MODELING SARS-CoV-2 SPREAD WITH DYNAMIC ISOLATION

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Abstract. Background: The SARS-CoV-2 pandemic is spreading with a greater intensity across the globe. The synchrony of public health interventions and epidemic waves signify the importance of evaluation of the underline interventions.

Method: We developed a mathematical model to present the transmission dynamics of SARS-CoV-2 and to analyze the impact of key nonpharmaceutical interventions such as isolation and screening program on the disease outcomes to the people of New Jersey, USA. We introduced a dynamic isolation of susceptible population with a constant (imposed) and infection oriented interventions. Epidemiological and demographic data are used to estimate the model parameters. The baseline case was explored further to showcase several critical and predictive scenarios.

Results and analysis: The model simulations are in good agreement with the infection data for the period of 5 March 2020 to 31 January 2021. Dynamic isolation and screening program are found to be potential measures that can alter the course of epidemic. A 7% increase in isolation rate may result in a 31% reduction of epidemic peak whereas a 3 times increase in screening rate may reduce the epidemic peak by 35%. The model predicts that nearly 9.7% to 12% of the total population of New Jersey may become infected within the middle of July 2021 along with 24.6 to 27.3 thousand cumulative deaths. Within a wide spectrum of probable scenarios, there is a possibility of third wave.

Conclusion: Our findings could be informative to the public health community to contain the pandemic in the case of economy reopening under a limited or no vaccine coverage. Additional epidemic waves can be avoided by appropriate screening and isolation plans.

1. Introduction

Public health communities are facing unprecedented challenges to control the SARS-CoV-2 pandemic, largely, due to the limitation of effective vaccines and lack of therapeutic treatment. In the absence of vaccines, nonpharmaceutical interventions such as screening, isolation, social distancing, quarantine, maintaining public hygiene (wearing mask and washing hands frequently) and contact tracing are in place to curtail the pandemic [7]. Although these measurements are highly potential to eliminate a pandemic, they are not socioeconomically friendly and may become impracticable for a long run. A lack of proper implementation of these interventions may turn the effort into a futile exercise as it has been seen from the current pandemic scenarios of SARS-CoV-2 in different countries [13].

Mathematical models have been used to assess the effectiveness of the control measures and to guide the public health policy. Models help to understand the dynamics of infectious diseases under the given circumstances and provide valuable information about how to control the disease. The impact of nonpharmaceutical interventions against the spread of SARS-CoV-2 can be seen in numerous studies [19 23 26]. Some studies showed that mitigation, plans and preparedness should be organized and...
deployed globally to prevent the progression of transmission rate, otherwise the basic reproduction number could reach up higher \[16, 34, 43, 44\]. A study on the basis of diagnosis and treatment resources indicated that a delayed diagnosis is somehow responsible for the increased transmission risk \[31\] whereas improvement of detection rate can rapidly and significantly lessen the death rate \[40\]. An investigation suggests that besides the medical facilities, the effectiveness of early media coverage may increase the public awareness \[45\]. A research focusing on the influenza type patients considered the seasonal pattern of SARS-CoV-2 into account and revealed that enhancement of mass influenza vaccination and public health interventions have positive impacts to contain the outbreak \[20\].

Studies found that implementation of quarantine strategies \[27\] and other important measures such as setting up complete lockdown with isolation, confirming media coverage and ensuring public hygiene can significantly mitigate the severity of the outbreak \[22\], more specifically, implementation of lockdown and centralized quarantine policy play a significant role in reducing the infection \[35\]. Recent models also pointed out some of the important control policies, for example, the effect of emergency and healthy sanitary measures \[1\], the impact of social distancing \[10, 13\], the outcome of estimating intensive care unit \[25\] and providing adequate medical resources like protective clothing, health workforce and necessary medicines \[39\] in order to reduce the community transmissions of SARS-CoV-2 infection. Besides nonpharmaceutical interventions, vaccination process is in progress and underway \[41\]. The current vaccination rates can minimize the infection but control policies also need to go on \[30\]. Moreover, strategies for optimum vaccine allocation depend on numerous factors \[11\].

In order to complement other studies, we would like to see the effect of population behaviour on the pandemic. An important aspect of the pandemic is the behaviour of the population due to the fear of severe consequences such as death or long term sickness. In general, the behaviour changes with the reported cases and incidence. People may go to self isolation and return from there subject to the intensity of these numbers. In contrast, an economy reopening program may increase the new infections through the elevated contacts. To contain the infection in a circumstance of the elevated contacts, the screening program may help to reduce infections (as it detects the asymptomatic cases and puts them in quarantine \[12\]) and can significantly mitigate the outbreak besides other protective measures \[4\]. We aim to identify the interplay of dynamic isolation, screening program and infection through a mathematical model.

To properly explore the effects of screening program and dynamic isolation, we develop a SARS-CoV-2 model that takes the Kermack-McKendrick form \[15\] with dynamic population movement. We use a SARS-CoV-2 data set of New Jersey, USA (cumulative reported deaths and cumulative reported cases) \[42\] to parameterize and validate the model. The remaining part of the paper is organized as follows: a mathematical model is developed in Section 2. Section 3 is dedicated to data collection, parameter estimation and data fitting. Section 4 presents the results and model simulations. Finally, Section 5 discusses the findings, consequences and uncertainties.

2. Model

This section is dedicated to develop a mathematical model for capturing the dynamics of SARS-CoV-2 infection. We also present an elementary analysis of the model and derive useful thresholds.

2.1. Model formulation. We consider \(N(t)\) as the total population and divide it into seven different classes (compartments): \(S(t)\), susceptible; \(A(t)\), asymptomatic (undetected); \(A_q(t)\), quarantined asymptomatic (detected through screening); \(S_o(t)\), isolated; \(I(t)\), infected (symptomatic but undetected); \(I_q(t)\), quarantined (symptomatic and detected); and \(R(t)\), recovered. Infection is spread by the individuals from \(A, A_q, I\) and \(I_q\) classes with different transmission rates. The susceptible population become infected due to effective contacts with the asymptomatic (both undetected and detected) and
the symptomatic individuals (infected and quarantined) who carry the pathogen. As a result, suscepti-
ble individuals (S), at first, move to the asymptomatic stage (A) with an effective transmission rate (β).
The individuals in the asymptomatic stage (A) are clinically silent and thus remain undetected unless
tested through a screening program. Individuals from the undetected asymptomatic stage may develop
symptoms and become fully infectious (undetected) in course of time, thus move to the infected stage
(I) at the rate of η1. A portion of the asymptomatic individuals undergo diagnosis through screening
program and become quarantined asymptomatic (Aq) with a rate σ. Individuals move from Aq to Iq
by disease progression at a rate η2 and from I to Iq through diagnosis at a rate τ. Due to immu-
nity or treatment, individuals who are in stages A, Aq, I and Iq may get recovery from the infection
with the recovery rates γ1, γ2, γ3 and γ4, respectively. We assume that a portion of total population
remains isolated (So) due to awareness or fear. The isolation continues with variation throughout the
observation period with a dynamic rate α+ subject to the number of reported cases. In other words,
individuals from susceptible class may go for isolation at any time due to fear or due to the regulations
(for example, a lockdown).

The isolation rate (α+) and the transmission rate (β) are considered to be nonlinear with respect to
the reported cases. The isolation rate is an increasing function of the reported cases and in contrast,
the effective transmission rate is a decreasing function of the reported cases. In particular, we consider
\[ α_+ = a_+ \exp(ψ_1 ζ), \quad β = β_0 \exp(-ψ_2 ζ) \]
where ζ is the daily reported cases, a_+ and β_0 are the initial values of isolation rate and effective
transmission rate and ψ_i : i = 1, 2 are constants.

We assume that isolated individuals are unlikely to get infection unless they move back to S class
with a rate of α−. Our assumptions also include that (i) there is no immigration (population size
does not change significantly over the observation period), (ii) vaccination is ignored (since vaccination
campaign is still in progress and underway), (iii) recovery gives a permanent immunity, which means,
the possibility of becoming second time susceptible after getting recovery from the disease is omitted
based on prior evidence [5, 18], (iv) death occurs only in I and Iq compartments due to the disease
with rates δ1 and δ2, respectively; other deaths are ignored and (v) quarantined individuals have very
little contribution to the reported cases (that is, ε1, ε2 << ε3).

The population movement discussed above is presented in Figure 1 and the descriptions of variables
and parameters are summarized in Tables 1 and 2, respectively. Considering the above assumptions, the
transmission dynamics of SARS-CoV-2 can be modeled by the following system of ordinary differential equations:

\[
\begin{align*}
\dot{S} &= -β(A + ε_1 A_q + ε_3 I + ε_2 I_q)S - α_+ S + α_S o \\
\dot{A} &= β(A + ε_1 A_q + ε_3 I + ε_2 I_q)S - (η_1 + σ + γ_1)A \\
\dot{A}_q &= σ A - (γ_2 + η_2) A_q \\
\dot{S}_o &= α_+ S - α_S o \\
\dot{I} &= η_1 A - (δ_1 + τ + γ_3)I \\
\dot{I}_q &= τ I + η_2 A_q - (δ_2 + γ_4) I_q \\
\dot{R} &= γ_1 A + γ_2 A_q + γ_3 I + γ_4 I_q
\end{align*}
\]

where \( N = S + A + A_q + S_o + I + I_q + R \).

To track the SARS-CoV-2 related deaths and cases (requisite for adjusting model (2.1) with realistic
data for predicting and measuring the public health impact of the disease), we define two state variables:
\( C_{rd} \), cumulative reported deaths; and \( C_{rc} \), cumulative reported cases. We assume that the data that
Table 1. Variables used in model (2.1).

| Variable | Description                        |
|----------|-------------------------------------|
| S        | Number of susceptible individuals   |
| A        | Number of asymptomatic individuals  |
| A_q      | Number of quarantined asymptomatic individuals |
| S_o      | Number of isolated individuals      |
| I        | Number of infected individuals      |
| I_q      | Number of quarantined individuals   |
| R        | Number of recovered individuals     |
| C_{rd}   | Cumulative reported deaths          |
| C_{rc}   | Cumulative reported cases           |
| N        | Total population                    |

Table 2. Parameters used in model (2.1).

| Parameter | Description                                                      |
|-----------|------------------------------------------------------------------|
| \beta_0   | Initial value of effective transmission rate                    |
| \epsilon_1 | Transmission rate for A_q                                      |
| \epsilon_2 | Transmission rate for I_q                                      |
| \epsilon_3 | Transmission rate for I                                        |
| \sigma_1  | Initial value of isolation rate                                 |
| \sigma_2  | Rate at which isolated individuals move back to S               |
| \sigma   | Screening program rate                                          |
| \eta_1    | Incubation rate                                                 |
| \eta_2    | Rate at which quarantined asymptomatic individuals move to I_q |
| \tau      | Transition rate from I to I_q                                   |
| \gamma_1  | Recovery rate of A                                             |
| \gamma_2  | Recovery rate of A_q                                           |
| \gamma_3  | Recovery rate of I                                             |
| \gamma_4  | Recovery rate of I_q                                           |
| \delta_1  | Disease induced death rate in I                                 |
| \delta_2  | Disease induced death rate in I_q                               |
| \psi_i    | Adjustment coefficients (i = 1, 2)                              |

are publicly available are based on the detected cases [42]. Our model (2.1) comprises with two detected compartments: \( A_q \) and \( I_q \). Thus, the dynamics of \( C_{rd} \) and \( C_{rc} \) can be obtained from model (2.1) as follows:

\[
\begin{align*}
\dot{C}_{rd} &= \delta_2 I_q, \\
\dot{C}_{rc} &= \sigma A + \tau I.
\end{align*}
\]
2.2. Well-posedness. The model (2.1) is a system of seven coupled equations. Following [28, 29], it can be shown that the state variables presented in the model yield non-negative values for \( t \geq 0 \) provided that the initial values stand non-negative. It also follows from model (2.1) that \( \dot{S}(t) + \dot{A}(t) + A_q(t) + \dot{I}(t) + \dot{I}_q(t) + \dot{R}(t) = -\delta_1 I - \delta_2 I_q \). That is, in the absence of infection, \( N = 0 \) (which means, \( N(t) \) is constant).

2.3. Basic reproduction number. The basic reproduction number is a threshold that determines whether an epidemic is in increasing or decreasing trends. It is usually denoted by the symbol \( \mathcal{R}_o \). If \( \mathcal{R}_o \) is larger than unity, then the number of reported cases remain in upward direction. For our model (2.1), there exists a disease free equilibrium point denoted by \( \xi_o = (\hat{S}, 0, 0, \hat{S}_o, 0, 0, 0) \) where \( \hat{S} = \frac{a_2}{a_1} \).

Using the next generation matrix approach [37], we can obtain the basic reproduction number (\( \mathcal{R}_o \)). It involves two major components, the new infection matrix (\( F \)) and the transfer matrix (\( V \)) which, for our model (2.1) at \( \xi_o \), are given by

\[
F = \begin{pmatrix}
\beta_o \hat{S} & \beta_o \epsilon_1 \hat{S} & \beta_o \epsilon_3 \hat{S} & \beta_o \epsilon_2 \hat{S} \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
\end{pmatrix}
\]

\[
V = \begin{pmatrix}
\eta_1 + \sigma + \gamma_1 & 0 & 0 & 0 \\
-\sigma & \gamma_2 + \eta_2 & 0 & 0 \\
-\eta_1 & 0 & \delta_1 + \tau + \gamma_3 & 0 \\
0 & -\eta_2 & -\tau & \delta_2 + \gamma_4 \\
\end{pmatrix}
\]

Then \( \mathcal{R}_o \) can be written as follows:

\[
\mathcal{R}_o = \frac{\beta_o \hat{S}}{c_1} + \frac{\beta_o \sigma \epsilon_1}{c_1 c_3} + \frac{\beta_o \eta_1 \epsilon_3}{c_1 c_2} + \frac{\beta_o \epsilon_2 (\tau \eta_1 c_3 + \sigma \eta_2 c_2)}{c_1 c_2 c_3 c_4}
\]  

(2.3)

or

\[
\mathcal{R}_o = \left( \frac{\beta_o}{c_1} + \frac{\beta_o \sigma \epsilon_1}{c_1 c_3} + \frac{\beta_o \eta_1 \epsilon_3}{c_1 c_2} + \frac{\beta_o \epsilon_2 (\tau \eta_1 c_3 + \sigma \eta_2 c_2)}{c_1 c_2 c_3 c_4} \right) \frac{a_- \hat{S}}{a_+}
\]  

(2.4)

where

\[ c_1 = \sigma + \gamma_1 + \eta_1, \quad c_2 = \tau + \gamma_3 + \delta_1, \quad c_3 = \gamma_2 + \eta_2 \quad \text{and} \quad c_4 = \gamma_4 + \delta_2. \]

Specifically from (2.4), we have the following:

\[
\mathcal{R}_o = \mathcal{R}_o^A + \mathcal{R}_o^A_v + \mathcal{R}_o^I + \mathcal{R}_o^I_q
\]  

(2.5)

The four terms on the right hand side of (2.5) demonstrate the transmission routes from asymptomatic (A) to susceptible (S), quarantined asymptomatic (A_q) to susceptible (S), infected (I) to susceptible (S) and quarantined (I_q) to susceptible (S), respectively. All these four modes of transmission contribute to \( \mathcal{R}_o \) and are collectively responsible to shape the total infection risk of SARS-CoV-2.

2.4. Final size. The final size (\( F \)) is a critical indicator for a pandemic. It shows the overall impact of the pandemic on the population. Thus, one would be interested to reduce the final size by controlling the model parameters. For a nonlinear model, the final size may not be expressed explicitly. In order to derive the final size of the pandemic, first we need to have the final size equation by introducing the number of susceptible individuals right at the end of the outbreak. We follow the method discussed in [3] to find the final size equation. We consider that \( S_\infty \) shapes the end of the outbreak which is the limit of \( S(t) \) as \( t \to \infty \). For such, let \( x \in \mathbb{R}^n \) be the set of infected components, \( y \in \mathbb{R}^m \) the set of susceptible component and \( z \in \mathbb{R}^k \) the set of isolated and recovered components. Thus from model (2.1), we have \( x(t) = (A(t), A_q(t), I(t), I_q(t))^T, y(t) = S(t) \) and \( z(t) = (S_o(t), R(t))^T \). Let \( b \) be
the row vector representing the horizontal transmission. Therefore, we have \( m = 1, n = 4, k = 2 \) and \( b = (1, \epsilon_1, \epsilon_3, \epsilon_2) \). Then, we obtain the following result:

**Theorem 2.1.** The final size equation of model (2.1) at \( \xi_o \) is given by

\[
\ln \left( \frac{y_o}{y_\infty} \right) = \Re_o \frac{y_o - y_\infty}{y_o} + \beta_o b V^{-1} x_o
\]  

(2.6)

Equivalently, we have

\[
\ln \left( \frac{\bar{S}_\infty}{\bar{S}} \right) = \Re_o \frac{\bar{S} - S_\infty}{\bar{S}} + \beta_o (A(0)g_1 + A_q(0)g_2 + I(0)g_3 + I_q(0)g_4)
\]  

(2.7)

where

\[
g_1 = \frac{1}{c_1} + \frac{\epsilon_1}{c_1 c_3} + \frac{\epsilon_3 \eta_1}{c_1 c_2} + \frac{(\tau \epsilon_3 \eta_1 + \sigma \epsilon_2 \eta_2)}{c_1 c_2 c_3 c_4},

g_2 = \frac{\epsilon_1}{c_3} + \frac{\epsilon_2 \eta_2}{c_3 c_4},

g_3 = \frac{\tau \epsilon_2}{c_2 c_4} + \frac{\epsilon_3}{c_2},

g_4 = \frac{\epsilon_2}{c_4}.
\]

Now following [24], the final size (\( F \)) of the pandemic (which is equal to the final size of the susceptible population (\( F_S \))) is the total number of individuals (either dead or recovered) who have experienced the SARS-CoV-2 infection. Therefore, we have

\[
F = F_S
\]  

(2.8)

where

\[
F_S = \bar{S} - S_\infty \text{ or } F_S = \frac{\alpha - \bar{S}_o}{\alpha} - S_\infty.
\]

Equation (2.8) can be used to control the final size of the pandemic by manipulating the control parameters. Details will be explored in Section 4.

### 3. Data and parameter estimation

3.1. **Data.** SARS-CoV-2 data set of New Jersey [42] is used to validate and parameterize the model (2.1). In particular, we extracted cumulative reported deaths and cumulative reported cases from the data set occurred in New Jersey from 5 March 2020 to 31 January 2021.

3.2. **Initial conditions and parameter values.** We consider the total population of New Jersey [36] as the initial population size, i.e., \( N(0) = 8882190 \). We set \( S = 6749674 \) and accordingly \( S_o = 2131726 \). From data fitting, we found \( A(0) = 788 \). Considering the reported cases of 5 March 2020, \( I(0) = 2 \) and \( R(0) = 0 \). At the beginning of the observation period, we consider that no infected individuals were in quarantine and therefore \( A_q(0) = 0 \) and \( I_q(0) = 0 \). The range of incubation period varies from 2 to 14 days [44]. Considering the mean incubation period of 7 days, we obtain \( \eta_1 = 1/7 \). Study shows that within 7 days (a median time) from the first symptom, patients move to hospital admission or quarantine [38], which yields \( \eta_2 = 1/7 \). On the other hand, it may take about two weeks to recover from the infections [31, 32, 44] and thus we obtain \( \gamma_1 = \gamma_2 = \gamma_3 = \gamma_4 = 1/14 \). It is also reported that the waiting time of the infected individuals for timely diagnosis ranges between 1 to 5 days. That means, the infected individuals move to quarantine within 1 to 5 days [31] and so we take 3 days for the transition period from \( I \) to \( I_q \) class, i.e., \( \tau = 1/3 \). The set of different parameter values is listed in Table 8.
Table 3. Values of the parameters.

| Parameter | Baseline Value | Unit   | Source |
|-----------|----------------|--------|--------|
| $\beta_o$ | $3.4 \times 10^{-8}$ | per day | Fitted |
| $\epsilon_1$ | 0.65 | per day | Fitted |
| $\epsilon_2$ | 0.43 | per day | Fitted |
| $\epsilon_3$ | 1.15 | per day | Fitted |
| $\alpha_+$ | 0.0011 | per day | Fitted |
| $\alpha_-$ | 0.0034 | per day | Fitted |
| $\sigma$ | 0.0011 | per day | Fitted |
| $\eta_1$ | 1/7 | per day | [44] |
| $\eta_2$ | 1/7 | per day | [38] |
| $\tau$ | 1/3 | per day | [31] |
| $\gamma_i; i = 1, 2, 3, 4$ | 1/14 | per day | [31] |
| $\delta_1$ | 0.01 | per day | Fitted |
| $\delta_2$ | 0.0075 | per day | Fitted |
| $\psi_1$ | $9.5 \times 10^{-4}$ | dimensionless | Fitted |
| $\psi_2$ | $3.5 \times 10^{-5}$ | dimensionless | Fitted |

3.3. **Data fitting.** The model (2.1) is fitted to the pandemic data set [42] so that the parameters $\beta_o, \epsilon_1, \epsilon_2, \sigma, \alpha_+, \alpha_-, \psi_1, \psi_2, \delta_1, \delta_2$ and the initial value $A(0)$ can be estimated. Since the asymptomatic cases were unknown, we found it reasonable to estimate its initial value. To estimate the unknowns, first, the model (2.1) is solved by using the MATLAB built-in function ode45 with some initial guesses. Then, the solutions are compared to the given data by fmincon (MATLAB routine) to estimate the parameters. More precisely, we minimize the following error function:

$$E = \sum_{i=1}^{333} \left[ (C_{rd}(t_i) - \hat{C}_{rd}(t_i))^2 + (C_{rc}(t_i) - \hat{C}_{rc}(t_i))^2 \right]$$

where $C_{rd}(t_i)$ and $C_{rc}(t_i)$ are the solutions of (2.2) computed numerically at time $t_i$ and $\hat{C}_{rd}(t_i)$ and $\hat{C}_{rc}(t_i)$ are the corresponding data. Here, $i = 1$ and $i = 333$ represent 5 March 2020 and 31 January 2021, respectively.

Due to the dynamic isolation rate and effective transmission rate described in Section 2, model (2.1) fits very well to the large data set (cumulative reported deaths and cumulative reported cases). The nonlinear functions used for the dynamic isolation rate and effective transmission rate are: $\alpha_+ = a_+ e^{\psi_1 [\sigma A + \tau]}$ and $\beta = \beta_o e^{-\psi_2 [\sigma A + \tau]}$, respectively. Figure 2 shows the fitting result of the model (2.1) to the cumulative reported deaths and cumulative reported cases occurred in New Jersey from 5 March 2020 to 31 January 2021. It is observed that the predictions given by the model (2.1) represent a trend which is very similar to the reported cases [42]. Therefore, dynamic isolation rate and effective transmission rate seem to be reasonable and realistic factors that need to be explored. Two pandemic waves of infection are seen from data fitting, one of which (first wave) occurred in April 2020 and another one (second wave) occurred in January 2021. Owing to the first and second waves of infection, nearly 0.7 million cumulative reported cases (which is 7.8% of the total population of New Jersey) and 22 thousand cumulative reported deaths are estimated on 31 January 2021. The results obtained through this data fitting are considered as the base case. If infection trend follows the same pattern after 31 January 2021 as it is in the base case, our model, in consequence, projects nearly 2.6 thousand additional deaths (24.6 thousand deaths in total) and 0.16 million additional cases (0.86 million cases in total which is 9.7% of the total population of New Jersey) within 18 July 2021. Such projection is considered as the current projection.
Figure 2. Model fitting to New Jersey data from 5 March 2020 to 31 January 2021. (a) The squares (blue) display the cumulative reported deaths and the solid curve (green) represents the model prediction. (b) The squares (red) display the cumulative reported cases and the solid curve (green) represents the model prediction.

4. Results

4.1. Sensitivity of $R_o$ on model parameters. Based on data fitting and estimated parameters, the basic reproduction number of our model (2.1) is: $R_o = 2.06$. Among the four infectious components ($A, A_q, I, I_q$), the largest magnitude of $R_o$ is observed in asymptomatic ($A$) to susceptible ($S$) transmission (i.e., $R_o^{A}$). Since asymptomatic individuals are clinically silent, they transmit the infection to others by coming in close contact unknowingly. The smallest magnitude of $R_o$ arises from quarantined asymptomatic ($A_q$) to susceptible ($S$) transmission (i.e., $R_o^{A_q}$). This is because of the screening program which detects the asymptomatic cases and immediately sends them to quarantine. The basic reproduction number includes several key parameters. The sensitivity analysis of $R_o$ could inform how significant each parameter is to the disease transmission [8, 25]. This analysis is generally useful to understand the robustness of model projections to the parameter values and to discover the specific parameters of a model which have high impacts on $R_o$. Such specific parameters can be targeted for control or intervention policies. To identify the critical parameters, first, we define the sensitivity index.

Definition 4.1. The normalized forward sensitivity index of $R_o$ is differentiable with respect to a specified parameter $p$ and is defined by

$$\gamma_{R_o}^p = \frac{\partial R_o}{\partial p} \frac{p}{R_o}$$

The parameter values from Table 3 are used to determine the sensitivity indices which are listed in Table 4. The positive indices in Table 4 indicate that the corresponding parameters will cause to increase $R_o$. On the contrary, the parameters with negative sensitivity indices will reduce $R_o$. This is explored in Figure 3 which demonstrates the significance of some important parameters to $R_o$. It is understood that $R_o$ can significantly be reduced through the implementation of isolation, acceleration of screening program and by minimizing the transmission rate. Moreover, the combined effects of isolation and screening program on $R_o$ is also noteworthy.

4.2. Computation of the final size. Equation (2.7) is used to see the effects of isolation and screening program on $S_\infty$ (see Figure 4). It is worth mentioning that $S_\infty$ will be larger if the values of isolation and screening parameters are increased and thus final size can eventually be reduced. The numerical value of $S_\infty$ for our model (2.1) is found to be $1.19 \times 10^6$ (which is the approximate number of susceptible individuals right at the end of the pandemic) for the baseline values of screening and isolation parameters. Using equation (2.8), the final size ($F$) of the pandemic is calculated to be $5.4 \times 10^6$, which means, nearly 60% of the total population is likely to be infected (both reported and unreported) by the end of the pandemic.
Table 4. Sensitivity of $R_o$.

| Parameter | Sensitivity index |
|-----------|-------------------|
| $\beta_o$ | +1.00000          |
| $\epsilon_1$ | +0.0159        |
| $\epsilon_2$ | +0.3176        |
| $\epsilon_3$ | +0.1891        |
| $\alpha_-$ | +1.0000        |
| $\sigma_+$ | −1.0000        |
| $\sigma$ | −0.0224          |
| $\eta_1$ | −0.1465          |
| $\eta_2$ | −0.0043          |
| $\tau$ | −0.0940          |
| $\gamma_1$ | −0.3171         |
| $\gamma_2$ | −0.0117         |
| $\gamma_3$ | −0.0840         |
| $\gamma_4$ | −0.2875         |
| $\delta_1$ | −0.0118         |
| $\delta_2$ | −0.0302         |
| $\psi_1$ | −0.0089          |
| $\psi_2$ | −0.0003          |

Figure 3. Contour plots of basic reproduction number ($R_o$) by (a) varying $\beta_o$ and $\sigma$, (b) varying $\beta_o$ and $a_+$, (c) varying $\epsilon_3$ and $\sigma$, (d) varying $\sigma$ and $a_+$. Base case is pointed with closed circles (black). The remaining parameter values are kept fixed, given in Table 3.
4.3. Effects of screening program. Screening is effective for detection of the asymptomatic cases. According to our model, a 3 times increase of screening compared to the base case from 5 March 2020 to 31 January 2021 could reduce the first wave of infection by 35% and second wave of infection by 25% relative to the base case (not shown in a Figure). Our model further predicts the possible impact of screening program on the epidemic from 31 January 2021 to 18 July 2021 (see Figure 5). It shows that a 73% increase of the screening program may reduce the cumulative reported deaths and cumulative reported cases by 4% and 9%, respectively for this period. The model also predicts that a 90% increase of screening program (not shown in a Figure) will possibly eliminate the infection fully and therefore cumulative reported deaths and cumulative reported cases can be minimized by 5% and 12%, respectively.

4.4. Effects of dynamic isolation. Isolation is a key tool to curve the epidemic. Our model estimates the effects of isolation with different schemes. A 7% increase of isolation compared to the base case (from 5 March 2020 to 31 January 2021) could reduce the first wave of infection by 31% and the second wave by 23% relative to the base case (not shown in a Figure). Figure 6 shows a scenario to demonstrate the effects of an increased isolation from 31 January 2021 to 18 July 2021. It reveals that a 16% increase of isolation from the base case may cause to eliminate the infection by 18 July 2021 (assuming the other interventions at the base line). Such additional isolation can reduce 4% of cumulative reported deaths and 10% of cumulative reported cases by 18 July 2021 compared to the base case scenario.

4.5. Combined effects of isolation and screening program. Figure 3(d) demonstrates the mutual effects of isolation and screening program on $R_0$. It shows that both isolation and screening rates should be increased in order to stop the spread of the infection. For example, if isolation is increased by 80% and screening by 9 times from the base case, then $R_0$ will be less than 1. Likewise, isolation and screening can be increased by 90% and 4 times, respectively from the base case to keep $R_0$ below 1. On the other hand, if isolation decreases, then screening rate needs to be increased so that $R_0$ can be made below 1. For example, if isolation rate is decreased by 5%, screening rate, at that time, should be increased by 50% to maintain the $R_0$ value. Similarly, while isolation drops about 10% from the base case, screening rate should be greater than 60% for $R_0$ to be less than 1.

4.6. Possibility of third wave. While the current epidemic appears to be an end by July 2021, there is a possibility of resurgence of epidemic if the undertaken measurements are loosened significantly. Figure 7 shows that a decline of 15% isolation rate after 31 January 2021 may trigger the infection
which can cause the third wave of SARS-CoV-2 pandemic in New Jersey with a possible pandemic peak in between 30 March 2021 to 11 April 2021. As a result, 2.7 thousand additional deaths and 0.21 million additional cases may occur by 18 July 2021 (compared to the current projection of 18 July 2021). A lack of screening program may also cause the resurgence of epidemic as shown in Figure 5. It shows that a 80% reduction of screening program (after 31 January 2021 till 18 July 2021) may cause to increase the infection rapidly in New Jersey with a possible pandemic peak in the middle of April 2021. According to our model simulations, nearly 2.68 thousand additional deaths and 0.18 million additional cases may occur within 18 July 2021 (compared to the current projection of 18 July 2021) for such reduction of screening program.

5. Discussion

This study evaluates some nonpharmaceutical interventions against the spread of SARS-CoV-2 through a mathematical model. The model is unique in a sense that it incorporates a natural phenomenon of population movement during a pandemic. It also shows an outstanding consistency with SARS-CoV-2 data set for a period of over ten months.

The results show that an accelerated screening program can reduce the infection significantly which is reasonable as the detected cases are taken to quarantine. However, it is important to quantify the required effort which is shown by our model that more than 70% acceleration of screening program may reduce the cumulative reported deaths and cumulative reported cases by 4% and 9%, respectively. Moreover, a 85% to 90% acceleration of screening program from the base case can fully eliminate the disease. These findings are consistent with a prior work [2].
Isolation is another critical factor for this pandemic as our findings indicate that a 16% increase of isolation from the base case may help to reduce 4% of cumulative reported deaths and 10% of cumulative reported cases over a five months period. Together with other results shown in Section 4, it is understood that isolation has a dramatic effect on the pandemic. This result is consistent with ongoing scenario in many places [12]. There have additional advantages of isolation as it can prevent other infections [9, 17].

Although isolation can mitigate the SARS-CoV-2 spread, but in reality, the number of isolated individuals should decrease over time due to the economy reopening or if the pandemic continues for a longer period (as it happened worldwide during the current pandemic situation) [33]. Consequently, isolated individuals may have to return to the susceptible pool in course of time which will possibly result in a massive increase of SARS-CoV-2. In order to curb such spread, a reasonable and oversized isolation policy is required [21] but this is challenging during economy reopening. In this scenario, the screening program could play a significant role [4, 6] as it detects the asymptomatic cases who are likely to transmit infections to others unknowingly. We suggest for an universal screening program if isolation can not be maintained.

In contrast to the positive results, there is a possibility of occurring a third wave of infection if isolation or screening is reduced to a certain extent. The model predicts that a reduction of 80% screening or 15% isolation from the base case may cause a resurgence of infection before 18 July 2021. Due to the third wave, 11% to 12% of the total population of New Jersey is likely to get infected by the end of July 2021 along with 27.3 thousand deaths. There may be additional waves too. So,
it’s important to know the approximate size of the infected population at the end of the pandemic. Therefore, the final size of our model, in that case, is an important threshold for the next possible prevention measurements.

Although our current model captures some important aspects of SARS-CoV-2 dynamics under screening program and dynamic isolation, it has limitations. First, our model does not incorporate any immigration. Since New Jersey is an open state, the individuals of New Jersey might come contact with the asymptomatic individuals of other states. As a result, there may be some variations in the results. Second, the model does not address vaccination. However, a fraction (subject to efficacy) of the vaccinated individuals can be considered as isolated and our results can be reinterpreted in accordance.

This study shows that dynamic isolation and screening program have been and will remain critical factors during this pandemic. While uncertainties remain in our results due to data gap and nonhomogeneity in population and their behaviour, the findings could be useful for a general understanding of the sensitivity of these interventions against the spread of SARS-CoV-2 or any upcoming pathogens.
Figure 8. Prediction of 3rd wave due to the slowdown of screening program. Model simulations from 5 March 2020 to 18 July 2021 for (a) susceptible class, (b) asymptomatic class, (c) quarantined asymptomatic class, (d) isolated class, (e) infected class, (f) quarantined class, (g) cumulative reported deaths and (h) cumulative reported cases. The solid curves (red) represent the base case whereas the dashed curves (magenta) represent the current projections following the pattern of base case and the dotted curves (blue) represent the projections up to 18 July 2021 due to 80% reduction of screening program from the base case. The parameter values are given in Table 3.

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