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COVID-19 dynamical evolution prediction in Mexico, decision making and social implementation: mid/low income countries study

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Abstract

A normal distribution approach is implemented to predict the evolution of the COVID-19 epidemic. The fit to the COVID-19 daily cases in Mexico, in the rising stage of the epidemic, is a very good continuous approximation to the data with $R^2 = 0.976$. The derivative of this function provides a measure of the increase/decrease or acceleration of new cases per day that are otherwise buried in the noise of the raw data. The predictions are depicted in a novel 3D way, so as to convey the evolution of the forecasts as data becomes available. The estimations are in accordance within standard deviation, with the logistic and Gompertz functions fitted to the corresponding epidemic models. This scheme can be used to model the epidemic and use it as an ancillary for decision making at a municipal or regional level. Simplicity with robust prediction is favoured, so that the model can be understood and implemented by local government advisors or personnel not familiar with specialized statistical methods.

Keywords: Epidemic models; Coronavirus; COVID-19; Infectious disease control;

1 Introduction

The evolution of epidemics has been modeled with diverse mathematical functions to predict the various features of the collective disease, in particular, the date when the infectious peak will occur and the maximum number of new cases. Different models have focused on diverse issues, for example, robustness under fluctuations from day-to-day data [1], international spreading [2], etc. For a recent historical account of epidemic models see [3]. The deterministic approach, from the mathematical point of view, establishes a set of partial differential equations, considering the most relevant features of the propagation of the disease. The solutions to this set of equations can be tackled analytically or numerically, depending on the complexity of the set (SIR, SIRS, SEIRS...) [4, 5]. In general, better fits to the data can be obtained with a larger number of parameters. Two highly relevant problems are the sensitivity of the differential equations to the initial conditions and the weighing of the factors according to different criteria or the available data. An example of the latter is the difficulty of accurately establishing the all important basic reproductive number R_0, in particular at the early stages of the epidemic [6].

To solely predict the future course of an epidemic, models with a fewer number of parameters can have some advantages over more sophisticated models. The number of coefficients that need to be known is greatly reduced or can even be avoided. Analytical solutions can be obtained for continuous-time models to describe the new or the cumulative number of cases. These analytic functions can be readily derived or integrated to obtain other quantities such as the acceleration of the spreading. Furthermore, the implementation and understanding of the model can be efficiently performed by non-specialists. These benefits have of course, a price. Besides the forecasting of the epidemic evolution as a function of time, no information is shed onto the underlying mechanisms nor the ways to modify them. Nonetheless, if the emphasis is laid on prediction, as in the present work, the assets can exceed the limitations for a rapid and reliable assessment of the epidemic forecasting.

Epidemic predictions are of paramount importance in order to implement different policies to lessen the impact of the disease [7]. On this basis, national and local governments, for example, increase the availability of the hospitals infrastructure, ban certain activities [8], recommend social distancing [9] and other schemes to prevent person-to-person transmission [10]. The relevance of flattening the curves when limited resources are available hardly needs to be stressed [11]. The lack of preparedness in mid/low income countries worldwide to face a large scale epidemic is evident from numerous reports [12]. The indirect increase of mortality due to potential disruption of health systems and decreased access to food could be devastating [13]. Severe problems undermine the readiness of countries in Latin America to face the spread of COVID-19 [14], in particular, due to very modest public healthcare systems in most countries of the region. The impact on the Caribbean, possibly except for Cuba, is expected to be severe [15]. The lack of investment in the last decades in the healthcare system in

Mexico has become evident with the emergency [16]. COVID-19 patients with associated chronic conditions and multimorbidity in Mexico, increase pneumonia and death rates [17]. Therefore, timely assessment and reliable prediction of the epidemic evolution at the various levels of governance is invaluable to ameliorate the handling of the health crisis.

In the present paper, a normal distribution is used to model the pandemic evolution. The reason for this choice is threefold, on the one hand, the derivative as well as the integral of the Gaussian function, permits the visualization of the change in the spreading speed as well as the total number of cases. The spreading acceleration is a variable that has been largely ignored, but, as we will show, it is a very sensitive function that can be of help in decision making. On the other hand, keeping the number of parameters to the minimum of three, the model leaves no room for parameters that can be hard to assess [18], in particular at the early stages of the epidemic. Thirdly, simplicity is favoured for the sake of clarity, so that the model can be understood and implemented locally by researchers or personnel that are not necessarily familiar with specialized mathematical procedures nor sophisticated statistical models.

The method is presented and exemplified here with COVID-19 data from Mexico, as the epidemic evolved from March to mid July. In section 2, results of the Gaussian fit to the number of new confirmed cases at a specific date are presented. The fit gives the maximum expected number of daily cases, the time when this maximum is expected and the foreseen duration of the disease. The cumulative cases function is obtained from direct integration of this curve. The derivative of the Gaussian curve is shown to be a valuable tool to establish how fast the spreading is increasing or decreasing. In section 3, rather than just a snapshot, the results are presented in a novel fashion, to show the way the outcome changed as a function of the time when the prediction was made. These time-time 3D plots show the dynamic evolution of the prediction as a function of data availability. In section 4, the possibilities of implementation of this technique at a local level and even within micro regions are explored. In the last section, the present approach is compared with other methods. Let us anticipate that the present model is surprisingly accurate compared with more sophisticated models.

2 Normal distribution fit to the COVID-19 evolution

The rate at which a disease is affecting a population can be measured with different parameters or criteria. The definitions vary according with the emphasis required, for example, geographical dissemination [19], percentage of infected population [20], etc. A further difficulty arises if case definitions are modified as the epidemic evolves, as has happened with COVID-19 in China, where seven versions were issued within three months [21]. A widely adopted definition is the number of new cases in a given interval, usually reported per day. This is the raw data used in this work. Daily confirmed new cases in Mexico were obtained from the 'Secretaría de Salud' of the Mexican government [22] and confirmed with other sources [23].

The number of new daily COVID-19 cases is considered a random variable. Due to the central limit theorem, the average of many observations with finite mean and variance is itself a random variable whose distribution converges to a normal distribution as the number of samples increases. This variable, in a stochastic Markovian epidemic model in continuous time with maximum entropy, will exhibit a normal distribution. The number of new daily COVID-19 cases is the result of many independent particular situations, and as such, its distribution is expected to be nearly normal. The continuous variable of daily confirmed new cases, labeled with the letter N, is modeled by a Gaussian function of the form

$$N = N_{\max} \exp\left(-\frac{(t - t_{\max})^2}{w^2}\right), \tag{1}$$

where $N_{\max}$ represents the prediction of the average maximum number of new cases at the highest infection rate, $t_{\max}$ the prediction of the time when the highest infection rate will occur, and w is a measure of the duration of the disease measured from the time when the infection rate grows from $1/e$ to its maximum value.

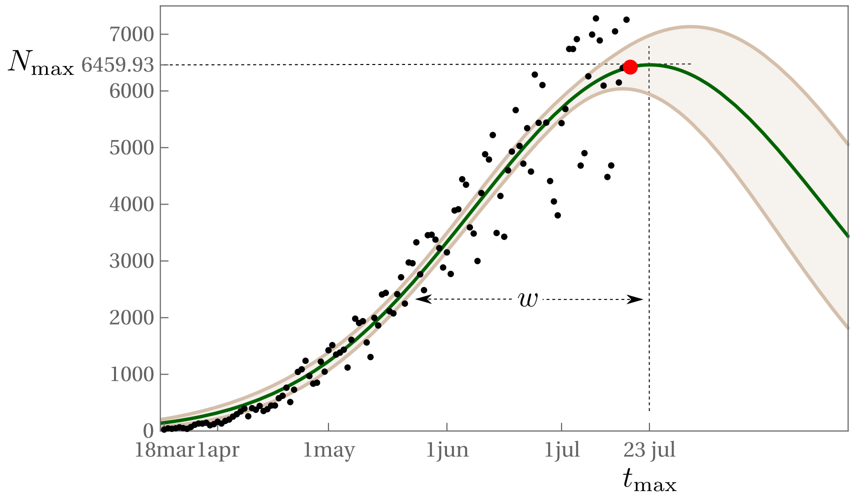

Figure 1: Gaussian fit (Green curve) to confirmed new COVID-19 cases in Mexico evaluated with data from 18 March up to 18 July (red dot) 2020. The three parameters obtained from the fit are the number of new confirmed cases at the peak $N_{\max}$, the date of maximum rate of new cases $t_{\max}$ and the duration of the disease w, measured half width at $1/e$. In this graph $2w$ is 130.6 days. Confidence bands at 95% for mean predictions are depicted in light brown.

The values of the three parameters N_{max}, t_{max} and w were obtained from a least squares fit of the Gaussian function to the data starting from 18 March 2020 to the indicated date. In Figure 1, the fit was performed with data up to 18 July. The R^2 value of the fit is a respectable 0.976, confirming that the Gaussian function is a good continuous approximation to the data. The parameters values with their uncertainties are shown in Table 1.

	Estimate	Std. error	P-value
N_{max}	6459.9 (cases per day)	263.5	1.5×10^{-48}
t_{max}	128.1 (days from 18 March)	5.1	3.1×10^{-49}
w	65.3 (days)	4.1	4.2×10^{-31}

Table 1: Parameter estimation diagnostics obtained for a linear regression fit to the Gaussian function shown in figure 1. Fit performed with 123 data points beginning 18 March.

The number of confirmed new cases per day N, is a measure of the spreading velocity of the infected cases. Thus, N_{max} represents the prediction of the average velocity of infections at the highest infection rate.

The Gaussian function integrates to the error function. This function has to be shifted, so that the initial condition corresponds to zero cases at $-\infty$, at least in the first appearance of the disease before successive outbreaks. The cumulative cases function is

$$N_{\text{cum}} = \int N\, dt = \frac{\pi}{2} N_{\text{max}}\, w\, \text{erf}\left(\frac{(t - t_{\text{max}})}{w}\right) - \frac{\pi}{2} N_{\text{max}}\, w\, \text{erf}\,(-\infty)\,, \tag{2}$$

where N_{cum} is the cumulative number of COVID-19 cases as shown in figure 2. This integral estimates the total number of cases from the Gaussian fit. This quantity can of course be obtained, without invoking the fit, from the sum of all cases up to date. Comparison of the total number of cases obtained from the raw data and the fit, gives a crude confirmation that the fit is being correctly evaluated. The cumulative number of cases from the raw data was 338,913 on 18 July [23]. Whereas the result from the integral of the fit given by Equation (2) is 339,887 cases, that amounts to a 0.3 % discrepancy.

2.1 Daily increase/decrease

An estimate of the new cases increase or decrease can be evaluated from the data by subtracting the number of new cases from two contiguous days. Some web sites, like the World Health Organization, actually show the 'Daily Increase/Decrease' directly in their tooltip [23]. This is plotted in figure 3. The daily reports have a large variability because data have to be collected from

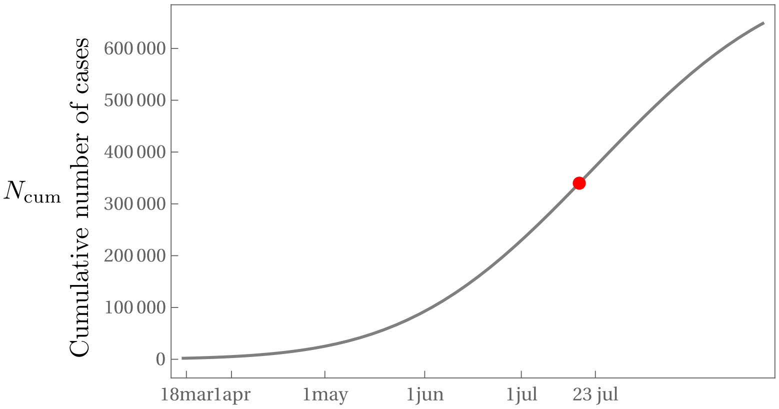

Figure 2: Prediction of cumulative COVID-19 cases in Mexico evaluated from the integral of the Gaussian function. Estimation on 18 July was 339,887 cases. The number of cumulative cases expected at the end of the disease $N_{\mathrm{cum}}(\infty)$, is 744,245.

different geographical regions with diverse infrastructure and communications. Weekdays or weekends as well as different time zones also play a role in the variations of these reports. The fluctuations in the day to day increase/decrease is so large, that hardly any information can be obtained from this plot. This is perhaps a reason why little attention has been paid to rate of change of new daily cases. Moreover, more sophisticated models usually have solutions whose derivatives are not so simple to evaluate. The derivative of the Gaussian function is

$$a = \frac{dN}{dt} = -2N_{\mathrm{max}} \frac{(t - t_{\mathrm{max}})}{w^2} \exp\left(\frac{(t - t_{\mathrm{max}})^2}{w^2} \right). \tag{3}$$

This function evaluates how fast is the rate of infections increasing or decreasing. The result obtained from the derivative of the fit gives a smooth curve as shown in Figure 4, in contrast with the discrete data shown in Figure 3. This curve is highly sensitive to the stage at which the pandemia has evolved. For example, the inflection points in the new cases curve (Figure 1) are readily spotted as the maximum and minimum in the derivative curve (Figure 4). In physics parlance, $a = \frac{dN}{dt}$ represents the acceleration (or deceleration) of new infections. However, we have to train a little bit to understand and read the graph correctly. Notice that the ordinates scale is more than an order of magnitude smaller than its counterpart obtained directly from the raw data. Suppose, as a mere exercise, that a given place has an infrastructure such that it can deal with, say, 1000 new patients per day. Consider one bed with the appropriate resources for each patient. For simplicity, consider that the number of discharged patients is the same as the incoming patients in the previous day. In a typical curve, shown in Figure 4, at the acceleration peak (7 June), 85 beds have to be increased

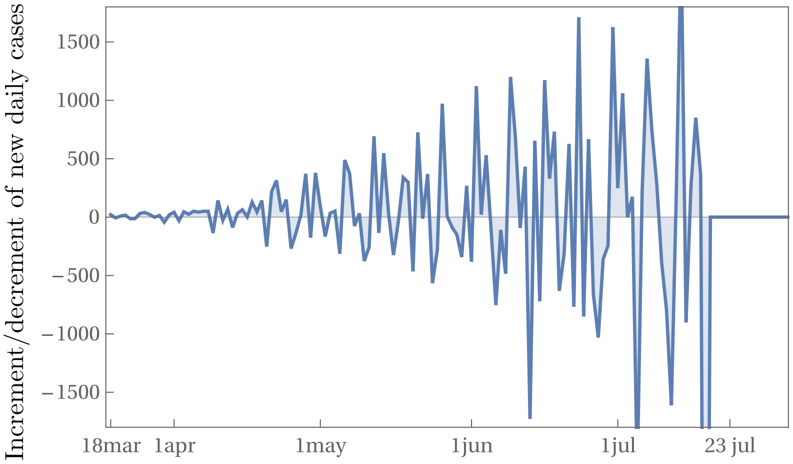

Figure 3: Increment/decrement raw data of new cases with respect to previous day from 18 March to 18 July. Scarce relevant information can be obtained from this plot due to the large daily variability. (Compare with figure 4, in particular the ordinates scale)

each day. At the maximum of new cases, i.e. the maximum of the bell shaped curve, the acceleration is zero and thus, no more beds need to be added to the infrastructure. The acceleration curve crosses the abscissas axis at this maximum, being very sharp about the moment when this happens (23 July in Figure 4). As the calamity evolves past the disease peak, the negative values of acceleration suggest that a number of COVID-19 beds that can be dismantled.

3 Prediction as a function of data availability

The predicted evolution of the epidemic is usually a snapshot at a given date evaluated with the latest available data. The prediction uncertainty is usually visualized by drawing bands surrounding the fit. This uncertainty, as it is well known, increases as the prediction curve lies further away from the evaluation time [24]. Day after day frozen images are produced as data becomes available each day or according with the interval when information is updated. Previous day or past predictions are discarded since the prediction becomes more accurate when more data are available. However, the way the prediction evolves is also important, in particular, if the results exhibit different behaviours at different stages of the epidemic.

A very interesting way of visualizing the dynamics of the prediction rather than just snapshots, is to consider the parameters of the fit as a function of the day when the prediction was performed. The primary parameters of the Gaussian fit are the maximum expected number of cases $N_{\max}$, the time $t_{\max}$ when the

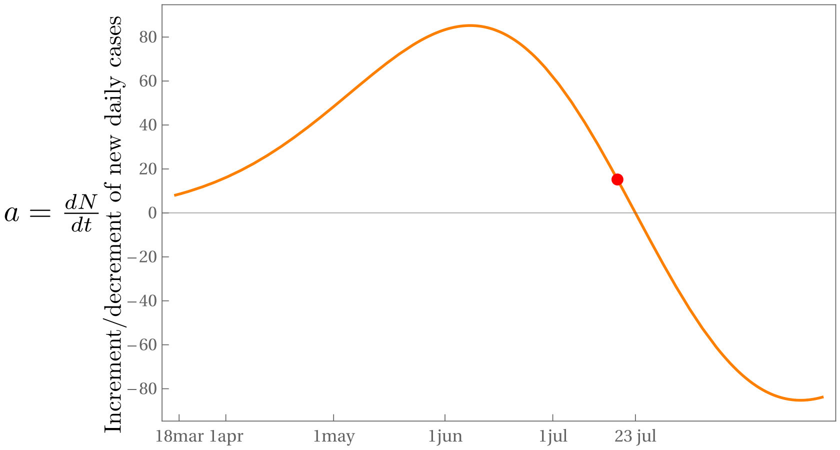

Figure 4: Increment/decrement of new cases prediction for Mexico as a function of time, obtained from the derivative of the new cases Gaussian fit. Typical acceleration curve evaluated on 18 July (red dot) corresponding to the parameters in Table 1 and Figure 1.

maximum is expected to be reached and the expected duration of the disease w.

In Figure 5, a three dimensional plot shows the way the predictions evolved from day to day. The expected maximum number of cases $N_{\max}$ and the date when this maximum is achieved $t_{\max}$ are plotted as a function of the day t_{eval}, when the prediction was made. Thus we have a time-time plot with height representing $N_{\max}$. The triad $(t_{\text{eval}}, t_{\max}, N_{\max})$, evinces the way the prediction changed as data was incorporated to the fit. The earliest data that we recorded for Mexico was 18 March 2020. For a time of evaluation t_{eval}, the number of data points is t_{eval} minus the initial recording date. In Figure 5, the first prediction was made 8 May 2020, with 53 data points; Whereas the last prediction is 18 July 2020, with 123 data points. There is a correlation between dates further away from the evaluation date and the maximum number of new cases. The maximum peak was expected around 10 May, in the evaluations performed during the first days of May. However, the peak date was shifted to the second fortnight in June in subsequent evaluations. The change in the maximum expectation date moved from mid July until the second fortnight in July.

4 Implementation of the model at micro level

There are global policies at a multinational level coordinated by the World Health Organization (WHO). At the next scale, nations establish their own policies, that it is worth mentioning, regarding the COVID-19 epidemic, have

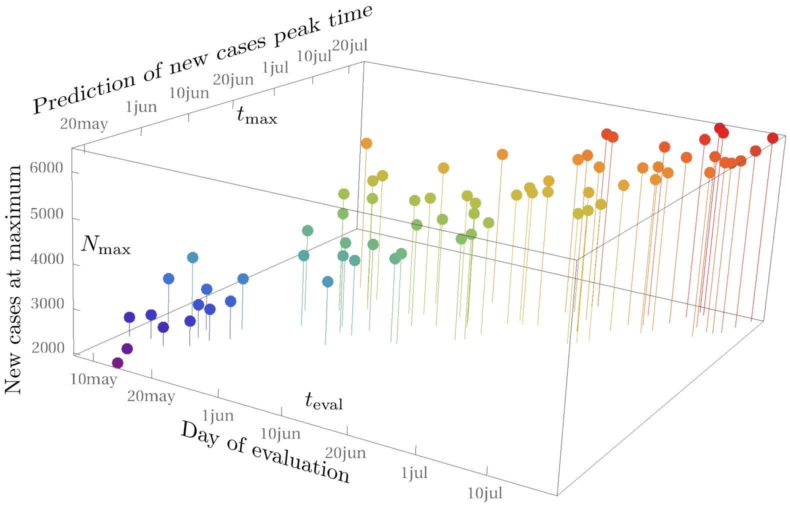

Figure 5: $N_{\max}$ and $t_{\max}$ predictions are plotted as a function of t_{eval}, the day when the prediction was made. These time-time plots evince the dynamical evolution of the predictions.

been quite diverse. Moving onto smaller units, depending on the geopolitical divisions of the countries, there are states, counties and other mid sized structures. These in turn are divided in municipalities or districts with a huge diversity of population and geographical sizes. The local attributes of the smaller structures vary enormously for different countries. Two examples in Latin America: Brazil currently has 5,570 municipalities and healthcare is in their responsibility [14]. In Mexico, there are 32 states and 2,457 municipalities; Healthcare and health decision making has been shifting to and from the national level to the state level with various degrees of success/failure. In a recent survey of Canadian municipalities, the aggressiveness of policy responses is strongly related to municipal population size and case totals and modestly related to province and local ideology [25].

In Mexico, most of the COVID-19 information is processed at a national level with the exception of some large metropolitan areas. Much fewer information, if any, is processed at the local municipal level. Nonetheless, some municipalities have taken local decisions regarding the COVID-19, for example, banning the entrance of people in the municipality or rejecting the installation of emergency COVID-19 mobile hospitals. Furthermore, few non government organizations or civil society members make use or generate local information to establish their stance at the problem or take the desirable or necessary measures to minimize the risks.

It is desirable that the local governments as well as the population have appropriate and opportune information regarding the disease. Decisions will be wiser if the local as well as the global information are adequately processed and expounded to the decision makers as well as the population. Central governments can process information at a global or intermediate level, but it is unfeasible to centrally process information at the micro-level. For these reasons, it is desirable that at the micro-level, people can make sense of the information that is being collected locally and be able to compare it with global trends. A deplorable practice all around the world at various government levels has been censorship and deliberate bias regarding the COVID-19 epidemic [26]. Locally generated knowledge can help to counteract banned or distorted information.

The present scheme could make a small but relevant contribution in order to evaluate the COVID-19 prospective at this micro-level. Locally generated knowledge can be a complementary information to the global trends, so that at the micro level, communities can understand what is happening in their immediate surroundings. This local knowledge can help decision makers at the micro level to make wiser decisions based on evidence and well founded prediction. With the present development of this work, it is necessary for some members of the local community to have rudiments of curve fitting and interpretation of graphs. Any mathematics software that can perform linear regressions and visualization is all that is required, in addition of course, of the local data of new infected cases. The program used in this work is cloned in the supplementary material. It is foreseeable that a web applet can be implemented so that micro communities could feed local data via a web browser and obtain prediction values and graphs over the internet. The former scheme requires a maths software whereas the latter requires an internet connection.

5 Comparison of results and discussion

At the Institute of Physics, UNAM, the peak of COVID-19 in Mexico with almost 6000 new cases was predicted to be 27 June, using the logistic function and considering data up to 23 May [24]. The peak prediction, with the normal distribution function in the present work for the same data set, was 1 July with 4448 new cases at the peak. There is a mere four day difference between these two estimations although $N_{\max}$ differs by 26%. Several groups working in close association with the Mexican government are CIMAT-Gompertz, CIMAT-IM-UNAM, CONACYT-CRIP, IMSS and CDMX epidemic model. The CIMAT-Gompertz group estimated the peak time at 29 June with just under 4000 new cases per day, evaluated up to 1 June [27]. The present model predicted the peak time at 26 June with 4694 new cases with data up to 4 June. The CDMX epidemic group approach is based on a SEIR model with nine coupled partial differential equations, in order to include hospital patients with different infrastructure requirements. Their published predictions are centered on the health infrastructure requirements in Mexico city area [28]. The CIMAT-IM AMA model is a compartmental SEIRD model aimed at forecasting hospital occupancy in metropolitan areas in the 32 states of the country [29]. Unfortunately their report does not include a national forecast. Comparison with publicly available results from the other groups come from the 'Secretaría de Salud' spokesman [30]. Roughly, in late April and early May, the peak was predicted around 10 May. However, it has been subsequently shifted towards late July. In view of the before mentioned comparisons, the present method shows peak time and maximum new cases predictions that are consistent with calculations by other models.

The expected duration of the epidemic is another matter. Behaviour past the maximum varies greatly depending on the region and the regional policies. While some places exhibit a plateau (i.e. Russian Federation), others have a steady exponential like decrease (i.e. Italy, that may nonetheless experience a different behavior in the coming weeks [31]), and yet others have a second outbreak shortly afterwards (i.e. Republic of Korea). If the propagation conditions are varied, quantities that are assumed constant in the models have to be modified. It is then necessary to solve the equations for time varying parameters (rather complex) or to evaluate piece-wise solutions for segments with constant parameters. The present method is not well suited for these purposes. The normal distribution is symmetric, although piece-wise asymmetric solutions can be implemented.

The normal fit to the COVID-19 daily cases in Mexico suggests that Gaussian fits can be successfully used to predict the peak number of new cases per day and the time the peak is likely to occur. The normal increase/decrease or acceleration curve of new cases per day provides a valuable tool to assess the pandemic evolution. Three dimensional plots showing the way forecasts evolve as data becomes available, exhibit the dynamical evolution of the predictions. The use of this model together with the data visualization tools are a complementary decision making instrument that should be encouraged. The simplicity of the model makes it a good candidate to be implemented at a municipal level, particularly in mid/low income countries where specialized human resources at a local level are scarce.

Contributors

Data analysis was led by MFG. SFE provided the data from online sources. LFE and SFE programmed the model and the corresponding visualizations. All authors contributed to processing and interpreted the study findings, contributed to writing the manuscript, and approved the final version for publication.

Declaration of interests

We declare no competing interests.

Data Availability Statement

The data that support the findings of this study are openly available in supplementary files.

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