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Mathematical modeling, analysis and numerical simulation of the COVID-19 transmission with mitigation of control strategies used in Cameroon

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A B S T R A C T

In this paper, we formulated a general model of COVID-19 model transmission using biological features of the disease and control strategies based on the isolation of exposed people, confinement (lock-downs) of the human population, testing people living risks area, wearing of masks and respect of hygienic rules. We provide a theoretical study of the model. We derive the basic reproduction number $R_0$, which determines the extinction and the persistence of the infection. It is shown that the model exhibits a backward bifurcation at $R_0 = 1$. The sensitivity analysis of the model has been performed to determine the impact of related parameters on outbreak severity. It is observed that the asymptomatic infectious group of individuals may play a major role in the spreading of transmission. Moreover, various mitigation strategies are investigated using the proposed model. A numerical evaluation of control strategies has been performed. We found that isolation has a real impact on COVID-19 transmission. When efforts are made through the tracing to isolate 80% of exposed people the disease disappears about 100 days. Although partial confinement does not eradicate the disease it is observed that, during partial confinement, when at least 10% of the partially confined population is totally confined, COVID-19 spread stops after 150 days. The strategy of massif testing has also a real impact on the disease. In that model, we found that when more than 95% of moderate and symptomatic infected people are isolated and isolated, the disease is also really controlled after 90 days. The wearing of masks and respecting hygiene rules are fundamental conditions to control the COVID-19.

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1. Introduction

The COVID-19, also known as the coronavirus pandemic, is an ongoing pandemic of coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus (SARS-CoV-2) [11]. The outbreak was first identified in Wuhan, China, in December 2019 [12,13]. The World Health Organization (WHO) declared the outbreak a Public Health Emergency of International Concern on 30th of January, and a pandemic on March 11 [14,15]. As of May 17, 2020, more than 463 million cases of COVID-19 have been reported in more than 188 countries and territories, resulting in more than 311,000 deaths. More than 1.69 million people have recovered [16].

The virus is primarily spread between people during close contact, most often via small droplets produced by coughing, sneezing, and talking [17–19]. The droplets usually fall to the ground or onto surfaces rather than traveling through air over long distances [17]. Less commonly, people may become infected by touching a contaminated surface and then touching their face [17,18]. It is most contagious during the first three days after the onset of symptoms, although the spread is possible before symptoms appear, and from people who do not show symptoms [17,18].

Common symptoms include fever, cough, fatigue, shortness of breath, and loss of smell [17]. Complications may include pneumonia and acute respiratory distress syndrome [20]. The time from exposure to onset of symptoms is typically around five days, but may range from two to fourteen days [21,22]. Actually, there is no
known vaccine or specific antiviral treatment [17]. Primary treatment is symptomatic and supportive therapy [23].

Furthermore, recommended preventive measures include hand washing, covering one’s mouth when coughing, maintaining distance from other people, wearing a face mask in public settings, and monitoring and self-isolation for people who suspect they are infected [17]. Authorities worldwide have responded by implementing travel restrictions, lock-downs, workplace hazard controls, and facility closures. Many places have also worked to increase testing capacity and trace contacts of infected persons.

Moreover, the pandemic has caused severe global economic disruption [24], including the largest global recession since the Great Depression [25]. It has led to the postponement or cancellation of sporting, religious, political, and cultural events [26], widespread supply shortages exacerbated by panic buying [27], and decreased emissions of pollutants and greenhouse gases [28]. Schools, universities, and colleges have been closed either on a nationwide or local basis in 186 countries, affecting approximately 98.5 percent of the world’s student population [29].

Besides, the COVID-19 pandemic was confirmed to have spread to Africa on February 14, 2020. The first confirmed case was in Egypt [30–31], and the first confirmed case in sub-Saharan Africa was in Nigeria [32]. Most of the identified imported cases have arrived from Europe and the United States rather than from China [33]. Most of the reported cases are from four countries: South Africa, Morocco, Egypt, and Algeria, but it is believed that there is widespread under-reporting in other African countries with less developed healthcare systems [34].

Thereby, the COVID-19 pandemic was confirmed to have spread to Cameroon, Central Africa on March 6, with its first confirmed case [35]. The infected person is a French national who arrived in the capital Yaoundé on February 24 [36]. On May 5, Cameroon had 2104 confirmed cases and 64 deaths [37] vs. 7392 confirmed cases on June 6, with 205 deaths [54]. On March 18, Cameroon Prime Minister Joseph Dion Ngute closed its land, air, and sea borders [38]. Then, on March 30, Cameroon’s Minister of Health announced the imminent launch of a coronavirus test campaign in the city of Douala. Dedicated teams will go door-to-door in the economic capital from April 2, to 6, says the minister [39]. On April 10, the government took 7 additional measures to stop the spread of COVID-19 in Cameroon. These measures take effect from Monday, April 13, 2020 [40]: wearing a mask in all areas open to the public; local establishment of specialized COVID-19 treatment centers in all regional capitals; intensification of the screening campaign with the collaboration of the Center Pasteur; intensification of the awareness campaign in urban and rural areas in both official languages; Continuation of activities essential to the economy in strict compliance with the Prime Minister directives of March 17, 2020; and sanction. On Tuesday, May 5, the Minister of Health announced the provision to healthcare personnel of 50,000 coveralls, 320,000 surgical masks, 220 backpack sprayers, 10,000 pairs of overalls [42].

Cameroon government choices control strategies based specially on; isolation of exposed or infected people, partial confinement, testing people of risk areas, and mandatory wearing of masks. Until now, no one mathematical model has been suggested modeling the real situation of COVID-19 propagation in Cameroon, to evaluate and to analyze various strategies used by the government to avoid hatching of COVID-19 disease in Cameroon. The present work is strongly motivated to suggest a general framework of COVID-19 simulation integrating real specificities of Cameroon and providing numerical evaluation and comparison of control strategies used by Cameroonian authorities. In literature, numerous general mathematical models have been published to analyze COVID-19 outbreaks in an effort to better understand the complex disease transmission [45–53,61–63]. But to our knowledge, few of these have specifically taken control actions into consideration [61].

In this paper, we formulated a mathematical model for the COVID-19 disease, which incorporates some key epidemiological and biological features of the disease such as variation infection form, control strategies taking account on some specificities of the Cameroonian population. The novelty of our model is based on his adequacy to the real situation of Cameroon. Since it is so difficult to confine totally population, government make many efforts to identify and isolate exposed peoples. From the 14th March 2020 Cameroonian government take some decisions to put the population in a context of partial confinement and total confinement for students. For instance, schools and universities are closed. Many administrations reduced their daily personal or/and the daily duration of their activities. That’s why it is important to consider the class of susceptible people who consider and apply these measures of partial confinement and total confinement. Another particularity of the model concerns variation of infection form which is very important on epidemiological view. The model suggested was deeply analyzed and numerical simulations have been performed to supported theoretical studies and to illustrate the effectiveness of each control strategy integrated. The sensitivity analysis of the model is carried out to identify the most influential parameters on the model output variables related to infected classes, which is the most robust estimations that are required.

The rest of the paper is organized as follows. After the formulation of the model in Section 2, we present its quantitative and qualitative analysis in Section 3. Numerical simulations are provided in Section 4. The last section is devoted to concluding remarks on how our work fits in the literature.

2. Model formulation

The proposed model classifies the human population according to the disease status and to the level exposition to the disease, namely: susceptible individuals S, quarantined individual Q, partially confined individuals C, totally confined individuals C, individuals in latency phase L, infected individuals with asymptomatic form Ia, infected individuals with benign (moderate) form Ib, infected individuals with serious form Is, quarantined infected individuals I and recovered individuals R. Thus, the total human population at time t denoted by N(t) is given by Eq. (1).

\[ N(t) = S(t) + Q(t) + C(t) + C(t) + L(t) + Ia(t) + Ia(t) + Is(t) + Is(t) + R(t). \] (1)

The population of coronavirus is denoted by V. The susceptible individuals are recruited through birth and immigration at a constant rate of \( \Lambda \). The disease can be transmitted directly through oral or nasal ingestion of droplets generated when an infected person coughs or sneezes, or indirectly through oral or nasal ingestion of droplets of saliva or discharge the nose of infected individuals left in environment [17–19]. Thus, the infection is regulated by the exposure with infected individuals at rates \( \beta_s(V/V + K) \) where \( \beta_s \) is the human-to-human per capita contact rate per unit time. Also, infection is regulated by the exposure with a free virus in nature at rates \( \beta_v \) per unit of time through the logistic dose-response function \( V(V + K) \) where \( K \) is a concentration of free virus that yields 50\% of chance for a susceptible individual to catch COVID-19. Thus, the force of infection is given in Eq. (2).

\[ \lambda_s = (1 - \pi) \left[ \beta_h \left( \frac{Ia + Is + R}{N} \right) + \beta_v \left( \frac{V}{V + K} \right) \right] \] (2)

where \( \pi \) is the proportion of infectious contact identified by public health workers.

In Cameroon, individuals partially confined are supposed able only to go work and market (for catering) but should avoid being where there are many people (more than 50) like mosques,
churches, beer-houses, snack bars, etc. [1,40,41]. The people partially confined are exposed to the disease through the force of infection \( \lambda_p = \epsilon \lambda_3 \) where \( \epsilon \) is the modification parameter which takes into account the fact that people partially confined are less exposed than the susceptible individuals. The susceptible individuals apply partial confinement rules at the rate \( p_3 \) and return to classical habits at rate \( p_1 \). When the situation becomes dramatic, the partial confinement could tend to the total confinement at the rate of \( t_2 \) and return to partial confinement \( t_1 \).

Susceptible individuals who have been known exposed with infected individuals or individuals in latency phases should be quarantined to observe their disease status and anticipate their treatment if it is necessary. This strategy control strategy reduces the expansion of the disease and its lethality. Thus, the force of infection, in this case, is given by Eq. (3).

\[
\lambda_q = \pi \beta_q \frac{\kappa L + L_a + I_b + I_s}{N}
\]

where the modification parameter \( 0 \leq \kappa \leq 1 \) accounts for the assumed reduction in transmissibility of latent individuals relative to infectious individuals. During isolation, if they have a negative test they will return in susceptible class. But if they have a positive test, they will be treated. They can heal at the rate of \( \alpha_q \) or die at the rate of \( d_1 \).

After the latency phase, most people with the COVID-19 will experience an asymptomatic form of infection at the rate of \( \omega_a \). In the two cases, they will recover without requiring special treatment \( \alpha_a \) and \( \alpha_b \) respectively. The older people and those with underlying medical problems like cardiovascular disease, diabetes, chronic respiratory disease and cancer are more likely to develop a serious illness at the rate of \( \omega_s \). Those who experience moderate respiratory illness may, at rate \( \sigma \), develop serious illness in case of superinfection or confection with malaria, influenza, or typhoid which are endemic diseases in Cameroon. The infected individuals who are not quarantined (\( I_b \), \( I_q \) and \( I_s \)) broadcast the virus in the environment at constant rates \( r_a \), \( r_b \) and \( r_t \) respectively. The pathogens are assumed to decay at a rate of \( \mu_v \). Through a test campaign launched by the Cameroonian government, most of those experiences moderate and serious can be tested and quarantined at the rate of \( v_b \) and \( v_t \) respectively. The infected individuals with serious form \( I_q \) and the quarantined infected individuals \( I_t \) can recover from the disease at constant rates \( \alpha_s \) and \( \alpha_t \) respectively. The infected individual who experiences a serious form of disease \( I_t \) can die because of disease at a constant rate of \( d_2 \). Infected individuals quarantined (\( I_q \) and \( I_t \)) could die due to the disease at the rate \( d_1 \) (which is supposed be less than \( d_2 \)). The human population is submitted to the natural mortality of \( \mu_h \).

The structure of the model is shown in Fig. 1. The dashed arrow indicates contamination of the environment by infected humans.

The dynamics of the disease can be described by the following system of non-linear differential equations:

\[
\begin{align*}
\dot{S} &= \lambda_p + p_1 C_p - (\lambda_q + \lambda_s + \mu_h + p_2) S, \\
C_p &= p_2 S + t_1 C_t - (\lambda_p + p_1 + t_2 + \mu_h) C_p, \\
C_t &= t_2 C_p - (t_1 + \mu_h) C_t, \\
Q &= \lambda_q S - (q + \alpha_q + \mu_h + d_1) Q, \\
\dot{L} &= \lambda_s S + \lambda_q C_p - (\omega_a + \omega_b + \omega_t + \mu_h) L, \\
\dot{I_b} &= \omega_a L - (\alpha_a + \mu_h) I_b, \\
\dot{I_q} &= \omega_b L - (\nu_b + \sigma + \alpha_b + \mu_b) I_b, \\
\dot{I_s} &= \nu_b I_b + \nu_t I_s - (\alpha_t + \mu_h + d_1) I_s, \\
\dot{I_t} &= \omega_s L + \sigma I_b - (\nu_t + \alpha_t + \mu_b + d_2) I_t, \\
\dot{R} &= \alpha_a I_a + \alpha_b I_b + \alpha_t I_t + \alpha_q Q - \mu_h R, \\
\dot{V} &= r_a r_b + r_s t_1 - \mu_V V,
\end{align*}
\]

We set \( k_1 = \mu_h + p_2, k_2 = p_1 + t_2 + \mu_h, k_3 = t_1 + \mu_h, k_4 = q + \alpha_q + \mu_h + d_1, k_5 = \omega_a + \omega_b + \omega_t + \mu_h, k_6 = \alpha_a + \mu_h, k_7 = \nu_b + \sigma + \alpha_b + \mu_h, k_8 = \alpha_t + \mu_h + d_1, \) and \( k_9 = \nu_t + \alpha_t + \mu_h + d_2. \)

The parameter values of system (4) used for numerical simulations are given in Table 1.
3. Mathematical analysis

3.1. Basic properties

3.1.1. Positivity of solutions

We investigate the asymptotic behavior of orbits starting in the nonnegative cone \( \mathbb{R}_+^1 \). Obviously, model (4) which is a C\( \infty \) differential system, admits a unique maximal solution for any associated Cauchy problem.

Theorem 3.1. Let \( (t_0 = 0, X_0 = (S(0), C_1(0), C_2(0), Q(0), L(0), I_2(0), I_3(0), I_4(0), L(0), R(0), V(0))) \in \mathbb{R} \times \mathbb{R}_+^1 \) and for \( T \in (0, +\infty) \), \( [0, T], X = (S(t), C_1(t), C_2(t), Q(t), L(t), I_2(t), I_3(t), I_4(t), L(t), R(t), V(t))) \) the maximal solution of the Cauchy problem associated to model (4). Then, \( \forall t \in [0, T], X(t) \in \mathbb{R}_+^1 \).

Proof: Let 

\[
\Delta = \left\{ t \in [0, T] \mid S(t) > 0, C_1(t) > 0, C_2(t) > 0, Q(t) > 0, L(t) > 0, I_2(t) > 0, I_3(t) > 0, L(t) > 0, R(t) > 0, V(t) > 0, \forall t \in [0, T] \right\}.
\]

By continuity of functions \( S, C_1, C_2, Q, L, I_2, I_3, L, R \) and \( V \) one can see that \( \Delta \neq \emptyset \). Let \( \bar{T} = \sup \Delta \). Now, we are going to show that \( \bar{T} = T \). Suppose \( \bar{T} < T \), then one has that \( S, C_1, C_2, Q, L, I_2, I_3, L, R \) and \( V \) are non negative on \([0, \bar{T}]\). At \( \bar{T} \), at least one of the following conditions is satisfied \( S(\bar{T}) = 0, C_1(\bar{T}) = 0, C_2(\bar{T}) = 0, Q(\bar{T}) = 0, L(\bar{T}) = 0, I_2(\bar{T}) = 0, I_3(\bar{T}) = 0, L(\bar{T}) = 0, R(\bar{T}) = 0 \) and \( V(\bar{T}) = 0 \). Suppose \( S(\bar{T}) = 0 \). Then from the first equation of model (4), one has

\[
\frac{d}{dt} \left( S^0 \left( \frac{\lambda_1 I(t) + \lambda_2 I(t) + p_2 + \mu_h}{S(t)} \right) dt \right) = \left( \Lambda + q Q(t) + p_1 C_2(t) \right) e^{\int_0^t \left( \frac{\lambda_1 I(t) + \lambda_2 I(t) + p_2 + \mu_h}{S(t)} \right) dt}.
\]

Integrating Eq. (5) from 0 to \( \bar{T} \) yields

\[
S(\bar{T}) = e^{-\int_0^\bar{T} \left( \frac{\lambda_1 I(t) + \lambda_2 I(t) + p_2 + \mu_h}{S(t)} \right) dt} \left( S(0) + \int_0^\bar{T} \left( e^{\int_0^t \left( \frac{\lambda_1 I(t) + \lambda_2 I(t) + p_2 + \mu_h}{S(t)} \right) dt} \right) dt \right).
\]

\[
(\Lambda + q Q(t) + p_1 C_2(t) dt) > 0.
\]

Similarly, one can show that \( C_1(\bar{T}) > 0, C_2(\bar{T}) > 0, Q(\bar{T}) > 0, L(\bar{T}) > 0, I_2(\bar{T}) > 0, I_3(\bar{T}) > 0, L(\bar{T}) > 0, R(\bar{T}) > 0 \) and \( V(\bar{T}) > 0 \). This is a contradiction. Then, \( \bar{T} = T \) and consequently the maximal solution \( S(t), C_1(t), C_2(t), Q(t), L(t), I_2(t), I_3(t), L(t), R(t), V(t)) \) of the Cauchy problem associated to model (4) is positive. This achieves the proof.

\[\square\]

3.1.2. Boundness of solutions

We first split the model (4) into two parts, the human population, and the virus population. Then, using a model (4), the dynamics of the total human population satisfy

\[
\dot{N} = \Lambda - \mu_h N - d_1 (Q + I_4) - d_2 I_3 \leq \Lambda - \mu_h N.
\]

Integrating the above differential inequality yields

\[
0 \leq N(t) \leq \Lambda \mu_h + \left( N(0) - \frac{\Lambda}{\mu_h} \right) e^{-\mu_h t}, \quad \forall t \geq 0,
\]

where \( N(0) \) is the initial value of \( N(t) \). It implies that \( 0 \leq N(t) \leq \frac{\Lambda}{\mu_h} \) for all \( t \geq 0 \) if \( N(0) \leq \frac{\Lambda}{\mu_h} \).

Now, suppose that \( N(0) \leq \frac{\Lambda}{\mu_h} \). Using the fact that \( I_2(t) + I_3(t) \leq \Lambda/\mu_h \), the dynamics of virus satisfies

\[
V \leq \frac{r \Lambda}{\mu_h - \mu_v} V,
\]

where \( r = \max(\tau_a, \tau_b, \tau_s) \). Integrating Eq. (7) gives

\[
0 \leq V(t) \leq \frac{r \Lambda}{\mu_v \mu_h} \left( V(0) - \frac{r \Lambda}{\mu_v \mu_h} \right) e^{-\mu_v t}, \quad \forall t \geq 0,
\]
where \(V(0)\) represents the initial value of \(V(t)\). It implies that \(0 \leq V(t) \leq \frac{rA}{\mu_v \mu_h}\) for all \(t \geq 0\) if \(V(0) \leq \frac{rA}{\mu_v \mu_h}\).

It then follows that
\[
N(t) + V(t) \leq \max \left( N(0) + V(0), \frac{\Lambda}{\mu_h} \left(1 + \frac{r}{\mu_v}\right)\right), \quad \forall t \geq 0. \tag{8}
\]

Thus, the region:
\[
\Omega = \left\{ (S, C, C_p, Q, L, I_a, I_b, I_c, I, R, V) \in \mathbb{R}^{11}_+, \ N \leq \frac{\Lambda}{\mu_h}, \ V \leq \frac{rA}{\mu_v \mu_h} \right\}, \tag{9}
\]
is positively invariant and attracting for model (4). Then, it is sufficient to consider the dynamics of the flow generated by model (4) in \(\Omega\).

**Remark 3.1.** Each maximal solution of model (4) is global.

**3.2. Asymptomatic stability of the disease-free equilibrium**

Model (4) has a disease-free equilibrium (DFE) obtained by setting the right-hand side of equations in model system (4) to zero with \(Q = L = I_a = I_b = I_c = V = 0\). The disease-free equilibrium is
\[
\mathcal{E} = (S_0, C_0^p, C_0^q, 0, 0, 0, 0, 0, 0, 0) \tag{10}
\]
where \(S_0\), \(C_0^p\) and \(C_0^q\) are given by
\[
\begin{align*}
S_0 &= \frac{k_\Lambda (\mu_h + p_1) + t_\mu \Lambda}{[k_\mu + (k_1 + p_1)k_\Lambda] \mu_h}, \\
C_0^p &= \frac{k_\mu k_3}{(k_1 + (k_1 + p_1)k_\Lambda) \mu_h}, \\
C_0^q &= \frac{k_\mu k_3}{(k_1 + (k_1 + p_1)k_\Lambda) \mu_h}.
\end{align*} \tag{11}
\]

Note that the total human population at the DFE, \(\mathcal{E}\), satisfies
\[
N_0 = S_0 + C_0^p + C_0^q = \frac{\Lambda}{\mu_h}. \tag{12}
\]

The basic reproduction number, which is very important for the qualitative analysis of the model, is determined here below by using the method of the next generation matrix used in van den Driessche and Watmough [44]. Following notations in van den Driessche and Watmough [44], matrices \(F\) and \(V\) for the new infection terms and the remaining transfer terms are, respectively, given by
\[
F = \begin{pmatrix}
0 & \frac{S_0 k_1}{N_0} & \frac{S_0 k_2}{N_0} & \frac{S_0 k_3}{N_0} & 0 & \frac{S_0 k_4}{N_0} \\
0 & 0 & \frac{1}{\Lambda} & \frac{1}{\Lambda} & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 \\
\end{pmatrix},
\]
and
\[
V = \begin{pmatrix}
k_4 & 0 & 0 & 0 & 0 & 0 \\
0 & k_5 & 0 & 0 & 0 & 0 \\
0 & 0 & -v_a & k_6 & 0 & 0 \\
0 & 0 & 0 & -v_b & k_7 & 0 \\
0 & 0 & 0 & 0 & k_8 & 0 \\
0 & 0 & 0 & 0 & 0 & k_9 \\
0 & 0 & 0 & 0 & 0 & -r_a - r_b - r_c \\
\end{pmatrix},
\]

The basic reproduction number denoted by \(R_0\) is defined as the average number of secondary cases produced in a completely susceptible population by a typical infected individual during its entire period of being infectious [43,44]. Mathematically, \(R_0\) is the spectral radius of the next-generation matrix, \(FV^{-1}\). After further simplification, we obtain
\[
R_0 = (1 - \pi) \left[ \frac{\beta_h (S_0 + C_0^q)}{N_0 k_5} + \frac{\omega_2 (C_0^q)}{k_7 k_9} + \frac{\omega_3 (C_0^q)}{k_5} + \frac{\omega_4 (C_0^q)}{k_6} \right] + \beta_i \left[ \frac{\omega_2 (C_0^q)}{k_7 k_9} + \frac{\omega_3 (C_0^q)}{k_5} + \frac{\omega_4 (C_0^q)}{k_6} \right] \tag{13}
\]

Thanks to Theorem 2 in van den Driessche and Watmough [44], we claim the following result.

**Lemma 3.1**. The DFE, \(\mathcal{E}\), of model (4) is locally asymptotically stable (LAS) if \(R_0 < 1\) and unstable if \(R_0 > 1\).

The biological implication of Lemma 3.1 is that a sufficiently small flow of infectious individuals will not generate an outbreak of the disease unless \(R_0 > 1\). For better control of the disease, the global asymptotic stability (GAS) of the DFE is needed. Actually, enlarging the
basin of attraction of $\hat{e}$ to be the entire $\Omega$ is, for the model under consideration a more challenging task involving relatively new results. We use the result of Kamgang and Sallet [55] for the global stability of the disease-free equilibrium for a class of epidemiological models.

Using the result of Kamgang and Sallet [55], model system (4) can be written in the following form:

$$\begin{align*}
\dot{X}_S &= A_1(X)(X_S - X_S^0) + A_{12}(X)X_I \\
\dot{X}_I &= A_2(X)X_I
\end{align*}\tag{14}$$

where $X_S$ represents the class of non infected individuals $(S, C_p, C_i)$ and the vector $X_I$ represents the class of infected individuals $(Q, L, I_a, I_b, I_q, I_v, V)$. Here, we have $X_S = (S, C_p, C_i)^T$, $X_I = (Q, L, I_a, I_b, I_q, I_v, V)^T$, $X = (X_S, X_I)^T$ and $X_S^0 = (S_0, C_{p}^0, C_{i}^0)^T$.

with

$$A_1(X) = \begin{pmatrix}
-k_1 & p_1 & 0 \\
p_2 & -k_2 & t_1 \\
0 & t_2 & -k_3
\end{pmatrix},$$

$$A_{12}(X) = \begin{pmatrix}
q & 0 & \zeta \psi \beta_h \zeta_\nu \frac{\zeta_\nu}{\zeta_\phi} & \zeta \psi \beta_h \zeta_\nu \frac{\zeta_\nu}{\zeta_\phi} & \zeta \psi \beta_h \zeta_\nu \frac{\zeta_\nu}{\zeta_\phi} & 0 & 0 \\
0 & -\zeta h \beta_h \zeta_\nu \frac{\zeta_\nu}{\zeta_\phi} & -\zeta \psi \beta_h \zeta_\nu \frac{\zeta_\nu}{\zeta_\phi} & 0 & -\zeta \psi \beta_h \zeta_\nu \frac{\zeta_\nu}{\zeta_\phi} & -\zeta \psi \beta_h \zeta_\nu \frac{\zeta_\nu}{\zeta_\phi} & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0
\end{pmatrix},$$

and

$$A_2(X) = \begin{pmatrix}
-k_4 & -k_5 & 0 & 0 & 0 & 0 & 0 \\
-k_5 & k_4 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & \omega_4 & -k_6 & 0 & 0 & 0 \\
0 & 0 & -k_6 & \omega_4 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \nu_b & -k_8 & \nu_5 \\
0 & 0 & 0 & 0 & \nu_b & -k_8 & \nu_5 \\
0 & 0 & r_a & r_b & 0 & r_s & -\mu_v
\end{pmatrix},$$

with $\psi := 1 + \varepsilon$ and $\zeta := 1 - \pi$.

A direct computation shows that the eigenvalues of $A_1(X)$ are real and negative. Thus the system $\dot{X}_c = A_1(X)(X_S - X_s^0)$ is globally asymptotically stable at the equilibrium $X_S^0 = (S_0, C_p^0, C_i^0)$. Note also that $A_2(X)$ is a Metzler matrix, i.e. a matrix such that off diagonal terms are non negative [56,57].

Let us consider the bounded set $D$:

$$D = \{X_S, X_I\} \in \Omega, \quad X_S \neq 0\tag{15}.$$ 

Let us recall the following theorem [55]

**Theorem 3.2.** Let $D \subset \mathbb{V} = \mathbb{R}^3 \times \mathbb{R}^7$. The system (14) is of class $C^1$, defined on $\mathbb{V}$. If

1. $D$ is positively invariant relative to (14).
2. The system $\dot{X}_c = A_1(X)(X_S - X_s^0)$ is globally asymptotically stable at the equilibrium $X_S^0 = (S_0, C_p^0, C_i^0)$ on the canonical projection of $D$ on $\mathbb{R}^3$.
3. For any $x \in D$, the matrix $A_2(X)$ is Metzler irreducible.
4. There exists a matrix $A_2$, which is an upper bound of the set $M = \{A_2(x) : x \in D\}$ with the property that if $\dot{A}_2 \in M$, for any $x \in D$, such that $\dot{A}_2(x) = A_2$, then $\bar{A}_2 \in \mathbb{R}^3 \times \{0_{3x}\}$.
5. The stability modulus of $\dot{A}_2$,

$$\alpha(\dot{A}_2) = \max_{\lambda \in \partial D} \Re(\lambda)$$

satisfied $\alpha(\dot{A}_2) < 0$.

Then the DFE is GAS in $D$. (See [55] for a proof).

Let us now verify the assumptions of the previous theorem: it is obvious that conditions (1–3) of the theorem are satisfied. An upper bound of the set of matrices $A_2$, which is the matrix $\dot{A}_2$ is given by

$$\dot{A}_2 = \begin{pmatrix}
-k_4 & -k_5 & 0 & 0 & 0 & 0 & 0 \\
0 & -k_5 & \xi \beta_h & 0 & 0 & 0 & 0 \\
0 & -k_5 & \xi \beta_h & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & -k_8 & \nu_5 & 0 & 0 \\
0 & 0 & 0 & 0 & \nu_5 & 0 & 0 \\
0 & 0 & r_a & r_b & 0 & r_s & -\mu_v
\end{pmatrix}.$$

To check condition (5) in Theorem 3.2, we will use the following useful lemma [55] which is the a characterization of Metzler stable matrices:

**Lemma 3.2.** Let $M$ be a square Metzler matrix written in block form $A \begin{pmatrix} A & B \\ C & D \end{pmatrix}$ with $A$ and $D$ square matrices. $M$ is Metzler stable if and only if matrices $A$ and $D - CA^{-1}B$ are Metzler stable.

Using Lemma 3.2, matrix $\dot{A}_2$ can be express in the form of the matrix $M$ with:
$$A = \begin{pmatrix} -k_8 & \pi \beta_n & \pi \beta_n & \pi \beta_n \\ 0 & -k_9 & \zeta \beta_n & \zeta \beta_n \\ 0 & \omega_a & -k_6 & 0 \\ 0 & \omega_b & 0 & -k_7 \end{pmatrix}, \quad B = \begin{pmatrix} 0 & \pi \beta_n & 0 & 0 \\ 0 & \zeta \beta_n & 0 & 0 \\ 0 & 0 & \sigma & 0 \\ 0 & 0 & \mu & \sigma \end{pmatrix}, \quad C = \begin{pmatrix} 0 & 0 & 0 & \nu_b \\ 0 & \omega_a & 0 & \sigma \\ 0 & \omega_b & \rho & \sigma \end{pmatrix}$$

$$D = \begin{pmatrix} -k_8 & \nu_b & 0 & 0 \\ 0 & -k_9 & 0 & 0 \\ 0 & \tau_s & -\mu & 0 \end{pmatrix}.$$ 

Clearly, $A$ is a stable Metzler matrix. Then, after some computations, we obtain $D - CA^{-1}B$ is a stable Metzler matrix if and only if

$$R_0^{\text{max}} = (1 - \pi) \frac{1}{N_0} \left( \beta_h \frac{\omega_a}{k_9} + \frac{\omega_b}{k_7} + \frac{\omega_c}{k_0} \right) + \beta_p \left( \frac{S_0 + \varepsilon C_0}{\mu} \right) \leq 1$$

Thus we claim the following result

**Theorem 3.3.** If $R_0^{\text{max}} \leq 1$, then the disease-free equilibrium $\hat{\xi}$ is globally asymptotically stable in $D$.

**Remark 3.2.** Note that the condition (16) is equivalent to

$$R_0 \leq R_c = \frac{(S_0 + \varepsilon C_0)}{\beta_h \mu} \left( \frac{\beta_p (S_0 + \varepsilon C_0)}{\beta_h \mu \mu + \beta_p (S_0 + \varepsilon C_0)} \right) R_2$$

where $R_1 = \frac{\omega_a}{k_9} + \frac{\omega_b}{k_7} + \frac{\omega_c}{k_0}$ and $R_2 = \frac{\omega_a}{k_9} + \frac{\omega_b}{k_7} + \frac{\omega_c}{k_0}$

Theorem (3.3) means that for $R_0 < R_c \leq 1$, the DFE $\hat{\xi}$ is the unique equilibrium in $D$ which is GAS. If $R_c < R_0 \leq 1$, the backward bifurcation phenomenon may occur in $\Omega$, i.e., the DFE $\hat{\xi}$, may coexist with two endemic equilibrium, one asymptotically stable and one unstable.

The epidemiological significance of the phenomenon of backward bifurcation is that the requirement of $R_c < R_0 < 1$ is, although necessary, no longer sufficient for disease eradication when the initial condition is taken in $\Omega$. In such a scenario, disease elimination would depend on various initial sizes of the population (state variables) chosen $\Omega$. That is, the presence of backward bifurcation in the COVID-19 transmission model (4) suggests that the feasibility of controlling COVID-19 when $R_c < R_0 < 1$ always be dependent on the initial sizes of the population even if they are chosen in $\Omega$.

To confirm whether or not the backward bifurcation phenomenon occurs in this case, one could use the approach developed in van den Driessche and Watmough [44], Castillo-Chavez and Song [59], which is based on the general centre manifold theory [58].

**Theorem 3.4.** The model (4) undergoes a backward bifurcation at $R_0 = 1$ when the parameters satisfy the condition

$$\frac{A_1 + A_2}{A_3} < 1.$$ 

where

$$A_1 = 2 \zeta (\chi_1 \chi_6 + \chi_1 \chi_7 + \chi_1 \chi_9) \frac{\beta_h}{N_0} \left( (1 - \epsilon) C_0 + C_0 \right) + 2 \zeta \epsilon (\chi_2 \chi_6 + \chi_2 \chi_7 + \chi_2 \chi_9) C_0 \frac{\beta_h}{N_0} + 2 \zeta \chi_1 \chi_2 \frac{\beta_p}{K} \left( \chi_1 + \epsilon \chi_2 \right),$$

$$A_2 = 2 \zeta (\chi_6 \chi_7 + 2 \chi_6 \chi_9 + 2 \chi_7 \chi_9 + \chi_5 + \chi_7 + \chi_9) \times \frac{(S_0 + \varepsilon C_0)}{N_0^2} + \zeta \chi_1 \chi_2 \frac{2 \beta_p (S_0 + \varepsilon C_0)}{K^2}.$$ 

$$A_3 = 2 \zeta \left( 1 - \epsilon \beta_p S_0 \right) \left( \chi_2 \chi_6 + \chi_2 \chi_7 + \chi_2 \chi_9 \right).$$

**Proof:** The theorem is the direct application of Theorem 4.1 in Castillo-Chavez and Song [59]. To check the existence of backward bifurcation of the model (4) at $R_0 = 1$, we use the center manifold theorem [58]. For this purpose, we introduce the following change of variables.

$$S = x_1, \quad C_p = x_2, \quad C_3 = x_3, \quad Q = x_4, \quad L = x_5, \quad I_a = x_6, \quad I_b = x_7, \quad I_q = x_8, \quad I_r = x_9, \quad R = x_{10} \quad \text{and} \quad V = x_{11}$$

so that

$$N = x_1 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8 + x_9 + x_{10}, \quad \lambda_s = (1 - \pi) \left[ \frac{\beta_h}{N} \frac{x_6 + x_7 + x_9}{N} + \beta_p \frac{x_{11}}{x_{11} + K} \right]$$

$$\lambda_p = \epsilon \lambda_s \quad \text{and} \quad \lambda_q = \pi \beta_p \frac{K x_5 + x_6 + x_7 + x_9}{N}$$

Further, by using the vector notation $x = (x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9, x_{10}, x_{11})^T$, model (4) can be written in the form $\dot{x} = f(x)$ with $f = (f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8, f_9, f_{10}, f_{11})^T$, as follows:

$$\begin{align*}
\dot{x}_1 &= \lambda_q x_1 - \lambda_s x_1 - \lambda_p x_2 - \frac{\mu x_1}{x_1}, \\
\dot{x}_2 &= \mu x_2 + \mu x_3 - \lambda_q x_2, \\
\dot{x}_3 &= \lambda_q x_2 - \lambda_p x_3, \\
\dot{x}_4 &= \lambda_p x_1 - \lambda_q x_4, \\
\dot{x}_5 &= \lambda_p x_1 + \lambda_p x_2 - \lambda_p x_5, \\
\dot{x}_6 &= \mu x_6 - \mu x_6, \\
\dot{x}_7 &= \mu x_7 - \mu x_7, \\
\dot{x}_8 &= \mu x_8 + \mu x_9 - \mu x_8, \\
\dot{x}_9 &= \mu x_9 + \mu x_9 - \mu x_9, \\
\dot{x}_{10} &= \lambda_q x_4 + \lambda_p x_4 + \lambda_p x_7 + \lambda_p x_8 + \lambda_q x_9 - \mu x_9, \\
\dot{x}_{11} &= \lambda_p x_6 + \mu x_7 + \mu x_9 - \mu x_9
\end{align*}$$

(20)
The Jacobian of system (20) at the DFE $\varepsilon$ is

$$J = \begin{bmatrix}
-k_1 & p_1 & 0 & q & -\pi \frac{\beta_S S_0}{N_0} & -\pi \frac{\beta_S S_0}{N_0} & -\pi \frac{\beta_S S_0}{N_0} & 0 & -\pi \frac{\beta_S S_0}{N_0} & 0 & -\frac{(1-\pi)\beta_S S_0}{N_0} \\
-p_2 & -k_2 & t_1 & 0 & 0 & -\pi \frac{\beta_S S_0}{N_0} & -\pi \frac{\beta_S S_0}{N_0} & 0 & -\pi \frac{\beta_S S_0}{N_0} & 0 & -\frac{(1-\pi)\beta_S S_0}{N_0} \\
0 & t_2 & -k_4 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & -k_4 & \pi \frac{\beta_S S_0}{N_0} & \pi \frac{\beta_S S_0}{N_0} & \pi \frac{\beta_S S_0}{N_0} & 0 & \pi \frac{\beta_S S_0}{N_0} & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \kappa \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \kappa \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \kappa \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \kappa \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \kappa \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \kappa
\end{bmatrix}.$$ 

where $\xi = 1 - \pi$.

The basic reproduction number of the transformed (linearized) model system (20) is the same as that of the original model given by Eq. (4). Therefore, choosing $\beta_h$ as a bifurcation parameter by solving for $\pi$ when $R_0 = 1$, one obtains

$$\beta_h^* = \left[ \frac{1}{1 - \pi} - \beta_v \left( \frac{S_0 + \pi \bar{c}_B^0}{k \mu_k k_5} \frac{\mu_k}{k_5} + \frac{\omega_k \mu_k}{k_5} + \frac{\omega_k p_0}{k_5} \right) \right]^{-1} \left( \frac{S_0 + \pi \bar{c}_B^0}{k \mu_k k_5} \frac{\mu_k}{k_5} + \frac{\omega_k \mu_k}{k_5} + \frac{\omega_k p_0}{k_5} \right).$$

It follows that the Jacobian $J(\varepsilon)$ of system (20) at the DFE $\varepsilon$, with $\beta_h = \beta_h^*$ denoted by $J_\beta$, has a simple zero eigenvalue (with all other eigenvalues having negative real parts). Hence, the Center Manifold theory [58] can be used to analyze the dynamics of the system (20). In particular, the theorem in Castillo and Song [59], reproduced below for convenience, will be used to show that when $R_0 > 1$ there exists an endemic equilibrium of system (20) which is locally asymptotically stable for $R_0$ near 1 under certain conditions.

**Theorem 3.5.** (Castillo-Chavez and Song [59]): Consider the following general system of ordinary differential equations with a parameter $\Phi$:

$$\frac{dz}{dt} = f(x, \Phi), f : \mathbb{R}^n \times \mathbb{R} \rightarrow \mathbb{R} \text{ and } f \in C^2(\mathbb{R}^n, \mathbb{R}),$$

where $0$ is an equilibrium point of the system (that is, $f(0, \Phi) = 0$ for all $\Phi$) and assume

1. $A = D_2 f(0, 0) = \left( \frac{\partial^2 f_k}{\partial x_i \partial x_j} \right)_{i,j=1}^n$ is the linearization matrix of system (22) around the equilibrium point $0$ with $\Phi$ evaluated at $0$. Zero is a simple eigenvalue of $A$ and other eigenvalues of $A$ have negative real parts;
2. Matrix $A$ has a right eigenvector $u$ and a left eigenvector $v$ (each corresponding to the zero eigenvalue). Let $f_k$ be the $k$th component of $f$ and

$$a = \sum_{k,i,j=1}^n v_k u_i \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0, 0) \text{ and } b = \sum_{k,i,j=1}^n v_k u_i \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0, 0).$$

then, the local dynamics of the system around the equilibrium point $0$ is totally determined by the signs of $a$ and $b$.

1. $a > 0$, $b > 0$. When $\Phi < 0$ with $|\Phi| \ll 1$, $0$ is locally asymptotically stable and there exists a positive unstable equilibrium; when $0 < \Phi < 1$, $0$ is unstable and there exists a negative, locally asymptotically stable equilibrium;
2. $a < 0$, $b < 0$. When $\Phi < 0$ with $|\Phi| \ll 1$, $0$ is unstable; when $0 < \Phi < 1$, $0$ is locally asymptotically stable equilibrium, and there exists a positive unstable equilibrium;
3. $a > 0$, $b < 0$. When $\Phi < 0$ with $|\Phi| \ll 1$, $0$ is unstable and there exists a locally asymptotically stable negative equilibrium; when $0 < \Phi < 1$, $0$ is stable, and a positive unstable equilibrium appears;
4. $a < 0$, $b > 0$. When $\Phi$ changes from negative to positive, $0$ changes its stability from stable to unstable. Correspondingly a negative unstable equilibrium becomes positive and locally asymptotically stable.

In order to apply the above theorem, the following computations are necessary (it should be noted that we are used $\beta_h^*$ as the bifurcation parameter, in place of $\Phi$ in Theorem 3.5).

**Eigenvectors of $J_\beta$:** For the case when $R_0 = 1$, it can be shown that the Jacobian of system (20) has a right eigenvector $U = (u_1, u_2, u_3, u_4, u_5, u_6, u_7, u_8, u_9, u_{10}, u_{11})^T$ verifying $J_\beta U = 0$ given by:

$$u_1 = -\chi_1 u_5, \quad u_2 = -\chi_2 u_5, \quad u_3 = \chi_3 u_5, \quad u_4 = \chi_4 u_5, \quad u_5 = u_5 > 0, \quad u_6 = \chi_6 u_5, \quad u_7 = \chi_7 u_5, \quad u_8 = \chi_8 u_5, \quad u_9 = \chi_9 u_5,$$

where

$$\chi_6 = \frac{\omega_5}{k_6}, \quad \chi_7 = \frac{\omega_5}{k_7}, \quad \chi_8 = \frac{1}{k_8} \left( \frac{v_k \omega_5}{k_7} + \frac{v_k \omega_5}{k_7} + \frac{v_k \omega_5}{k_7} \right), \quad \chi_9 = \frac{1}{k_9} \left( \frac{\omega_5 + \omega_5}{k_7} \right),$$

$$\chi_{11} = \frac{1}{\mu_h} \left( \frac{r_0 \omega_5}{k_6} + \frac{r_0 \omega_5}{k_7} + \frac{r_0 \omega_5}{k_7} \right), \quad \chi_4 = \frac{\pi \beta_h S_0}{k_4 N_0} \left( k + \frac{\omega_5 \dot{S}_0}{k_7} + \frac{\omega_5}{k_7} + \frac{\omega_5}{k_7} \right),$$

$$\chi_{10} = \frac{1}{\mu_h} \left( \omega_5 \chi_4 + \omega_5 \chi_6 + \omega_5 \chi_7 + \omega_5 \chi_8 + \omega_5 \chi_9 \right).$$
\[ \chi_1 = \frac{1}{\lambda} \left[ \Gamma \left( \sum_1 \frac{\beta_0 S_0}{N_0} (\chi_6 + \chi_7 + \chi_9) + \frac{\beta_0 S_0}{K} \chi_{11} \right) + p_1 e \sum_1 \right] \]

\[ \chi_2 = \frac{1}{\lambda} \left[ \left( \sum_1 \frac{\beta_0 S_0}{N_0} (\chi_6 + \chi_7 + \chi_9) \right) + \frac{1}{\lambda} \sum_1 \right] \]

where \( \Delta = \frac{k_1 k_2 k_3 - k_1 k_2 - p_1 k_1 p_3}{k_3} \gt 0, \quad \Gamma = \frac{k_1 k_2}{k_3} > 0 \) and \( \Psi = k_4 - q > 0 \).

Similarly, the components of the left eigenvectors \( \mathbf{V} = (v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8, v_9, v_{10}, v_{11}) \) of \( f_0 \) verifying \( \mathbf{V} f_0 = 0 \) are given by

\[ v_1 = 0, \quad v_2 = 0, \quad v_3 = 0, \quad v_4 = 0, \quad v_5 = v_7 > 0, \quad v_6 = \partial_6 v_5, \quad v_7 = \partial_7 v_5, \quad v_8 = 0, \quad v_9 = \partial_9 v_5, \quad v_{10} = 0 \) and \( v_{11} = \partial_{11} v_5 \)

where

\[ \partial_6 = \frac{1}{k_6} (A + \frac{B \varepsilon}{\mu_v}), \quad \partial_7 = \frac{1}{k_7} (A + \frac{B \varepsilon}{\mu_v}) \]

\[ \partial_9 = \frac{1}{k_9} (A + \frac{B \varepsilon}{\mu_v}) \quad \partial_{11} = \frac{B}{\mu_v} \]

\[ \text{Computation of } a: \text{ The bifurcation coefficient } a \text{ at the DFE is given by} \]

\[ a = \sum_{i,j,k=1}^{11} u_i u_j \frac{\partial^2 f_k}{\partial x_i \partial x_j} (\varepsilon_0, \beta_0) \]

\[ = 2 v_5 \left( u_1 u_6 \frac{\partial^2 f_5}{\partial x_1 \partial x_6} + u_1 u_7 \frac{\partial^2 f_5}{\partial x_1 \partial x_7} + u_1 u_9 \frac{\partial^2 f_5}{\partial x_1 \partial x_9} + u_1 u_{11} \frac{\partial^2 f_5}{\partial x_1 \partial x_{11}} \right) \]

\[ + 2 v_5 \left( u_2 u_6 \frac{\partial^2 f_5}{\partial x_2 \partial x_6} + u_2 u_7 \frac{\partial^2 f_5}{\partial x_2 \partial x_7} + u_2 u_9 \frac{\partial^2 f_5}{\partial x_2 \partial x_9} + u_2 u_{11} \frac{\partial^2 f_5}{\partial x_2 \partial x_{11}} \right) \]

\[ + 2 v_5 \left( u_3 u_6 \frac{\partial^2 f_5}{\partial x_3 \partial x_6} + u_3 u_7 \frac{\partial^2 f_5}{\partial x_3 \partial x_7} + u_3 u_9 \frac{\partial^2 f_5}{\partial x_3 \partial x_9} + u_3 u_{11} \frac{\partial^2 f_5}{\partial x_3 \partial x_{11}} \right) \]

\[ + v_5 \left( u_4 u_6 + u_4 u_7 + u_4 u_9 + u_4 u_{11} \right) \]

\[ = - (A_1 + A_2) + A_3 \mid u_5 u_7^2 \mid \]

where

\[ A_1 = 2 \xi (\chi_1 \chi_6 + \chi_1 \chi_7 + \chi_1 \chi_9) \frac{\beta_0}{N_0} ((1 - \varepsilon) C_0 + C_1) + 2 \xi \varepsilon (\chi_2 \chi_6 + \chi_2 \chi_7 + \chi_2 \chi_9) C_0 \frac{\beta_0}{N_0} \frac{\beta_0}{N_0} + 2 \xi \chi_1 \frac{\beta_0}{K} \chi_1 + \chi_2 \]

\[ A_2 = 2 \xi (\chi_6 \chi_7 + \chi_6 \chi_9 + \chi_6^2 + \chi_7^2 + \chi_8^2) \times \frac{(S_0 + \varepsilon C_1)}{N_0} + \frac{\chi_1^2}{N_0} \frac{\beta_0}{K} \]

\[ A_3 = \frac{(1 - \varepsilon) \beta_0 S_0}{N_0} (\chi_2 \chi_6 + \chi_2 \chi_7 + \chi_2 \chi_9) \]

Thus, \( a > 0 \iff \frac{A_3 + A_4}{A_3} < 1 \).

\[ \text{Computation of } b: \text{ The second bifurcation coefficient } b \text{ is given by} \]

\[ b = v_5 u_6 \frac{\partial^2 f_5}{\partial x_6 \partial x_7} (0, \beta_0) + v_5 u_7 \frac{\partial^2 f_5}{\partial x_7 \partial x_8} (0, \beta_0) + v_5 u_9 \frac{\partial^2 f_5}{\partial x_9 \partial x_{10}} (0, \beta_0) \]

\[ = (1 - \varepsilon) \frac{S_0 + \varepsilon C_1}{N_0} (\chi_6 + \chi_7 + \chi_9) u_5 u_7 > 0 \]

Thus, depending on the values of the parameters of the model system (4), the value of \( a \) can be positive or negative. So, if \( b > 0 \), if \( a > 0 \), model system (4) undergoes the phenomenon of backward bifurcation (see Theorem 3.5, item (1)). Also, if \( a < 0 \) (by Theorem 3.5, item (4)), we have established the result about the local stability of the endemic equilibrium of model system (4) for \( R_0^* > 1 \) but close to 1. This concludes the proof of Theorem 3.4 \( \square \)

4. Numerical simulation

4.1. Sensitivity analysis of model’s parameters

The sensitivity analysis of the model parameters done in this section aims to measure firstly the correlation between model's parameters (4) and state variables of infected people (see Table 2) and secondly the correlation between model's parameters (4) and threshold parameters \( R_0, R_0^{max} \) and \( R_c \) (see Table 5). After this, we compute the sensitivity index of threshold parameters \( R_0, R_0^{max} \) and \( R_c \) with respect to model's parameters (4).
We compute the partial ranking correlation coefficient (PRCC) of parameters against the model’s variables \( Q, l_0, l_1, l_2, l_3 \) and \( V \). A positive (negative) correlation coefficient corresponds to an increasing (decreasing) monotonic trend between the model’s variable and the parameter under consideration.

The results in Table 2 show values of PRCCs at time \( t = 3000 \) days of simulation. Each row in the table contains the coefficients for the corresponding parameter against the variables in columns. Note that, one parameter in Table 2 is said “significantly correlated to one state variable” if absolute value of PRCC is more than 0.5 and \( p - \text{value} < 0.001 \). We present in Table 3 the list of parameters which are significantly correlated to state variable \( Q, l_0, l_1, l_2, l_3 \) and \( V \) of model (4).

The parameters \( \beta_6 \) (exposure rate to infected people) and \( \alpha_a \) (recovery rate of asymptomatic infected people) are those significantly correlated to state variables \( Q, l_0, l_1, l_2, l_3 \) which are related to infected people. This suggests that an effective control strategy should aim to reduce significantly human contact and to quickly identify asymptomatic infected people in order to isolate and treat them.

The relevance of the basic reproduction ratio of \( R_0 \) is due to the Lemma 3.1. It is one important key parameter for controlling the disease. The parameters \( R_0^{\alpha_{max}} \) and \( R_0 \) are also important to determine conditions of the global stability of DF. From the previously sampled parameter values, we compute the PRCC between \( R_0, R_0^{\alpha_{max}} \) and \( R_0 \) and each parameter of the model (4). The parameters with large PRCC values (> 0.5 or < −0.5) statistically have the most influence [60]. The straightforward computations give on Table 4 the results concerning computation of parameter PRCCs with \( R_0, R_0^{\alpha_{max}} \) and \( R_0 \) thresholds.

On Table 5 we give the list of parameters of model (4) more correlated to \( R_0, R_0^{\alpha_{max}} \) and \( R_0 \). It is clear that the parameter \( \beta_6 \) is the one-parameter strongly correlated to \( R_0, R_0^{\alpha_{max}} \) and \( R_0 \).

The previous computation (PRCC) give us the parameters correlated to \( R_0, R_0^{\alpha_{max}} \) and \( R_0 \). We want now to evaluate quantitatively how the parameters of the model can increase or decrease the values of threshold quantities \( R_0, R_0^{\alpha_{max}} \) and \( R_0 \). This should be useful to identify the parameters that should be taken into consideration when considering an intervention strategy. Since the parameters \( R_0, R_0^{\alpha_{max}} \) and \( R_0 \) are differentiable functions of the parameters, the sensitivity index may alternatively be defined using partial derivatives. For instance, the computation of the sensitivity index of \( R_0 \) with respect to \( p \) is defined as follows:

\[
\gamma_{R_0}^{p} = \frac{\partial R_0}{\partial p} \cdot \frac{p}{R_0}.
\]

The result concerning the computation of the sensitivity index of \( R_0, R_0^{\alpha_{max}} \) and \( R_0 \) with respect to each parameter is given in the Table 6.

The parameters whose sensitivity index has negative sign decrease the value of the corresponding threshold as their values increase, while those with positive sensitivity index increase the value of the corresponding threshold as they increase. For instance, if the parameter value of \( \epsilon \) increase for 10% then the value of \( R_0 \) will increase for 4.9%. We summarize in Table 7 the list of model's

**Table 2**

| Parameters | Range | \( Q \) | \( l_0 \) | \( l_1 \) | \( l_2 \) | \( l_3 \) | \( V \) |
|------------|-------|---------|---------|---------|---------|---------|-------|
| \( \Lambda \) | [1−100] | 0.1831  | 0.1852  | 0.1843  | 0.0053  | 0.3033  | 0.0076 |
| \( \mu_b \) | 0.001–0.999 | −0.0022 | 0.0605  | 0.0023  | −0.1409 | 0.0600  | 0.1167 |
| \( \beta_s \) | 0.001–0.999 | 0.6824** | 0.5938** | 0.6105** | 0.6789** | 0.5557** | 0.6269** |
| \( \beta_t \) | 0.001–0.999 | 0.0088  | −0.1213 | −0.0573 | 0.0010  | 0.0106  | 0.0585 |
| \( q \) | 0.001–0.999 | 0.1424  | 0.0493  | 0.2514  | 0.0128  | 0.1226  | 0.0175 |
| \( p_t \) | 0.001–0.999 | −0.5764** | −0.2188 | −0.5455 | −0.3697 | −0.3160 | −0.2981 |
| \( \lambda_1 \) | 0.001–0.999 | 0.0112  | −0.0113 | −0.0888 | 0.0391  | −0.0329 | −0.2615 |
| \( \pi_1 \) | 0.001–0.999 | 0.1641  | 0.0893  | 0.1295  | 0.0286  | −0.0643 | 0.2058 |
| \( \pi_t \) | 0.001–0.999 | 0.0611  | −0.0583 | 0.0500  | 0.0774  | −0.1312 | 0.2500 |
| \( d_1 \) | 0.001–0.999 | −0.0916 | 0.0074  | 0.0222  | 0.0628  | 0.1065  | 0.0749 |
| \( d_2 \) | 0.001–0.999 | 0.0125  | −0.1768 | 0.0716  | 0.1505  | −0.3062 | −0.2022 |
| \( K \) | [1−10^8] | 0.1961  | −0.1444 | 0.1738  | −0.2030 | 0.0651  | 0.0613 |
| \( \omega_q \) | 0.001–0.999 | 0.0003  | 0.0823  | 0.0369  | 0.2173  | 0.2012  | 0.2489 |
| \( \omega_p \) | 0.001–0.999 | 0.0091  | 0.0458  | 0.0906  | 0.0406  | 0.0634  | 0.0583 |
| \( \alpha_a \) | 0.001–0.999 | 0.0348  | 0.0974  | 0.0991  | 0.0046  | 0.0206  | 0.1799 |
| \( \sigma \) | 0.001–0.999 | 0.0112  | 0.2058  | 0.0994  | 0.0046  | 0.0206  | 0.1799 |

**Table 3**

| Variables | \( Q \) | \( l_0 \) | \( l_1 \) | \( l_2 \) | \( l_3 \) | \( V \) |
|-----------|---------|---------|---------|---------|---------|-------|

Correlated parameters significantly

\( \beta_s, \alpha_a, p_t \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

| Correlated parameters significantly | \( \beta_s, \alpha_a, p_t \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) | \( \beta_t, \alpha_a \) |
|-----------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

\( \beta_t, \alpha_a \)

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\( \beta_t, \alpha_a \)
parameters which significantly affect (sensitivity index > 0.5 or < -0.5) the threshold parameters \( R_0, R_0^{\text{max}} \) and \( R_c \).

It is clearly observed from Table 7 that the parameters \( \pi \) and \( \beta_3 \) are those modify quickly the threshold parameters \( R_0, R_0^{\text{max}} \) and \( R_c \). This means that it is firstly urgent for Cameroonian authorities to improve strategies to identify exposed people in order to isolate them. Secondly, maximise the strategies to reduce human and environmental transmission.

### 4.2. General dynamics

Numerical simulations using a set of reasonable parameter values in Table 1 is carried out to support analytical results and to evaluate numerically efficiency of control strategies.

The Fig. 2 illustrate global stabilities of disease equilibrium of model (4) using various initial conditions when \( \Lambda = 10, K = 10^6 \) (so that \( R_0 = 0.6910 < 1 \)). All other parameter values are as in Table 1. As it is expected the solutions of (4) converge toward disease equilibrium.

The Fig. 3 shows time series of model (4) using various initial condition when \( \Lambda = 100, K = 10^3 \) (so that \( R_0 = 4.01 > 1 \)) and all other parameters are as in Table 1. As it is expected the solutions of (4) converge toward endemic equilibrium.

### 4.3. Impact of controls strategies

Now, numerical simulations are carried out to investigate the impact of control strategies well known and actually applied over the world:

**Isolation:** It is important to isolate exposed people, individuals traveling from affected countries or potential carriers as it is applied carefully by Cameroonian authorities. This control strategy increases the value of parameter \( \pi \) which concerns the proportion of infectious contact identified. We simulated a model (4) for \( \pi = 0.8(R_0 = 0.89), \pi = 0.6(R_0 = 1.78) \) and \( \pi = 0.5(R_0 = 2.22) \) when \( \Lambda = 100, K = 10^3 \) and all other parameter values are as in Table 1. As we can see in Fig. 4, isolation has a real impact on COVID-19 transmission. When...
efforts are made through tracing to isolate 80% of exposed people the disease disappears about 100 days. It is then vital to isolate those who have been exposed to the disease or those coming from affected countries. That’s why many countries used contact tracing to identify exposed people to isolate them. Dr Laura Breeher is medical director of occupational health services at the Mayo Clinic (U.S) and she said: “Contact tracing, it’s having a moment of glory right now with COVID-19 because of the crucial importance of identifying those individuals who have been exposed quickly and isolating or quarantining them” [8].

**Confinement:** Partial confinement in Cameroon consist to avoid social gathering, imposing travel restrictions and to maintain social distancing [1]. The WHO recommend early execution of this strategies when the disease is detected [9]. The implementation of this control action matches with the increasing of the value of $p_2$ in our model (4). As we supposed in our model, those who are partially confined have 50% ($\epsilon = 0.5$ in Table 1) less than those that are not confined to be infected. We simulated model (4) for $p_2 = 0.94(R_0 = 3.03)$, $p_2 = 0.54(R_0 = 3.08)$ and $p_2 = 0.04(R_0 = 4.01)$ when $\Lambda = 100$, $K = 10^3$ and all other parameters values are as in Table 1. As we can see in Fig. 5 partial confinement does not have effective impact. Total confinement reduce strongly movement of population. In that context, every human contacts is strongly pro-

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**Fig. 2.** Simulation of model (4) using various initial conditions when $\Lambda = 10$, $K = 10^6$ and all parameters values are as in Table 1 (so that $R_0 = 0.69 < 1$). (a) Infected people and (b) Virus density.

**Fig. 3.** Simulation of model (4) using various initial conditions when $\Lambda = 100$, $K = 10^3$ and all parameters values are as in Table 1 (so that $R_0 = 4.01 > 1$). (a) Infected people and (b) Virus density.

**Fig. 4.** Simulations of model (4) showing impact of control strategy based on isolation of exposed people (a) Infected people and (b) Virus density.
with replications, so that the value of \( t_2 \) increases. But people totally confined are supposed to be partially confined first. We simulated model (4) for \( t_2 = 0.1(\mathcal{R}_0 = 0.947) \), \( t_2 = 0.01(\mathcal{R}_0 = 2.5) \) and \( p_2 = 0.001(\mathcal{R}_0 = 3.03) \) when \( \Lambda = 100, K = 10^5 \). \( p_2 = 0.94 \) and all other parameters values are as in Table 1. The Fig. 6 illustrate that when at least 10% of those partially confined are totally confined, the disease can disappear after 130 days.

**Testing**: Testing people for the COVID-19 is important in helping to knowing who has been infected and where can allow the health service to plan, and more effectively cope. Efficient and timely virus testing is a crucial prerequisite for early identification, reporting, isolation, diagnosis, and treatment. Testing casts a direct impact on the effectiveness of epidemic prevention and control. The WHO has called on all countries to ramp up testing programs. Dr Tedros, Director-General of the WHO, made it clear at the media briefing in Geneva on March 16, "We have a simple message for all countries: test, test, test. Test every suspected case." Individuals who have positive tests should be isolated. In Cameroon for example, systematic testing is achieved to those coming at the hospital for medical consultation. This action should increase quickly the value of \( v_b \) and \( v_s \) in model (4). We simulated model (4) for \( v_b = v_s = 0.1(\mathcal{R}_0 = 4.01) \), \( v_b = v_s = 0.5(\mathcal{R}_0 = 1.44) \) and \( v_b = v_s = 0.95(\mathcal{R}_0 = 0.89) \) when \( \Lambda = 100, K = 10^5 \) and all other parameters values are as in Table 1. Fig. 7 illustrates the advantages of testing. If more than 95% of moderate and symptomatic infected people are identified and isolated, the disease is controlled after 100 days.
Mask and hygiene rules: Some studies to Hong Kong with hamsters showed that the transmission of COVID-19 was reduced by more than 60% when the masks are massively used [10]. What should be happened for human population? Otherwise this recommendation is always coupled with the strict respect for hygienic rules. These should really reduce the value of $\beta_h$ and $\beta_v$. We simulated model (4) for $\beta_h = \beta_h = 0.18 (R_0 = 4.01)$, $\beta_v = \beta_v = 0.09 (R_0 = 2.00)$ and $\beta_h = \beta_v = 0.018 (R_0 = 0.40)$ when $\Lambda = 100$, $K = 10^3$ and all other parameters values are as in Table 1. It is obvious to see that reduction for 10% for example of $\beta_h$ and $\beta_v$ reduce also 10% values of $R_0$. Fig. 8 confirm the real impact of these parameters.

5. Conclusion

We presented a mathematical model for the dynamics of COVID-19 whose first 508 cases were reported in December 2019 in Wuhan-China and the first case was confirmed in Cameroon on March 6, [35]. On June 20, Cameroon reported 10,638 confirmed cases and 282 deaths [54]. In this work, we proposed a COVID-19 model with the mitigation of control strategies used in Cameroon. The aim was to evaluate the impact of controls strategies based on isolation of exposed people, confinement of human population, testing people living risks area, wearing of masks, and respect of hygienic rules to curtail the spread of COVID-19 disease. Most of the mathematical models existing in literature are focused on modeling and predicting the disease [45–53,61–63].

We suggest a model that takes into account biological and epidemiological facts known of the disease and the control actions used in Cameroon. A qualitative analysis of the model has been presented. Our findings on the long term dynamics of the system can be summarized as follows: (1) we computed the disease-free equilibrium and derived the basic reproduction number $R_0$ that determines the outcome of COVID-19; (2) we proved that there exists a threshold parameter $R_C$ such that the disease-free equilibrium is globally asymptotically stable whenever $R_0 < R_C < 1$, while when $R_C < R_0 < 1$ the model can exhibit the phenomenon of backward bifurcation; (3) the sensitivity analysis of the system has been performed. We found that state variables related to infected people are most sensitive to exposure rates to infected people and the recovery rate of asymptomatic infected people. This suggests that effective control strategies should reduce significantly human contact and to quickly identify asymptomatic infected people in order to isolate and treat them; (4) numerical simulation has been presented to illustrate the theoretical results on the general dynamics of the model. A numerical evaluation of control strategies has been performed. We found that isolation has a real impact on COVID-19 transmission. When efforts are made through tracing to isolate 80% of exposed people the disease disappears about 100 days. Although partial confinement does not eradicate the disease it is observed that, during partial confinement, when at least 10% of the partially confined population is totally confined, COVID-19 spread stops after 150 days. The strategy of testing has also a real impact on the disease. In that model, we found that when more than 95% of moderate and symptomatic infected people are identified and isolated, the disease is also really controlled after 90 days. The wearing of mask and respecting hygiene rules are fundamental conditions to control the COVID-19. In fact, we can see in Fig. 8 and by sensitivity analysis, the parameters $\beta_h$ greatly influence the parameter $R_0$ more than other parameters. The disease disappear after 75 days when $\beta_h = 0.018$.

The theory and applications of fractional calculus have become extremely useful and important in modeling of biological processes [65] and [66]. Some recent works use fractional calculus compartmental for modeling of infectious disease dynamics [64] and [67]. There are some improvements and extensions of the model (4) on which we are planning to work: the introduction of fractional derivatives and eventually the parameter and state estimation by using available data. We are actually using the fractional derivatives approach in the case of Cholera.

Credit author statement

All authors equally contributed in this manuscript.

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.

References

[1] Services du premier ministre. Déclaration spéciale du Premier Ministre, Chef du Gouvernement ce 17 mars 2020: https://www.pcm.gov.cm.
[2] World statistics. Cameroon. http://www.statistiques-mondiales.com/cameroun.htm.
[3] Jean-Christophe L., Sandrine R., Quitterie R., Nathalie F., Loc B. Syndrome respiratoire aigu sévère Coronavirus 2 (COVID-19), Hospices Civils Lyons.
[4] Ministry of public health of cameroon. COVID-19 STATISTICS http://covid19.minsante.cm.
[5] Pateron D., Raphael M., Trinh-Duc A., COVID-19 Diagnostic et Prise en charge thérapeutique. Elsevier.
[6] Présidence de la république du cameroun. Coronavirus: mesures instruites par le Président Paul BIYA https://www.prc.cm.
[7] Présidence de la république du cameroun. Reprise des cours https://www.prc.cm.
[8] TIME. What is contact tracing?Here’s How It Could Be Used to Help Fight Coronavirus.2020.
Novel coronavirus “China”. World Health Organization (WHO)2020;https://www.who.int/csr/don/12-12-2020-new-coronavirus-china-en/.

Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, et al. “Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China”. Lancet 2020;395(10223):497–506. doi:10.1016/S0140-6736(20)30183-5. PMC 7159299. PMID 31986296.

World Health Organization (WHO). “Statement on the second meeting of the international health regulations (2005) emergency committee regarding the outbreak of novel coronavirus (2019-nCoV)”. 2020a. Archived from the original on 31 January 2020. Retrieved 30 January 2020.

World Health Organization (WHO). 2020b. 11 March 2020. WHO Director-General’s opening remarks at the media briefing on COVID-19.

ArcGIS. “COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU)”. Johns Hopkins University; 2020.

World Health Organization (WHO). Okra on coronaviruses (COVID-19). 2020c. Archived from the original on 14 May 2020. Retrieved 14 May.

Centers for Disease Control and Prevention (CDC). How COVID-19 spreads. 2020a. Archived from the original on 3 April 2020. Retrieved 3 April.

European Centre for Disease Prevention and Control. Okra on COVID-19. 2020.

U.S. Centers for Disease Control and Prevention (CDC). Interim clinical guidance for management of patients with confirmed coronavirus disease (COVID-19). 2020b. Retrieved 11 April 2020.

U.S. Centers for Disease Control and Prevention (CDC). Symptoms of novel coronavirus (2019-nCoV). 2020c. Retrieved 11 February 2020.

Yelavani TP, Meyer CG. The COVID-19 epidemic. Tropical Med Int Health 2020;25(3):278–80. doi:10.1111/tmi.13383. PMC 7168770. PMID 32052514.

U.S. Centers for Disease Control and Prevention (CDC). Prevention. Caring for yourself at home. 2020d. Retrieved 23 March 2020.

Editorial. The New York Times. Here comes the Coronavirus Pandemic: Now, after many fire drills, the world may be facing a real fire. 2020. Retrieved 1 March 2020.

IMF Blog. The Great Lockdown: Worst Economic Downturn Since the Great Depression. 2020.

A List of What’s Been Canceled Because of the Coronavirus. 2020. Retrieved 11 April 2020. The New York Times.

Scipioni J. Why there will soon be tons of toilet paper, and what food may be scarce, according to supply chain experts. CNBC; 2020.

Watts J, Kommenda N. Coronavirus pandemic leading to huge drop in air pollution. The Guardian; 2020. ISSN 0261–3077.

UNESCO. COVID-19 educational disruption and response. 2020. Retrieved 28 March 2020.

BBC News. Beijing orders 14-day quarantine for all returnees. 2020a. Retrieved 24 March 2020.

Egyt T. Egypt announces first coronavirus infection. 2020.

BBC News. Nigeria confirms first coronavirus case. 2020b. Retrieved 24 March 2020.

Maclean R. Africa braces for coronavirus, but slowly. The New York Times; 2020.

Burke J, Mumin AA. Somali medics report rapid rise in deaths as COVID-19 spreads. The Guardian; 2020.

Kouagheu J. Cameroon confirms first case of coronavirus. Reuters; 2020.

Lukong P, Wousou K. Cameroon, togo report first confirmed cases of coronavirus. Bloomberg; 2020.

Le M. Au cameroun, sur la piste du coronavirus dans les quartiers de douala. 2020. In French.

TVSMONDE (in French). Coronavirus: le cameroun ferme ses frontières. Retrieved 10 April 2020a.

RFI (in French). Coronavirus: au cameroun, le silence de paul biya, face l’épidémie, fait parler. 2020b.

CRTWeek 9 April 2020. 7 mesures supplémentaires contre la propagation du COVID-19 au camerounee mesure 1 : port du masque obligatoire. 2020. (Tweet) in French. Retrieved 10 April 2020 – via Twitter.