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COVID-19 PANDEMIC: A NOVEL THEORETICAL APPROACH TO EPIDEMICS

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Key words: *biased Gaussian distribution, COVID-19 model, Markovian process, pandemic spreading model, stochastic model*
Ключові слова: *зміщений гаусівський розподіл, модель COVID-19, марковський процес, модель поширення пандемії, стохастична модель*

Abstract. COVID-19 Pandemic: a novel theoretical approach to epidemics. Saglam Ugur. *The coronavirus pandemic 2019 (COVID-19) has completed numerous global spreading waves. Several models categorized as compartmental, growth, and distributional have been derived and are intended to determine the spread dynamics of the pandemic and behavioral patterns. However, it seems that a more generalized theoretical approach to this phenomenon can be derived via distributional models, especially the Gaussian distribution. For this reason, we aim to approach the problem as a stochastic phenomenon, considering that the spread and the related outcomes of the epidemic occur randomly and exhibit stochastic behavior. In this way, we can predict the course of the pandemic by detecting the spreading wave patterns using stochastic instruments and methods. The purpose of our study is to present a phenomenological model that helps us understand the general outbreak behaviors that determine the characteristic parameters of the pandemic and behavioral patterns in spreading waves. To achieve the goal, we have developed a theoretical approach that obtains a stochastic differential equation or a master equation called the Fokker-Planck equation by starting with a stochastic difference equation or a random walk model. Thus, as a solution to this master equation, we get a time-dependent Gaussian distribution with a shifted center, which is a good instrument to determine the characteristic spreading parameters of COVID-19 and the general behavior patterns for all pandemic diseases. The model uncovers thoughts on preventative mechanisms and sheds light on most criticisms about the importance of individual isolation, recovery treatments, remedies, and vaccine development.*

Реферат. Пандемія COVID-19: новий теоретичний підхід до епідемій. Саґлам Угур. *Пандемія коронавірусу 2019 року (COVID-19) завершила численні глобальні хвилі поширення. Було розроблено декілька моделей, які належать до категорій компартментальних, моделей зростання та розподільчих, які призначені для визначення динаміки поширення пандемії та поведінкових моделей. Однак, мабуть, загальніший теоретичний підхід до цього явища може бути отриманий за допомогою розподільчих моделей, особливо гаусівського розподілу. З цієї причини ми прагнемо підійти до проблеми як до стохастичного явища, враховуючи, що поширення та пов'язані з ним результати епідемії відбуваються випадково й демонструють стохастичну поведінку. Таким чином, ми можемо передбачити перебіг пандемії, виявляючи моделі поширення хвиль за допомогою стохастичних інструментів та методів. Мета нашого дослідження – створити феноменологічну модель, що допоможе нам зрозуміти загальну поведінку спалахів, яка визначає характерні параметри пандемії і поведінкові моделі у хвилях, що поширюються. Для досягнення цієї мети ми розробили теоретичний підхід, що дозволяє отримати стохастичне диференціальне рівняння (рівняння Фоккера-Планка), виходячи зі стохастичного різницевого рівняння або моделі випадкового блукання. Таким чином, як розв'язання цього рівняння ми отримуємо гаусівський розподіл, що залежить від часу, зі зміщеним центром, який є хорошим інструментом для визначення характерних параметрів поширення COVID-19 і загальних закономірностей поведінки всіх пандемічних захворювань. Модель розкриває ідеї про превентивні механізми та висвітлює більшість критичних зауважень щодо важливості індивідуальної ізоляції, відновного лікування, засобів правового захисту та розроблення вакцин.*

In mid-December 2019, the huge threat to public health, COVID-19, first emerged in Wuhan, China, and started spreading worldwide. The disease is claimed to live along with ongoing confirmed and suspected cases. Many alternative treatments or vaccines for the disease have been developed thus far. High and low-risk groups have been determined and enforced severe strategic prohibitions to restrain the disease spread rate [1, 2]. Until a significant regression in the pandemic is developed, the spreading behavior of COVID-19 has to be determined to minimize deaths and potential cases. The course of cases could have been foreseen through a disease model that must estimate the future situation and verify the current situation. Therefore, many modeling studies have been developed in the early and late eras of the pandemic.

Several classifications such as mechanistic, compartmental, phenomenological, deterministic, and stochastic have been generated for the mathematical epidemics models in the literature [3, 4]. However, we can propose a new relatively simple branching hierarchy from a different viewpoint for epidemic research methodologies. This branching hierarchy, as seen in Fig. 1 comprises categories such as compartmental models (CM), growth models (GM), and distributional models (DM), and models such as the Suspected-Infected-Recovered (SIR) model and its modified variations (mSIR) [5], Logistic Growth Model (LGM), Richard Growth Model (RGM), Generalized Growth Model (GGM), Gaussian Mixture Model (GMM), and Gaussian Noise Model (GNM).

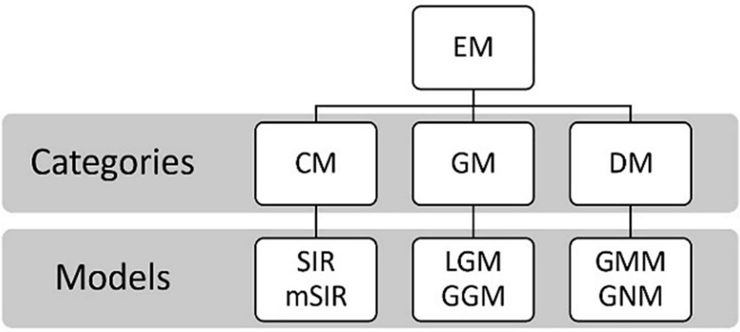

Fig. 1. Branching hierarchy of epidemic modeling over categories and corresponding models

The modeling studies conducted on CM, GM, and DM-type categories can be represented through a holistic approach that is usable for interpreting the behavioral patterns of pandemics. This holistic approach can be developed and characterized via the Gaussian Distribution (GD) model parameters, which can be assumed as a phenomenological and stochastic assessment of mathematical epidemic modeling studies. Thus, the categories of CM and GM can be grouped into the relevant Gaussian-type behavioral patterns such as truncated-complete-cumulative distributions as seen in Fig. 2. These relevant behavioral groups can be determined via mutual or independent variables and their known or predefined behavioral patterns.

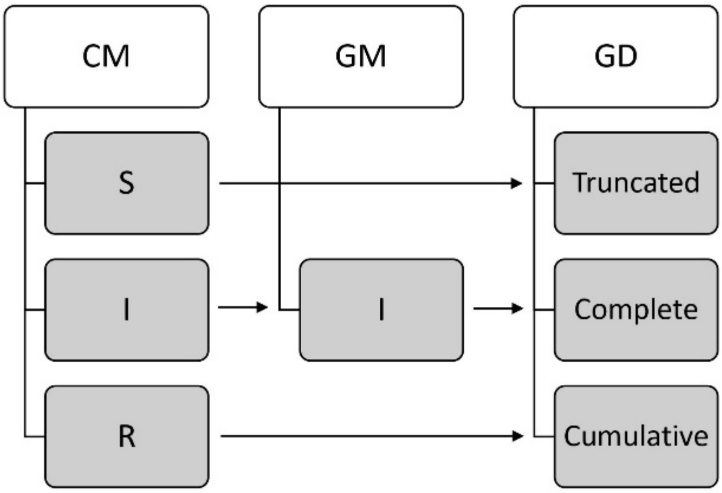

Fig. 2. The relation scheme among CM and GM with GD

For the most general purposes, we can mention that epidemics can be categorized into two main research methodologies: the mutual behavior pattern of relevant disease variables or compartments, or the independent characteristic parameters of each variable or compartment. For this purpose, many models and their variations have been derived and applied to epidemics to determine the spreading dynamics that can be expressed over some disease variables and characteristic parameters. Spreading variables have been defined in many models as the SIR model or LGM and some variations [6, 7, 8, 9, 10]. Still, no modeling study has been mentioned on the independent characteristic parameters of spread dynamics. To determine the characteristic parameters, we can consider each variable independently and develop a theoretical approach for the predefined spreading characteristics of the variables.

Current studies mostly use the LGM or SIR model and its variations to interpret the cumulative behavior of variables or the predefined mutual compartmental variables, respectively, only over time. Although time is a variable of spread dynamics, different disease parameters should also exist to determine the spreading behavior and correlated processes. Certain characteristic parameters should be revealed to understand the spread dynamics of each predefined variable independently and improve some consistent and proper responses to the disease course.

The current models are developed on only the cumulative behavior of some variables as seen in LGM or the behavior of the mutual variables or compartments as seen in SIR and their respective related models. However, we can independently interpret the spreading process over the variables to determine characteristic parameters instead of doing so as in the current models. When the current models and real data are carefully examined, three types of general behavior can be assumed to exhibit a truncated, complete, or cumulative distribution as seen in Fig. 3 that is expected from the whole natural consecutive processes, and they can be considered to have Gaussian-like behavior that may also be heavy- or long-tailed distribution in the stretched form to interpret nonlinear stochastic processes. Therefore, the pandemic phenomenon can be assumed to be a linear stochastic process, and the characteristics of disease dynamics can be defined over the parameters of the classical form of the Gaussian distribution. From this viewpoint, we ask to develop a theoretical approach to determine the disease dynamics as a random process using stochastic instruments.

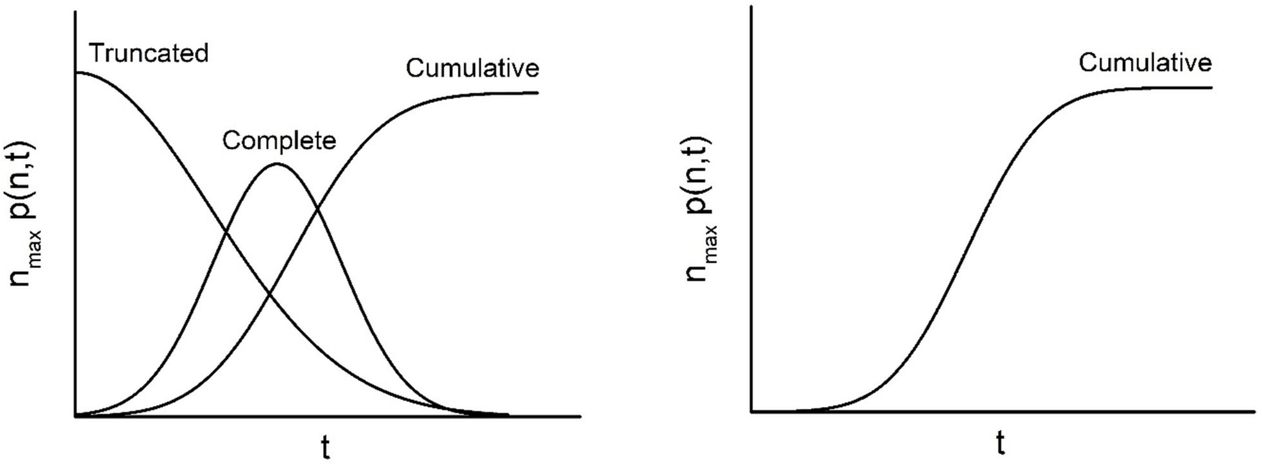

Fig. 3. The relevant Gaussian-like distribution plots of SIR and LG Models

Stochastic modeling studies have many applications in science, such as biology [11], ecology [12], neuroscience [13], physics [14, 15], signal processing, information theory, cryptography, and telecommunication. A random behavior can be defined as a stochastic process via some stochastic differential equations. The spreading of a disease among people is a stochastic process referred to as a randomly changing system [16, 17]. This random system can be assumed to be a continuous-time Markovian process derived mostly from random walk approximations that exhibit memoryless and well-behaved patterns. Besides, the spreading behavior has a transmission gradient from infected to healthy among people. Therefore, it is concluded that this random process also has an external bias.

In light of the behavioral, methodological, and mathematical analysis above, it can be concluded that a more comprehensive and basic theoretical approach can be derived to determine the characteristics and spreading patterns of pandemics. The purpose of our study is to present a phenomenological model through a novel theoretical foundation to get a generalized perception of the spreading dynamics and patterns of outbreaks.

MATERIALS AND METHODS OF RESEARCH

A model for each compartmental variable behavior independently can be derived among the mutually changing disease variables, such as suspected, infected, exposed, recovered, and death. Although many models examine the mutual behavior of variables over time, no model analyzes the behavior of each variable independently and tries to find characteristic disease parameters. Thus, we study to explore the independent behaviors of each variable in the current models to find some characteristic parameters for the disease dynamics.

Each compartment variable exhibits a complete, truncated, or cumulative distribution. Thus, we can use a confirmed method with variables with Gaussian behavior results to determine some characteristic disease parameters. On the other hand, natural phenomena have intrinsic random processes with variables with normal distributions and variations, which can also be defined via the instruments of stochastic dynamics. We can apply stochastic dynamics to construct a stochastic disease model and determine the characteristic parameters for each variable.

We evaluate a stochastic model of the disease's spread mechanism by assuming a time-dependent death probability behavior. In this process, the number of deaths tends to fluctuate due to disease dynamics such as susceptible, exposed, infected, recovered, quarantined, and isolated individuals. The disease dynamics vary as the number of deaths gradually decreases via isolated and recovered individuals and increases via susceptible and exposed individuals. Thus, the model is developed to estimate the fluctuation of deaths according to time through the disease mentioned above dynamics.

The spread from infectious to healthy people and from sickening to dying can be considered a total stochastic process. We can model this stochastic behavior as a random walk process to determine the epidemic dynamics and the parameters that affect the stage of the disease. Therefore, the spreading patterns can be assumed as a stochastic process, and a biased random walk model is developed via stochastic instruments and approaches.

We consider the fluctuation in the number of deaths behavior a stochastic process resulting from disease spread. Thus, we can determine the spreading parameters to show that n is the number of deaths based on the epidemic, t is the time, Δn and Δt are the changes in the number of deaths and time, r and d are the probability of rising and decreasing in the number respectively. Hence, we have the equation:

$$p(n, t+\Delta t) = p(n-\Delta n, t)r + p(n+\Delta n, t)d + p(n, t)(1-d-r)$$

We can express the equation as a series expansion that gives the differential equation,

$$\frac{\partial p}{\partial t} = -\frac{(\Delta n)\epsilon}{\Delta t}\frac{\partial p}{\partial n} + \frac{\delta(\Delta n)^2}{2(\Delta t)}\frac{\partial^2 p}{\partial n^2} + \mathcal{O}((\Delta t)^2, (\Delta n)^3)$$

We can neglect the higher-order terms and redefine the coefficients in the limit state.

$$\mu = \lim_{(\Delta n),(\Delta t)\to 0} \epsilon\frac{\Delta n}{\Delta t}, \qquad \zeta = \lim_{(\Delta n),(\Delta t)\to 0} \delta\frac{(\Delta n)^2}{2\Delta t}$$

Here μ and ζ are bias and diffusion coefficients, respectively. We get a stochastic differential equation called the master equation, the special case of the Fokker-Planck equation [18].

$$\frac{\partial}{\partial t}p(n,t) = -\mu\frac{\partial}{\partial n}p(n,t) + \zeta\frac{\partial^2}{\partial n^2}p(n,t)$$

In this case, the spread can be considered locally steady in time. The solution of the Fokker-Planck equation gives the probability density function (PDF), which is the Gaussian distribution with a shifted center.

$$p(n,t) = \frac{1}{\sqrt{4\pi\zeta t}}\exp\left(-\frac{(n-\mu t)^2}{4\zeta t}\right)$$

The mean and mean squared values are as below.

$$\langle n\rangle = \mu t, \langle n^2\rangle = \mu^2 t^2 + 2\zeta t$$

We obtain the shifted distribution with three characteristic parameters that define the spreading wave behavior in detail.

Here, the characteristic parameters of GD are expressed as that μ is the mean number of deaths per day, t defines the elapsed time through a spreading wave, and ζ takes value depending on the preventative mechanisms as seen in Figure 4. Pandemic behavioral patterns can be simulated via the characteristic parameters of the GD model and this approach makes the spread dynamics more clearly understood.

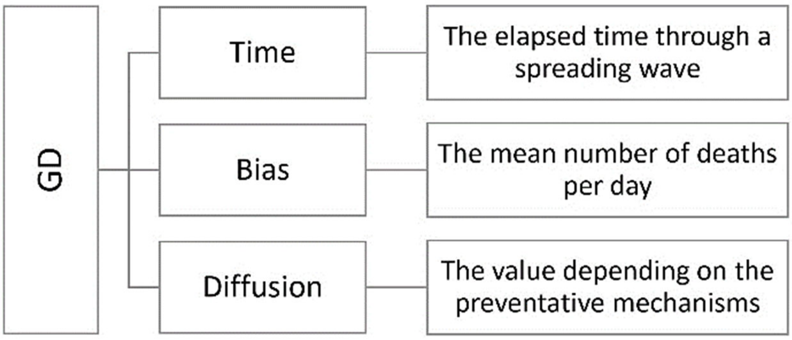

Fig. 4. The characteristic parameters of spreading waves in GD model

We have concluded that a stochastic model helps us understand the outbreak behavior and simplify it to determine disease dynamics. The new model is a biased random walk model, a master equation called the Fokker-Planck equation, and the resultant behavior is a time-dependent Gaussian distribution. Time-dependent Gaussian behavior is a good instrument for explaining the characteristics of spreading waves, guessing the number of deaths, and indicating the importance of preventative mechanisms.

RESULTS AND DISCUSSION

We have developed a phenomenological approach to the problem of the COVID-19 pandemic via stochastic dynamics by assuming that the process exhibits a Markovian randomly changing behavior. All epidemics exhibit the same stochastic behavior and can be modeled as a random process to determine the spread mechanism dynamics. For the present pandemic, three parameters are obtained to clarify the spread dynamics and are sufficient to demonstrate the graphical results that coincide with the current experimental data.

Certain relations exist among the parameters, distribution patterns, and means, and can be summarized through that table in Figure 5. The spreading parameters have exact effects on the distribution patterns through shifting peaks or changes in mean and the wave's width or fluctuation. The time shifts the peak and changes the width; the bias affects only the peak, while the diffusion impacts only the width of the distribution wave. Thus, the time and the bias affect the mean, while diffusion does not.

		Changes in distribution pattern	
		Peak(Mean)	Width(Deviation)
Parameters	t	☑	☑
	μ	☑	☒
	ζ	☒	☑
		Change	Not Change
		Expectation of distribution	

Fig. 5. The relational table among the spreading parameters, distribution wave patterns, and means

Figure 6 monitors two spreading waves at different times, biases, and diffusion values. The spreading parameters have behavioral effects on the wave, such as shifting the peak of the distribution, changing the width of the wave, and fluctuating the probability. The elapsed time through spreading shifts the peak directly and affects the width of the waves. Thus, an increase in time exhibits a wide and outnumbered shifted distribution. The different bias values cause variation in the mean but do not affect other wave characteristics. The different diffusion values affect the width of the spreading wave but do not change the mean.

Since mid-2019, many phenomenological approaches have been evaluated to model the spread of the disease and estimate the probable outcomes as exposed, infected, recovered, or dead individuals. There are many commonly used deterministic mathematical models such as SIR, SEIR, SEIRD, LGM, RGM, and GGM in the recent literature about the COVID-19 pandemic. In some papers, it is mentioned that though stochastic models are more realistic and mostly provide proper prediction results, they are much more complicated to analyze and sometimes difficult to determine the fundamental dynamics of the process. Even so, we have developed a theoretical approach using stochastic dynamics to understand and interpret the variables of the pandemic spread phenomenon.

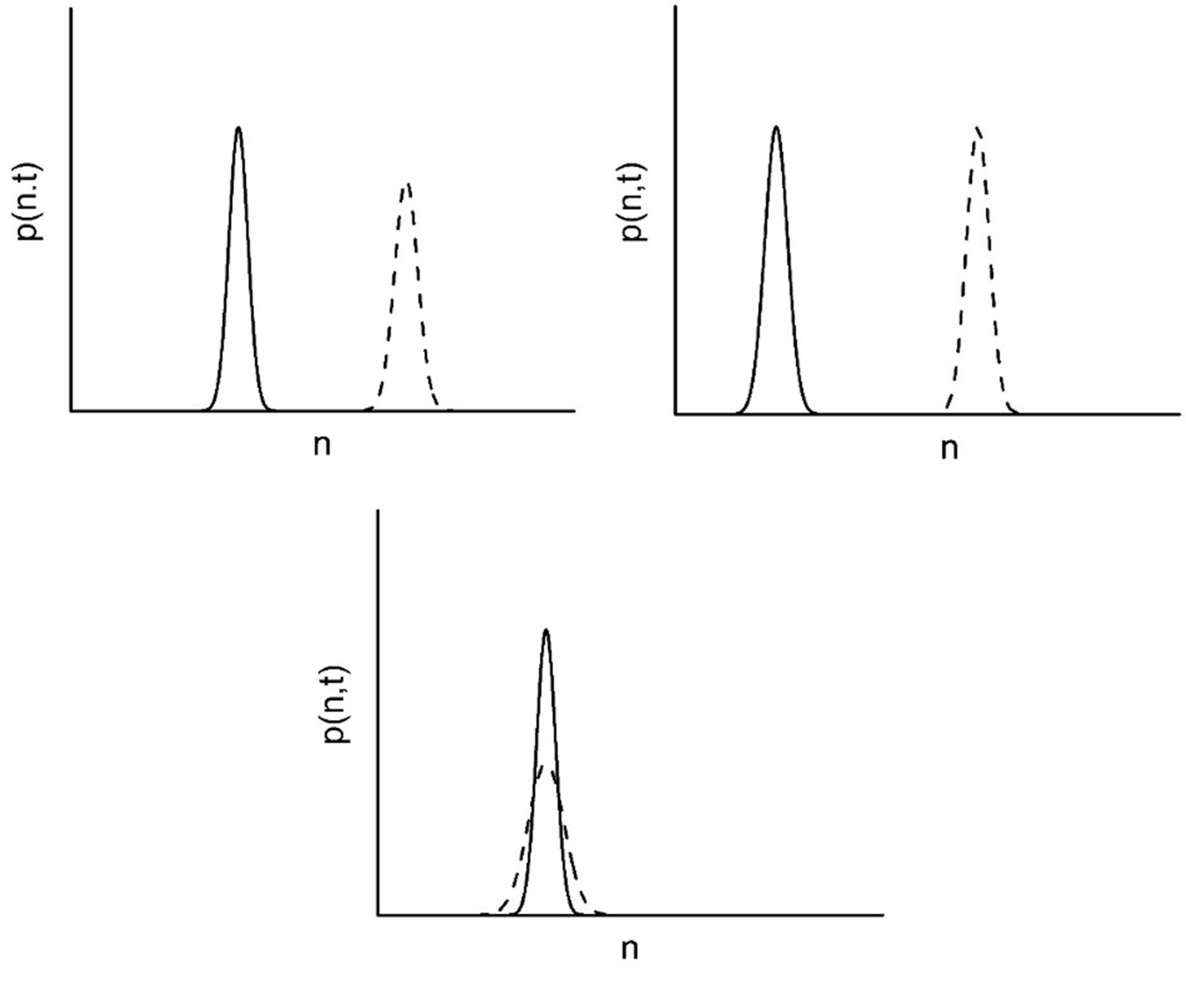

Fig. 6. Spreading wave patterns plotted in different time, bias, and diffusion

This paper provides a novel approach to model the pandemic from an alternative viewpoint to the current deterministic epidemic models and a simplified type of master equation: the time evolution of the probability density function (PDF) derived from the master equation. It has also verified the random nature of the spreading process via the stochastic model and estimated the behavioral patterns of the pandemic consistent with the current public data. We have represented the process over three basic parameters, monitored the independent effects of the parameters on different spreading waves, and interpreted most of the criticism about the preventative mechanisms.

CONCLUSIONS

1. Most criticism reveals the distribution behavior such as the importance of individual isolation, treatments, remedies, or vaccine development. The first

shifted distribution peak rises with the first spreading wave but the other peaks occur in time due to disease dynamics. The bias denoted as μ is the transmission parameter that depends on the gradient between infectious and healthy people. Earlier, the bias gets the biggest value, then decreases gradually to the equilibrium condition. Diffusion, denoted as ζ, depends on the spreading preventative mechanisms such as isolation, social distancing, public hygiene measures, etc. The diffusion takes lower values depending on how the spread preventative mechanisms are enforced strictly.

2. The bias coefficient takes different values due to the transmission gradient between infectious and healthy people. The bias gradually decreases until all healthy people struggle with the disease. Thus, the diffusion coefficient related to the preventative mechanisms only protects people from the wide-spreading waves that have the additional probability of increasing deaths. The diffusion coefficient only reduces the number of deaths in one spreading wave but does not change the mean. A remedy, vaccine, or treatment has to be developed to save more people from such a disease. Preventive measures must be strictly enforced to protect people from the higher-order spreading waves until remedial research gives successful results.

3. This model presents an alternative phenomenological approach to estimate the spreading behaviors of pandemic outbreaks by explaining disease dynamics via the spreading parameters μ, ζ, and t. Simplifying outbreaks over a master equation and a Gaussian distribution provides some advantages in understanding and determining disease dynamics and behavioral patterns. Therefore, we can perceive the critical importance of prohibition and restrictions or vaccine and remedy development works better.

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Conflict of interests. The author declares no conflict of interest.

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