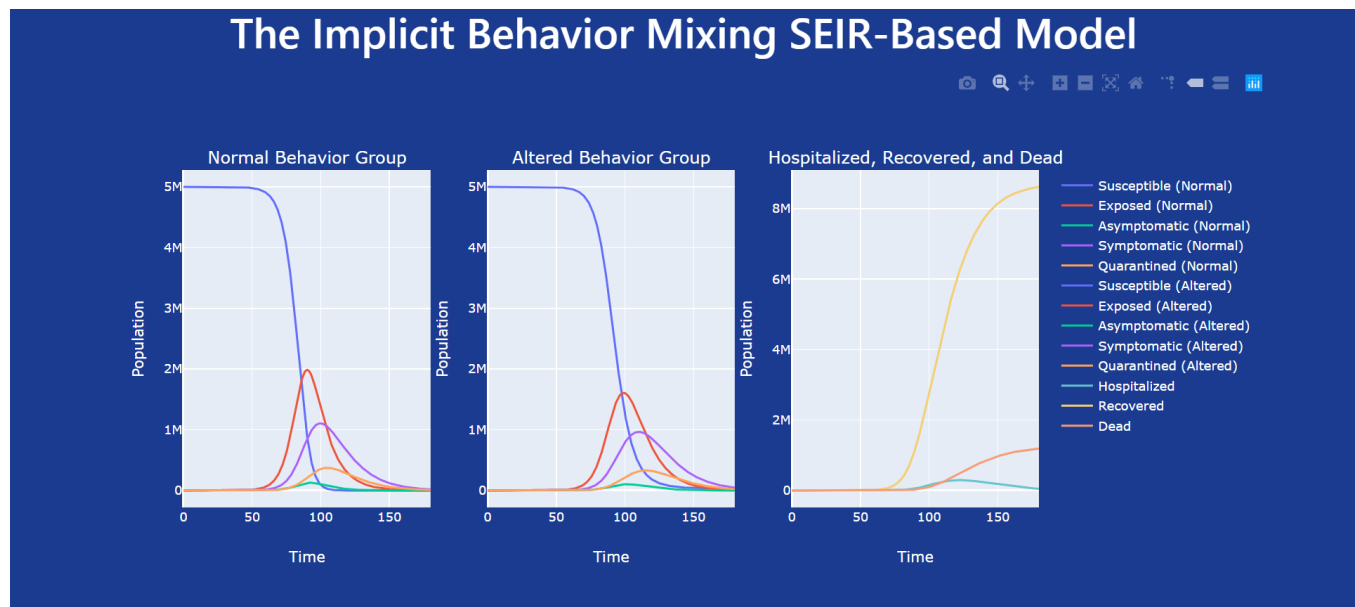


Figure 9: Three graphs found in top portion of Dashboard.

Initial Conditions

Susceptible (Normal Behavior):	5000000	Susceptible (Altered Behavior):	5000000	Hospitalized:	0
Exposed (Normal Behavior):	5	Exposed (Altered Behavior):	5	Recovered:	0
Asymptomatic (Normal Behavior):	0	Asymptomatic (Altered Behavior):	0	Dead:	0
Symptomatic (Normal Behavior):	0	Symptomatic (Altered Behavior):	0		
Quarantine (Normal Behavior):	0	Quarantine (Altered Behavior):	0		

Behavior Parameters

Proportion of Inner Group Mixing (Normal): 0.50

Number of contacts (Normal): 1.00

Proportion of Inner Group Mixing (Altered): 0.50

Number of contacts (Altered): 0.50

Figure 10: Portion of dashboard with input boxes for initial values and sliders for behavior-related parameters.

Other Parameters

Rate of Incubation: 0.08

Rate at which Asymptomatic Individuals Develop Symptoms or Recover: 0.50

Rate at which Hospitalized Individuals Recover: 0.08

Lethality Rate: 0.04

Fraction of Hospitalized individuals out of Quarantined individuals: 0.19

Rate at which Symptomatic Individuals Quarantine: 0.07

Rate at which Quarantined Individuals Hospitalize or Recover: 0.20

Rate at which Hospitalized Individuals Die: 0.07

Fraction of Symptomatic individuals out of Exposed individuals: 0.60

Fraction of Recovered individuals out of Asymptomatic individuals: 0.80

Number of Days:

Number of Beds:

Figure 11: Portion of dashboard for input boxes and sliders for parameter values.

ulation. Furthermore, we showed that mixing patterns had little effect on the normal behavior group. On the contrary, greater proportions of inner-group mixing and a lower number of contacts improved the disease dynamics of COVID-19 within the altered behavior group. In fact, out of the three types of mixing, like-with-like mixing resulted in the lowest maximum number of infected cases. Furthermore, in this paper, we present an interactive dashboard for our model. In the future, we may expand our model to include risk perception and irrational behavior. We will also incorporate stochasticity, especially in our behavior terms, to explore the influence of randomness on our model. Moreover, in the future, we will use our model to study the effects of COVID-19 on other public health concerns.

Appendix: Literate Programming

Literate programming is a style of documenting computer code developed by Donald E. Knuth. The goal of literate programming is to produce a program that is understandable to the reader by weaving text to explain the code [9]. In this section, we use literate programming to demonstrate how we develop the code to implement our model.

First, we import specific packages related to our implementation, specifically `numpy` and `scipy`, which are commonly used Python packages for data and mathematical analysis. For our work, `numpy` is used to manage and manipulate arrays and `scipy` is used to implement the Runge-Kutta method.

```
import numpy as np
from scipy import integrate
```

Next, we define certain parameters for our model from system (4).

```
ti, tf = 0, 210 #initial time, final time
```

```
sigma = 1/6
omega = 1/14
gamma = 1/5
alphaR = 1/12
alphaD = 1/14
```

```
p = 0.6
q = 0.19
v = 0.8
x_hat = 0.04
xi = 0.5
```

```
pi_n = 0
pi_a = 0
c_n = 0.8
```

```
c_a = 0.5

if pi_n == 1:
    f_n = 0
else:
    f_n = (1-pi_n)*c_n*N_n/
        ((1-pi_n)*c_n*N_n + (1-pi_a)*c_a*N_a)
if pi_a == 1:
    f_a = 0
else:
    f_a = (1-pi_a)*c_a*N_a/
        ((1-pi_n)*c_n*N_n + (1-pi_a)*c_a*N_a)

f_nn = pi_n + (1-pi_n) * f_n
f_na = (1-pi_n) * f_a
f_an = (1-pi_a)*f_n
f_aa = pi_a + (1-pi_a)*f_a

b_nn = f_nn * c_n * y
b_na = f_na * c_n * y
b_an = f_an * c_a * (1-y)
b_aa = f_aa * c_a * (1-y)

b_n = b_an - b_nn
b_a = b_aa - b_na
```

We also define our initial conditions for the simulation, which are set inside a `numpy` array called `compartments`. This array will be treated as a vector and used to initialize our integrator.

```
S = 9_999_990
y = 0.99
```

```
S_n = S*y #susceptible (normal)
E_n = 5 #exposed (normal)
Ia_n = 0 #asymptomatic (normal)
Is_n = 0 #symptomatic (normal)
Q_n = 0 #quarantined (normal)
```

```
S_a = S*(1-y) #susceptible (altered)
E_a = 5 #exposed (altered)
Ia_a = 0 #asymptomatic (altered)
Is_a = 0 #symptomatic (altered)
Q_a = 0 #quarantined (altered)
```

```
H = 0 #hospitalized
R = 0 #recovered
D = 0 #dead
```

```
compartments = np.array([S_n, E_n, Ia_n, Is_n,
                        Q_n, S_a, E_a, Ia_a, Is_a, Q_a,
                        H, R, D, y])
                        #vector of compartment values
```

Afterwards, we write the system of equations (4) as a function called `behavior_mixing`, which takes in time t

and a vector of values corresponding to each compartment. For simplicity, we define each element within the vector, so we can write the equations for our model in familiar terms.

```
def behavior_mixing(t, vector):
    """Differential Equations for the
    Social Behaviors Model"""
```

```
    S_n = vector[0]
    E_n = vector[1]
    Ia_n = vector[2]
    Is_n = vector[3]
    Q_n = vector[4]
    S_a = vector[5]
    E_a = vector[6]
    Ia_a = vector[7]
    Is_a = vector[8]
    Q_a = vector[9]
    H = vector[10]
    R = vector[11]
    D = vector[12]
    y = vector[13]
```

```
    S = S_n + S_a
    Ia = Ia_n + Ia_a
    Is = Is_n + Is_a
    E = E_n + E_a
    Q = Q_n + Q_a
```

Since x is a function of time t , we must also define $x(t)$ within **behavior_mixing**.

```
def x(t):
    x_hat = 0.04
    B = 2700

    if H <= B:
        return (x_hat)
    else:
        return ((x_hat*B+H-B)/H)
```

We write out the system of differential equations (4) and end **behavior_mixing** with a statement that returns these values as an array.

```
dS_n = -(beta_nn * S * (Ia_n + Is_n)/N_n
        + beta_na * S * (Ia_a + Is_a)/N_a)
dE_n = -dS_n - sigma*E_n
dIa_n = (1-p)*sigma*E_n - omega*Ia_n
dIs_n = p*sigma*E_n + (1-v)*omega*Ia_n
        - xi*Is_n
dQ_n = xi*Is_n - gamma*Q_n

dS_a = -(beta_an * S * (Ia_n + Is_n)/N_n
        + beta_aa * S * (Ia_a + Is_a)/N_a)
dE_a = -dS_a - sigma*E_a
dIa_a = (1-p)*sigma*E_a - omega*Ia_a
```

```
dIs_a = p*sigma*E_a + (1-v)*omega*Ia_a
        - xi*Is_a
dQ_a = xi*Is_a - gamma*Q_a
```

```
dH = q*gamma*Q - (((1-x(t))*alphaR)
        + (x(t)*alphaD))*H
dR = v*omega*Ia + (1-q)*gamma*Q
        + (1-x(t))*alphaR*H
dD = x(t)*alphaD*H
```

```
dy = y*(1-y)*(b_n*(Ia_n + Is_n)/N_n
        + b_a*(Ia_a + Is_a)/N_a)
```

```
return (np.array([dS_n, dE_n, dIa_n, dIs_n,
                  dQ_n, dS_a, dE_a, dIa_a,
                  dIs_a, dQ_a, dH, dR,
                  dD, dy]))
```

Finally, we create a solver function to numerically solve our model using the Runge-Kutta method. We define this function **ode_solver** to take in an initial time value, **ti**, final time value, **tf**, and the initial conditions for the model. Ultimately, at the end of **ode_solver**, we want to return an array of time values and an array of compartment values. Within **ode_solver**, we create a object using SciPy's **integrate.RK45** class called **solver**. The **solver** object accepts various parameters, including a system of equations, time bounds, and initial conditions. Thus, we input **behavior_mixing**, **ti**, **tf**, **initial_values**.

```
def ode_solver(ti, tf, initial_values):
    solver = integrate.RK45(behavior_mixing, ti,
                            initial_values, tf)
```

We create two empty arrays for time (**t_values**) and Compartmental values (**c_values**). The **t_values** array contains the times and the **c_values** values for each sub-population at each time step. In order to fill these arrays, we create a while loop to perform a series of integration steps. The while loop runs as long as the integration is incomplete and terminates when the solver is complete. To perform one integration step, we write **solver.step()**. Once this step is complete, we add our new time value **solver.t** and new compartment values **solver.y** to **t_values** and **c_values**, respectively. However, we want the array of compartmental values to be two-dimensional, so that the number of rows correspond to the number of integration steps and the number of columns correspond to the number of compartments, 14. We want a two-dimensional array because it would make it easier to manipulate it later for generating graphs. So, we count the number of integration steps with the variable **steps**. Each iteration of the while loop increases **steps** by 1. Thus, after the while loop, we can reshape **c_values** with the number of integration steps and 14. Lastly, we return **t_values** and **c_values**.

```
t_values = np.array([])
c_values = np.array([])
steps = 0
```

```

while solver != 'finished':
    solver.step()
    t_values = np.append(t_values, solver.t)
    c_values =
    np.append(c_values, solver.y)
    steps+=1
    if solver.status == 'finished':
        break
c_values=c_values.reshape(steps, 14)
return (t_values, c_values)

```

Now, whenever we call `ode_solver`, we can have an array of time values and solutions, which we can analyze. In fact, for the figures discussed in Section 3, we used `Matplotlib` package to create graphs.

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