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 coronavirus has spread worldwide, causing an epidemic in Argentina. We implement an SEIR model to analyze the evolution of the disease in Buenos Aires and neighbouring cities (RMBA) with 15 million inhabitants. The parameters of the model are calibrated by using as data the number of casualties officially reported. Since infinite solutions honour the data, we show a set of cases by considering different situations. The first set of parameters yields initially a reproduction ratio $R_0 = 3.33$ decreasing to 0.95 in April 8, after the lockdown, but increasing to 1.55 after April 27, most probably due to an increase of the contagion in highly populated slums. The infection fatality rate (IFR) is 1.88 % and the predicted number of casualties is 173000 deaths with 9 million people infected at the end of the epidemic. However, keeping $R_0 = 0.95$ after April 27, would cause only 1881 casualties and 92955 infected individuals. Other cases, assuming the present trend, predict smaller incubation periods (4-5 days) and yield between 20000 and 70000 deaths and IFRs between 0.5 % and 1.1 %. We also consider doubling the number of casualties, with a death toll of 44000 individuals and 5.1 million infected individuals. Other choices of parameters

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also provide a good fit of the data, indicating the uncertainty of the results, which may differ from reported values. The analysis allows us to study how isolation and social distancing measures affect the time evolution of the epidemic.

1 Introduction

An outbreak of pneumonia caused by a novel coronavirus (COVID-19) began (officially) in Argentina in March 9, 2020, with the number of newly reported cases still increasing (the time of writing is May 21, 2020). Most of the mathematical models to simulate an epidemic divide the population into classes and assumptions about the time rate of transfer from one class to another (Hethcote, 2000; Brauer, 2017). We refer to Hethcote (2000), Keeling and Rohani (2008) and Diekmann et al. (2013) for detailed mathematical analyses of this kind of models. Here, we use a Susceptible-Exposed-Infected-Removed (SEIR) model consisting of a first-order in time system of ODE’s, to describe the spread of the virus, compute the number of infected individuals, including the IFR to model the death toll. It is important to clarify that the E class is infected but has not the symptoms of the disease, because they are incubating it. 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 serious danger COVID-19 poses is reflected in the high number of cases of transmission to health-care workers, more than 20 % in Italy. The SEIR model has been applied by Carcione et al. (2020) to simulate the epidemic in the Lombardy Region (Italy), with approximately 15000 casualties reported to date.

The model is calibrated using the number of dead individuals to date, which we consider more reliable than the number of infectious individuals to predict the behaviour of the epidemic. The experience in China, European Union and USA shows that combining isolation measures and rapid diagnosis has a strong impact on the dynamics of the epidemic. Thus, it is important to analyze and quantify the effectiveness of these isolation measures (e.g., Chowell et al., 2003). Hou et al., (2020) used a SEIR model to study the spread of the COVID-19 disease in the city of Wuhan, China. Also, Dekhordi et al., (2020) presented a case study of COVID-19 using an statistical analysis of data from countries in Asia and Europe like China, USA, Italy and Spain, among others, to characterize the dynamics of the pandemia.

Then, the objective of the numerical simulation is to determine the number of infected, recovered and dead individuals using as parameters the number of contacts, probability of the disease transmission, incubation and infectious periods and fatality rate. In this
manner, the peak of the infected and dead individuals per day as a function of time can be predicted provided that the births and natural deaths are balanced, which is a reasonable assumption due to the relatively short period being analyzed. The ODE’s system is solved using a forward Euler scheme (e.g., Carcione, 2014).

2 The SEIR differential model

This work uses the SEIR epidemic model (Hethcote, 2000; Al-Showaikh and Twizell, 2004; Keeling and Rohani, 2008; Diekmann et al., 2013; 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 classes: 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’s system is formulated as follows:

$$
\begin{align*}
\dot{S} &= \Lambda - \mu S - \beta S \frac{I}{N}, \\
\dot{E} &= \beta S \frac{I}{N} - (\mu + \epsilon) E, \\
\dot{I} &= \epsilon E - (\gamma + \mu + \alpha) I, \\
\dot{R} &= \gamma I - \mu R,
\end{align*}
$$

with initial conditions $S(0), E(0), I(0)$ and $R(0)$. In equation (1) $N = S + E + I + R \leq N_0$, where $N$ is the number of live individuals at time $t$, and the dot above a variable denotes time derivative.

The choice $\Lambda = \mu = 0$ and $\epsilon = \infty$ gives the classical SIR model (e.g., Kumar et al., 2020), while if $\Lambda$ and $\mu$ are not zero, the model is termed endemic SIR model (e.g., Allen, 2017). However, the SIR model has no latent stage (no exposed individuals) and then it is inappropriate as a model for diseases with an $\epsilon$ such as that of the COVID-19.

The coefficients in (1), all having units of (1/T), with T: time, are as follows: $\Lambda$ and $\mu$ are the per-capita birth and natural death rates, respectively, $\alpha$ is the induced average fatality rate (its inverse is the life expectancy of an individual in the infected class) and $\beta$ is the probability of disease transmission per contact (dimensionless) times the number of contacts per unit time. Moreover, $1/\gamma$ and $1/\epsilon$ are the infection and incubation periods, respectively.

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 $\epsilon$ and infected recover ($R$) with a rate $\gamma$. Since lifelong immunity is assumed, people in the
The basic reproduction ratio, $R_0$, gives the average number of secondary cases of infection generated by an infectious individual. It can be used to estimate the growth of the virus infection, giving a threshold for the stability of the disease-free equilibrium point. When $R_0 < 1$, the disease dies out; when $R_0 > 1$, an epidemic occurs. Al-Sheikh (2012) analyzes in detail the behavior of the SEIR models in terms of $R_0$. For the SEIR model, $R_0$ is given by

$$R_0 = \frac{\beta \epsilon}{(\epsilon + \mu)(\gamma + \alpha + \mu)}$$

(e.g., Zhang et al., 2013).

The infection fatality rate (IFR) is defined as

$$\text{IFR} \, (\%) = 100 \cdot \frac{D_\infty}{R_\infty + D_\infty},$$

where $R_\infty + D_\infty$ represents the final number of infected individuals, with the subscript referring to the end of the epidemic ($t \to \infty$).

Using the last equation (1) (with $\mu = 0$) and equation (2), we obtain

$$\text{IFR} \, (\%) = 100 \cdot \frac{\alpha}{\alpha + \gamma} \approx 100 \cdot \frac{\alpha}{\gamma},$$

where this relation holds at all times, not only at the end of the epidemic. Another usually reported (time-dependent) coefficient is the case fatality rate (CFR), such that $\text{CFR} > \text{IFR}$, 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 discrete solution $(S^n, E^n, I^n, R^n) = (S, E, I, R)(n\Delta t)$, $n \geq 1$ of this time discretization procedure yields positive and bounded solutions (e.g., 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 $t \to \infty$.

A sensitivity analysis of the model to changes in its parameters is presented in Carcione et al. (2020), assuming that the parameters do not vary during the epidemic. It is observed that higher values of the incubation period ($\epsilon^{-1}$) delay the epidemic, while 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.
The COVID-19 epidemic in the RMBA

Next, we attempt to model the COVID-19 epidemic in the RMBA, comprising the city of Buenos Aires and neighbouring cities, with a population \( N_0 = 14839026 \) individuals. For this purpose, we use as reliable data the total number of casualties from day 1 (March 9, 2020) to day 74 (May 21). 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 can be an under-ascertainment of deaths, but the error is much smaller than the error related to the infected individuals. The number of dead individuals reported officially could possibly be underestimated due to undeclared cases. Thus, we also consider a case with 100% more dead people, compared to the official figures.

Predictions of high accuracy are not possibily 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. Parameter \( \beta \) varies as a piecewise constant function in time intervals \([t_0, t_1], [t_1, t_2], \ldots, [t_{L-1}, \infty]\), with changes associated with administrative measures (such as lockdown) taken by the state 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.

Fitting the casualities with the model parameters is an inverse problem with infinite solutions. In order to accomplish the fit, we use a simulated annealing algorithm developed by Goffe et al. (1994). The Fortran code can be found in: https://econwpa.ub.uni-muenchen.de/econ-wp/prog/papers/9406/9406001.txt. The fit is based on the \( L^2 \)-norm and yields \( \alpha, \beta, \epsilon, E(0) \) and \( \gamma \) on each time interval from the beginning of the epidemic (day 1, March 9, 2020) to date (day 74, May 21). For each fit, the parameters \( \alpha, \epsilon, E(0) \) and \( \gamma \) remain constant on the whole simulation time, while \( \beta \) varies in the intervals \([t_0, t_1], [t_1, t_2] \) and \([t_2, \infty]\), as mentioned above.

Table 1 shows the constraints, initial values and results for different cases, which honour the data. All the cases assume an initial number of infectious individual \( I(0) = 100 \), although this value may also affect the result. The last column do not correspond to variables but indicates the infected individuals at the end of the epidemic, i.e., \( I_\infty = R_\infty + D_\infty \approx R_\infty \), the day of the last infected individual (the end of the epidemic in theory), and the death toll \( D_\infty \). 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. The tragic situation predicted by the model is strongly
influenced by the behaviour of $R_0$ during the latter period, after day 50. Therefore, a reduction of $R_0$ is essential to avoid this situation.

Figure 1 and 2 show the fit and extended curves corresponding to Case 1, which predicts an initial $R_0 = 3.33$, decreasing to 0.95 in April 8, after the lockdown, and increasing to 1.55 after April 27, most probably due to an increase of the contagion in highly populated slums. This case, which is characterized by a long incubation period of approximately 11 days, predicts an IFR = 1.88 % and a very high death toll (nearly 173 K) and 9 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, maintaining the value of $R_0 = 0.95$ after April 27 yields only 1881 casualties and 92955 infected individuals. In the situation shown in Case 1, the maximum number of infected individuals is approximately 400000 people at day 300 (January 02, 2021). If only 1 % of this individuals requires intensive care, this amounts to 4000 humans, a number that can overload the capacity of the hospitals. The other cases honour the data with smaller incubation periods between 4 and 5 days, and predict less than 1/2 of casualties, compared to Case 1, with IFR between 0.5 % and 1.13 % approximately. For instance, Case 4 (Figure 3) has a peak of 80 thousand infected individuals approximately, which implies 800 patients if 1 % requires intensive care, a more tractable amount. Since the reported number of deceased people could possibly be underestimated due to undeclared cases, we also consider a case with 100 % more casualties to date (Case 5 in Table 1), giving IFR = 0.83 % and values of the other parameters and infected and dead individuals similar to those of Cases 2, 3 and 4. Figure 4 shows the results of Case 1 but keeping $R_0 = 0.95$ from day 31 (April 8). As can be seen, the epidemic is under control with a minimum death toll (1881 individuals) and a minimum number of infected humans at the end of the epidemic, approximately 93 thousand people.

The values in Table 1 can be compared to figures reported in the literature. The fatality rate and IFR depend on the age of the population. Verity et al. (2020, Table 1) estimate for China an IFR = 0.657 % but over 60 yr age this rate is 3.28 %. If the number of infected people is several times higher than the reported cases, the fatality rate could be considerably less than the official one, suggesting that this disease is less deadly than SARS and MERS, although much more contagious. Read et al. (2020) report a mean value $R_0 = 4$, while Wu et al. (2020) obtain values between 1.8 and 2. According to Chowell et al. (2003), IFR = 4.8 % for SARS, and Verity et al. (2020) state that the average case fatality rate (CFR) of SARS is higher than that of COVID-19, with the latter approximately 1.38 % (their IFR is 0.657 %). However, this virus seems to
be much more contagious. The meaning of $\alpha^{-1}$ is the life expectancy of an individual in the infectious class, i.e., if $\alpha = 0.00285$/day (Case 1), the expectancy is 351 days.

An extended approach consists in using time derivatives of fractional order to generalize the diffusion process. Such models include in a natural way both memory and non-local effects (Mainardi, 2010; Zeb et al., 2014; Ahmed and El-Saka, 2017; Chen et al., 2020). Indeed, the replacement of the first-order temporal derivative by a Caputo fractional derivative of non-natural order provides an additional parameter to fit the data (Caputo et al., 2011). This modelling can be performed by using fractional derivatives computed with the Grünwald-Letnikov approximation, which is a generalization of the finite-difference derivative (Carcione et al., 2002; 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 (e.g., Naheed et al., 2014; Qin 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 (e.g., Santos and Gauzellino, 2017). Alternatively, the Fourier pseudospectral method, to compute the spatial derivatives, combined with time-domain fractional derivatives, can be used to solve the space-time diffusion equation of the epidemic (Carcione et al., 2013; Carcione, 2014). 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 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).

4 Conclusions

The SEIR epidemic model is implemented to simulate the time evolution of the COVID-19 epidemic in Argentina, specifically the “Región Metropolitana de Buenos Aires” (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, but we found that the reproduction ratio first decreased and then increased,
causing a drastic prediction of the death toll if this trend persist in the future. In
general, the incubation and infectious periods are in the range 4-5 days and 3-4 days,
respectively, and the infection fatality rate (IFR) between 0.5 % and 2 %. A case with
an incubation period of 11 days yields approximately three times more casualties at
the end of the epidemic, and the infected individuals will be between 5 million and 9
million people if the increasing $R_0$ trend is not inverted.

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 fatality rate.

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Table 1. Constraints and initial–final values of the inversion algorithm.

| Case | Variable | $\alpha$ (day$^{-1}$) | $\beta_1$ (day$^{-1}$) | $\beta_2$ (day$^{-1}$) | $\beta_3$ (day$^{-1}$) | $\epsilon^{-1}$ (day) | $\gamma^{-1}$ (day) | $E(0)$ | $I_\infty$ (K) | $L$ (day) | $D_\infty$ (K) |
|------|----------|------------------------|------------------------|------------------------|------------------------|------------------------|------------------------|--------|----------------|---------|-------------|
| 1.1  | Lower bound | $10^{-5}$ | $10^{-6}$ | $10^{-6}$ | $10^{-6}$ | 2 | 2 | 1 | 8997 | July 28 (2022) | 173 |
| 1.2  | Upper bound | $10^{-1}$ | $10^3$ | $10^3$ | $10^3$ | 20 | 20 | $10^4$ | 5382 | Feb 02 (2022) | 58 |
| 1.3  | Initial value | 0.006 | 0.7 | 0.7 | 0.7 | 10 | 10 | 100 | 5850 | Jan 18 (2022) | 68 |
| 2.1  | Final value | 0.00285 | 0.50478 | 0.14343 | 0.23339 | 11.06 | 6.74 | 162 | 4017 | April 07 (2022) | 19 |
| 2.2  | $IFR$ | 1.88 % | 3.33 | 0.95 | 1.55 | 4.29 | 3.31 | 44 | 5144 | March 24 (2022) | 44 |
| 2.3  | $R_0$ | 1.06 % | 0.57999 | 0.31000 | 0.37999 | 4.29 | 3.31 | 44 | 5144 | March 24 (2022) | 44 |
| 3.1  | Final value | 0.00322 | 0.58999 | 0.25000 | 0.36000 | 4.44 | 3.58 | 10 | 5850 | Jan 18 (2022) | 68 |
| 3.2  | $IFR$ | 1.14 % | 1.90 | 1.01 | 1.24 | 4.44 | 3.58 | 10 | 5850 | Jan 18 (2022) | 68 |
| 3.3  | $R_0$ | | 1.90 | 1.01 | 1.24 | | | | | | |
| 4.1  | Final value | 0.00152 | 0.50000 | 0.36000 | 0.37500 | 3.45 | 3.13 | 490 | | |
| 4.2  | $IFR$ | 0.47% | 0.50000 | 0.36000 | 0.37500 | 3.45 | 3.13 | 490 | | |
| 4.3  | $R_0$ | | | 1.56 | 1.12 | 1.17 | | | | | |
| 5.1  | Final value(s) | 0.0023 | 0.53000 | 0.28999 | 0.34000 | 4.65 | 3.65 | 500 | | |
| 5.2  | $IFR$ | 0.83 % | 1.92 | 1.05 | 1.23 | | | | | | |
| 5.3  | $R_0$ | | | | | | | | | |

$I(0) = 100$

(*) Doubling the number of casualties.

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

$I_\infty$ indicates the total infected individuals at the end of the epidemic.

$L$, the day of the last infected individual is obtained when $I < 1$.

$D_\infty$ is the death toll at the end of the epidemic.

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

Lauer et al. (2020) report $\epsilon^{-1} = 5.1$ days.

Ferguson et al. (2020) estimate an average IFR = 0.9 %.

$I(0) = 100$

(*) Doubling the number of casualties.

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

$I_\infty$ indicates the total infected individuals at the end of the epidemic.

$L$, the day of the last infected individual is obtained when $I < 1$.

$D_\infty$ is the death toll at the end of the epidemic.

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

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Ferguson et al. (2020) estimate an average IFR = 0.9 %.
Fig. 1 RMBA case history. Dead individuals (a) and number of deaths per day (b), where the red symbols dots represent the data. The solid line corresponds to Case 1 in Table 1.
Fig. 2 Number of individuals (a) and deaths (b), corresponding to Case 1 in Table 1. The black and blue curves refer to the accumulated deaths and deaths per days. The peak of infected individuals (and deaths per day) occurs at approximately day 300 (January 02, 2021).
Fig. 3 Number of individuals (a) and deaths (b), corresponding to Case 4 in Table 1. The black and blue curves refer to the accumulated deaths and deaths per day. The peak of infected individuals (and deaths per day) occurs at day 194 (September 18, 2020).
Fig. 4 Number of individuals (a) and deaths (b), corresponding to Case 1 in Table 1, but maintaining the reproduction ratio $R_0 = 0.95$ after day 31, i.e., $\beta_3 = \beta_2$. The black and blue curves refer to the accumulated deaths and deaths per days. The peak of infected individuals (and deaths per day) occurs at day 45 (April 22, 2020).