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The sooner strict public health strategies are applied the lower the peak of the epidemics: The SARS-CoV-2 case

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Summary

An epidemiological model is proposed to analyze the COVID-19 epidemics when control interventions are being applied to reduce the speed of the disease. The analyzed model includes parameters that describe control strategies such as behavioral changes of susceptible individuals to reduce the transmission of the disease, rates of diagnosis of the infectious individuals, and other control measures as cleaning and disinfection of contaminated environments. The proposed model is calibrated using Bayesian statistics and the official cumulative confirmed cases for COVID-19 in Mexico. We show which public health strategies contribute the most to the variation of R_0. A central result is the fact that the peak of the epidemics can drastically be changed depending on the time when the control strategies are introduced.

KEYWORDS:
SARS-CoV-2, COVID-19, Epidemic Model, Public health strategies, Parameter estimation

1 | INTRODUCTION

The COVID-19 pandemic has been the centre of intense epidemiological research in the last months. The COVID-19 has infected at least 9.3 million of people in the world, and there have been at least 497,000 deaths from December, 2019 to June 26, 2020. Since the beginning of the epidemic in Wuhan, China, the Surveillances Epidemiological Systems of all countries have been alerted and have taken control measures against the disease. Despite this, there have been abundance COVID-19 cases in many countries. In this sense, the COVID-19 disease was declared, by the WHO, an international emergency on January 30, 2020, and it was declared a pandemic in March 11, 2020; see[23]. Since the WHO emitted the COVID-19 alert, the interventions for controlling the spread of COVID-19 have differed from one country to another. Those public health strategies differ from each other not only in the kind of intervention for controlling the epidemic outbreak but also in the time when they are applied to the population.

The transmission of COVID-19 may occur by different routes. Some of them are human-to-human contacts while others are humans-to-contaminated environments. In the former case, an effective infectious contact occurs when someone inhales respiratory droplets that are produced by an infectious individual, who can show symptoms or not; see[2]. In the second case, an effective infectious contact may occur if one susceptible individual touches a contaminated surface, and then he touches his own mouth, nose, or eyes. It has been suggested that COVID-19 virus is spreading more efficiently than influenza; however, it is spreading less efficiently than measles.

On the other hand, the COVID-19 has revealed gaps in the health systems in many countries because almost all intensive care beds are being taken. This saturation of the healhtcare systems occurs because symptoms related to COVID-19 can cause from mild or moderate respiratory illness to severe respiratory illness, septic shock, or other characteristic that require intensive care as mechanical ventilation; see[14].

These reasons make us think of the importance of analyzing how control interventions can smooth the epidemic curve for the healthcare systems not to be saturated. The control interventions range from travel restriction, social distancing, including banning public gatherings, to hand hygiene; see[21,13].

In this race against the spread of the coronavirus SARS-CoV-2, the epidemiological models have been used to understand and forecast the horizon of the epidemics[8,11,20,24,10]. Compartmental epidemiological models are frequently used as basic structure to model the spread of an infectious disease; see[7,22]. These models are used for calculating some epidemiological parameters such as infectiousness rates and the basic reproduction number that is denoted by R_0.

In this work, the spread of COVID-19 is analyzed through one compartmental epidemic model that shows how the number of infectious individuals changes due to the application of control strategies into a population. Epidemiological parameters are estimated for the cases of COVID-19 in Mexico, which occurred from March 09, 2020 to May 07, 2020; see[12]. With this parameters, plausible scenarios are shown as function of the control interventions at an specific time. Also, Sobol's indices are calculated to find which model parameters must be chosen such that their election allows to reduce R_0 below 1, so that the epidemic outbreak will be controlled.

For this purpose, in Section 2, the epidemic model with adjusted-incidence is constructed to analyze the COVID-19 spread in a totally susceptible population; also, the basic reproduction number is calculated. In Section 3, epidemiological parameters are estimated using Bayesian statistics for COVID-19 cases in Mexico. In Section 4, Sobol's indices for basic reproduction number of the proposed model are calculated. In Section 5, plausible scenarios are shown as function of one specific time when the public health intervention strategies to control the coronavirus disease are applied. Finally, Section 6 presents a discussion of the obtained results.

2 | MODEL CONSTRUCTION AND R_0

In this section, a compartmental epidemic model with adjusted-incidence is proposed to describe the evolution of an infectious disease when the total population is divided in epidemiological classes and there is one compartment to describe free-virus in the environment. For this purpose, the model proposed in[16] is extended.

2.1 | The model

In the model are considered two possible ways of infection: human-to-human and human-vector-human contagion. The former occurs when a susceptible individual has contact with one infectious individual. The latter occurs when susceptible individuals are living in one contaminated environment[6], and they touch a surface with SARS-CoV-2 coronavirus. Also, the model captures certain phenomenology related to some public health strategies which are being applied into a susceptible population to control the COVID-19 outbreak.

In the formulation of the model, natural vital rates (birth and death rates) are not considered since the model dynamics is of interest only in the short-term as the life cycle of the coronavirus has been associated with a short time period. A model without vital rates is simpler but still allows to describe the evolution of the disease, particularly, the model analysis allows to find parameter conditions for an epidemic outbreak to occur.

The human population is divided as follows. $N(t) = S(t)+S_c(t)+E(t)+A(t)+I(t)+D(t)+R(t)$. We are interested mainly in the effects of two epidemiological classes, $S_c(t)$ and $D(t)$, the parameter related with these classes, and the public health strategies related to them. $S_c(t)$ denotes the cautious susceptible individuals, that is, the susceptible individuals who changed their behavior and became prudent susceptible individuals. $D(t)$ denotes diagnosed individuals who are isolated and treated. For the description of all the variables and parameters of the model see Tables 1 and 2 . Because there are isolated individuals, new human-to-human infections are described by the term $\frac{\beta_A A+\beta_I I}{N-D-\delta S_c} S$, where $0 < \delta < 1$. The term $\frac{A+I}{N-D-\delta S_c} = \frac{A+I}{S(t)+(1-\delta)S_c(t)+E(t)+A(t)+I(t)+R(t)}$ describes the infectious fraction of the circulating population. This term is called adjusted-incidence and it is used to describe the effect in the evolution of the disease due to the isolation of individuals. Notice that, when the incidence is modeled using adjusted-incidence, the number of contacts is maintained. This kind of incidence describes scenarios where some individual are forced to stay in quarantine but they are replaced by other individuals. For example, during the COVID-19 contingency, people belonging to risk classes were put into quarantine, and they were replaced by individuals without comorbidities. In particular, medical professionals were hired to help during the contingency; however, even though the number of contacts are maintained, there are more contacts between susceptible and infectious individuals; see[7]. The term δS_c in the adjusted-incidence can be interpreted as certain invisibility degree of cautious susceptible individuals. That is, they are not noted by infectious individuals because they follow in a strict way the instruction of social distancing, for example. Being more specific, cautious susceptible individuals reduce the infectiousness rate by implementing social distancing strategies, staying at home during contingency, using mouth covers, cleansing and disinfecting. So, with all these assumptions the model proposed is shown here.

$$\begin{aligned}
\dot{S} &= -\frac{(\beta_A A+\beta_I I)}{N-D-\delta S_c} S - \beta_V V S - \alpha S,\\
\dot{S}_c &= -\frac{(\beta_A A+\beta_I I)}{N-D-\delta S_c} \theta S_c - \beta_V \theta V S_c + \alpha S,\\
\dot{E} &= \frac{(\beta_A A+\beta_I I)}{N-D-\delta S_c} \left(S + \theta S_c\right) + \beta_V V S + \beta_V \theta V S_c - \sigma E - d_1 E,\\
\dot{A} &= (1-p)\sigma E - d_1 A - \gamma_A A,\\
\dot{I} &= p\sigma E - d_2 I - \gamma_I I - \mu I,\\
\dot{D} &= d_1(E+A) + d_2 I - \gamma_D D - \mu D,\\
\dot{R} &= \gamma_A A + \gamma_I I + \gamma_D D,\\
\dot{V} &= c_1 A + c_2 I - (\mu_V + m) V.
\end{aligned} \tag{1}$$

As mentioned earlier, there are two pathways of infection. In this sense, the rates β_A and β_I are the product of the average number of contacts between asymptomatic infectious or symptomatic infectious individuals and susceptible individuals per unit of time, and the probability that those encounters result in new infections. In analogous way, β_V is the average number of contacts between susceptible individuals and contaminated surfaces, multiplied by the probability that those encounters result in new infections. Also, in the last equation in (1) parameter c_1 and c_2 are the contribution rates of coronavirus to the contaminated environment by asymptomatic infectious and symptomatic infectious individuals respectively; see[24].

Parameter	Parameter description
$S(t)$	Susceptible individuals
$S_c(t)$	Cautious susceptible individuals
$E(t)$	Exposed/latent individuals
$A(t)$	Asymptomatic individuals
$I(t)$	Symptomatic individuals
$D(t)$	Diagnosed individuals
$R(t)$	Recovered individuals
$V(t)$	Free SARS-CoV-2 in the contaminated environment

TABLE 1 Model variables for model (7).

To analyze the behavior of the solutions of (1), we start by analyzing R_0, the basic reproduction number, using the next generation matrix; see[4,22]. The disease-free equilibrium, for model (1), that is given by $E_0 = (0, N_0, 0, 0, 0, 0, 0, 0)$ is needed for

Parameter	Parameter description
β_A	Asymptomatic infection rate
β_I	Symptomatic infection rate
β_V	Infection rate of hosts in a contaminated environment
σ	Transfer out rate of the exposed class
γ_A	Recovery rate of asymptomatic individuals
γ_I	Recovery rate of symptomatic individuals
μ	Induced-death rate of the disease
p	probability of one exposed individual becoming asymptomatic
c_1	Virus reproduction rate by asymptomatic individuals
c_2	Virus reproduction rate by symptomatic individuals
μ_V	Loss rate of virus in the environment
α	Rate in which susceptible individuals become cautious susceptible individuals
θ	$\theta \in (0, 1)$ reduction factor of the infectious rate
d_1	Diagnosis rate of exposed and asymptomatic individuals
d_2	Diagnosis rate of symptomatic individuals
γ_D	Recovery rate of diagnosed individuals
m	Induced-death rate of virus in the environment

TABLE 2 Model parameters for model (1).

analyzing the progression of the number of infectious individuals at the beginning of the epidemic. The matrix F and V that are defined in[22] are given by

$$F = \begin{bmatrix} 0 & \frac{\beta_A \theta}{1-\delta} & \frac{\beta_I \theta}{1-\delta} & \theta \beta_V N_0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{2}$$

and

$$V = \begin{bmatrix} \sigma + d_1 & 0 & 0 & 0 \\ -(1-p)\sigma & \gamma_A + d_1 & 0 & 0 \\ -p\sigma & 0 & d_2 + \gamma_1 + \mu & 0 \\ 0 & -c_1 & -c_2 & \mu_V + m \end{bmatrix}. \tag{3}$$

Calculating the spectral radius of the next generation matrix FV^{-1}, the basic reproduction number is obtained. It is given by

$$R_0 = (1-p)R_0^A + pR_0^I. \tag{4}$$

Where

$$R_0^A = \frac{\sigma}{(d_1 + \gamma_A)(\sigma + d_1)} \left(\frac{\beta_A}{(1-\delta)} + \frac{c_1 \beta_V N_0}{\mu_V + m} \right) \theta \tag{5}$$

and

$$R_0^I = \frac{\sigma}{(d_2 + \gamma_I + \mu)(\sigma + d_1)} \left(\frac{\beta_I}{(1-\delta)} + \frac{c_2 \beta_V N_0}{\mu_V + m} \right) \theta \tag{6}$$

Note that R_0 is independent of the rates γ_D and α. Independence of the parameter γ_D can be explained using the argument that people in the diagnosed class is isolated during the mean period $\frac{1}{\gamma_D}$. During this period, new infections do not occur due to isolated individuals; also, after people are moved out the diagnosed class, they are no longer infectious individuals. Even though the basic reproduction number does not depend on α, its effects are included in the factor θ, which is a reduction factor of the infectiousness rate.

The decomposition of R_0 in the components R_0^A and R_0^I allows to measure the contributions of the asymptomatic and symptomatic class to the progression of infected individuals. So, R_0 is a function of the new transmissions due to the asymptomatic and symptomatic individuals. That is, R_0 for model 1 is the weighted sum of the new infections associated to the two infectious classes; asymptomatic and symptomatic individuals. Each components of the basic reproduction number takes into account the contributions of human-to-human contagions and the human-to-contaminated environment contagions as a function of the class, that is, R_0^A measures the contribution of the asymptomatic individuals to R_0 while R_0^I measures the contribution of the symptomatic individuals to R_0. Observe that, R_0 increases with δ. That is, δ increases the effect of the infectiousness rates β_A and β_I in R_0. In other words, δ compensates the effects of the adjusted-incidence.

The behavior of the solutions of model (1) are described by the following result.

Theorem 1. The free-disease equilibrium for system (1) is locally asymptotically stable if and only if $R_0 < 1$.

3 | PARAMETER ESTIMATES

In this section, some parameters of the model without intervention control are estimated. In the evolution of the COVID-19 epidemic there are epidemiological and demographic parameters involved that can be known; however, parameters related to the transmission rates are so difficult to estimate because there are many social and environmental drivers involved. In this sense, model 1 without control interventions will be used to estimate some parameters. This is shown here.

$$\begin{aligned}
\dot{S} &= -\frac{\beta_A SA + \beta_I SI}{N} - \beta_V SV, \\
\dot{E} &= \frac{\beta_A SA + \beta_I SI}{N} + \beta_V SV - \sigma E, \\
\dot{A} &= (1-p)\sigma E - \gamma_A A, \\
\dot{I} &= p\sigma E - \gamma_I I - \mu I, \\
\dot{R} &= \gamma_A A + \gamma_I I, \\
\dot{V} &= c_1 A + c_2 I - \mu_V V.
\end{aligned} \tag{7}$$

In this case, the population is given by $N(t) = S(t) + E(t) + A(t) + I(t) + R(t)$, and the parameters $\alpha, \delta, \theta, d_1, d_2, \gamma_D$ for model 1 are zero.

The basic reproduction number for model 7 is given by

$$R_0 = (1-p)R_0^A + pR_0^I, \tag{8}$$

where

$$R_0^A = \left(\frac{\beta_A}{N_0} + c_1\frac{\beta_V N_0}{\mu_V}\right)\frac{1}{\gamma_A} \tag{9}$$

and

$$R_0^I = \left(\frac{\beta_I}{N_0} + c_2\frac{\beta_V N_0}{\mu_V}\right)\frac{1}{\gamma_I + \mu}. \tag{10}$$

Then, an stability result of the equilibrium point $(N_0, 0, 0, 0, 0, 0)$ for model (7) is enunciated as follows:

Theorem 2. The free-disease equilibrium for system (7) si locally asymptotically stable if and only if $R_0 < 1$.

To calibrate model (7), the unknown parameters $\phi = (\beta_A, \beta_I, \beta_V, c_1, c_2)$ will be estimated using a Bayesian approach based on MCMC (Markov Chain Monte Carlo). This estimation uses the pytwalk implementation on Python; see[3]. For this, some parameter values that appear in the epidemiological literature will be used (see Table 3).

Parameter	Value	Units	Source
σ	0.15325	day^{-1}	1
γ_A	0.13978	day^{-1}	19
γ_I	0.33029	day^{-1}	19
γ_D	0.1162	day^{-1}	19
μ	1.7826×10^{-5}	day^{-1}	19
p	0.868343	$dimensionless$	19
μ_V	1	day^{-1}	9

TABLE 3 Values of some epidemiological parameters for model (7).

It is assumed that data $y = (y_0, y_1, ..., y_n)$ consisting on the cumulative daily cases of infected individuals can be modeled as

$$y_t = C(t; \phi) + \eta_t \tag{11}$$

where $t = 0, ..., n$, and η_t are independent identically distributed random variables with normal distribution with mean 0 and unknown variance κ^2.

$$C(t; \phi) = \sum_{i=0}^{t} I(i; \phi) = y_0 + \sum_{i=1}^{t} I(i; \phi) \tag{12}$$

where $I(i; \phi)$ is the solution of the ODE's system 7 for the I compartment given a fixed vector of parameters ϕ with initial values $(S_0, E_0, A_0, I_0, R_0, V_0)$. That is, $I(i; \phi)$ are the infected individuals at time i given ϕ.

The prior distribution for the unknown parameters assumes independence among them. We propose different Gamma distributions for the infection rates and the shedding rates; see (14). To take into account the possible asymmetry of the parameter distribution and plausible values concentrated towards zero, we propose gamma distributions for the parameters β_A, β_I and β_V with expected values in agreement with the results presented in[19,24] to allow the parameters to take values in all positive real numbers. Also, we consider different scales of magnitude for the parameters β_A, β_I and β_V, and for the parameters c_1 and c_2. Therefore:

$$\pi(\phi, \kappa^2) = \pi_1(\beta_A)\pi_2(\beta_I)\pi_3(\beta_V)\pi_4(c_1)\pi_5(c_2)\pi_6(\kappa^2). \tag{13}$$

Where

$$\begin{aligned}
\beta_A &\sim \Gamma(1, 10^7)\\
\beta_I &\sim \Gamma(1, 10^7)\\
\beta_V &\sim \Gamma(1, 10^7)\\
c_1 &\sim \Gamma(\tfrac{121}{24}, \tfrac{11}{24})\\
c_2 &\sim \Gamma(\tfrac{121}{24}, \tfrac{11}{24})\\
\kappa^2 &\sim \Gamma(1, 10^2)
\end{aligned} \tag{14}$$

With a gamma distribution with shape parameter α and inverse scale parameter β, where $z \sim \Gamma(\alpha, \beta)$ means $E(z) = \frac{\alpha}{\beta}$ and $Var(z) = \frac{\alpha}{\beta^2}$.

The pytwalk based on MCMC was simulated in Python for 200, 000 samples with 100, 000 burnin. It returns posterior parameter distributions shown in Figure 1 . The maximum a posteriori estimators (MAP), the posterior mean and credible intervals, which were calculated with the library ArviZ, are shown in Table 4 .

Parameter	MAP estimate	Posterior mean	95% credible interval
β_A	0.114492365	0.011419836	$(4.48 \times 10^{-5}, 0.071054381)$
β_I	0.020927934	0.107460168	$(0.008764924, 0.190194056)$
β_V	2.70×10^{-6}	2.84×10^{-6}	$(2.73 \times 10^{-6}, 2.92 \times 10^{-6})$
c_1	0.000898382	0.00230416	$(0.001092413, 0.003184447)$
c_2	0.001474126	0.000821253	$(0.000324343, 0.001458102)$

TABLE 4 Estimated values of the infectious rates and shedding rates for model (7) with its credible intervals.

The estimated values of the infection rates β_A, β_I, and β_V seem to be far from the estimated rates that were calculated in[24,19]; however, β_V is very close to parameter value calculated in[24,19].

Analyzing the MAP estimated rates it turns out the infectiousness rate corresponding to symptomatic infectious individuals is less than the one corresponding to the asymptomatic infectious individuals. This agrees with the fact that asymptomatic infectious individuals are not isolated and symptomatic individuals are isolated when they are diagnosed. On the other hand, comparing the shedding rates we see that $c_2 > c_1$. That is, symptomatic infectious individuals contribute more than asymptomatic ones to the environmental contamination.

The R_0 estimation as well as using the maximum a posteriori (MAP) and the mean posterior estimates are given by $R_0^{MAP} = 1.630414577$ and $R_0^{M} = 1.566609364$ respectively. These values of R_0 agree with the values calculated in[19,24,15].

Using the parameters given in Tables 3 4 , the cumulative cases of infected individuals $I(t)$ for the MAP and the mean posterior estimates and the data per data are showed in the Figure 2 .

4 | SENSITIVITY ANALYSIS

Calculating the basic reproduction number for one model is not enough to design control interventions because the effect of each parameter over the threshold parameter R_0 is unknown. In this sense, it would be better for the public health strategies to take into consideration the parameters to which R_0 is more sensitive.

In this section, the Sobol's indices for the basic reproduction number for the model with control interventions (model 1) will be calculated; see[17,18,15]. The Sobol's indices will be used to measure the variation of the basic reproduction number given by

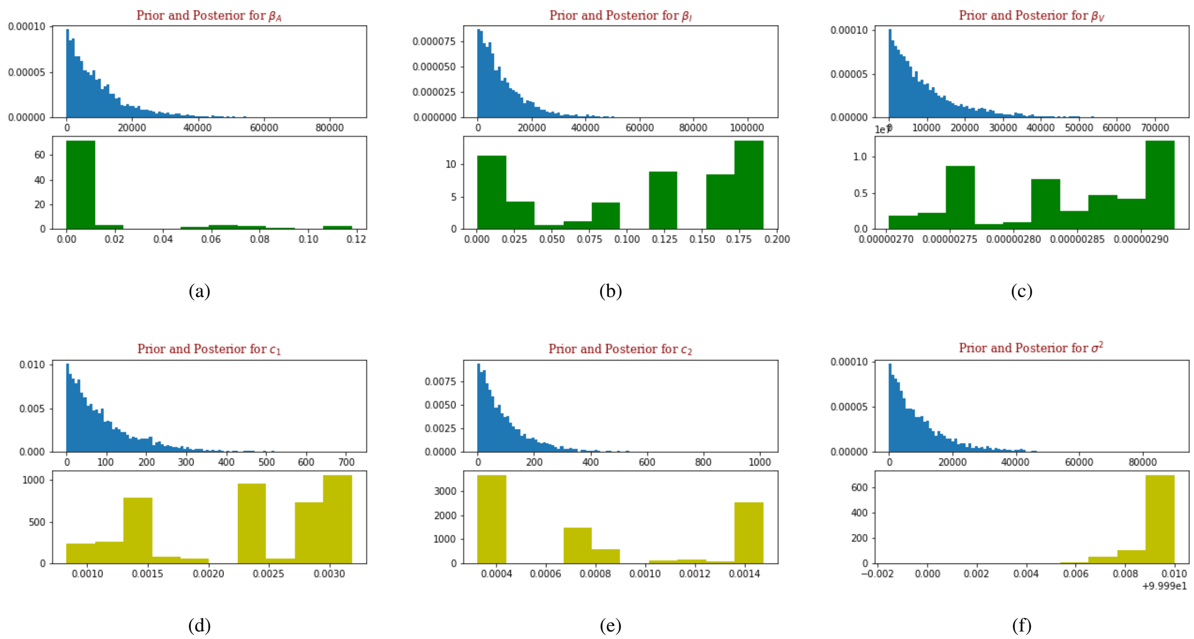


FIGURE 1 Posterior distributions for the parameters obtained.

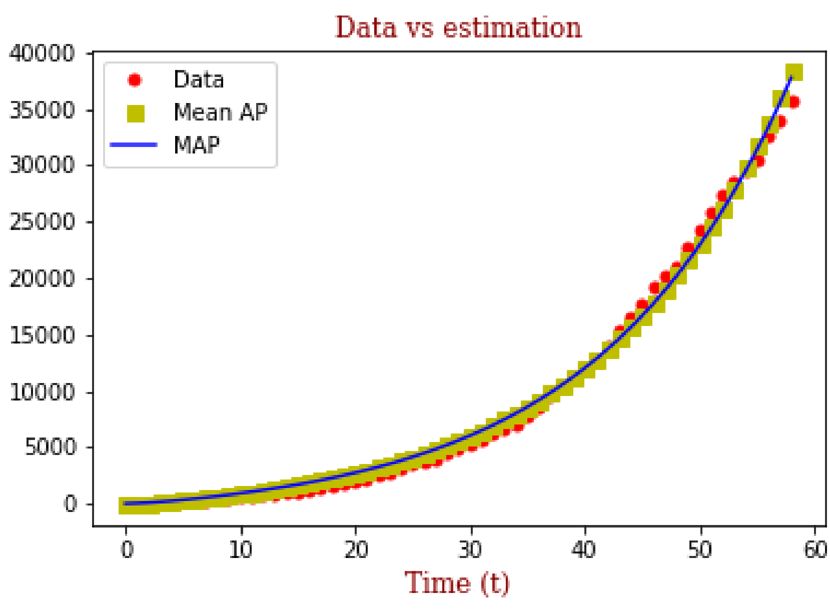


FIGURE 2 Figure shows the cumulative infections $C(t;\phi)$ for the basic model using the estimated MAP, the mean from the posterior distribution for ϕ, and the confirmed cases for COVID-19 in Mexico from March 09, 2020 to May 07, 2020.

(4) as a function of the relative contribution of the parameters involved in the control interventions. For this, the parameters were ranged in the intervals shown in Table 5 .

Figure 3 shows the direct contribution of each parameter on R_0. It also shows the combined contribution of several parameters.

Scenario A) shows that when cautious individuals are extremely cautious, i. e. having a reduction of the infection rate higher than 50%, $0 \leq \theta \leq 0.5$, the parameter θ contributes in 52%. At the same time the parameters associated to the diagnostic rates

d_1 and d_2 contribute to the variation of R_0 less than 25%, while cleaning and disinfecting contribute no more in 10% to the variation of R_0. On the opposite scenario case B), i. e. when $0.5 \leq \theta \leq 1$ other contribution prevail. The added contribution of d_1 and d_2 is bigger than 45%, while changes in m contribute less than in 20% to the variation of R_0.

Cases C) and D) show scenarios for which the viruses' mortality rate, m is big so that the viruses in the environment degrade rapidly. In particular, scenario C) shows that if the infectiousness rate reduction is less than 50% ($0 \leq \theta \leq 0.5$), the other parameters can not be neglected, because the sum of their total-order sensibility by Sobol's indices is above 37%. Case D) shows that if $\theta > 0.5$, the contribution of the other parameters to the variation of R_0 is less than 20% in the first as well as in the total orders.

Cases E) and F) show scenarios for which the cautious susceptible individuals do not reduce the infection rate massively (a poor reduction of the infection, $0.8 \leq \theta \leq 1$) and there is a bad cleaning and disinfection of surfaces. In case E), the diagnostic rate of infectious individuals contributes to the variation of R_0 in at least 80% in the first and total order of the Sobol's indices. Notice that, in this scenario, the contribution of the parameters d_1, θ and m to variations in R_0 may be neglected. Case F) shows the scenario of which the asymptomatic individuals are diagnosed with a big rate. Note that, the cases of diagnosed asymptomatic individuals contribute less than 40% to the $R_0's$ variation, and the diagnosed symptomatic individuals contribute less than 45% to the variation of R_0. Observe that, in real world scenarios diagnosing asymptomatic individuals implies a higher effort due to the difficult of finding them.

In all analyzed cases, the Sobol indices of δ is null. That is, the number of cautious susceptible individuals who are subtracted from the population $N(t)$ in the adjusted-incidence rate does not affect to the possible values of the basic reproduction number; see Figure 3 .

	d_1	d_2	θ	m	δ
Case A)	[0.0,0.0505]	[0.0,0.505]	[0,0.5]	[0.0,1]	(0, 1)
Case B)	[0.0,0.0505]	[0.0,0.505]	[0.5,1]	[0.0,1]	(0, 1)
Case C)	[0.0,0.0505]	[0.0,0.505]	[0,0.5]	[0.0,10]	(0, 1)
Case D)	[0.0,0.0505]	[0.0,0.505]	[0.5,1]	[0.0,10]	(0, 1)
Case E)	[0.0,0.0505]	[0.0,0.505]	[0.8,1]	[0.0,0.156]	(0, 1)
Case F)	[0.0,0.2]	[0.0,0.505]	[0.8,1]	[0.0,0.156]	(0, 1)

TABLE 5 Variation ranges for the analysis of the Sobol's indices for the parameters of R_0 for model (7).

5 | NUMERICAL SIMULATIONS

In this section we show numerical solutions of the model 1. The numerical simulations show scenarios for which control interventions are applied at diverse moments after March 09, 2020. In this date, there were recorded 25 diagnosed infectious cases in Mexico City. To simulate scenarios for the epidemic outbreak, we use the values of the parameters given in the Tables 3 and 4 and hypothetical values for the parameters associated with control interventions.

Figure 4 shows plausible scenarios when lax control interventions to control the epidemic outbreak are applied with a delay from 1 to 12 weeks after March 09, 2020. The values of the parameter used to describe lax control interventions are $\alpha = 1.0 \times 10^{-12}$, $\theta = 0.999$, $d_1 = 2.0 \times 10^{-5}$, $d_2 = 2.0 \times 10^{-4}$, $m = 1.0\times^{-6}$, $\delta = 1.0 \times 10^{-9}$. We choose small values for α, m, δ and $(1-\theta)$ to describe that the intervention controls are not strict, and we choose d_1 and d_2 close to zero to describe the scenario for which very few infectious individuals are being diagnosed and treated. In Mexico, according to some early reports, only 10 percent of mild suspected cases were tested for COVID-19[5]. On the other hand, for severe cases, 100 percent of patients were tested. Hence, we assume $10d_1 = d_2$.

Figure 5 shows the evolution of the number of infected individuals for a scenario for which public health strategies are applied in a population and a different one without control interventions. Figure 6 shows two plausible scenarios: in the first case public health strategies are being strictly applied for cautious susceptible individuals and more infectious individuals are

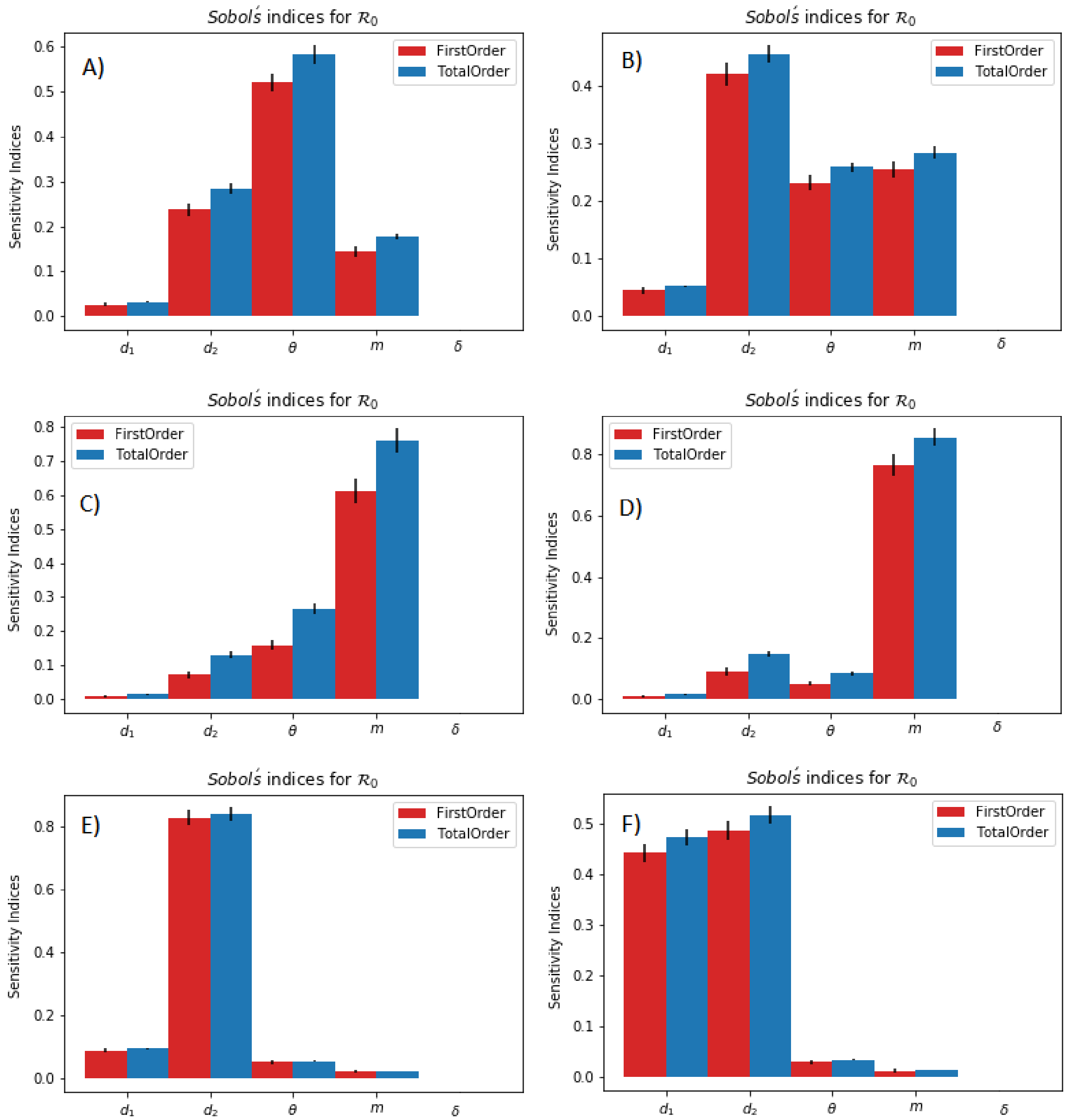
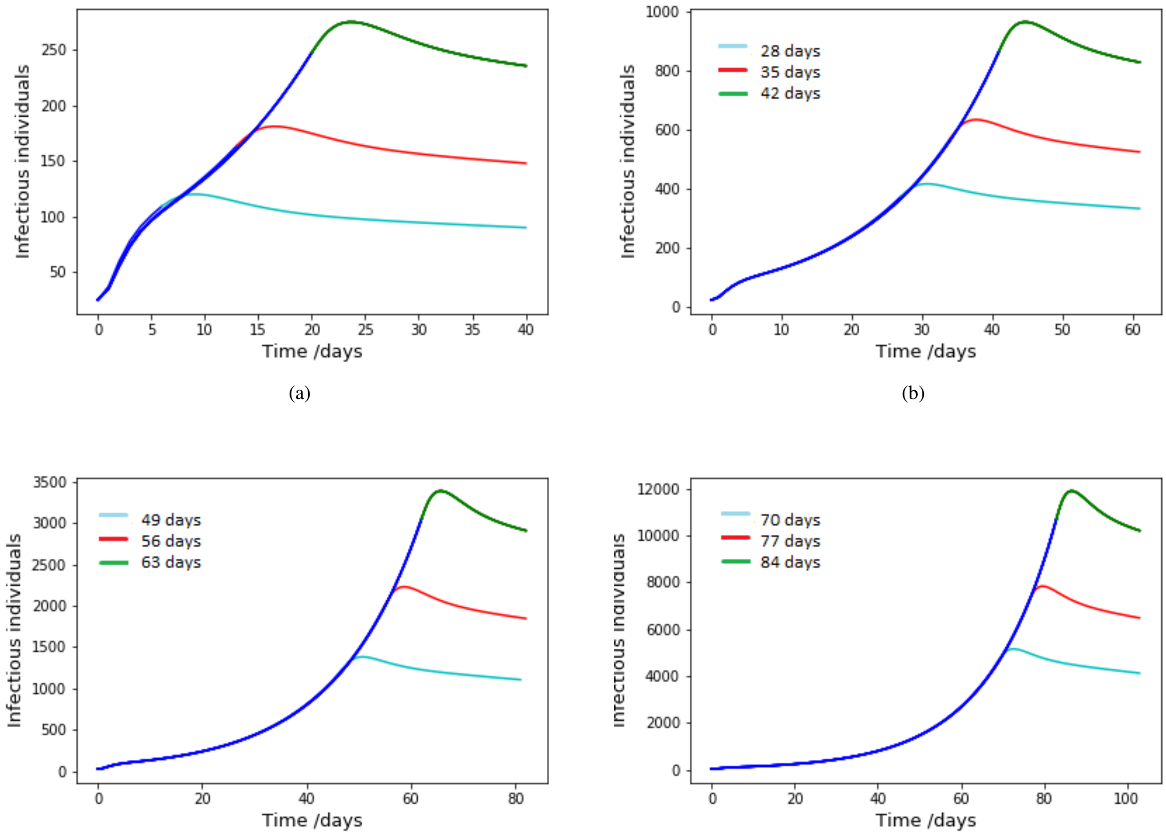


FIGURE 3 Sobol's indices for the basic reproduction number R_0, for the first and total orders. The Sobol's indices were explored in the ranges showed in Table 5 .

diagnosed. For this scenario, the parameter values are $\alpha = 0.8, \theta = 0.001, d_1 = 0.02, d_2 = 0.2, m = 10, \delta = 0.9$. In this scenario, $m = 10$ describes the case for which the life expectancy of the virus is rapidly reduced to zero because contaminated surfaces were rapidly disinfected. Since $\frac{1}{\mu_V + m}$ describes the mean period that the virus is in the contaminated environment before it is cleaned.

The second scenario describes the case for which the intervention controls are not strict, and the values of the parameters are the same as in the scenarios shown in Figure 4 .



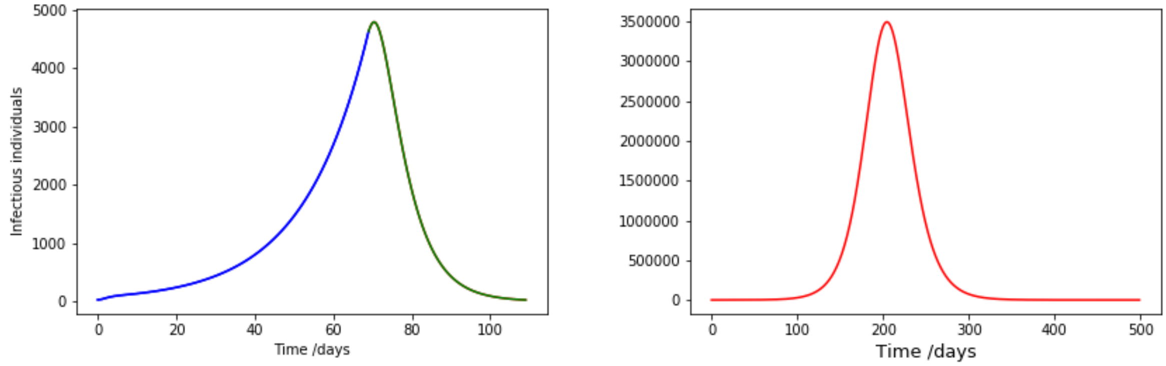
(a) (b) (c) (d)

FIGURE 4 Figure shows the effect exerted in the number of infectious individuals when the control interventions begin at day 7, 14, 21, 28, 35, 42, 49, 56, 63, 70, 77, and 84 after the beginning of the epidemic.

6 | DISCUSSION

The implications of the occurrence of epidemic outbreaks such as the Covid-19 have a great social and economic impact. That is why all new knowledge of its dynamics can leads to understanding, controlling, and even forecasting the spread of COVID-19 in future times. In this work, we focus on how the control interventions affect the evolution of the disease. We present a mathematical model for Covid-19 that explicitly incorporates the asymptomatic individuals category and the possibility of a contaminated environment. We also include the role played by behavioral changes of the individual due to external as well as internal decisions. It could include reacting to a large number of cases by staying home, being more cautious in general or just washing hands more often. In a different setting it includes restrictions set by a central authority. In any case it is of great interest to know the effect of each parameter on the outcome of the epidemics. In particular we found that personal care and personal protection together with regular environmental cleansing can strongly reduce the need for regular screening, which is not affordable in some setting or at least may be more expensive than education. We found in the case of lax restrictions or careless behaviour that the screening requirements for controlling the epidemics can dramatically grow.

Since the parameter associated to the cautious individuals, θ, is located in the numerator of R_0, the results suggest that changes in the behavioral conducts have a big impact in the spread of the infectious disease. When susceptible individuals turn cautious, they decrease their chances of being infected which has a big impact in the evolution of the COVID-19 epidemic. This agrees with results of the sensitivity analysis since the Sobol's indexes indicate that the parameters θ and m have a higher contribution to the variation of R_0. In particular, when the efforts are concentrated in increasing θ and m, the contributions of the other parameters such as the diagnostic rates d_1 and d_2 decrease. Notice that increasing θ and m has to do with human behavior



(a) (b)

FIGURE 5 Case a) shows the solution of the combined model for an horizon of 175 days. Case b) shows the solution of the basic model for a horizon of 250 days.

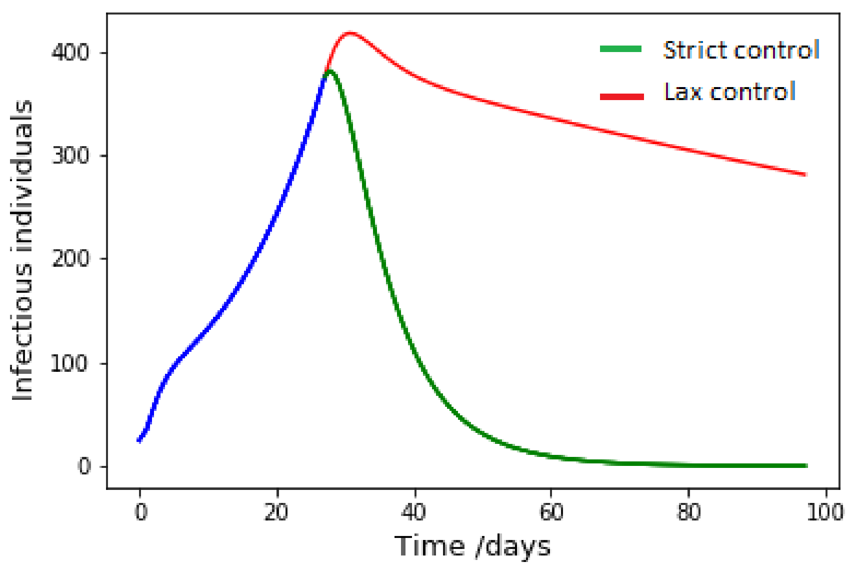


FIGURE 6 Figure shows the effect in the shape of the epidemic curve when the suggested parameters by the Sobol's analysis given by the Sobol's indices are changed. For the scenario with strict intervention controls the parameters are $\alpha = 0.8, \theta = 0.001, d_1 = 0.02, d_2 = 0.2, m = 10, \delta = 0.9$ while, for the lax scenario, the parameters are the same that the values used for the scenarios showed in Figure 4 .

more than with economical issues, whereas diagnostic requires not only an economical but a social effort. In particular, the diagnosis of asymptomatic individuals needing to find them before they can be tested. Therefore, it is of paramount importance that susceptible individuals boost their awareness about public health strategies in which they can contribute to decrease the speed of the propagation of the SARS-CoV-2. Those control interventions include, hand hygiene practices, cleaning and disinfection of contaminated surfaces, safe management of health care waste associated with infected individual, environmental cleansing, social distancing, etc. The system is highly sensitive to the moment the control strategies are introduced. The sooner control strategies are applied the lower the epidemic peak will be. Figure 4 shows that the smallest epidemic peak is associated with the shortest reaction time, and this peak is smaller in many orders of magnitude. Figure 5 shows the solutions $I(t)$ for the model when the intervention controls are applied 10 week after the start of the epidemic (March 09, 2020), and without intervention controls. Note that any health care system can collapse if the epidemic follows its natural spread, while it is not the case when there are opportune control interventions and the epidemic outbreak can be administered.

Figure 6 shows that the shape of the solutions $I(t)$ for model (1) are drastically changed as a function of the parameters that describe the public health strategies. Note that the epidemic curve suffers changes in its shape depending whether the intervention controls are lax or strict. In both cases, the number of new infectious individuals decrease until the epidemic outbreak is controlled. Since, the sooner public health strategies are applied the lower number of infectious individuals will be, it follows that the epidemic peak can be drastically decreased further if strict interventions strategies to control the spreading of the SARS-CoV-2 are used. So, the central statement we can share is the fact that the sooner a public health strategy is applied the stronger its effect on the reduction of the peak reached in the outbreak. This means, promt allocation of resources as an early response can save huge amounts later on. This might be of relevance for future waves of Covid-19 or any similar diseases.

Ongoing work, by the authors is looking into the effect of periodical behavioral changes of the susceptible individuals in the evolution of the spread of the infectious disease.

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