



Pandemic Equation for Describing and Predicting COVID19 Evolution

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Abstract

The purpose of this work is to describe the dynamics of the COVID-19 pandemics accounting for the mitigation measures, for the introduction or removal of the quarantine, and for the effect of vaccination when and if introduced. The methods used include the derivation of the Pandemic Equation describing the mitigation measures via the evolution of the growth time constant in the Pandemic Equation resulting in an asymmetric pandemic curve with a steeper rise than a decrease and mitigation measures. The Pandemic Equation predicts how the quarantine removal and business opening lead to a spike in the pandemic curve. The effective vaccination reduces the new daily infections predicted by the Pandemic Equation. The pandemic curves in many localities have similar time dependencies but shifted in time. The Pandemic Equation parameters extracted from the well advanced pandemic curves can be used for predicting the pandemic evolution in the localities, where the pandemics is still in the initial stages. Using the multiple pandemic locations for the parameter extraction allows for the uncertainty quantification in predicting the pandemic evolution using the introduced Pandemic Equation. Compared with other pandemic models our approach allows for easier parameter extraction amenable to using Artificial Intelligence models.

Keywords COVID19 · Pandemic · Mitigation · Quarantine

1 Introduction

The management of the COVID-s19 pandemics requires a difficult trade-off between limiting the spread of the disease and trying to control and limit the horrendous damage to the economy. Opening the USA could limit the damage to the economy and relieve

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economic and psychological pressures but could also lead to a spike in the COVID-19 infections. To address this problem, many states have chosen a partial opening. For example, most of the state of Virginia was open on May 14, 2020. However, Northern Virginia, Richmond, and Accomack County were all granted 2-week delays.

The predictive models could guide the pandemic response by learning from the past [1]. Some are based on Lotka-Volterra (prey-predator) equation [2], others use comparisons with previous epidemics [3]. There are many attempts to address more specific issues, such as a lockdown impact [4] or explore the evolution of Intensive Unit bed availability [5] or effects of tracing [6]. Some of the models focus on predicting the average number of infections caused by an infected person [7], the effects of the social contact patterns [8] and estimating the severity of the coronavirus disease [9]. The models range from those assessing the global impact of the COVID-19 pandemic [10] to the models focusing on European countries [11] [12], Asia [13] (including China) [14] and on the low- and middle-income countries [15] [16], with the latter addressing opposing effects of the limited health care options and having a younger population on the pandemic trends. The pandemic models also address the effects of the seasonal variations on the pandemic growth [17]. Many of the COVID-19 models are presented at the Center for Disease Control and Prevention COVID-19 forecasting site [18] and ForecastHub [19]. Predictive mathematical models of the COVID-19 Pandemic are reviewed in Reference [20] It has been even claimed that simulations drive the world's response to COVID-19 [21]. Models, such as Advanced Autoregressive Integrated Moving Average (ARIMA) Model [22], have been used to predict the trends of the COVID-19 pandemic for the most affected countries. The factors affecting the accuracy of such models have been widely discussed (see, e.g., [23] and references therein). They include uncertainties in estimating asymptomatic infections and time lag between infections and deaths, possible underestimation of the COVID-19 deaths [24] [25], issues related to establishing COVID-19 recovery [26], and strikingly different patterns of the pandemic in different countries and even in the different regions of the same country [27] [28]. The challenging problem is to account for the balance between controlling the pandemic growth and negatively affecting the economy [29] [30]. These difficulties and uncertainties highlight the case for the development of the unified model with an established parameter extraction procedure and parameters that have a clearly understood meaning and could be related to the factors, such as mitigation measures or factors specific to a given locality.

I now propose a unified model based on a new equation that I call the Pandemic Equation. This equation has as simple analytical form but could accurately fit different pandemic evolution curves and account for the effects of mitigation measures and/or of opening and closing the economy. This allows for establishing a balance between limiting the spread of the virus and the economic hardship. The equation could be used to predict pandemic trends. The predictive time range of the Pandemic Equation could be estimated by using a partial set of the fitted pandemic data for the prediction of the pandemic evolution. The calculated results could be then compared with the entire available data set. The results of such a procedure could be used for the uncertainty quantification of the future pandemic evolution. The parameter extraction and the uncertainty quantification procedures could be incorporated into trainable Artificial Intelligence models for the big data processing approach to the pandemics.

2 Pandemic Equation

The unique feature of our model is having a limited number of the pandemic curve evolution parameters with an easily understood meaning and well-defined parameter extraction procedure. The model parameters are directly linked to the mitigation measures, such as the introduction or removal of the quarantine, and to the effect of vaccination when and if introduced. The quarantine removal and business opening lead to a spike in the pandemic curve predicted by Pandemic equation. The effective vaccination reduces the new daily infections described by the Pandemic equation. The pandemic curves in many localities have similar time dependencies but shifted in time. The Pandemic Equation parameters extracted from the well-advanced pandemic curves can be also used for predicting the pandemic evolution in the localities, where the pandemics is still in the initial stages or having a rebound. Using the multiple pandemic locations for the parameter extraction allows for the uncertainty quantification in predicting the pandemic evolution. Future work will use artificial intelligence to train the Pandemic Equation model for the parameter optimization based on the history of multiple pandemic locations.

The Pandemic Equation could be applied to other pandemics using different parameter sets. It could be also find applications for describing other processes, such as stock price evolution that could be correlated with the market conditions and management changes.

Table 1 summarizes the parameters of the Pandemic Equation curve and relates these parameters to specific events and measures during the pandemic.

Table 1 Pandemic Equation curve parameters and related characteristics

Parameter	Unit	Meaning	Comment
N		Number of people infected from pandemic start	
N_t	–	Total number of people who could be infected	.
N_o		Number of infected people at pandemic start	Typical values 1 to 20
f_o	–	Initial infection ratio	$f_o = N_o/N_t$
τ_o	day	Initial growth time constant	Typical values from 2 to 5 days
τ	day	Time dependent growth time constant	$\tau = \tau_o + \alpha t$
α	–	Curve flattening parameter($\tau = \tau_o + \alpha t$)	α is extracted from pandemic peak time, t_m
$\beta_1, \beta_2 \dots \beta_n$	–	Mitigation parameters for 1, 2, ...n Mitigation events	Negative β correspond to lifting restrictions. Typical values –3 to 1
$t_{\beta 1}, t_{\beta 2} \dots t_{\beta n}$	day	Times of mitigation events	Typically larger than the pandemic peak time
$\tau_{\beta 1}, \tau_{\beta 2} \dots \tau_{\beta n}$	day	Time constants of mitigation events.	Typically very small From $1/N_t$ to $10/N_t$
t_m	day	Time of the pandemic peak	Time of the first peak for multiple peaks

As seen from Table 1, all parameters of the Pandemic Equation have a very clear meaning and, as shown below, their y extraction from the pandemic evolution data is straightforward.

We start from the standard rate equation (see, for example [31, 32],) that we generalize to obtain the Pandemic Equation.

$$\frac{dN}{dt} = \frac{(1-N/N_i)N}{\tau_o} \quad (1)$$

Here N is the total number of infections (not of the infected people because some infected people recovered and some, unfortunately died), τ_o is the characteristic time of the pandemic growth, and N_i is the total number of people who could be infected (the infection pool). N_i is smaller than the number of people N_p in the population because some people could have genetic immunity to the virus or isolated from the community. The herd immunity ratio

$$f_{herd} = N_i/N_p < 1 \quad (2)$$

was estimated to be 60–70% [33], but it could strongly depend on a specific locality, since it depends on the transmission ratio that varies a great deal depending on the population's habit (e.g., it could be much smaller in South Korea, where people have been used to wearing masks than in the USA).

From Eq. (1), the ratio of the total infection to the infection pool $f = N/N_i$ is

$$\frac{df}{dt} = \frac{(1-f)f}{\tau_o} \quad (3)$$

The solution of Eq. (3) is

$$f = \frac{\exp(t/\tau_o)}{\exp(t/\tau_o) + \exp(C_1)} \quad (4)$$

Here C_1 is the integration constant to be determined from the initial conditions $f(0) = f_o$

$$f_o = (1 + e^{C_1})^{-1} \quad (5)$$

Since $f_o \ll 1$, $f_o \approx e^{-C_1}$ and Eq. (4) becomes

$$f = \frac{f_o \exp(t/\tau_o)}{f_o \exp(t/\tau_o) + 1} = \frac{f_o \exp(x)}{f_o \exp(x) + 1} \quad (6)$$

Hence, the total number of the infected people N_{io} is given by

$$N = \frac{N_t f_o \exp(x)}{f_o \exp(x) + 1} \tag{7}$$

Here $x = t/\tau$. For following the pandemic evolution, the daily number of the new infections ΔN is more important than the total number of infections to date. From Eq. (7)

$$\Delta N = \frac{dN_{to}}{dt} = \frac{N_{to} f_o e^{t/\tau_o}}{(1 + e^{t/\tau_o} f_o)^2 \tau_o} \tag{8}$$

As seen from Fig. 1, this approach to modeling pandemic might only work at the initial stage of the pandemics (during its exponential growth).

The maximum of this symmetric curve is reached at

$$t_{mo} = \tau \ln(1/f_o) \tag{9}$$

The pandemic evolution should be described by a more complex time dependence of the new infections with a typical asymmetrical curve. This could be accounted for by making the pandemic growth time constant τ and the infection pool N_t to be a slow (on the scale of τ_o) functions of time:

$$\Delta N_i = \frac{N_t(t) f_o e^{t/\tau(t)}}{(1 + f_o e^{t/\tau(t)})^2 \tau(t)} \tag{10}$$

This approach is similar to the adiabatic approximation in the quantum theory of solids of allowing two time scales for slow (atomic) and rapid (electronic) motion [34]. We call Eq. (10) the **Pandemic Equation**.

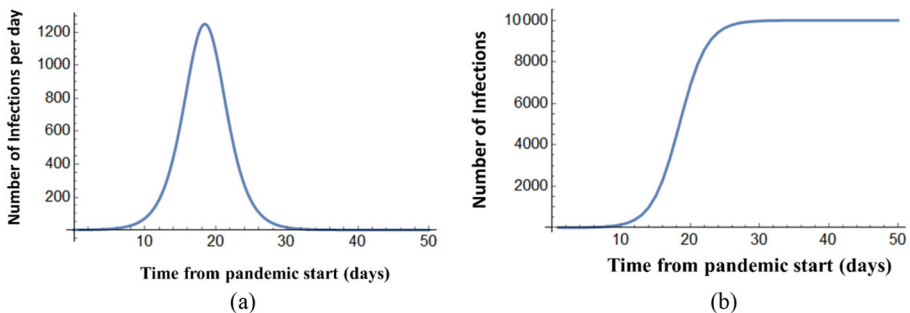


Fig. 1 Solutions of the rate equation: the number of infected people and the number of people infected per day as a function of time from pandemic start

The total number of the infected people as a function of time is then given by

$$N_i(t) = \int_0^t \Delta N_i(t') dt' \tag{11}$$

We will show that we could fit a variety of data using the following function

$$\tau = \tau_o + \alpha t \tag{12}$$

leading to

$$\Delta N_i = \frac{N_{I\alpha}(\alpha) f_{\alpha} e^{t/(\tau_o + \alpha t)}}{(1 + f_{\alpha} e^{t/(\tau_o + \alpha t)})^2 (\tau_o + \alpha t)} \tag{13}$$

Here α is the flattening parameter responsible for “flattening the curve” as illustrated by Fig. 2(a) showing an asymmetric pandemic curves reproduced using the time dependence of τ .

The maxima of the daily infections reached at approximately

$$t_m \approx \frac{\tau_o \ln(1/f_o)}{1 - \alpha \ln(1/f_o)} \tag{14}$$

This expression is obtained from Eq. (13) assuming that $\alpha < \tau_o/t_m$, so that the terms αt are only kept in the exponential functions in Eq. (13). Figure 2(b) shows the dependence given by Eq. (14). As seen, Eq. (14) agrees well with the position of the maxima in Fig. 2(a) and it could be used for the parameter extraction. Our numerical calculations show that Eq. (14) works as a reasonable approximation if $\alpha < \tau_o/t_m = \ln(1/f_o)$. As seen from Fig. 2(a), varying the curve flattening parameter α reproduces well different degrees of the curve flattening and, as seen from Fig. 2(b) could be easily

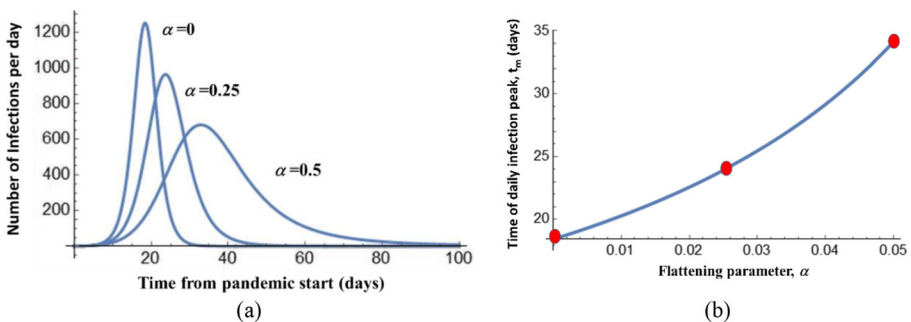


Fig. 2 **a** Number of people infected per day as a function of time from pandemic start. **b** Time of the pandemic peak versus flattening parameter (solid line calculated using Eq. (14), dots are calculated numerically) (b). Parameters used in the calculation: $N_I = N_{I\alpha} = 10,000$, $f_{\alpha} = 1/N_{I\alpha}$, $\tau_o = 2$ days

extracted based on the initial time constant of the pandemic growth and the time of the first pandemic peak.

We now introduce the effect of the mitigation measures, such as contact tracing, closing or opening the economy, introduction or removal of the quarantine, and requiring wearing masks and social distancing in public places. Now the Pandemic Equation becomes

$$\Delta N_{\beta}(t) = \Delta N_i(t, \alpha) \left(1 - \beta / \left(1 + \exp\left(\frac{t_{\beta} - t}{\tau_{\beta}}\right) \right) \right) \tag{15}$$

Here β is the mitigation parameter, τ_{β} is the characteristic time constant of the control measures introduction, and t_{β} is the characteristic time of the control measures introduction (the effect of the measures starts at approximately $t_{\beta} - 3\tau_{\beta}$ and finishes at approximately $t_{\beta} + 3\tau_{\beta}$).

The Pandemic Equation could be further generalized to account for multiple government mitigation events as follows

$$\Delta N_{\beta_1, \beta_2, \dots, \beta_n}(t) = \Delta N_i(t, \alpha) \left(1 - \frac{\beta_1}{1 + \exp((t - t_{\beta_1}) / \tau_{\beta_1})} \right) \times \tag{16}$$

$$\left(1 - \frac{\beta_2}{1 + \exp((t - t_{\beta_2}) / \tau_{\beta_2})} \right) \dots \left(1 - \frac{\beta_n}{1 + \exp((t - t_{\beta_n}) / \tau_{\beta_n})} \right)$$

3 Results and Discussion

We start from simulating different mitigation effects using the Pandemic Equation and then discuss the parameter extraction that we apply to the COVID19 data for New City and the Commonwealth of Virginia.

Figure 3 shows the simulated effect of vaccination for different vaccine efficiencies represented by the values of the mitigation parameter $\beta = 0.1, 0.5,$ and 1 . The value of $\beta = 1$ corresponds to the limiting case of the totally effective vaccination. The ability of our model to account for the vaccination effectiveness is very important. Typically, for

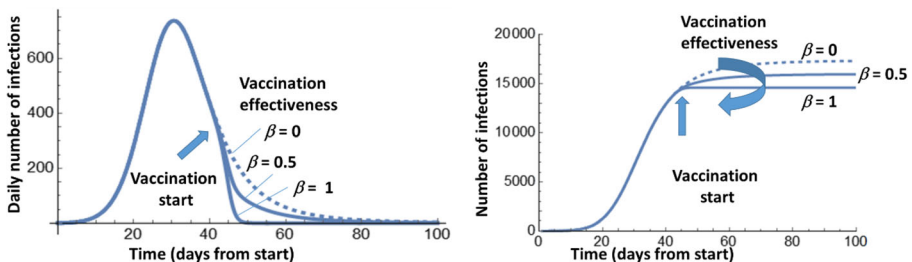


Fig. 3 Simulated effect of vaccination for different vaccine efficiencies represented by $\beta = 0.1, 0.5,$ and 1

a flu vaccination, the vaccine effectiveness is between 40 and 60% according to CDC [35]. Recent reports estimate the COVID-19 vaccine effectiveness to be approximately 90%. However, the US public, for example, is divided over whether to get the COVID-19 vaccine [36]. All these factors could be accounted for by the values of the mitigation parameter corresponding to vaccination and could be reproduced by varying the mitigation parameter. It is also important that the model accounts for the characteristic time of the vaccine deployment.

Figure 4 shows the simulated effects of relaxing the COVID-19-induced restrictions and opening the economy. We could relate the values of $\beta = -1$ and $\beta = -2$ to Phase 1 and Phase 2 of lifting the COVID-19-related restrictions.

Figure 5 shows relaxing the simulated combined effect of lifting and re-introducing restrictions, such as opening and the closing down economy. As seen, the Pandemic Equation reproduces well the complicated shapes of the pandemic evolution by accounting for multiple events corresponding to positive and negative values of the mitigation parameter and related time constants.

We now use the Pandemic Equation for fitting the pandemic evolution curves for the Commonwealth of Virginia and New York City. The parameter extraction for the Pandemic Equation starts from plotting the number of the natural log of the total infections as a function of time. This dependence is linear at the beginning of the pandemic. The slope and intercept of this line yield τ_o and f_o , respectfully. From the time of the first peak, we estimate parameter α using Eq. (17)

$$\alpha \approx \frac{t_m - \tau_o \ln(1/f_o)}{t_m \ln(1/f_o)} \tag{17}$$

Parameter N_t is then extracted from fitting the peak value of the daily infections. Finally, we choose the values of parameters β, t_β and τ_β . Figure 6 and Fig. 7 show the resulting fits.

The Pandemic Equation is capable of reproducing the pandemic evolution curves with multiple events leading to the second spike. However, a more important application of the Pandemic Equation in its predictive capability to be endowed by the parameter extraction and interpretation from the localities, where the pandemic has run its course or at least the pandemic is far enough on the decreasing slope. Future work should include developing the AI approach to train the Pandemic Equation model

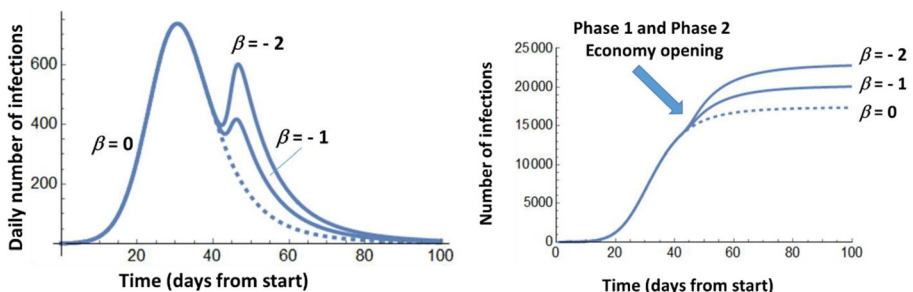


Fig. 4 Simulated effects of relaxing the COVID19 induced restrictions and opening the economy

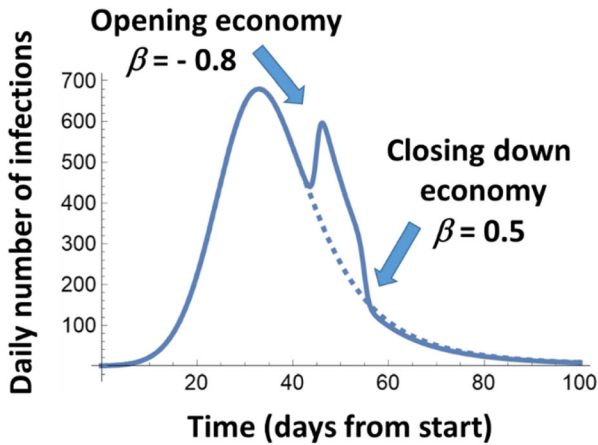


Fig. 5 Combined effect of lifting and re-introducing restrictions, such as opening and the closing down economy

for the parameter optimization based on the history of multiple pandemic locations with well advanced pandemic history.

Fitting the data for New York City and Commonwealth of Virginia pandemic evolution revealed interesting trends. The fitted values of the population pools for the infection (10^5 for NYC and 2.4×10^4 for Commonwealth of Virginia) are much smaller than the total New York and Virginia populations, respectively. Also, the curve flattening parameters are quite large (0.067 for Virginia and 0.0631 for NYC). We speculate that these results could be explained by having loosely connected infection

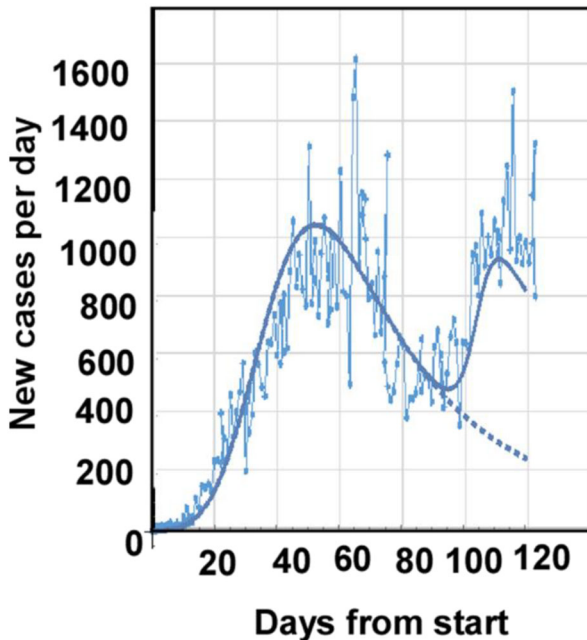


Fig. 6 Fitting the Commonwealth of Virginia pandemic evolution (solid line: the Pandemic Equation fit)

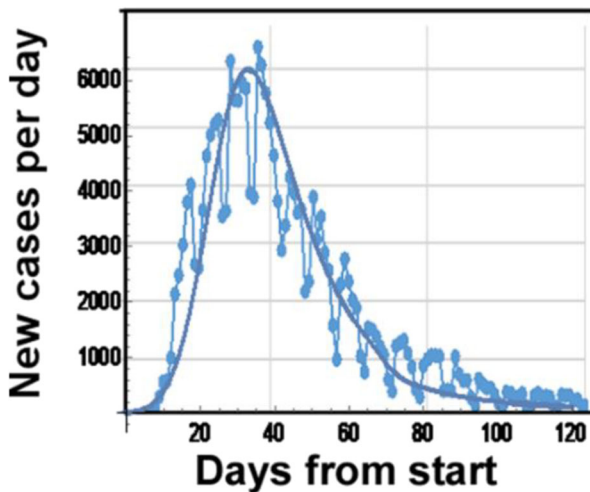


Fig. 7 Fitting the NYC pandemic evolution (solid line: the Pandemic Equation fit)

clusters. One such cluster could be international fliers who brought the initial infection from China or Italy and their friends and relatives belonging to the NYC more affluent society. Another cluster might be low-income population that includes waiters, porters, and cab drivers getting infected serving the original infected people. Still another cluster in NYC is the nursing home population. A large fraction of the population has remained relatively unaffected. It is also possible that more affected individuals transmit the disease at a higher rate but they die or recover first making the transmission less likely. The NYC data also reveal a very long low infection rate tail. The duration of this tail allows to estimate the low limit of the acquired immunity, which seems to exceed four months. More fitting by the Pandemic Equation for different localities and longer periods of time might prove or disprove these speculations but they show that presenting the noisy pandemic data by a few clear parameters driving the pandemic is very useful for the analysis of the trends and predicting our future.

The evolution of the new cases for Virginia (see Fig. 6) is very different. If we again apply the cluster hypothesis to the pandemic evolution a much smaller per capita first peak for the Virginia pandemic means that the intra-cluster herd immunity has not been reached in contrast to the New York situation and the rebound potential was higher when the state was opening up.

4 Conclusion

The Pandemic Equation is the modified rate equation with slowly varying parameters. This approach is similar to the adiabatic approximation in quantum theory of solids. The Pandemic Equation describes the pandemic evolution curves accounting for curve flattening and mitigation measures, such as the introduction or removal of the quarantine and for the effect of vaccination when and if introduced. Extracting these parameters from the well-advanced pandemic curves allows for reaching conclusions about the pandemic trends and might enable the Pandemic Equation to predict the pandemic

evolution for the locations where the pandemics is not yet very advanced including the effects of different mitigation measures.

Future work should include linking the model parameters to different measures and events affecting pandemic. The simplicity and relative ease of the parameter extraction should make this model to be a tool that could be widely used by local governments and communities for understand the past and trying to predict the future trends. This work could be supplemented by an artificial intelligence model to be trained to recognize the features of the pandemic curves and automatically extract the model parameter, similar to how it was done for extracting the image features during integrated circuit testing [37].

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Compliance with Ethical Standards

Conflicts of Interest/Competing Interests The author has not conflicting interests and no competing interests.

Code Availability custom code.

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