ADV MATH SCI JOURNAL
Advances in Mathematics: Scientific Journal **11** (2022), no.9, 741–757
ISSN: 1857-8365 (printed); 1857-8438 (electronic)
https://doi.org/10.37418/amsj.11.9.1

MATHEMATICAL MODELING AND SIMULATION OF EARLIER STAGES OF THE COVID-19 EPIDEMIC IN MALI

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ABSTRACT. In this paper, we propose a mathematical model to predict the spread of the coronavirus disease (COVID-19) in Mali. Official data on the number of confirmed cases over 30 days are used to calibrate the model to the Malian context. The positivity, the boundness, the existence and the uniqueness of the solution of the system of differential equations constituting the model have been proven. The basic reproduction number R_0 was calculated and its analysis against the parameters of the model was made. The numerical value of R_0 allowed us to calculate the final size of the epidemic in the absence of any intervention measures. The results of the numerical simulations showed that on the one hand, the peak of the epidemic can be reached on the 184th day with an average of 4 million infected if the barrier measures are not rigorously applied. But on the other hand, they support that the disease can be controlled by adherence to barrier measures, mass screening or a combination of both.

1. INTRODUCTION

The COVID-19 disease appeared in China in late 2019. It is caused by SARS-Cov-2, a virus which belongs to the coronavirus family. At the origin of deadly

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2020 *Mathematics Subject Classification.* 34A12, 37N25, 65L04, 92B05.
Key words and phrases. Epidemic model, COVID-19, Mathematical analysis, Basic reproduction number, epidemic prediction, epidemic peak, numerical simulations.
Submitted: 12.08.2022; *Accepted:* 27.08.2022; *Published:* 12.09.2022.

epidemics, these viruses can cause a simple cold as well as a severe respiratory infection such as pneumonia. It has been officially declared as a pandemic on March 11, 2020 by the World Health Organization (WHO). On March 18, 2020, the government of Mali announced several measures with immediate effect while no cases have yet been recorded, namely the suspension until further notice of commercial flights from affected countries, with the exception of cargo flights, the closure of all public, private, and religious schools from kindergarten to higher education and the suspension until further notice of all public gatherings, including workshops, conferences, seminars, and popular meetings.

These measures were reinforced on March 25 by the establishment of a state of health emergency and a curfew from 9 p.m. to 5 a.m., effective from March 26, 2020. In Mali, the first cases (two in number) were reported on March 25, 2020, at which time the incidence, i.e. the daily number of new confirmed cases is strictly positive. The incidence data plotted in Figure 1 are not estimated but were obtained from the Malian Ministry of Health and Social Affairs.

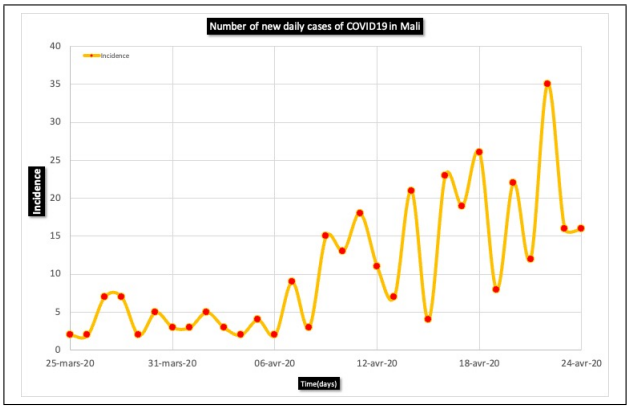


FIGURE 1. Number of new confirmed cases of COVID-19 in Mali from March 25 to April 24, 2020.

In epidemiology, mathematical modeling plays an important role in understanding the dynamics of infectious diseases in a population and is widely used to successfully predict the outcome of an epidemic. The most commonly used epidemic models are the SIS, SIR and SEIR models [3]. The SIR model is a very well established and widely used model for various epidemics [9]. Several mathematical

models have been proposed to study the dynamics of epidemic diseases. Mathematical models that analyze the spread of COVID-19 have begun to appear in published articles and online resources [2, 9, 10].

Several compartmental models have already been proposed and analyzed for the COVID-19 epidemic in different countries [5, 11]. For example, the compartments corresponding to suspected cases, which consisted of individuals with similar symptoms but were not confirmed cases, and directly infected individuals were incorporated in [5]. The modified SEIR model that included asymptomatic and treatment compartments for occurrences in Wuhan (in China), the city where the epidemic began, and outside Wuhan was used in [5]. An alternative approach that consists in separating the compartment for quarantined individuals in the SIR model to account for the containment measures applied by the public was introduced in [6]. The stability of epidemic models has been widely studied in the literature [4, 12]. In this paper, we consider the SLIHR model which is an extension of the SEIR model describing the spread of COVID-19 disease in the Malian population.

2. Mathematical model

The spread of infectious agents such as COVID-19 is a dynamic phenomenon where the number of susceptible, latent, infectious and removed individuals evolves over time and contacts between susceptible and infected individuals. This phenomenon can be described by mathematical models. These models, which are an approximation of reality, have proven to be effective in predicting epidemics such as influenza, Ebola and many others. They are generally used as decision-making tools. In this work, we will use this practical tool for understanding the evolution of people tested positive for COVID-19 in Mali. One of the basic models commonly used in the literature to predict the spread of an epidemic in a given population is the SIR model. It was introduced by KERMACK and McKENDRICK in [7] for studying the dynamics of the plague epidemic occurred in Bombay in 1905-1906. In order to improve and adapt this original approach of the SIR model to our study so that it best fits the reality, we modified it by adding two new compartments.

In our model, the total population is divided into five disjoint compartments. Susceptible individuals S are those who are not infected with the disease but are

at risk of becoming infected. Latent individuals L are individuals who are in the incubation period after being infected with the disease, and who have no visible clinical signs, i.e. they are infected but not yet infectious. After the incubation period, latent individuals move into the compartment of infectious individuals I representing infected individuals who have developed the symptom of the disease. We assume that infectious individuals will be immediately sent to designated hospitals for isolation and treatment, so they move into the inpatient compartment H. Finally, recovered individuals R are those individuals who have recovered from the disease, died, or been transferred. We denote by β the transmission rate at which susceptible individuals acquired the Covid-19 infection through contact with infectious individuals. The latent individuals become infectious and join the infectious compartment with the proportion γ_1. The parameter γ_2 is the average rate at which infectious individuals become hospitalized and γ_3 is the recovery rate of hospitalized individuals. We assume that all these parameters are positive. The total constant population over time t denoted by N(t) is given by:

$$N(t) = (t) + L(t) + I(t) + H(t) + R(t).$$

This life cycle of the virus can be represented using the flow diagram shown in Figure 2, in which, the boxes represent the different compartments and the arrows illustrate the transition between compartments.

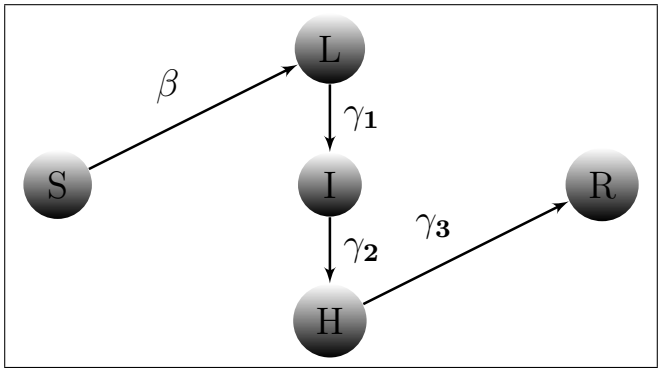


FIGURE 2. Flow diagram of the SLIHR model of COVID-19 in Mali.

Using the above representation, we formulate the corresponding dynamical model as follows:

$$\frac{dS}{dt} = -\beta\frac{I}{N}S \tag{2.1a}$$

$$\frac{dL}{dt} = \beta\frac{I}{N}S - \gamma_1 L \tag{2.1b}$$

$$\frac{dI}{dt} = \gamma_1 L - \gamma_2 I \tag{2.1c}$$

$$\frac{dH}{dt} = \gamma_2 I - \gamma_3 H \tag{2.1d}$$

$$\frac{dR}{dt} = \gamma_3 H \tag{2.1e}$$

The system (2.1a)-(2.1e) is completed with the following initial conditions:

$$\begin{aligned} &S(0) = S_0 > 0, \quad L(0) = L_0 \geq 0, \quad I(0) = I_0 > 0, \\ &H(0) = H_0 = 0, \quad R(0) = R_0 = 0. \end{aligned} \tag{2.2}$$

All the parameters of the model are reported in Table 1.

TABLE 1. Description of model parameters.

Parameters	Description
β	Transmission rate
γ_1	Proportion of latent individuals leaving the compartment
γ_2	Proposition of infected individuals become hospitalized
γ_3	Recovery rate of hospitalized patients

3. MATHEMATICAL ANALYSIS OF THE MODEL

3.1. **Positivity and boundedness.** An important feature of a relevant epidemiological model is the positivity and boundedness of its solutions. Therefore, it is important to prove that all variables are nonnegative for all time t> 0. This implies that any solution that has positive initial values will remain positive for all time t> 0. We begin by determining the biologically feasible set for the system (2.1).

Theorem 3.1. *The closed region* $\Omega = \left\{X = (S, L, I, H, R) \in \mathbb{R}^5_+ : 0 < N = S + L + I + H + R = K\ (K \in \mathbb{N})\right\}$ *is positively invariant set for the system* (2.1).

Proof.

(1) **Positivity of X(t)=$\Big($S(t), L(t), I(t), H(t), R(t)$\Big)$ for all t ≥ 0:** we show by absurd that for all $t \geq 0$, $X(t) \geq 0$. Suppose that for a time t′ > 0, we have X(t') < 0. The function X(t) being continuous, from the intermediate value theorem, there exists a time $t_1 \in]0, t'[$ such that $X(t_1) = 0$. Consider the equations of the system (2.1) and let:

$$f_1(t) = \exp\left(\int_0^t \frac{\beta I(s)}{N(s)} ds\right),\ f_2(t) = \exp(\gamma_1 t),\ f_3(t) = \exp(\gamma_2 t),$$
$$f_4(t) = \exp(\gamma_3 t) \text{ and } f_5(t) = 1.$$

By differentiating each of the expressions $S(t)f_1(t)$, $L(t)f_2(t)$, $I(t)f_3(t)$, $H(t)\ f_4(t)$ and
$R(t)f_5(t)$ with respect to time t, we obtain:

$$\frac{dSf_1}{dt} = 0, \quad \frac{dLf_2}{dt} = \frac{\beta}{N} f_2 SI, \quad \frac{dIf_3}{dt} = \gamma_1 f_3 L, \quad \frac{dHf_4}{dt} = \gamma_2 f_4 I, \quad \frac{dR\ f_5}{dt} = \gamma_3 H. \tag{3.1}$$

By integrating each equation of (3.1) between 0 and t_1, it holds:

$$S(t_1) = \frac{1}{f_1(t_1)} > 0 \tag{3.2}$$

$$L(t_1) = \frac{1}{f_2(t_1)} \left(L(0) + \int_0^{t_1} f_2(t)\beta \frac{I(t)}{N(t)} S(t)\ dt\right) > 0 \tag{3.3}$$

$$I(t_1) = \frac{1}{f_3(t_1)} \left(I(0) + \int_0^{t_1} f_3(t)\gamma_1 L(t)\ dt\right) > 0 \tag{3.4}$$

$$H(t_1) = \frac{1}{f_4(t_1)} \left(H(0) + \int_0^{t_1} f_4(t)\gamma_2 I(t)\ dt\right) > 0 \tag{3.5}$$

$$R(t_1) = R(0) + \int_0^{t_1} \gamma_3 H(t)\ dt > 0 \tag{3.6}$$

From (3.2)-(3.6), it follows that $X(t_1) > 0$. It is a contraction according to the starting hypothesis. Then, $\forall t \geq 0$, $X(t) \geq 0$. Therefore, all solutions initiated in $\mathbb{R}^5_+$ are positive.

(2) **Boundedness of X(t)=$\Big($ S(t), L(t), I(t), H(t), R(t)$\Big)$ for all t ≥ 0:** the total population in the model is

$$N(t) = S(t) + L(t) + I(t) + H(t) + R(t).$$

Then, by differentiating N with respect to time t, we obtain:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dL}{dt} + \frac{dI}{dt} + \frac{dH}{dt} + \frac{dR}{dt} = 0 \tag{3.7}$$

Integrating (3.7) using the initial condition, we obtain N(t) = N(0) = K. This achieves the proof.

□

3.2. **Existence and uniqueness.** Let us start by recalling the Cauchy-Lipschitz theorem as presented in [8].

Cauchy-Lipschitz theorem: *Let $F : \mathbb{R}_+ \times \mathbb{R}^n \longrightarrow \mathbb{R}^n$ be a piecewise continuous function with respect to t and satisfying:*

$$\|F(t,X_1) - F(t,X_2)\| \leq C\|X_1 - X_2\|.$$

Then the equation $\dot{X} = F\left(t, X\right)$ with $X(t_0) = X_0$ admits a unique solution for $t \in [t_0, t_1]$.

Theorem 3.2. *The SLIHR model described by the system* (2.1) *admits a unique solution for all time $t \in \mathbb{R}_+$.*

Proof. Let us associate the function F : $\mathbb{R}_+ \times \mathbb{R}_+^5 \longrightarrow \mathbb{R}_+^5$ defined by

$$\mathrm{F(t,X)} = \left(-\beta\frac{SI}{N}, \quad \beta\frac{SI}{N} - \gamma_1 L, \quad \gamma_1 L - \gamma_2 I, \quad \gamma_2 I - \gamma_3 H, \quad \gamma_3 H\right)$$

to the SLIHR model described by the system (2.1). According to the fact that all norms are equivalent in $\mathbb{R}^n$, and in particular for $n = 5$, let us prove that the function F is Lipschitz with respect to X for the norm 1.

$$\|\mathrm{F(t,\,X_1) - F(t,\,X_2)}\|_1 = \left\| \begin{pmatrix} \frac{\beta}{N}(S_2I_2 - S_1I_1) \\ \frac{\beta}{N}(S_1I_1 - S_2I_2) - \gamma_1(L_1 - L_2) \\ \gamma_1(L_1 - L_2) - \gamma_2(I_1 - I_2) \\ \gamma_2(I_1 - I_2) - \gamma_3(H_1 - H_2) \\ \gamma_3(H_1 - H_2) \end{pmatrix} \right\|_1$$

$$
\begin{aligned}
&= \frac{\beta}{N}\Big|S_2I_2 - S_1I_1\Big| + \Big|\frac{\beta}{N}\big(S_1I_1 - S_2I_2\big) - \gamma_1(L_1 - L_2)\Big| \\
&\quad + \Big|\gamma_1(L_1 - L_2) - \gamma_2(I_1 - I_2)\Big| + \Big|\gamma_2(I_1 - I_2) - \gamma_3(H_1 - H_2)\Big| \\
&\quad + \Big|\gamma_3(H_1 - H_2)\Big| \\
&\leq \frac{\beta}{N}\Big|S_1I_3 - S_2I_2\Big| + \frac{\beta}{N}\Big|S_1I_1 - S_2I_2\Big| + \gamma_1\Big|L_1 - L_2\Big| + \gamma_1\Big|L_2 - L_2\Big| \\
&\quad + \gamma_2\Big|I_1 - L_2\Big| + \gamma_2\Big|I_1 - I_2\Big| + \gamma_3\Big|H_1 - H_2\Big| + \gamma_3\Big|H_1 - H_2\Big| \\
&\leq 2\frac{\beta}{N}\Big|S_1I_1 - S_2I_2\Big| + 2\gamma_1\Big|L_1 - L_2\Big| + 2\gamma_2\Big|I_1 - I_2\Big| + 2\gamma_3\Big|H_1 - H_2\Big| \\
&\leq 2\beta\frac{|I_1|}{N}\Big|S_1 - S_2\Big| + 2\beta\frac{|S_2|}{N}\Big|I_1 - I_2\Big| + 2\gamma_1\Big|L_1 - L_2\Big| + 2\gamma_2\Big|I_1 - I_2\Big| \\
&\quad + 2\gamma_3\Big|H_1 - H_2\Big|
\end{aligned}
$$

or

$$
\begin{aligned}
&\|F(t, X_1) - F(t, X_2)\|_1 \\
&\leq 2\Big(\beta\Big|S_1 - S_2\Big| + \gamma_1\Big|L_1 - L_2\Big| + \big(\beta + \gamma_2\big)\Big|I_1 - I_2\Big| + \gamma_3\Big|H_1 - H_2\Big|\Big) \\
&\leq 2\max\Big[\beta, \gamma_1, \big(\beta + \gamma_2\big), \gamma_3\Big]\left(\Big|S_1 - S_2\Big| + \Big|L_1 - L_2\Big| + \Big|I_1 - I_2\Big| + \Big|H_1 - H_2\Big|\right) \\
&\leq C\|X_1 - X_2\|_1
\end{aligned}
$$

with $C = 2\max\Big[\beta, \gamma_1, \big(\beta + \gamma_2\big), \gamma_3\Big]$.

Furthermore, the function F is piecewise continuous over $\mathbb{R}_+$. So, according to the Cauchy Lipschitz theorem, the SLIHR model defined by the system (2.1) admits a unique solution for all time $t \in \mathbb{R}_+$. □

4. Estimation of epidemiological parameters

4.1. **Estimation of model parameters by adjustment.** We conducted our study on the population of Mali, estimated to N=20243609 in 2020, see [13]. In order to simulate the evolution of COVID-19 infection in this population, a good knowledge of the biological parameters involved in the SLIHR model is necessary. Thus, to calibrate the model to the dynamics of COVID-19 in Mali, we will use an approach based on the adjustment of the model parameters by optimization.

It consists in comparing the real data with theoretical models in order to define one that fits better the observation. To do this, we define a distance between two curves and we try to minimize this distance by varying the parameters of the theoretical model. This operation is facilitated by Excel which allows to minimize a function thanks to its solver. We will use it to minimize the sum of the square of the difference between each point of the theoretical and experimental models. As experimental model, we use the data of the first 30 days of infection in Mali, namely from March 25, 2020 to April 23, 2020. These data are summarized in Table 2.

TABLE 2. Source: Ministry of Health and Social Affairs of Mali.

Day	Confirmed	Recovered	Positive	Day	Confirmed	Recovered	Positive
1	2	0	2	16	74	23	51
2	4	1	3	17	87	29	58
3	11	1	10	18	105	29	76
4	18	1	17	19	116	31	85
5	20	2	18	20	123	36	87
6	25	2	23	21	144	47	97
7	28	3	25	22	148	47	101
8	31	3	28	23	171	47	124
9	36	3	33	24	190	47	143
10	39	3	36	25	218	54	164
11	41	3	38	26	224	59	219
12	45	3	42	27	246	78	168
13	47	6	41	28	258	79	179
14	56	14	42	29	293	98	195
15	59	18	41	30	309	98	211

The results obtained from this adjustment of the parameters by optimization are plotted in Figure 3. On one side, the representative curves of the model (in red) and the real data (in black) of the infectious inpatients are shown. On the other side, we can see the representative curves of the model (in green) and the real data (in black) of the recovered individuals. The estimated values of the biological parameters of our model are summarized in Table 3.1.

4.2. **Basic reproduction number.** The basic reproduction number is an important threshold condition in the analysis of an infectious disease. It determines

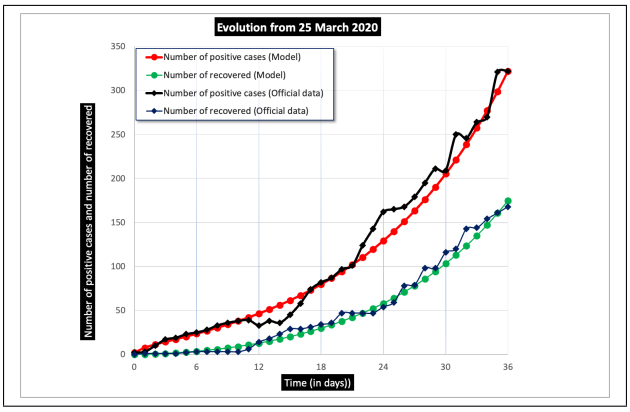


FIGURE 3. Adjustment of biological parameters.

TABLE 3. Estimated values of biological parameters from adjustment.

Parameters	Description	Value
β	Transmission rate	0.3965
γ_1	Proportion of latent individuals leaving the compartment	0.522871
γ_2	Proposition of infected individuals become hospitalized	0.2729
γ_3	Recovery rate of hospitalized patients	0.05

whether the disease will die out or persist in the population over time. We calculate the basic reproduction number R_0 of the system by applying the next generation matrix method used in [5, 6]. The first step in obtaining R_0 is to rewrite the model equations starting with the newly infected compartments:

$$\frac{dL}{dt} = \beta\frac{I}{N}S - \gamma_1 L \tag{4.1}$$

$$\frac{dI}{dt} = \gamma_1 L - \gamma_2 I \tag{4.2}$$

$$\frac{dH}{dt} = \gamma_2 I - \gamma_3 H. \tag{4.3}$$

Using the principle of next-generation matrix, the Jacobian matrices at DFE = $(S_e, L_e, I_e, H_e, R_e)$ = (N, 0,0,0,0) of the SLIHR model described by the system (2.1)

is given by

$$\mathrm{J} = \begin{pmatrix} -\gamma_1 & \beta & 0 \\ \gamma_1 & -\gamma_2 & 0 \\ 0 & \gamma_2 & -\gamma_3 \end{pmatrix} = \mathrm{F} - \mathrm{V}$$

where

$$\mathrm{F} = \begin{pmatrix} 0 & \beta & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad \text{and} \quad \mathrm{V} = \begin{pmatrix} \gamma_1 & 0 & 0 \\ -\gamma_1 & \gamma_2 & 0 \\ 0 & -\gamma_2 & \gamma_3 \end{pmatrix}.$$

The next-generation matrix is defined by:

$$\mathrm{F\,V}^{-1} = \begin{pmatrix} \frac{\beta}{\gamma_2} & \frac{\beta}{\gamma_2} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

The basic reproduction number is computed as

$$\mathrm{R}_0 = \rho(\mathrm{F\,V}^{-1}) = \frac{\beta}{\gamma_2}.$$

This number R_0 is a threshold parameter that represents the average number of infections caused by an infectious individual when introduced into the susceptible population [11]. According to the biological parameters of our model it holds:

$$\mathrm{R}_0 = \frac{\beta}{\gamma_2} = \frac{0.3965}{0.2729} = 1.45.$$

4.3. **Sensitivity analysis of R_0.** Based on each parameter of R0, a sensitivity analysis is performed to check the sensitivity of the basic reproduction number. As reported by Arriola and Hyman [1], we calculate the normalized sensitivity index as a function of each parameter of R_0. The normalized sensitivity index of a variable R0 with respect to a given parameter m is defined as follows:

$$\mathrm{A}_m^{\mathrm{R}_0} = \frac{\partial \mathrm{R}_0}{\partial \mathrm{m}} \times \frac{\mathrm{m}}{\mathrm{R}_0}.$$

The sensitivity indices of R_0 with respect to the parameters β and γ_2 are then computed as:

$$\mathrm{A}_\beta^{\mathrm{R}_0} = \frac{\partial \mathrm{R}_0}{\partial \beta} \times \frac{\beta}{\mathrm{R}_0} = \frac{1}{\gamma_2} \times \frac{\beta}{\mathrm{R}_0} = \frac{\beta}{\gamma_2} \times \frac{1}{\mathrm{R}_0} = \frac{\mathrm{R}_0}{\mathrm{R}_0} = 1 > 0.$$

$$A_{\gamma_2}^{R_0} = \frac{\partial R_0}{\partial \gamma_2} \times \frac{\gamma_2}{R_0} = -\frac{\beta}{\gamma_2^2} \times \frac{\gamma_2}{R_0} = -\frac{\beta}{\gamma_2} \times \frac{1}{R_0} = -\frac{R_0}{R_0} = -1 < 0.$$

From the above calculations, it is obvious that the reproduction number R_0 is sensitive to changes in β and γ_2. An increase in β will cause an increase in R_0 by the same amount, and a decrease in β will cause a decrease in R_0 by the same amount. The parameter γ_2 has an inversely proportional relationship with R_0, i.e. an increase in gamma will cause a decrease in R_0.

4.4. **Total size of epidemic.** Let us consider the SLIHR model described by the system (2.1) and determine what the final size of the epidemic will be in the complete absence of intervention. From equation (2.1a), it follows that:

$$\frac{dS}{S} = -\frac{\beta}{N} I(t)dt.$$

Integrating this equation from $t = 0$ to $t = +\infty$, we obtain:

$$S(\infty) = S_0 \exp\left(-\frac{\beta}{N}\int_0^{\infty} I(t)dt\right), \tag{4.4}$$

where $S(\infty)$ denotes the limit when $t \longrightarrow +\infty$ of the function $S(t)$.

From equation (2.1d), it follows that:

$$\frac{dH}{dt} = \gamma_2 I(t) - \gamma_3 H(t).$$

Integrating this equation from $t = 0$ to $t = +\infty$:

$$H(\infty) = \gamma_2 \int_0^{\infty} I(t)dt - \gamma_3 \int_0^{\infty} H(t)dt, \tag{4.5}$$

where $H(\infty)$ denotes the limit when $t \longrightarrow +\infty$ of the function $H(t)$.

From equation (2.1e), it follows that:

$$\frac{dR}{dt} = \gamma_3 H(t).$$

Integrating this equation from $t = 0$ to $t = +\infty$, we obtain:

$$R(\infty) = \gamma_3 \int_0^{\infty} H(t)dt, \tag{4.6}$$

where $R(\infty)$ denotes the limit when $t \longrightarrow +\infty$ of the function $R(t)$.

Using (4.5) in (4.6), we get

$$\mathrm{R}(\infty) = \gamma_2 \int_0^{\infty} \mathrm{I(t)dt} - \mathrm{H}(\infty). \tag{4.7}$$

Moreover, we have at any time $t \geq 0$, S(t)+L(t)+I(t)+H(t)+R(t)=N. When $t \longrightarrow +\infty$, the epidemic ends up stopping so that L(t), I(t) and H(t) tend towards 0. At the limit, there are only those individuals who escaped the epidemic and those who were recovered after being infected.

$$\mathrm{S}(\infty) + \mathrm{R}(\infty) = \mathrm{N} \tag{4.8}$$

By combining (4.4), (4.7) and (4.8), it holds:

$$\mathrm{N\text{-}R}(\infty) = \mathrm{S}_0 \exp\Big(- \frac{\beta}{\gamma_2} \frac{\mathrm{R}(\infty)}{\mathrm{N}} \Big).$$

At the start of the epidemic, there are only a few infected individuals in the population, so $\mathrm{S}_0 \approx \mathrm{N}$. The equation can be written as

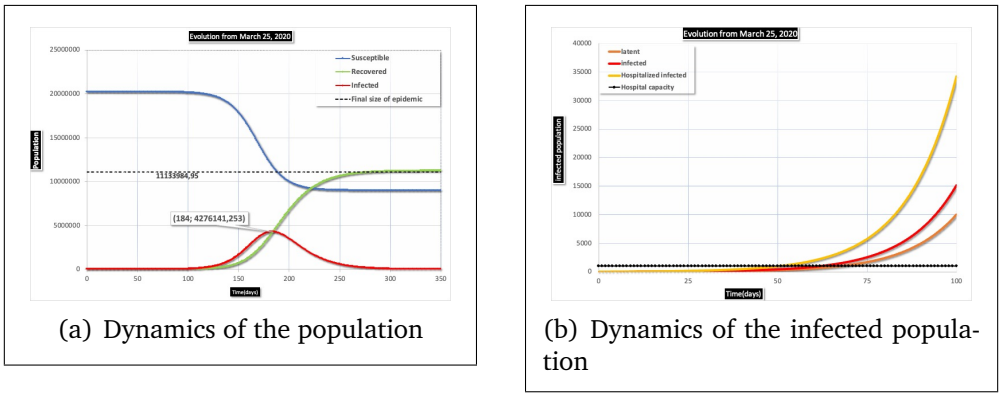
$$1 - \frac{\mathrm{R}(\infty)}{\mathrm{N}} \approx \exp\Big(- \mathrm{R}_0 \frac{\mathrm{R}(\infty)}{\mathrm{N}} \Big).$$

We find numerically $\frac{\mathrm{R}(\infty)}{\mathrm{N}} \approx 55\%$ of the N population, or approximately 11 million individuals infected at the end of the epidemic.

5. Numerical simulations and discussion

In this section, we examine the model and studied the effects of the combined strategies for controlling disease transmission. In all the numerical simulations, the curves were first fitted to the official data to set the correct rate of spread of the epidemic. This rate of spread is fixed here from the first 30 days of the epidemic, and then we evolve these curves over time.

5.1. **Prediction and epidemic peak and curves.** In Figure 4(a) are represented the curves of susceptible individuals (in blue), of all infected individuals, including latent, infectious and hospitalized infectious, (in red) and recovered individuals (in green). We can see that the epidemic peak (red curve) is expected around the 184th day with an average of 4 million infected. This is due to the fact that the basic reproduction number R_0 is assumed to be constant, i.e. there is no intervention and the barrier measures are not strictly enforced. Finally, as shown



(a) Dynamics of the population

(b) Dynamics of the infected population

FIGURE 4. Prediction and epidemic peak and curves.

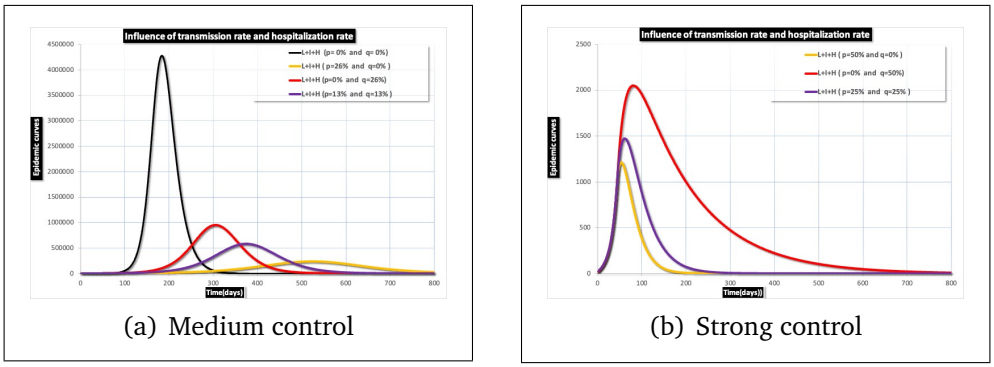
in section 4, the epidemic stops once the 55% of the population (materialized by the black dotted line) is reached.

In Figure 4(b), where infected individuals are plotted, we see that the epidemic grows exponentially. It can also be observed that the majority of the hosts are in the compartment H, which is where they stay the longest according to the model. Finally, we can see that the proportion of infected individuals detected (in yellow) rapidly exceeds the capacity of our hospitals, estimated here to 1000 beds and represented by the black dotted line.

5.2. **Epidemic curve with control scenarios.** Here we modeled the implementation of a public health policy with different scenarios for controlling the epidemic. It aims to reduce the basic reproduction rate R_0 from its value β/γ_2 to another value $\beta'/\gamma_2' = (1-\mathrm{p})\beta/(1+\mathrm{q})\gamma_2$, where p is the proportion of the transmission rate β reduced by the effects of the public health policies and q is the proportion of the hospitalization rate γ_2 increased by the effects of the public health policies.

One goes from β to β' by increasing p through measures such as social distancing, containment, wearing masks or closing certain places. We go from γ_2 to γ_2' by increasing q through mass screening.

In Figure 5(a), the epidemic curve is represented in the different scenarios: the black curve illustrates the scenario 0, the yellow curve the scenario 1, the red curve the scenario 2 and the purple curve the scenario 3. As can be seen, this strategy does not prevent the spread of the epidemic. But unlike in scenario 0, the peak of the curve is lower and occurs much later for the scenarios 1, 2 and 3. These are



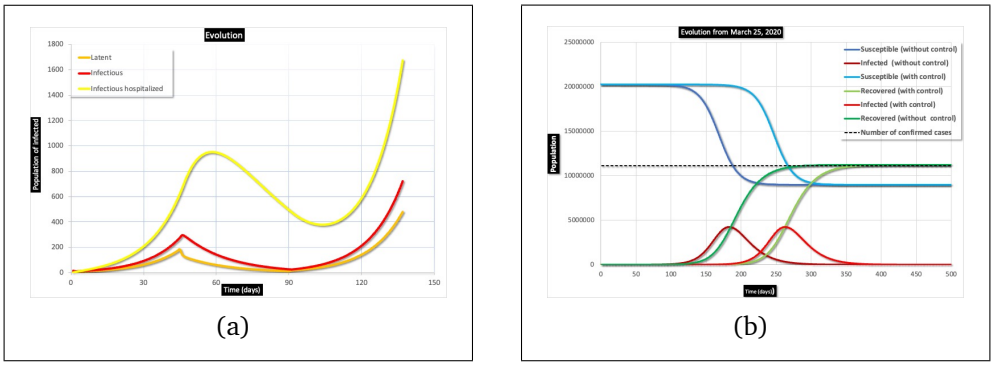
(a) Medium control (b) Strong control

FIGURE 5. Epidemic curves with persistent scenarios.

therefore scenarios for which the curve is more spread out over time. Similarly, the total proportion of the infected population becomes lower compared to the case of scenario 0.

This public health policy makes it possible to flatten the epidemic curve in order to allow the health system to absorb the influx of infected people over a slightly longer period. Comparing the effectiveness of the different scenarios of this strategy, it can be seen that in scenario 1, the curve is much flatter (14% of the total infected population) compared to scenario 3 (20% of the total infected population). The scenario 2 is the one in which the peak of the curve is the highest (25% of the total infected population) apart from scenario 0. In conclusion, the scenario 1 seems to be the most efficient.

It is shown in Figure 5(b) the epidemic curves for the scenarios 1, 2 and 3. This policy consists in stopping the epidemic, i.e. to lower R_0 below 1.



(a) (b)

FIGURE 6. Curves with strong control but of limited duration.

It is shown in Figure 6(a) the epidemic curves of the population when scenario 1 is applied from the 45th of the epidemic for a limited period of 45 days. We see that the epidemic is well suppressed during the strategy period. Unfortunately, once the measures taken are lifted, the epidemic resumes very strongly. In the end, this strategy shifted the epidemic peak from scenario 0, as illustrated in Figure 6(b). However, the total number of confirmed cases remains the same.

6. Conclusions and perspectives

In this paper, we formulated and studied a five-compartment mathematical model of the COVID-19 disease that is transmitted from human to human. Official data from Mali on COVID-19 were used to estimate the different parameters of the model. In order to study the dynamics of our model, we calculated the basic reproduction number R_0, analyzed its sensitivity with respect to the parameters and established a relationship between R_0 and the final size. The numerical simulations showed that if the barrier measures are not rigorously applied, the epidemic peak will be reached around the 184th day with an average of 4 million infected. Thus, until the end of the epidemic, the total number of infected individuals will be around 11 million and the number of hospitalized infectious patients will very quickly exceed the capacity of our public health facilities. On the other hand, the rigorous application of barrier measures and the persistence of mass screening will make it possible to stop the epidemic, which will eventually disappear in a short time. However, it can be seen from numerical simulations that if the barrier measures are rigorously applied for some time and lifted before the disease disappears completely from the population, the epidemic will start again very quickly. The epidemic peak will be shifted, but the total proportion of the population infected will be the same as when the measures are not strictly enforced.

As perspectives, we can note that this model, despite the fact that it allowed us to study the impact of barrier measures on the evolution of the coronavirus disease (COVID-19) in Mali, is very simple in its structure. We plan for future work to modify it for taking into account certain specificities of the epidemic such as the flanking transmission which plays an important role in its propagation. Some additional parameters such as the age of the individuals (mortality by COVID-19 infection increases with age), comorbidity (aggravating factor for COVID-19 patients), and the demographic patterns will be added to the model.

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