

## A NUMERICAL SIMULATION OF THE COVID-19 EPIDEMIC IN ARGENTINA USING THE SEIR MODEL

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**Abstract**— A pandemic caused by a new corona virus has spread worldwide, affecting Argentina. We implement an SEIR model to analyze the disease evolution in Buenos Aires and neighboring cities. The model parameters are calibrated using the number of casualties officially reported. Since infinite solutions honor the data, we show different cases. In all of them the reproduction ratio  $R_0$  decreases after early lockdown, but then raises, probably due to an increase in the community circulation of the virus. Therefore it is mandatory to reverse this growing trend in  $R_0$  by applying control strategies to avoid a high number of infectious and dead individuals. The model provides an effective procedure to estimate epidemic parameters (fatality rate, transmission probability, and infection and incubation periods) and monitor control measures during the epidemic evolution.

**Keywords** – COVID-19, SEIR model, reproduction ratio, fatality rate.

### I. INTRODUCTION

In March 9, 2020, the start of the new coronavirus (COVID-19) epidemic in Argentina was officially reported by the Argentinean Ministry of Health. By today, September 30, 2020, the number of cases is still rising. The majority of mathematical models that replicate illnesses outbreaks splits the population into categories, to analyze how long will it take for one group to evolve into another (Hethcote, 2000; Brauer, 2017). The mathematical details of these models can be seen in Hethcote (2000) and Keeling and Rohani (2008). Here, we use a SEIR model, consisting of a system of first-order ODE to describe the spread of the virus, compute the number of infected individuals and estimate the death toll. As examples, the SEIR model has been successfully applied to study the transmission dynamics of tuberculosis (Athithan and Ghosh, 2013) and varicella (Zha *et al.*, 2020). It is important to clarify that the  $E$  class is incubating the disease and has not symptoms. They will have symptoms when they pass to class  $I$ . Individuals in class  $I$  may not have symptoms (asymptomatic), but they are

infectious, while those in class  $E$  are not. Moreover, individuals in class  $E$  can move to  $R$  without showing symptoms, but they are infectious when they are in class  $I$ .

The SEIR model has been applied by Carcione *et al.* (2020) to simulate this epidemic in the Lombardy Region (Italy), with approximately 16800 casualties reported to date. The significant threat COVID-19 carries finds its meaning in the elevated number of infected health-care workers, such as 20 % of the cases in Italy.

In order to analyze the epidemic's behavior, the model is calibrated using the number of dead individuals to date, which we consider more reliable than the number of infectious individuals. The model parameters are: probability of transmission per contact, incubation and infectious periods and fatality rate.

Based on China, USA and European Union's experience, we are certain that combining rapid diagnosis with isolation measures has a substantial effect on the epidemic's dynamics. Evaluating and quantifying the effectiveness of these methods is extremely important (Chowell *et al.*, 2003) and numerical simulators contribute to achieve this goal. Dekhordi *et al.* (2020) presented a case study of COVID-19 using a statistical analysis of data from countries in Asia and Europe like China, Italy and Spain to characterize the dynamics of the pandemia.

Summarizing, the numerical simulation aim is to provide an effective procedure to model the virus diffusion over time and to analyze the effectiveness of administrative measures. The ODE system solution is obtained employing a forward Euler scheme (Carcione, 2014) and we assume that natural deaths and births are balanced (Brauer, 2008; d'Onofrio *et al.*, 2015; Carcione *et al.*, 2020). In this way the peak of infected and dead individuals per day as a function of time can be predicted based on the parameters estimated during calibration.

### II. THE SEIR DIFFERENTIAL MODEL

This work uses the SEIR (Susceptible-Exposed-Infected-Removed) epidemic model (Hethcote, 2000; Keeling and

Rohani, 2008; Zha *et al.*, 2020) to study the time evolution of the COVID-19 epidemic in Argentina. The model considers a total (initial) population,  $N_0$ , composed of four compartments: susceptible,  $S(t)$ , exposed,  $E(t)$ , infected,  $I(t)$  and recovered,  $R(t)$ , with  $t$  being the time variable. The initial value problem for the SEIR ODE system is formulated as follows:

$$\begin{aligned}\dot{S} &= \Lambda - \mu S - \beta S \frac{I}{N}, \\ \dot{E} &= \beta S \frac{I}{N} - (\mu + \varepsilon)E, \\ \dot{I} &= \varepsilon E - (\gamma + \mu + \alpha)I, \\ \dot{R} &= \gamma I - \mu R,\end{aligned}\quad (1)$$

with initial conditions  $S(0)$ ,  $E(0)$ ,  $I(0)$  and  $R(0)$ . In Eq. (1) the time derivative is denoted by a dot above the variable and  $N$  is the number of live individuals at time  $t$ , e.g.  $N = S + E + I + R \leq N_0$ . The coefficients in Eq. (1) are: the birth rate  $\Lambda$ , the natural per-capita death rate  $\mu$ , the virus induced average fatality rate  $\alpha$  and the probability of disease transmission per contact  $\beta$ . Moreover,  $1/\gamma$  and  $1/\varepsilon$  are the infection and incubation periods, respectively. All of these coefficients have units of (1/time).

The traditional SIR (Susceptible-Infected-Removed) model (Kumar *et al.*, 2020) is obtained selecting  $\Lambda = \mu = 0$  and  $\varepsilon = \infty$  while if  $\Lambda$  and  $\mu$  are not zero, the model is termed endemic SIR (Allen, 2017). However, as the SIR model has no exposed compartment, then it would not be proper using it for infections with  $\varepsilon$  values such as those of the COVID-19. Concerning the meaning of the variables in (1),  $S$  is the number of humans susceptible to be exposed and  $E$  is the actual number of exposed individuals (individuals in which the disease is latent; they are infected but not infectious). Individuals move from  $S$  to  $E$  depending on the number of contacts with  $I$  individuals, multiplied by the probability of infection ( $\beta$ ). Furthermore, exposed ( $E$ ) become infected ( $I$ ) with a rate  $\varepsilon$  and infected become recovered ( $R$ ) with a rate  $\gamma$ . Since lifelong immunity is assumed, people in the  $R$  class do not move back to the  $S$  class. Because of the relatively short period of the epidemic, it is assumed that  $\Lambda = \mu N$ , so that the deaths balance the newborns. The deceased individuals  $D(t)$  are computed as  $D(t) = N_0 - N(t)$ , therefore the dead people per unit time  $\dot{D}(t)$  can be obtained as (De la Sen *et al.*, 2014):

$$\dot{D} = \alpha I(t), \quad (2)$$

if the deaths balance the newborns.

An important measure to quantify the virus expansion is the basic reproduction ratio,  $R_0$ , which estimates the average number of secondary cases caused by an already infected person. For the SEIR model,  $R_0$  is given by (Zhang *et al.*, 2013):

$$R_0 = \frac{\beta \varepsilon}{(\varepsilon + \mu)(\gamma + \alpha + \mu)} \quad (3)$$

The basic reproduction ratio is used to estimate the virus spread, establishing  $R_0 = 1$  as a stability limit: if  $R_0 > 1$  the disease invades the population while if  $R_0 < 1$  the disease disappears.

Another measure is the *infection fatality rate* (*IFR*),

$$IFR(\%) = 100 \frac{D_\infty}{R_\infty + D_\infty} \quad (4)$$

where  $R_\infty + D_\infty$  represents the final number of infected individuals ( $t \rightarrow \infty$  refers to the epidemics ending).

Using the last line in Eq. (1) (with  $\mu = 0$ ) and Eq. (2), we obtain

$$IFR(\%) = 100 \frac{\alpha}{\alpha + \gamma}, \quad (5)$$

where this relation is always valid, not just at the epidemics ending.

A third usually reported coefficient is the *case fatality rate* (*CFR*), such that  $CFR > IFR$ , since this rate underestimates the number of infected individuals.

Equations (1) are discretized using a forward Euler discretization scheme with a time step  $\Delta t = 0.01$  day. The solution  $(S^n, E^n, I^n, R^n) = (S, E, I, R)(n\Delta t)$ ,  $n \geq 1$ , this time discretization procedure yields positive and bounded solutions (Brauer, 2017). Furthermore, the solution converges to an equilibrium, i.e.,  $S^n + R^n + D^n = S_\infty + R_\infty + D_\infty = N_0$  for  $t \rightarrow \infty$ .

A sensitivity analysis of the model to changes in its parameters is presented by Carcione *et al.* (2020). It is observed that higher values of the incubation period ( $\varepsilon^{-1}$ ) delay the epidemic, and increasing the infectious period ( $\gamma^{-1}$ ) induces the same effect. Furthermore, when more individuals are initially exposed ( $E(0)$ ), the intensity of the peak does not change, but anticipates the epidemic. Other results indicate that if  $R_0$  does not change during the epidemic, the peak of infected people is hardly sensitive to the initial number of infected individuals, and an earlier lockdown highly reduces the number of dead individuals.

### III. THE COVID-19 EPIDEMIC IN THE RMBA

Next, we attempt to model the COVID-19 epidemic in the RMBA (Región Metropolitana de Buenos Aires), comprising the city of Buenos Aires and neighboring cities, with a population  $N_0 = 14,839,026$  individuals. For this purpose, we use as reliable data the total number of casualties from day 1 (March 9, 2020) to day 206 (September 30, 2020). The reported infected people cannot be used for calibration, since at present the number of asymptomatic, undiagnosed infectious individuals is unknown. The number of death individuals is also uncertain, since there were delays in the upload of official data. In order to overcome this limitation, we consider 22% more casualties in the estimation (average percentage chosen for Argentina based on our data and general underestimation of COVID-19 mortality; Kung *et al.*, 2021). Predictions of high accuracy are not possibly due to the lack of information about the probability of the disease transmission, characteristics of the disease and initial conditions of the SEIR model. We assume  $\mu^{-1} = 3.6 \times 10^{-5}$  / day, corresponding to a life expectancy of 76 years (available at <https://datatopics.worldbank.org/world-development-indicators/>). Parameter  $\beta$  varies as a piecewise constant function in time intervals  $[t_0, t_1)$ ,  $[t_1, t_2)$ , ...,  $[t_{L-1}, \infty)$ , with changes associated with administrative measures taken by the state (such as lockdown) and behavior of the population. In this case,  $t_0 =$

1 day,  $t_1 = 31$  day and  $t_2 = 50$  day, i.e.,  $L = 3$ , since after  $t_1$  (April 8), home isolation, social distancing and partial Nation lockdown started to be effective, as indicated by an inflection point in the curve of casualties, and after  $t_2$  (April 27), the situation became worst with an increase in the slope of the curve. The SEIR model parameters,  $\alpha$ ,  $\beta$ ,  $\varepsilon$ ,  $\gamma$ , together with the initial exposed individuals  $E(0)$  are estimated fitting the number of fatal victims. This constitutes an inverse problem with infinite solutions. A Quasi Newton approximation technique for nonlinear least squares problem with the formula of Broyden-Fletcher Goldfarb-Shanno is applied. This technique was successfully applied to estimate parameters in reservoir engineering (Savioli and Bidner 1994, Savioli and Fernández Berdaguer, 2007). The L2-norm of the differences between simulated and measured casualties is minimized and yields  $E(0)$  and the model parameters on each time interval. In fact, while  $\alpha$ ,  $\varepsilon$  and  $\gamma$  remain constant throughout the entire simulation,  $\beta$  varies in the intervals  $[t_0, t_1)$ ,  $[t_1, t_2)$ ,  $[t_2, \infty)$ . We present the results of four different cases that honor the data. Computational implementation is done by writing Fortran codes and plotting with gnuplot public software. The parameters constraints are shown in Table 1 (Carcione *et al.*, 2020; Lauer *et al.*, 2020; Read *et al.*, 2020), while initial values and results for the four cases are displayed in Table 2. All the cases assume an initial number of infectious individual  $I(0) = 100$ , although this value may also affect the result. The last four files in Table 2 are: date of the peak of infected individuals, day of the last infected individual (the end of the epidemic in theory), total number of infected individuals at the end of the epidemic, i.e.,  $I_\infty = R_\infty + D_\infty$ ; and death toll  $D_\infty$  (note that the end of the epidemic is predicted by the model without considering that effective vaccines or treatments are developed).

The results are very sensitive to variations of the parameter  $\beta$  and, consequently, those of  $R_0$ , mostly due to the impact of the performed intervention strategies.

In fact, the model predictions are strongly influenced by the behavior of  $R_0$  during the last period, after day 50. Therefore, a reduction of  $R_0$  is essential to avoid a tragic situation.

Figures 1 and 2 show the fit and extended curves corresponding to Case 1, which predicts an initial  $R_0 = 1.70$ , decreasing to 0.74 in April 8, after the lockdown, and increasing to 1.23 after April 27, most probably due to an increase of the community circulation of the virus.

This case predicts an  $IFR = 0.94\%$ , a high death toll (nearly 49 k) and 5.16 million infected individuals at the end of the epidemic. However, this is due to the last  $R_0$  trend that can be inverted by implementing more isolation. In fact, if the value of  $R_0 = 0.74$  had been maintained after April 27 only 575 casualties and 61,400 infected individuals would have occurred. In the situation shown in Case 1, the maximum number of infected individuals is approximately 113,300 people at day 228 (October 22, 2020). If only 5% of these individuals require intensive care, this amounts to 5,665 humans. Besides, the end of the epidemic is predicted by January 27, 2022.

The other cases honor the data with smaller fatality rate  $\alpha$ , and, consequently, predict less casualties, compared to Case 1, with  $IFR$  between 0.3% and 0.5% approximately. For instance, Case 2 (Fig. 3) which predicts an initial  $R_0=3.17$ , decreasing to  $R_0 = 1.03$  (approximately the stability limit) in April 8, and increasing to 1.40 after April 27.

Table 1 – Parameter constraints applied in the estimation procedure

Variable	Lower bound	Upper bound
$\alpha$ (day <sup>-1</sup> )	$1 \times 10^{-5}$	$1 \times 10^{-2}$
$\beta$ (day <sup>-1</sup> )	0.1	0.9
$\varepsilon^{-1}$ (day)	3	9
$\gamma^{-1}$ (day)	3	9
$E(0)$	10	1000

Table 2 - Initial values and results of the estimation procedure

	Case 1 Final (initial)	Case 2 Final (initial)	Case 3 Final (initial)	Case 4 Final (initial)
$\alpha$ (day <sup>-1</sup> )	0.003128 (0.003)	0.0006(0.003)	0.001408 (0.003)	0.001407 (0.004)
$\beta_1$ (day <sup>-1</sup> )	0.5713 (0.5)	0.5102 (0.5)	0.5349 (0.58)	0.4590 (0.5)
$\beta_2$ (day <sup>-1</sup> )	0.2471 (0.3)	0.1655 (0.3)	0.3600 (0.31)	0.3809 (0.3)
$\beta_3$ (day <sup>-1</sup> )	0.4140 (0.4)	0.2243 (0.4)	0.3760 (0.4)	0.4491 (0.4)
$\varepsilon^{-1}$ (day)	4.38 (6)	4.10 (6)	4.25 (4)	6.31 (5)
$\gamma^{-1}$ (day)	3.01 (6)	6.25 (6)	3.42 (4)	3.01 (5)
$E(0)$	925 (500)	14 (200)	260 (300)	3426 (200)
$R_{01}$	1.70	3.17	1.82	1.37
$R_{02}$	0.74	1.03	1.22	1.14
$R_{03}$	1.23	1.40	1.28	1.34
$IFR(\%)$	0.94	0.37	0.48	0.42
Peak of Infected	October 22, 2020	September 21, 2020	September 22, 2020	September 23, 2020
End of epidemic	January 27, 2022	December 5, 2021	November 11, 2021	November 22, 2021
$I_\infty(k)$	5156	7466	5934	6794
$D_\infty(k)$	49	28	29	29

$I(0) = 100$ . The values of  $\beta$  refer to the periods (in days):  $[1, 31)$ ,  $[31, 50)$  and  $[50, \infty)$  (in days).

$I_\infty$ : the total infected individuals at the end of the epidemic, obtained when  $I < 1$ .  $D_\infty$  is the death toll at the end of the epidemic.

Read *et al.* (2020) report the mean values  $\varepsilon^{-1} = 4$  days and  $\gamma^{-1} = 3.6$  days.

Lauer *et al.* (2020) report  $\varepsilon^{-1} = 5.1$  days. Ferguson *et al.* (2020) estimates an average  $IFR = 0.9\%$

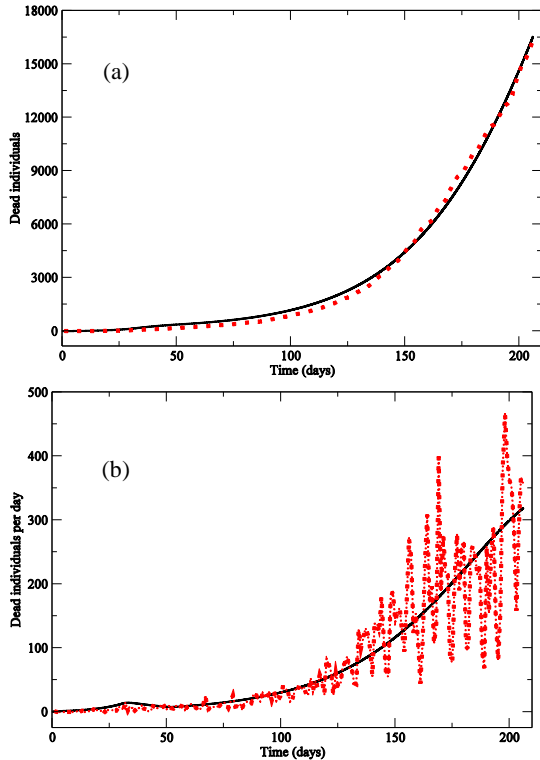


Figure 1. RMBA case history. Dead individuals (a) and dead individuals per day (b). The dots represent the data and the solid line corresponds to Case 1-Table 2.

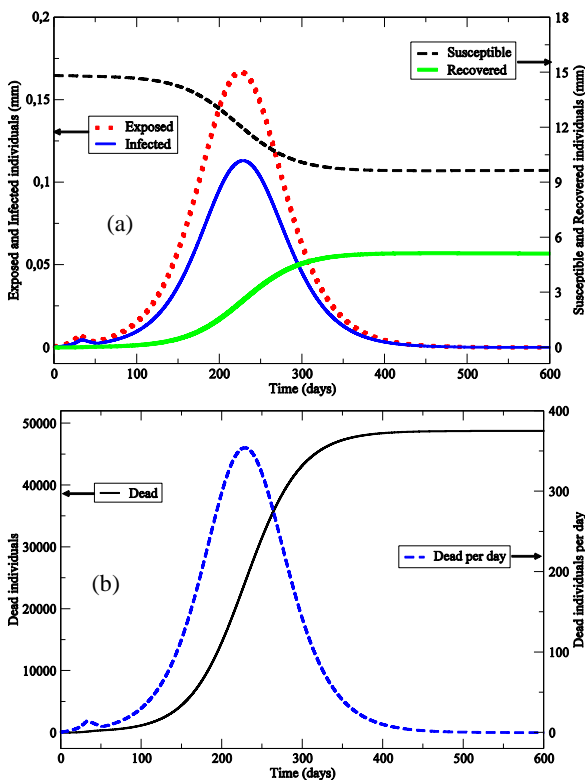


Figure 2. Number of individuals in each class (a) and deaths (b), corresponding to Case 1 in Table 2. In (b) the solid and dashed curves refer to the accumulated deaths and deaths per day. The peak of infected individuals (and deaths per day) occurs at approximately day 228 (October 22, 2020).

Case 2 estimates the highest peak of infected individuals, 400 thousand at 197 days (September 21, 2020), as can be seen in Fig. 3 (a). This amount implies 20,000 patients if 5 % require intensive care, a number that can overload the capacity of the hospitals. This situation is related with the infectious period  $\gamma^{-1}$ , which is higher than 6 days. Also the total number of infected individuals at the end of the epidemic,  $I_{\infty}$  is the highest, 7466 thousand people. Keeping  $R_0=1.02$  from day 31 (April 8), the epidemic would be under control with a minimum death toll (4477 individuals) and a minimum number of infected humans at the end of the epidemic (1131 thousand people).

Besides the last three cases predict similar dates of occurrence of the peak of infected individuals (September 21-23, 2020) and of the end of the epidemic (November 11, 2021 to December 5, 2021).

Data provided by literature can be compared with the values shown in Table 2. The population’s age affects the IFR and fatality rate. As an example an estimated IFR of 0.657 % for the whole Chinese population grows to 3.28 for population over 60 yr. age (Verity *et al.*, 2020 – Table I). If the amount of infected people is considerably superior than the reported cases, the mortality rate could be substantially lower than the official one, indicating COVID-19 is less lethal than SARS and MERS, despite of being far more contagious. Read *et al.* (2020) states an average value  $R_0=4$ , whereas Wu *et al.* (2020) get values within 1.8 and 2. As reported by Chowell *et al.* (2003) IFR = 4.8 % for SARS, and Verity *et al.* (2020) state that CFR of SARS is superior to that of COVID-19, with approximately 1.38 %. Again, COVID-19 appears to be far more contagious.

An extended approach consists in using time derivatives of fractional order to generalize the diffusion process. Such models include both memory and non-local effects in a natural way (Mainardi, 2010). Indeed, replacing the first-order temporal derivative by a Caputo fractional derivative of non-natural order (Caputo *et al.*, 2011) we obtain a new parameter to adjust the data: the derivative order. This modeling can be performed by using fractional derivatives computed with the Grünwald-Letnikov approximation, which is a generalization of the finite-difference derivative (Carcione, 2014) or solving the differential equations in the frequency domain (Gauzellino *et al.*, 2014, Santos and Gauzellino, 2017). Furthermore, the model can be made two-dimensional by including the spatial diffusion of the virus (Naheed *et al.*, 2014) to model local outbreaks and be able to isolate them. The approach can be based on a finite-element method in the space-frequency domain with domain decomposition. This numerical procedure has already been applied to wave propagation in 2D and 3D media in geophysics (Santos and Gauzellino, 2017). Moreover, there are more complex versions of the SEIR model as, for instance, including a quarantine class and a class of isolated (hospitalized) members (Brauer, 2017). Finally, since signals propagate instantaneously in diffusion equations, the model predicts that there are more infectious humans ( $I$

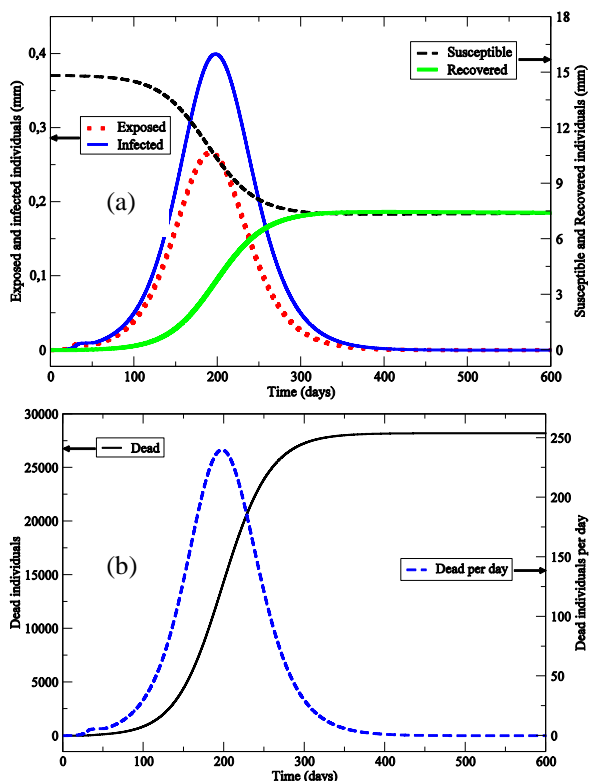


Figure 3. Number of individuals in each class (a) and deaths (b), corresponding to Case 2 in Table 2. In (b) the solid and dashed curves refer to the accumulated deaths and deaths per day. The peak of infected individuals (and deaths per day) occurs at day 197 (September 21, 2020).

class) than actual before the latent period and at late stages of the epidemic. Solutions to this problem can be found, for instance, in Keeling and Rohani (2008) – Section 3.3.

#### IV. CONCLUSIONS

The SEIR epidemic model is implemented to simulate the time evolution of the COVID-19 epidemic in Argentina, specifically in the RMBA, where the situation is more critical compared to other parts of the country. We calibrate the model parameters by using the number of officially reported casualties, considered more reliable than the number of infected individuals. The simulation attempts to provide a simple but effective procedure to model the virus diffusion over time, in view of the lack of knowledge of many variables related to the epidemic. At present, the epidemic in the Buenos Aires area is under control due to the early lockdown, because most predictions have estimated the peak of infected individuals by the end of September, and the health system was not collapsed. But we found that the reproduction ratio first decreased and then increased, causing a drastic prediction of the death toll if this trend persists in the future. In general, the incubation and infectious periods are in the range 4-7 days and 3-7 days, respectively, and the infection fatality rate (IFR) between 0.4 % and 1.0 %. A case with a high infectious period yields a high peak of infected individuals that can overload the intensive care capacity. The total amount of infected individuals will be between 5.0 million and 7.5 million people if the increasing  $R_0$

trend is not inverted. In general, the results indicate that the peak of infected individuals in RMBA has occurred approximately at September 22th, but other predictions delay this peak to October 22th. We show how the effectiveness of the lockdown, the incubation and infectious periods, the probability of transmission and the initially exposed individuals affect the evolution of the epidemic. More complex models, i.e., with more classes or compartments and considering spatial diffusion, can be used in the future when some of the properties of the virus can be established more accurately, mainly the incubation and infectious periods and the fatality rate.

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