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# Mathematical Analysis of a COVID-19 Compartmental Model with Interventions

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**Abstract.** Mathematical models of the COVID-19 pandemic have been utilized in a variety of settings as a core component of national public health responses. Often based on systems of ordinary differential equations, compartmental models are commonly used to understand and forecast outbreak trajectories. In view of the primarily applied nature of COVID-19 models, theoretical analysis can provide a global and long-term perspective of key model properties, and relevant insights about the infection dynamics they represent. This work formulates and undertakes such an investigation for a compartmental model of COVID-19, which includes the effect of interventions. More specifically, this paper analyzes the characteristics of the solutions of a compartmental model by establishing the existence and stability of the equilibrium points based on the value of the basic reproductive number $R_0$. Our results provide insights on the possible policies that can be implemented to address the health crisis.

## INTRODUCTION

The coronavirus disease 2019 (COVID-19) is an infectious disease caused by the recently discovered severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The disease first emerged late 2019 in Wuhan, China, which eventually led to an outbreak that spread to many countries around the globe. Declared as a global pandemic in March 2020 by the World Health Organization, COVID-19 has gone on to infect over 29 million individuals as of early September 2020, resulting in over 900,000 deaths worldwide [1].

The tremendous negative impact brought by this disease necessitates the development of comprehensive strategies to control its spread. Researchers and public health officials have looked towards mathematical models to understand the nature and the effect of this disease in their communities and inform data-driven policy responses [2, 3]. Compartmental models, in particular, have been useful in analyzing the dynamics of transmission of infectious diseases such as COVID-19. Several studies on the outbreak of this disease in Wuhan [3, 4, 5, 6] and in other countries such as India, Italy and the US [7, 8, 9] have valuably considered variations of the SEIR compartmental model. Under this classical setup, the spread of an infectious disease is viewed in terms of the transition of human populations across susceptible (S), exposed (E), infectious (I), and recovered (R) categories. Such models are used to forecast number of cases over time, and incorporate the effect of state-initiated interventions such as community quarantines and travel restrictions, as well as the adherence of the public to the health protocols such as social distancing and wearing of face masks [10, 11, 12, 13, 14, 15].

This paper presents a mathematical analysis of a compartmental model used to describe the spread of COVID-19. The model includes the effect of interventions, and is characterized by modified SEIR dynamics with bilinear incidence rates. Here, we derive the basic reproduction number and use it to analyze the stability of the equilibrium points. We utilize theoretical insights from this paper to draw out practical implications for understanding the dynamics of COVID-19 as a disease as well as formulating effective strategies for controlling ongoing and future outbreaks.

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## THE MATHEMATICAL MODEL

### Model Formulation

We formulated a compartmental model in which members of a population belong to one of the six compartments depending on their status in relation to the disease: susceptible $(S)$, exposed $(E)$, infectious $(I)$, treated $(T)$ and recovered $(R)$. Susceptible individuals are those who have not been infected with the COVID-19 disease. Compartment $E$ consists of individuals who have been infected, but still incapable of infecting others, to account for the latent period of the disease. Compartment $I$ consists of individuals who are infectious but have not been clinically diagnosed and documented. Individuals in compartment $T$ are those who have been confirmed positive with COVID-19 disease. It is assumed in this model that individuals in $T$ are undergoing treatment and are properly isolated; hence, they cannot infect the susceptible individuals. Lastly, compartment $R$ consists of individuals who have recovered from the disease. Since the possibility of reinfection has yet to be established, it is assumed in this model that those who have recovered from the disease have acquired lifelong immunity and are are no longer infectious. This may be considered as a limitation of our model.

Individuals move from one compartment to another based on the assumed model parameters such as the coefficient of disease transmission $\beta_0$, detection rate $\delta$ of infectious individuals, and the recovery rates $r$ and $\theta$ of treated and undetected infectious individuals, respectively.

In several countries, community quarantine at different restriction levels was imposed by the government in order to curb the spread of the disease. Aside from this, minimum health standards such as proper hygiene, social distancing and wearing of face mask and face shield have been intensified to stop the virus from spreading further. All these measures help to reduce the transmissibility of the disease. This reduction is reflected in the parameter $\lambda$, with the corresponding transmission rate now given by $\beta_0(1-\lambda)$.

A constant recruitment rate $A$ in the susceptible compartment is assumed, mainly through birth. When susceptible individuals are exposed to an infectious person, they may become infected, which will lead to their transition towards the $E$ compartment. After some time $\tau$, exposed individuals will become infectious $(I)$. Among infectious cases, some will be confirmed positive and promptly be isolated and treated, while others will recover directly at a rate $\theta$. Finally, deaths are accounted for in the model through transition rates describing deaths from natural causes $(\mu)$, and deaths due to the disease among the undetected $(\varepsilon_I)$ and detected cases $(\varepsilon_T)$.

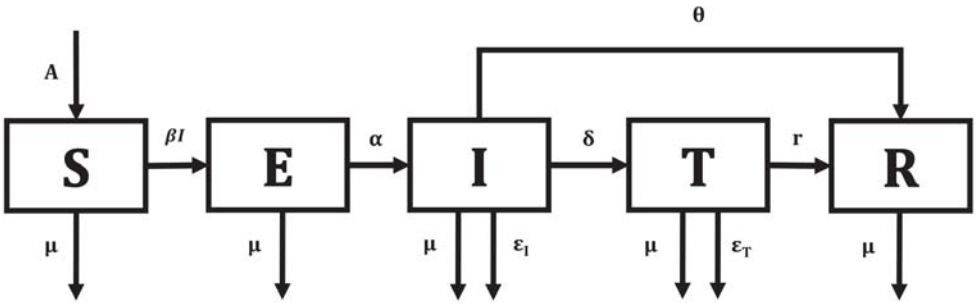


**FIGURE 1.** Movement of individuals through the different compartments in relation to the disease.

We can describe the above model through a system of ordinary differential equations

$$S'(t) = A - \beta S(t)I(t) - \mu S(t) \tag{1}$$
$$E'(t) = \beta S(t)I(t) - (\mu + \alpha)E(t) \tag{2}$$
$$I'(t) = \alpha E(t) - (\mu + \delta + \varepsilon_I + \theta)I(t) \tag{3}$$
$$T'(t) = \delta I(t) - (\mu + r + \varepsilon_T)T(t) \tag{4}$$
$$R'(t) = \theta I(t) + rT(t) - \mu R(t), \tag{5}$$

where $\beta = \beta_0(1-\lambda)$, $\alpha = 1/\tau$, and the real-valued functions $S, E, I, T$, and $R$ are differentiable on $\mathbb{R}$. The model also uses positive constant parameters. For this paper's discussion, the system of equations (1)-(5) will be referred to as system (C).

Consider the biologically feasible region

$$\Phi = \left\{ (S,E,I,T,R) \in \mathbb{R}^5_{0+} : S+E+I+T+R \leq \frac{A}{\mu} \right\}.$$

The existence of a unique solution to system (C) having initial condition $\phi \in \Phi$ follows from the standard fundamental results in ordinary differential equations [16, 17] . Moreover, it can easily be shown that such solution is bounded and nonnegative on $[0,+\infty)$.

## The Basic Reproduction Number and Equilibrium Points

One of the fixed points of system (C) is given by

$$\mathbf{E}_{dfe} = (S_{df}, E_{df}, I_{df}, T_{df}, R_{df}) = \left( \frac{A}{\mu}, 0, 0, 0, 0 \right),$$

referred to as the disease-free equilibrium.

We now derive the basic reproduction number $R_0$ using the next generation matrix approach [18]. Suppose $Z = (E,I,T)^{tr}$. Then

$$\frac{dZ}{dt} = \mathscr{F} - \mathscr{V},$$

where

$$\mathscr{F} = \begin{bmatrix} \beta SI \\ 0 \\ 0 \end{bmatrix} \text{ and } \mathscr{V} = \begin{bmatrix} (\mu+\alpha)E \\ (\mu+\varepsilon_I+\theta+\delta)I - \alpha E \\ (\mu+\varepsilon_T+r)T - \delta I \end{bmatrix}.$$

The Jacobian matrices of $\mathscr{F}$ and $\mathscr{V}$ evaluated at $\mathbf{E}_{dfe}$ are, respectively, given by

$$F = \begin{bmatrix} 0 & \frac{\beta A}{\mu} & \frac{\beta A}{\mu} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \mu+\alpha & 0 & 0 \\ -\alpha & \mu+\varepsilon_I+\theta+\delta & 0 \\ 0 & -\delta & \mu+\varepsilon_T+r \end{bmatrix}.$$

The largest eigenvalue of $FV^{-1}$ gives the value of $R_0$, that is,

$$R_0 = \frac{\beta A \alpha}{\mu(\alpha+\mu)(\mu+\varepsilon_I+\delta+\theta)}.$$

As shown in the succeeding theorems, the existence and stability of the fixed points of system $(C)$ depends on the value of $R_0$. If $R_0 > 1$, then another fixed point, referred to as endemic equilibrium, exists and is given by $\mathbf{E}_{ee} = \{S_*, E_*, I_*, T_*, R_*\}$, where

$$S_* = \frac{(\mu+\alpha)(\mu+\varepsilon_I+\delta+\theta)}{\beta\alpha} \tag{6}$$

$$E_* = \frac{\mu(R_0-1)(\mu+\varepsilon_I+\delta+\theta)}{\beta\alpha} \tag{7}$$

$$I_* = \frac{\mu(R_0-1)}{\beta} \tag{8}$$

$$T_* = \frac{\delta I_*}{\mu+\varepsilon_T+r} \tag{9}$$

$$R_* = \frac{\theta I_* + r T_*}{\mu}. \tag{10}$$

## Stability Analysis

It can be observed that equations (1), (2) and (3) are not dependent on the compartments $R$ and $T$. Hence, in establishing the stability of the equilibrium points, it suffices to consider the following subsystem $(C_R)$:

$$S'(t) = A - \beta S(t)I(t) - \mu S(t) \tag{11}$$
$$E'(t) = \beta S(t)I(t) - (\alpha+\mu)E(t) \tag{12}$$
$$I'(t) = \alpha E(t) - (\delta+\varepsilon_I+\mu+\theta)I(t). \tag{13}$$

Clearly, the disease-free equilibrium for system $(C_R)$ exists, and is given by $\mathbf{E}_{dfe_R} = \left(\frac{A}{\mu},0,0\right)$. Moreover, the system has the unique endemic equilibrium $\mathbf{E}_{ee_R} = (S_*,E_*,I_*)$ when $R_0 > 1$.

For system $(C_R)$, we shall consider the region

$$\Phi_R = \left\{(S,E,I) \in \mathbb{R}^3_{0+} : S+E+I \leq \frac{A}{\mu}\right\}.$$

It should be noted that for any initial condition $\phi \in \Phi_R$, the corresponding initial value problem will yield a unique solution that is bounded and nonnegative on $[0,+\infty)$.

**Theorem 1.** *If $R_0 < 1$, then the disease-free equilibrium $\left(\frac{A}{\mu},0,0\right)$ of system $(C_R)$ is globally asymptotically stable.*

Proof. Consider the Lyapunov function $V : \Phi_R \to \mathbb{R}$ defined by

$$V(S,E,I) = V_1(S,E,I) + V_2(S,E,I),$$

where

$$V_1(S,E,I) = \alpha E \quad \text{and} \quad V_2(S,E,I) = (\alpha+\mu)I.$$

Observe that $V$ is nonnegative and continuous on $\Phi_R$. Furthermore, $V(S,E,I) = 0$ if and only if $S = \frac{A}{\mu}$, $E = 0$, and $I = 0$.

We evaluate the derivative of $V$, as a function of $t$, along the solutions of system $(C_R)$ with initial condition $\phi \in \Phi_R$. Note that

$$\frac{d}{dt}V_1(t) = \alpha\left[\beta S(t)I(t) - (\mu+\alpha)E(t)\right],$$
$$\frac{d}{dt}V_2(t) = (\mu+\alpha)\left[\alpha E(t) - (\delta+\varepsilon_I+\mu+\theta)I(t)\right].$$

Accordingly,

$$\begin{aligned}\frac{d}{dt}V(t) &= \alpha\left[\beta S(t)I(t) - (\mu+\alpha)E(t)\right] + (\mu+\alpha)\left[\alpha E(t) - (\delta+\varepsilon_I+\theta+\mu)I(t)\right] \\ &\leq \alpha\beta\frac{A}{\mu}I(t) - (\mu+\alpha)(\delta+\varepsilon_I+\theta+\mu)I(t) \\ &= (\mu+\alpha)(\delta+\varepsilon_I+\theta+\mu)\left[R_0-1\right]I(t) \\ &\leq 0,\end{aligned}$$

since $R_0 < 1$. Thus, $V'(t) = 0$ for all $t$ if and only if $S(t) = \dfrac{A}{\mu}$, $E(t) = 0$, and $I(t) = 0$ for all $t$. Accordingly, by La Salle's Invariance Principle, $\mathbf{E}_{dfe_R}$ is globally asymptotically stable. □

**Theorem 2.** *If $R_0 > 1$, then the disease-free equilibrium $\left(\frac{A}{\mu},0,0\right)$ of system $(C_R)$ is unstable.*

Proof. We linearized the system $(C_R)$ at the disease-free equilibrium $\mathbf{E}_{dfe_R}$. The resulting Jacobian matrix was shown to have a positive eigenvalue; hence, the result follows. □

**Theorem 3.** *If $R_0 > 1$, then the endemic equilibrium $(S_*,E_*,I_*)$ of system $(C_R)$ is globally asymptotically stable.*

Proof. Consider the Lyapunov function $V : \Phi_R \to \mathbb{R}$ given by

$$V(S,E,I) = V_1(S,E,I) + V_2(S,E,I) + V_3(S,E,I),$$

where

$$\begin{aligned}
V_1(S,E,I) &= S(t) - S_* - S_* \ln \frac{S(t)}{S_*} \\
V_2(S,E,I) &= E(t) - E_* - E_* \ln \frac{E(t)}{E_*} \\
V_3(S,E,I) &= \frac{\beta S_* I_*}{\alpha E_*} \left[ I(t) - I_* - I_* \ln \frac{I(t)}{I_*} \right].
\end{aligned}$$

It can be shown that $V$ is nonnegative and continuous on $\Phi_R$. Furthermore, $V(S,E,I) = 0$ if and only if $S = S_*$, $E = E_*$, and $I = I_*$.

Observe that, along the solutions of system $(C_R)$ with initial condition $\phi \in \Phi_R$,

$$\frac{d}{dt} V_1(t) = \left(1 - \frac{S_*}{S(t)}\right) [A - \beta S(t) I(t) - \mu S(t)].$$

Because $A = \mu S_* + \beta S_* I_*$, we then have

$$\frac{d}{dt} V_1(t) = \left(1 - \frac{S_*}{S(t)}\right) [-\mu(S(t) - S_*) + \beta S_* I_*] - \beta S(t) I(t) + \beta S_* I(t).$$

Note also that $(\delta + \mu + \theta + \varepsilon_I) I_* = \alpha E_*$ and $(\alpha + \mu) E_* = \beta S_* I_*$. Hence,

$$\begin{aligned}
\frac{d}{dt} V_2(t) &= \left(1 - \frac{E_*}{E(t)}\right) [\beta S(t) I(t) - (\alpha + \mu) E(t)] \\
&= \beta S(t) I(t) - \beta S_* I_* \frac{E(t)}{E_*} - \beta S(t) I(t) \frac{E_*}{E(t)} + \beta S_* I_*, \\
\frac{d}{dt} V_3(t) &= \frac{\beta S_* I_*}{\alpha E_*} \left(1 - \frac{I_*}{I(t)}\right) [\alpha E(t) - (\delta + \mu + \theta + \varepsilon_I) I(t)] \\
&= \beta S_* I_* \frac{E(t)}{E_*} - \beta S_* I(t) - \beta S_* I_* \frac{I_*}{I(t)} \frac{E(t)}{E_*} + \beta S_* I_*.
\end{aligned}$$

Accordingly,

$$\begin{aligned}
\frac{d}{dt} V(t) &= -\frac{\mu [S(t) - S_*]^2}{S(t)} + \beta S_* I_* \left[ 3 - \frac{S_*}{S(t)} - \frac{S(t)}{S_*} \frac{I(t)}{I_*} \frac{E_*}{E(t)} - \frac{I_*}{I(t)} \frac{E(t)}{E_*} \right] \\
&\leq 0.
\end{aligned}$$

Thus, $V'(t) = 0$ if and only if $S(t) = S_*$, $E(t) = E_*$, and $I(t) = I_*$. Accordingly, by La Salle's Invariance Principle, $E_{ee_R}$ is globally asymptotically stable. □

## Numerical Simulations

Several studies have shown that $R_0$ in the initial stages of the COVID-19 pandemic is greater than one [19, 20]. Theorem 2 and Theorem 3 say that if this remains the case, and unless a vaccine is made available, then the fight against the pandemic is far from over. Theorem 1, on the other hand, gives insights on how to address the health crisis. Recall that $R_0 = \frac{\beta A \alpha}{\mu(\alpha+\mu)(\mu+\varepsilon_I+\delta+\theta)}$. Among the parameters that define $R_0$, the transmission rate $\beta$, which is equal to $\beta_0(1-\lambda)$, and the detection rate $\delta$ are the ones that can be controlled so as to achieve the condition that $R_0 < 1$.

In this section, we examine the results of the theorems through numerical simulations. Using illustrative parameter values summarized in Table 1, we show differences in outbreak trajectories of COVID-19 cases in the Philippines

**TABLE 1.** Parameter values for simulation.

| Parameter | Value | Reference |
|---|---|---|
| $A$ | $7.6968 \times 10^{2}$ | [21, 22] |
| $\beta$ | $9.2010 \times 10^{-9}$ | Assumed in Fig. 2 simulation |
| $\mu$ | $4.0548 \times 10^{-5}$ | [21] |
| $\theta$ | 0.0714 | [23] |
| $\tau$ | 5.0000 | [23] |
| $\varepsilon_I$ | 0.0031 | [24] |
| $\varepsilon_T$ | 0.0031 | [24] |
| $r$ | 0.0404 | [24] |

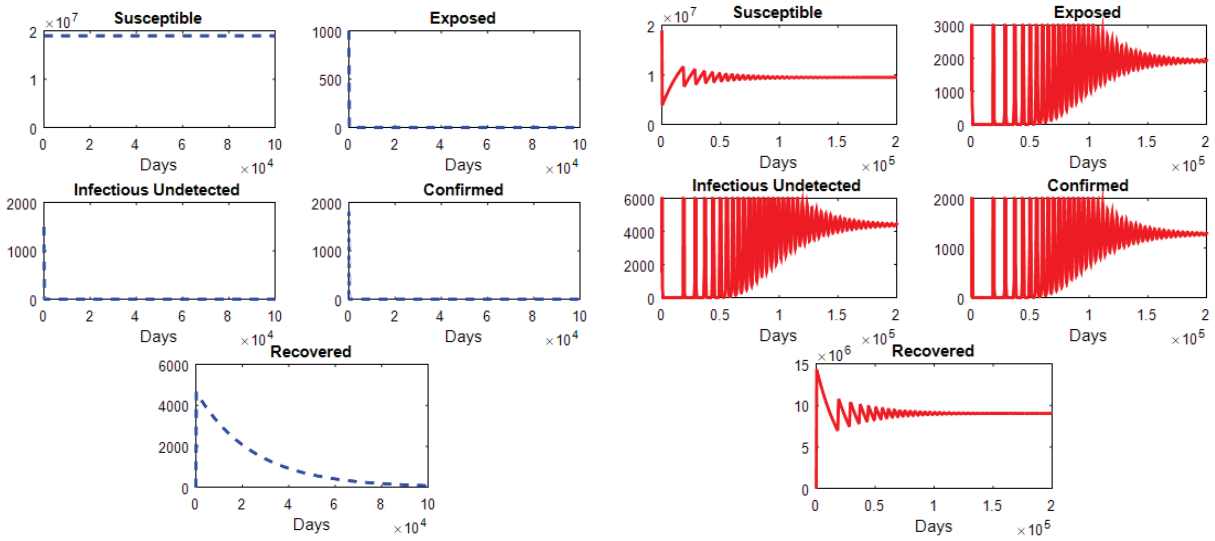


**FIGURE 2.** Numerical simulations confirm the stability of the disease-free equilibrium ($\mathbf{E}_{df}$) if $R_0 < 1$ (blue-dashed line) and the stability of the endemic equilibrium ($\mathbf{E}_{ee}$) if $R_0 > 1$ (red solid line). Parameters used are summarized in Table 1 and $R_0$ is varied by changing the value of parameter $\delta$ (0.2743 and 0.0127 respectively).

based on different values of $R_0$. Figure 2 depicts changing compartment values over time in the cases of $R_0 < 1$ and $R_0 > 1$. It can be seen that when $R_0 < 1$ (see blue graphs), the solution approaches the disease-free equilibrium; when $R_0 > 1$ (see red graphs), the solution approaches the endemic equilibrium. Solutions to the system were obtained and visualized using Runge-Kutta methods on MATLAB.

From a more general standpoint, we also consider how different values of $\lambda$ and $\delta$ can be combined resulting in different values of $R_0$. All other parameters held equal, Fig. 3 shows that a linear boundary is observed between cases where $R_0 > 1$ and $R_0 < 1$. This may be seen by setting the derived expression for $R_0$ to 1 and solving for $\lambda$ as a function of $\delta$. In particular, we see that the linear boundary has negative slope given by $\dfrac{-\mu(\alpha+\mu)}{\beta_0 A\alpha}$.

## CONCLUSION AND RECOMMENDATIONS

In this paper, we developed a compartmental model to describe the spread of COVID-19 disease in the community. Through the use of a next generation matrix, we also derived a formula for the basic reproduction number $R_0$. This quantity is important in establishing the existence and stability of equilibrium points, namely, the disease-free equilibrium and endemic equilibrium.

Based on the formula for $R_0$, the parameters that can be changed through interventions in order to achieve the condition that $R_0 < 1$ are $\delta$ and $\lambda$. Changes in $\lambda$ may lower the transmission rate through government policies

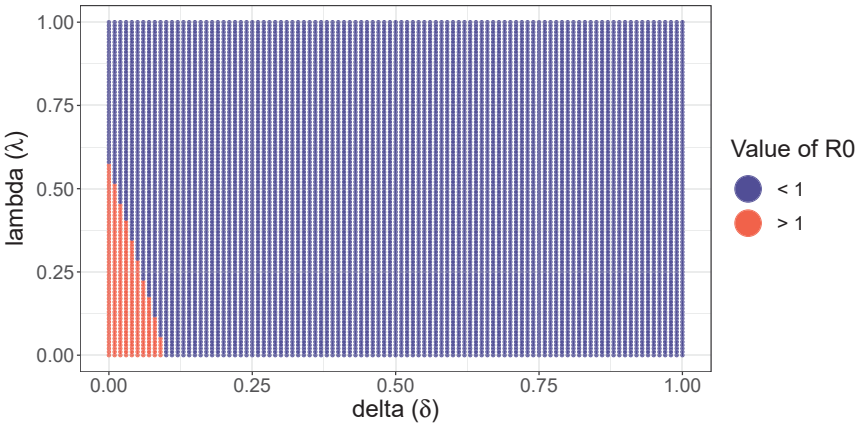


**FIGURE 3.** Variations in values of $R_0$ based on values of $\lambda$ and $\delta$.

on non-pharmaceutical interventions such as imposing community quarantine, adjustment in the type of community quarantine based on bi-weekly or monthly health outcomes and intensifying the compliance of the public to minimum health standards. Community quarantine, however, can have very high economic costs; furthermore, they entail population control at a large-scale level, enforcing blanket lockdowns for entire areas. Improving minimum health standards can offer an effective alternative if enforced in a targeted and efficient manner.

The detection rate $\delta$ should thus also be increased. This parameter covers a whole package of health system capacity, which includes contact tracing, testing, immediate isolation, and proper treatment. To increase the value of $\delta$, more tests should be conducted so that those who turn out positive will be promptly isolated and treated. Moreover, adequate facilities and support should be prepared to accommodate the increased need for isolation and treatment. Intensifying this measure offers a more viable and cost-effective alternative to imposing a community quarantine.

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