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Mathematical analysis of the effects of controls on transmission dynamics of SARS-CoV-2

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Abstract COVID-19, an infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), starting from Wuhan city of China, plagued the world in the later part of 2019. We developed a deterministic model to study the transmission dynamics of the disease with two categories of the Susceptibles (ie Immigrant Susceptibles and Local Susceptible). The model is shown to have a globally stable disease-free equilibrium point whenever the basic reproduction number \( R_0 \) is less than unity. The endemic equilibrium is also shown to be globally stable for \( R_0 > 1 \) under some conditions. The spread of the disease is also shown to be highly sensitive to use of PPEs and personal hygiene \((d)\), transmission probability \((\beta)\), average number of contacts of infected person per unit time (day) \((c)\), the rate at which the exposed develop clinical symptoms \((d)\) and the rate of recovery \((\rho)\). Numerical simulation of the model is also done to illustrate the analytical results established.

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1. Introduction

Coronavirus (COVID-19) is an infectious disease caused by a new strain of a virus discovered by scientists. Covid-19 began to spread from China, Wuhan, in late part of 2019. Since then there have been reported outbreaks in other parts of the world mostly due to immigration. The World Health Organisation (WHO) declared it as a pandemic because of the rate of infection, spread and mortality of the infected individuals. Two pandemics in the last two decades caused by similar viruses have been experienced; the severe acute respiratory syndrome (SARS) in 2003 and the Middle East respiratory syndrome (MERS) in 2012 [1].

Globally an increasing trend of COVID-19 cases have been reported since the outbreak was declared on 31st December, 2019 and as of 21st April, 2020 at 18:00 CET, the total global confirmed cases reported were 2,402,250, which includes 163,097 deaths (Case Fatality Ratio (CFR): 6.8%) [2].

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In Africa, the virus has affected all Member States of WHO African Region [2]. As of 22nd April, 2020, South Africa had recorded 3,465 cases, Algeria – 2,811, Cameroon – 1,163 cases, Ghana – 1,042 cases, Côte d’Ivoire – 916 cases and Guinea – 688 cases. These six countries account for 66% of the cases reported in the region [2]. Overall, in the African continent a total of 24,137 cases and 1,171 deaths (Case Fatality Ratio [CFR]: 4.9%) had been reported as of 21st April, 2020 including 15,394 cases and 716 deaths in Member States from the WHO African Region and 8,743 cases and 455 deaths in Member States from the WHO Eastern Mediterranean Region [2].

Human-to-human has been the main mode transmission of COVID-19. The transmission of infection is by directly ‘sufficiently close’ host-to-susceptible contact or by infecting the environment and a susceptible individual makes ‘sufficiently close’ contact with the environment where in this context, the meaning of environment includes the curtains, cutlery, door holding etc of the household as well as the ambient air. With increased air travel, the entire world population became affected. The first reported cases in all the African countries were imported via air travels.

An infected individual takes between 5 to 14 days to show symptoms which may include fever, tiredness, dry cough, arches and pain, sore throat and nasal congestion [3]. There is not yet a specific vaccine or drug for the treatment of COVID-19.

Due to its relatively short period of existence, not so much is known about the disease and researchers all over the world are conducting research to find a lasting solution to the pandemic. Huang et al. [3] collected data on all patients with suspected COVID-19 who were admitted to a designated hospital in Wuhan. The data was analysed on patients with laboratory-confirmed COVID-19 infection by real-time RT-PCR and next-generation sequencing. They accordingly obtained the data with standardised data collection forms shared by WHO and the International Severe Acute Respiratory and Emerging Infection Consortium from electronic medical records. Patients and their families had direct communication with researchers to ascertain epidemiological and symptom data. Outcomes were also compared between patients who had been admitted to the intensive care unit (ICU) and those who had not. They found out that all 41 patients had pneumonia with abnormal findings on chest CT. Complications included acute respiratory distress syndrome.

The focus of this study is on the transmission dynamics of COVID-19 in Africa and the impact of relevant factors on disease transmission and control. This is crucial for further surveillance and control of the outbreak. In this study we employed Mathematical modelling which has been used extensively to study the dynamics of other infectious diseases and COVID-19, see the following sorted articles and the references therein [4–16]. In terms of mathematical models related to the African continent; the work by Asamoah et al. [17] discusses COVID-19 dynamics in a 10 compartmental structure for Ghana and Egypt. They calculated the control and basic reproduction numbers for both countries. Projections for the disease control in Ghana and Egypt were presented. The sensitivity analysis of their studies suggests that: a continuous increase in the rate of diagnoses, the rate of quarantine through doubling enhanced contact tracing, and stringent safety measures in hospitals (and/or isolation centres); with a constant supply of effective personal protective equipment’s (PPEs) will help reduce the control reproduction number $R_c$, to less than unity. Furthermore, they stated that, adding natural recovery to the model shows that an increase in natural recovery from the asymptomatic stage reduces the control reproduction number; also, they noticed that the choice of a force of infection influences the control reproduction number. Zhao et al. [18], presented an improved SEIR model to study the COVID-19 dynamics in South Africa, Egypt, Algeria, Nigeria, Senegal, and Kenya. Musa et al. [19] systematized presented estimation of exponential growth rate and basic reproduction number of the coronavirus disease 2019 (COVID-19) in Africa. Hammoumi et al. [20] studied the impact assessment of containment measure against COVID-19 spread in Morocco; their model gave an estimated basic reproduction number as 2.9949, with confidence interval (2.6729–3.1485) for Morocco, reflecting a high speed of spread of the epidemic. Their model further shows that compulsory containment can be efficient if more than 73% of population are confined. Fahmy et al. [21] used generalized SEIR model to analysis of COVID-19 in Egypt, Qatar and Saudi Arabia. Their model project that, the pandemic will resolve in the countries for their investigation in February 2021, January 2021 and 28th August 2020 with total death cases of 9,742, 5,600 and 185 and total cases of 187,600, 490,000 and 120,000 respectively. The Mathematical model used in this study is developed in the next section and some basic qualitative properties (including boundedness and positivity of solutions, stability of equilibria and Sensitivity) are discussed in Section 3. Numerical experiment of the model is carried out in Section 4 to illustrate the analytical results obtained. In Section 5 some basic conclusions are drawn from the study.

2. Model formulation

In Africa COVID-19 is often transmitted from humans to humans. In this paper, an outbreak of COVID-19 is considered in a population of size $N(t)$ at time $t$. The population is compartmentalized into Susceptible individuals, people who are exposed (latently infected), individuals showing clinical symptoms $I(t)$, those who are hospitalized $H(t)$ and individuals who have recovered from the infection $R(t)$. The Susceptible and Exposed individuals are segmented into two groups each of Susceptible Immigrants $S_M(t)$, those who migrate into Africa, and Susceptible Locals, $S_L(t)$, individuals who stay in Africa for the period under consideration, Exposed Immigrants, $E_M(t)$, individual who are latently infected and migrate into Africa and Exposed Locals, $E_L(t)$, those who are latently infected within Africa. The Susceptible population is increased locally and by immigration through recruitment at rate $P_S$ and $P_M$ respectively. Susceptible persons contract the disease through effective contact with viral sources $(E_M, E_L, I, H)$ at rate $\lambda = \frac{\beta (E_M + E_L + I + H)}{N}$, where $\beta$ is the transmission probability from a viral source to a Susceptible individual, $c$ is the average number of contact persons per unit time (day) of a typical viral source. Susceptibles are infected at rate $\lambda$ from infectious individuals. During the incubation period, which ranges from 1 to 14 days, the exposed are also infectious but develop clinical symptoms after the incubation period at the rate $\delta$. We assume that the infected persons are clinically detected and hospitalized (quarantine) and placed under treatment at rate $\theta$ as a curative measure which can lead to recovery at rate $\rho$. We also
assume that the exposed can recover without treatment at same recovery rate. The recovered are recruited into the population as local Susceptibles (without immunity) at the rate $\sigma$. Natural death rate is taken to be $\mu$, while COVID-19-induced death rate is $\mu_d$. Finally, apart from the fact that we are social animals, in some parts of Africa it is a custom for individuals to visit or show hospitality to relations and friends or foreigners who are immigrants, hence preventive measures $d$, of social distancing, regular hand washing with soap under running water, use of alcohol based hand Sanitizers and Personal Protective Equipment (PPEs), and restrictions on international travels are also considered. The following set of equations describe the dynamics of COVID-19 infection in Africa. Fig. 1 represents the transfer diagram of the compartmental model under study.

$$\begin{align*}
\frac{dS_M}{dt} &= P_M - (1 - d)\lambda S_M - \mu S_M \\
\frac{dE_M}{dt} &= (1 - d)\lambda S_M - (\delta + \rho + \mu)E_M \\
\frac{dS_L}{dt} &= P_L - (1 - d)\lambda S_L - \mu S_L + \sigma R \\
\frac{dE_L}{dt} &= (1 - d)\lambda S_L - (\delta + \rho + \mu)E_L \\
\frac{dI}{dt} &= \delta (E_L + E_M) - (\theta + \mu + \mu_d)I \\
\frac{dH}{dt} &= \theta I - (\rho + \mu + \mu_d)H \\
\frac{dR}{dt} &= \rho (H + E_M + E_L) - (\sigma + \mu) R
\end{align*}$$

with initial conditions, $(S(0), E_M(0), E_L(0), I(0), H(0), R(0)) \in \mathbb{R}^7_{\geq 0}$.

For convenience, where appropriate, we use the following notations $k_1 = \delta + \rho + \mu, k_2 = \theta + \mu + \mu_d, k_3 = \rho + \mu + \mu_d$ and $k_4 = \sigma + \mu$. The model parameters are presented in Table 1 with their baseline values for numerical purposes.

In the next section, we discuss some basic properties of the model (1).

3. Qualitative properties

3.1. Positivity and boundedness of model solution

The following result relates to positivity and boundedness of solutions of model (1).

Lemma 1. All solutions of (1) which start in $\Omega$ remain in $\Omega$ for all $t \geq 0$.

Also, the region $\Omega = \{(S_M, E_M, S_L, E_L, I, H, R) \in \mathbb{R}^7_{\geq 0} | N \leq \frac{\mu + \mu_d}{\mu_d}\}$ is a positively invariant set for the model (1).

Proof. Define $\zeta(x) = \{x(t) = 0\text{ and } (S_M, E_M, S_L, E_L, I, H, R) \in \mathbb{R}^7_{\geq 0} \}, \forall x \in \{S_M, E_M, S_L, E_L, I, H, R\}$.

Then from (1), we have;

$$\begin{align*}
\frac{dS_M}{dt}|_{(S_M)} &= P_M > 0, \\
\frac{dE_M}{dt}|_{(E_M)} &= (1 - d)\lambda (S_M) \geq 0, \\
\frac{dS_L}{dt}|_{(S_L)} &= P_L > 0, \\
\frac{dE_L}{dt}|_{(E_L)} &= (1 - d)\lambda (S_L) \geq 0, \\
\frac{dI}{dt}|_{(I)} &= \delta (E_M + E_L) > 0, \\
\frac{dH}{dt}|_{(H)} &= \theta (H) > 0, \\
\frac{dR}{dt}|_{(R)} &= \rho (H + E_M + E_L) > 0.
\end{align*}$$

Using Lemma 2 of [23], shows any solution of (1) is such that...
and the endemic equilibrium, completes the proof of the second part of the Lemma and hence the whole Lemma.

This proves that the COVID-19 model (1) is mathematically and epidemiologically well-posed inside of \( \Omega \) [24].

3.2. Equilibrium points of the model

The model (1) has two equilibria; the disease-free, \( \mathcal{E}_0 = (S_M, 0, S_I, 0, 0, 0, 0) \) (where \( S_M = \frac{P_M}{\mu} \) and \( S_I = \frac{P_I}{\mu} \)) and the endemic equilibrium, \( \mathcal{E}^* \).

The basic reproduction number [25] is obtained as

\[
R_0 = \frac{\beta c(k_2k_3 + \delta k_3 + \delta \delta)(1 - d)}{k_1k_2k_3}.
\]

Now, a typical endemic equilibrium point \( \mathcal{E}^* = (S_M, E_M, S_I, E_I, \Gamma, H^*, R^*) \) of the model (1) is given by:

\[
\begin{align*}
S_M &= \frac{P_M}{\mu(1 - \beta c)}, & E_M &= \frac{\beta c(1 - \beta c)}{\mu}, \\
S_I &= \frac{Q_1}{Q_2}, & E_I &= \frac{\beta c(1 - d)\rho_0}{Q_2}, \\
\Gamma &= \frac{Q_1Q_2}{Q_1 + Q_2}, & H^* &= \frac{Q_2(1 - \beta c)}{Q_2}, \\
R^* &= \frac{Q_1}{Q_2}, & Q_1 &= k_1k_3k_4(\mu + \delta)(1 - d) + 1, \\
Q_2 &= \mu k_3k_4k_5(\rho_0 - \delta - \delta d + \delta(1 - d)\rho_0).
\end{align*}
\]

Substituting (2) into the expressions of force of infection \( \lambda \) and solving for \( \lambda \) gives \( \lambda^* = 0 \) and \( \lambda^*_1 = \frac{\mu k_3k_4k_5(\rho_0 - \delta - \delta d + \delta(1 - d)\rho_0)}{k_1k_2k_3k_4k_5k_6k_7k_8k_9k_10}$, which correspond to the disease-free and endemic equilibria respectively. We note here that \( \lambda^*_1 > 0 \iff R_0 > 1 \) and hence the endemic equilibrium exists only when \( R_0 > 1 \).

We discuss the local stability of the equilibrium in the next section.

3.3. Local stability of equilibria

An equilibrium point of the model is said to be locally asymptotically stable if all eigenvalues of the Jacobian matrix \( J \) of the model have negative real parts.

It is easy to show that three \((\mu, -\mu \text{ and } -k_4)\) of the eigenvalues of Jacobian of the model at \( \mathcal{E}_0 \) are negative and the rest are the zeros of the following polynomial equation.

\[
x^3 + \Phi_1x^2 + \Phi_2x + \Phi_3 = 0
\]

Clearly, whenever \( R_0 < 1 \), then all coefficients of (3) are positive, and the following result is thus established.

**Theorem 1.** The disease-free equilibrium, \( \mathcal{E}_0 \) is locally asymptotically stable whenever \( R_0 < 1 \) and unstable otherwise.

Theorem 1 implies that the disease can be eliminated from the community (when \( R_0 < 1 \)) if the initial sizes of the sub-populations of the model are in the basin of attraction of the \( \mathcal{E}_0 \). To ensure that disease elimination is independent of the initial sizes of sub-populations, it is necessary to show that \( R_0 < 1 \) guarantees global asymptotic stability (GAS) of \( \mathcal{E}_0 \). This is investigated in the next section.

3.4. Global stability of \( \mathcal{E}_0 \)

Using the technique of Castillo-Chavez [26], let,

\[
X = (S_M, S_I, R) \text{ and } Z = (E_M, E_I, I, H),
\]

so that (1) can be re-written as

\[
\begin{align*}
\frac{dX}{dt} &= \mathcal{F}(X, Z), \\text{and} \\
\frac{dZ}{dt} &= \mathcal{G}(X, Z),
\end{align*}
\]

where

\[
\mathcal{F} = \left( \begin{array}{c}
\frac{P_M - (1 - \beta c)x_1x_2 - \beta c x_2 - \beta c x_1 - \beta c x_1}{N} - \mu S_M \\
\frac{P_L - (1 - \beta c)x_1x_2 - \beta c x_2 - \beta c x_1 - \beta c x_1}{N} - \mu S_L \\
\rho (H + x_3 + x_4) - \mu R
\end{array} \right)
\]

with

\[
\mathcal{G} = [\mathcal{F}]_3.
\]
Mathematical analysis of the effects of controls on transmission dynamics

The endemic equilibrium of the COVID-19 model

\[ \mathcal{G}_1 = \begin{bmatrix} (1-\delta)S_M \delta & (1-\delta)S_M \delta - k_1 \\ (1-\delta)S_M \delta & (1-\delta)S_M \delta - k_1 & \delta \\ \delta & \delta & 0 \\ 0 & 0 & 0 \end{bmatrix}, \]

and

\[ \mathcal{G}_2 = \begin{bmatrix} (1-\delta)S_M \delta & (1-\delta)S_M \delta - k_1 & (1-\delta)S_M \delta & (1-\delta)S_M \delta - k_1 \\ (1-\delta)S_M \delta & (1-\delta)S_M \delta - k_1 & (1-\delta)S_M \delta & (1-\delta)S_M \delta - k_1 \\ k_2 & 0 & 0 & 0 \\ \theta & k_3 & 0 & 0 \end{bmatrix}. \]

The following conditions, according to [26] guarantee global stability of $\mathcal{E}_0$.

H1: For $\frac{dX}{dt}|_{X=0}$, $X^*$ is globally asymptotically stable,

H2: $\mathcal{L} = D_2 \mathcal{G}(X,0)$ is the Jacobian of $\mathcal{G}(X, Z)$ with respect to $Z$ at $\mathcal{E}_0$.

Consider the reduced system of (1) given by

\[ \frac{dX}{dt}|_{Z=0} = \begin{bmatrix} P_M - \mu S_M \\ P_L - \mu S_L \\ -\mu R \end{bmatrix}. \]

The disease-free equilibrium point $X^* = \mathcal{E}_0$ is clearly a globally asymptotically stable point of the reduced system. Also, let

$\mathcal{L} = D_2 \mathcal{G}(X, Z)$, where

\[ \mathcal{L} = \begin{bmatrix} (1-\delta)E_M + E_L + \mu S_M - k_1 E_M \\ \delta (E_M + E_L) \delta - k_1 E_L \\ \delta (E_M + E_L) \delta - k_1 E_L \\ 0 \end{bmatrix} \]}

The components of $\mathcal{G}(X, Z)$ are obviously zeros at $\mathcal{E}_0$ and the condition H2 is satisfied. The global asymptotic stability of $\mathcal{E}_0$ is therefore guaranteed wherever $\mathcal{R}_0 < 1$. The following results is hence established.

**Lemma 2.** The disease-free equilibrium point $\mathcal{E}_0$ of the model is globally asymptotically stable whenever $\mathcal{R}_0 < 1$.

In the next section we prove the global stability of the endemic equilibrium using Lyapunov functions technique.

**3.5. Global stability of $\mathcal{E}^*$**

**Theorem 2.** The endemic equilibrium of the COVID-19 model (1) is globally asymptotically stable when $\mathcal{R}_0 > 1$.

**Proof.** Consider the Lyapunov function

\[ V = \left( S_M - S_M - S_M \ln \frac{S_M}{S_M} \right) + \left( S_M - S_M - S_M \ln \frac{S_M}{S_M} \right) + \left( S_M - S_M - S_M \ln \frac{S_M}{S_M} \right) + \left( E_M - E_M - E_M \ln \frac{E_M}{E_M} \right) + \left( E_M - E_M - E_M \ln \frac{E_M}{E_M} \right) + \left( E_M - E_M - E_M \ln \frac{E_M}{E_M} \right) + \left( H - H - H \ln \frac{H}{H} \right) + \left( R - R - R \ln \frac{R}{R} \right). \]

Taking the derivative of $V$ yields

\[ \dot{V} = -((1-d) + \mu) \frac{S_M}{S_M} \dot{S}_M - k_1 E_M + \delta (E_M + E_L) \delta - k_1 E_L + \mu R \]

\[ = -((1-d) + \mu) \frac{S_M}{S_M} \dot{S}_M - k_1 E_M + \delta (E_M + E_L) \delta - k_1 E_L + \mu R \]

\[ = -((1-d) + \mu) \frac{S_M}{S_M} \dot{S}_M - k_1 E_M + \delta (E_M + E_L) \delta - k_1 E_L + \mu R. \]

After some simplification we have

\[ \dot{V} = -((1-d) + \mu) \frac{S_M}{S_M} \dot{S}_M - k_1 E_M + \delta (E_M + E_L) \delta - k_1 E_L + \mu R. \]

Therefore $\dot{V} < 0$, at the same time

\[ 0 = \mathcal{A} \mathcal{B} = \Rightarrow \frac{dV}{dt} = 0, \]

if $S_M = S_M$, $E_M = E_M$, $S_L = S_L$, $E_L = E_L$, $L = L$, $H = H$, $R = R$. Therefore, the largest compact invariant set for (1) is $\{\mathcal{E}^*\}$. Hence from the Lyapunov-LaSalle’s stability theorem [27], we conclude that $\mathcal{E}^*$ is globally asymptotically stable in the positive region $\mathcal{B}_{\mathcal{R}_0}$ if $\mathcal{A} < \mathcal{B}$.
3.6. Sensitivity analysis of $R_0$

Model parameters greatly affect the dynamical behaviour of models because of errors in the measurement or unavailability of parameter values. It has become very necessary to study the impact of parameter changes on the behaviour of model, so that parameters that are observed to play significant roles will be given the needed attention in their measurement (in the case of data availability) or measuring them more accurately. This is the goal of sensitivity analysis. Also, we can then begin to manage these parameters in an effort to handling the pandemic. We employed the normalized forward sensitivity index as a proxy for the sensitivity analysis. The normalized forward sensitivity index of model output $x$ relative to parameter $p_i$ is given by $\frac{\partial x}{\partial p_i}$. We also employed the technique of [28] for finding the sensitivity indexes of endemic equilibria of models of the form $\frac{dx}{dt} = f(x, p)$ where $x$ and $p$ are vectors of state variables and parameters respectively. Since the expressions for these indexes are complex, we evaluate them in Table 2 at the baseline parameter values provided in Table 1.

A positive sensitivity index $\frac{\partial S}{\partial p}$ of model output $x$ with respect to model parameter $p$ means that a 1% increase (decrease) in $p$ will lead to a $\frac{\partial S}{\partial p} \%$ increase (decrease) in $x$. Similarly, negative sensitivity index $\frac{\partial S}{\partial p}$ of model output $x$ with respect to model parameter $p$ means that a 1% increase (decrease) in $p$ will lead to a $\frac{\partial S}{\partial p} \%$ decrease (increase) in $x$. Therefore, in Table 2 we show the relative importance of $d$, $\beta$, $c$, $\rho$, $\delta$, $\mu_d$, $\mu$ and $\theta$ on the prevalence or otherwise of COVID-19 in Africa. In Table 3, we arrange the parameters in decreasing order of influence on the endemic equilibrium states and $R_0$. Table 3 indicates that, social distancing helps to protect susceptible individuals from the disease. The rate of recruitment $P_M$, into the Population by immigration increases the number of exposed immigrants. The rate of recruitment into the Population by net births increases the local exposure of individuals to COVID-19 and the number of symptomatic individuals.

4. Numerical simulation

Using the baseline parameter values in Table 1, we performed numerical experiments to verify the analytical results established among others.

4.1. Stability of equilibria

To illustrate the stability of the equilibria, the Covid-19 model Eq. 1 is numerically solved with varying initial conditions for two the scenarios (when $R_0 < 1$ and $R_0 > 1$). The results in Fig. 2 illustrate that $E_0$ and $E^*$ are locally asymptotically stable whenever $R_0 < 1$ and $R_0 > 1$ respectively.

### Table 2 Local sensitivity indexes of $E^*$ and $R_0$.

| Par. | $R_0$ | $S_0^*$ | $E_0^*$ | $S_L^*$ | $E_L^*$ | $I^*$ | $H^*$ | $R^*$ |
|------|-------|--------|--------|--------|--------|------|------|------|
| $P_M$ | 0.0000 | 1.0000 | 1.0000 | 0.09414 | 0.09414 | 0.2308 | 0.2308 | 0.2308 |
| $d$  | -2.3333 | 3.0420 | -0.1705 | 2.936 | -0.277 | -0.2609 | -0.2609 | -0.2609 |
| $\mu$ | -0.08703 | -0.05427 | -0.1270 | -0.2106 | -0.2833 | -0.2805 | -0.3252 | -0.3832 |
| $\delta$ | -0.3091 | 0.08187 | -0.5944 | -0.1747 | -0.8509 | 0.1878 | 0.1878 | -0.629 |
| $\rho$ | -0.3691 | 0.4226 | -0.3599 | 0.7988 | 0.0163 | -0.04045 | -0.2437 | 0.9223 |
| $P_L$ | 0.0000 | 7.088e-17 | -1.232e-18 | 0.9059 | 0.9039 | 0.7692 | 0.7692 | 0.7692 |
| $\theta$ | -0.01526 | 0.02974 | -0.001667 | 0.07109 | 0.03968 | -0.596 | 0.404 | 0.1013 |
| $\mu_d$ | -0.2196 | 0.08351 | -0.004681 | -0.04545 | -0.1336 | -0.4639 | -1.216 | -0.3161 |
| $\beta$ | 1.0000 | -1.3040 | 0.07309 | -1.2580 | 0.1187 | 0.1118 | 0.1118 | 0.1118 |
| $c$  | 1.0000 | -2.596 | 0.01455 | -0.1809 | 0.09319 | 0.08133 | 0.08133 | -0.8072 |

### Table 3 Ordering of parameters in terms of impact of variables.

| $R_0$ | $S_0^*$ | $E_0^*$ | $S_L^*$ | $E_L^*$ | $I^*$ | $H^*$ | $R^*$ |
|------|--------|--------|--------|--------|------|------|------|
| $d$  | $d$ | $P_M$ | $d$ | $P_L$ | $P_L$ | $\mu_d$ | $\rho$ |
| $\beta$ | $\beta$ | $\delta$ | $\beta$ | $\delta$ | $\rho$ | $\mu$ | $\rho$ |
| $c$  | $c$ | $\rho$ | $c$ | $\mu$ | $\mu_d$ | $\theta$ | $P_L$ |
| $\rho$ | $\rho$ | $P_M$ | $d$ | $\mu$ | $\mu$ | $\delta$ | $P_L$ |
| $\delta$ | $\delta$ | $\mu_d$ | $\sigma$ | $\mu$ | $P_M$ | $\rho$ | $\delta$ |
| $\mu_d$ | $\sigma$ | $c$ | $\delta$ | $P_M$ | $\beta$ | $\delta$ | $P_M$ |
| $\theta$ | $\theta$ | $\delta$ | $c$ | $\beta$ | $\delta$ | $c$ | $\theta$ |
| $P_M$ | $\mu$ | $P_M$ | $\sigma$ | $c$ | $\beta$ | $\delta$ | $\theta$ |
| $P_L$ | $\theta$ | $\theta$ | $\theta$ | $\sigma$ | $c$ | $c$ | $\theta$ |
| $\sigma$ | $P_L$ | $P_L$ | $\mu_d$ | $\rho$ | $\rho$ | $\theta$ | $\theta$ |
4.2. Impact of control parameters

In order to illustrate, numerically, the impact of the controls $b$, $d$ and $h$, model (1) is solved for varying values of each control, keeping all other model parameters constant. The results of the simulations are presented in Figs. 3–5.

It is observed from Fig. 3 that an increase in $\beta$ will lead to more Susceptibles getting exposed, especially the locals,
which will lead to increase in Infected persons and subsequently the hospitalized. Therefore, efforts needed to reduce $\beta$ such as use of PPEs and observing personal hygiene should be made, which corresponds to the observation made in [17]. Eating food and supplements that are rich in boosting the immune system will be helpful so as to save the healthcare system not to be overwhelmed which will be disastrous. The impact of $d$ is opposite to that of $\beta$. Therefore, attempts at increasing $d$ should be made. Thus, the social distancing protocol should be maintained for as long as the disease lingers on. The hospitalization control $\theta$, has a similar impact as $d$ even though it is not as impactful as $\beta$ and $d$. Therefore, a better approach to the fight against the COVID-19 disease should include measures aimed at reducing $\beta$, and increasing $d$ and $\theta$.

5. Conclusions

In this paper, we proposed an ODE model to describe the dynamics of COVID-19 in a variable-sized population, taking into account immigration. Several basic qualitative analyses and some numerical simulation have been conducted on the model. The model reveals a unique disease-free equilibrium and a unique endemic equilibrium points, which are stable whenever $R_0 < 1$ and $R_0 > 1$ respectively. Sensitivity analysis revealed that the most important factors to consider in the fight against the spread of COVID-19 include use of PPEs and personal hygiene ($d$), transmission probability ($\beta$), average number of contacts of infected persons per unit time (day) ($c$), the incubation period ($\delta$) and the rate of recovery ($\rho$). Therefore, efforts (such as quarantine, isolation, restriction on international travels, lock-downs, use of personal protective equipments (PPEs)) aimed at reducing these factors should be implemented. Except ($\beta$) and $c$, increasing any of the other parameters on which $R_0$ depends leads to disease-spread. The following measures are therefore recommended to curtail the spread of COVID-19 virus disease:

1. Infected persons should quickly be identified and sent for treatment.
2. Contact tracing should be carried out when an infected person is identified.
3. Quarantine exposed persons while clinical test is carried out.
4. The rate of treatment of infected persons should be increased.
5. Social distancing should be enforced.
6. Use of PPEs should be mandatory.
7. Personal hygiene should be practised.
8. Immigration restrictions should be observed.
9. Diet of general population should include more immune boosters.

These recommendations will help decision makers to assess the preparedness of their controls of the pandemic.
Authors contributions

All authors contributed equally to the development of the article.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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