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Chapter

Propagation Analysis of the Coronavirus Pandemic on the Light of the Percolation Theory

Moez Guettari and Ahmed El Aferni

Abstract

Efforts to combat the Covid-19 pandemic have not been limited to the processes of vaccine production, but they first began to analyze the dynamics of the epidemic's spread so that they could adopt barrier measures to bypass the spread. To do this, the works of modeling, predicting and analyzing the spread of the virus continue to increase day after day. In this context, the aim of this chapter is to analyze the propagation of the Coronavirus pandemic by using the percolation theory. In fact, an analogy was established between the electrical conductivity of reverse micelles under temperature variation and the spread of the Coronavirus pandemic. So, the percolation theory was used to describe the cumulate infected people versus time by using a modified Sigmoid Boltzman equation (MSBE) and several quantities are introduced such as: the pandemic percolation time, the maximum infected people, the time constant and the characteristic contamination frequency deduced from Arrhenius equation. Scaling laws and critical exponents are introduced to describe the spread nature near the percolation time. The speed of propagation is also proposed and expressed. The novel approach based on the percolation theory was used to study the Coronavirus (Covid-19) spread in five countries: France, Italy, Germany, China and Tunisia, during 6 months of the pandemic spread (the first wave). So, an explicit expression connecting the number of people infected versus time is proposed to analyze the pandemic percolation. The reported MSBE fit results for the studied countries showed high accuracy.

Keywords: Percolation theory, reverse micelles, electrical conductivity, sigmoid Boltzmann equation (SBE), Coronavirus, spread

1. Introduction

In late December 2019, the emerging epidemic of Coronavirus, Sars-Cov-2 (Covid-19) first appeared in China. Then, it spread on a very large scale to most of the world's countries. For this reason the World Health Organization (WHO) has declared it a global pandemic. The main distinguishing characteristic of this pandemic is its very high contagion power and subsequently, which gives it a spectacular speed of propagation. Recently [1], it was associated with the Spanish flu of 1918 in this regard. For this reason, efforts to forecast, predict, and model the spread of Coronavirus (Covid-19) global pandemic are accumulating to understand its contamination mode [2–6]. The objective of these efforts is to explore ways for

predicting its evolution curve to be able to skirt the contamination, in the absence of an effective vaccine serving as an antidote against this disease.

In this context, in a recent study [7] on the spread of Covid-19 in 15 different countries, we have showed that the pandemic spread in a given population follows a sigmoidal law. Indeed, the curve of variation of the cumulative number of infected persons *I* is composed of 3 phases, a linear phase (slow growth) followed by second exponential phase (fast growth), then another stable phase (slow growth). Given that, in our laboratory, we are used to using the sigmoidal model to characterize the percolation phenomenon occurring in colloidal systems [8, 9]. We suggest in the present work to apply the theory of percolation theory on the cumulative number of infected people in order to better understand the dynamics of the virus spread.

Percolation is a mathematical model which first introduced by S.R Braodblent and J. Hammersely in 1957 [10]. As a geometric phase transition, he described largescale connectivity from other links that are randomly established on small scales. Such connectivity brought the studied system from one state of disorder to another more ordered state. This model has been widely applied to explain phase transitions in a very wide variety of physical systems such as alloys, complex fluids, semiconductors, communication networks, etc. As examples of the application of the percolation model, we can cite the following transitions: Insulating conductive composite material (Insulator/conductor), Glass transition (Liquid/glass), Polymer gels (Liquid/gels), Quarks in nuclear matter (confinement/non confinement) [11].

Meanwhile, in our laboratory, we used to study several kinds of colloidal systems, in particular, the microemulsions water in oil, so-called reverse micelles. These are nano-droplets of water surrounded by monolayers of surfactant and dispersed in oily phases. In these systems, a percolation phenomenon has often been highlighted and widely studied. In fact, in reverse micelle systems, the percolation phenomenon was manifested by a spectacular increase in the transport properties (viscosity, dielectric constant electrical conductivity, etc.) of the micelles for a volume fraction, ϕ_d or a well-determined temperature T_p [8, 9]. The critical micellar volume fraction and the temperature signaling the appearance of percolation phenomenon are called the percolation thresholds $(\phi_{d,c}, T_p)$. This increase has been explained by the fusion of neighboring micelles, a fusion which in turn leads to the formation of a percolating network and the exchange of charge carriers (or matter). In the bibliography, the studies were focused on the viscosity, the electrical conductivity [12] and, of the dielectric constant of the reverse micelles around the percolation threshold. Theoretically, two models have been proposed [13] to justify the percolation-related experimental observations: a static model and a dynamic model. In the static model, the sudden change in the conduction of the system is caused by the formation of a bicontinuous phase of the organic solvent and water at the percolation threshold. Otherwise, micellar fusions are established between the neighboring micelles giving rise to micellar exchanges of the charge and the material. Furthermore, concerning the dynamic model, it is a model that attributes this behavior to the Brownian movement of droplets. Such movement induces random mutual collisions between the different micelles accompanied by exchanges of charge and matter.

2. Electrical percolation versus Covid-19 pandemic percolation

2.1 Phenomenological description

It seems imperative to mention that we are dealing here with two systems with several similarities in dynamics. Regarding the reverse micellar systems, these are indeed spherical particles of nanometric sizes in Brownian (random) motion. This

movement leads to permanent inter-micellar collisions giving rise to mutual exchanges of matter and electrical charges. Therefore, reverse micelles transport phenomena such as viscosity η and electrical conductivity σ increase exponentially. On the other side, they are infected people circulating randomly (carriers of the virus). This circulation leads to the virus spread in various ways (contamination of surfaces, the spread of droplets carrying the virus, handshaking with contaminated people...) which giving rise to cumulative number of infected people I_c . We report in **Figure 1** the schematic behavior of two systems. We also present in **Table 1** the detailed analogy between the two systems.

From a qualitative viewpoint, we find that the evolution of the number of people infected over time followed the same curve as the evolution of the micelles' electrical conductivity as a function of temperature. These are two trays separated by an exponential progression. We have measured the electrical conductivity of water/ AOT/reverse micelles of composition $W_0 = \frac{[water]}{[AOT]} = 30, \phi_m = \frac{V_{AOT}}{V_{isooc tane}} = 0.1, 0.15, 0.2,$ with an increase in temperature. Results are reported in **Figure 2** and compared with the evolution of the cumulative number of detected cases of Covid-19 in china since the first case.

2.2 Theoretical background

2.2.1 Sigmoid Boltzmann equation

Authors [13, 16] are used to using the sigmoid Boltzmann equation (SBE) to model the percolation process in reverse micelles. It is important to elucidate some notions on the SBE equation so that both the relevance of this equation and the definitions of both of its terms are understood.



Schematic representation of the analogy between reverse micelles and the virus spread.

Electrical percolation of reverse micelles	Spread of the virus (Covid-19)
σ : Electrical conductivity	<i>N</i> : Number of people infected
Reverse micelles: charge carriers	Infected people: carriers of the virus
Electrical charge (the Na ⁺ ion)	Virus
Nature of movement: Brownian (random)	Random
Micellar collision	Contamination of surfaces, spread of droplets carrying the virus, handshaking with contaminated people.

Table 1. Detailed similarities between reverse micelles and the pandemic spread.



(a) Electrical conductivity of water/AOT/isooctane reverse micelles ($W_0 = 30, \phi_m = 0.1, 0.15, 0.2$ vs Temperature (b) Confirmed cases of infected persons with covid-19 since the first case in China.

To describe the evolution of a quantity evolving as a function of a variable, the Sigmoid-Boltzmann equation (SBE) has the following form:

$$y = \frac{y_i - y_r}{1 + \exp(x - x_0) / \Delta x} + y_r$$
(1)

Rearranging Eq. (1),

$$y = y_r \left[1 + \left(\frac{y_i - y_r}{y_r} \right) \times \{ 1 + \exp(x - x_0) / \Delta x \}^{-1} \right]$$
 (2)

where y is the measured magnitude of the system which depends on x, y_i and y_r are the left and right asymptotes of y, x_0 is the center (where y returns the mean of y_i and y_r), and Δx is the constant interval of the independent variable that controls the rise profile or decrease from y_i to y_r (for a large Δx , the rise is gradual while for small Δx , the rise is rapid).

The equation therefore essentially deals with the switching of a variable from an initial state (state of y_i) to a final state (state of y_r) through a transition x_0 .

2.2.2 Application for electrical percolation of reverse micelles

By applying this equation to the electrical conductivity of the inverse micelles, σ , evolving as a function of temperature, T, the equation, therefore, deals with the switching of the conductivity from an initial state, σ_i , to a final state, σ_f , passing through the transition, T_p , (percolation temperature).

$$\sigma = \sigma_f \left[1 + \left(\frac{\sigma_i - \sigma_f}{\sigma_f} \right) \times \left\{ 1 + \exp\left(T - T_p \right) / \Delta T \right\}^{-1} \right]$$
(3)

From an experimental point of view, it is often convenient to use the logarithmic scale to better highlight the variations. The equation therefore becomes:

$$\log \sigma = \log \sigma_f \left[1 + \left(\frac{\log \sigma_i - \log \sigma_f}{\log \sigma_f} \right) \times \left\{ 1 + \exp \left(T - T_p \right) / \Delta T \right\}^{-1} \right]$$
(4)

2.2.3 Application of SBE to the cumulative number of infected persons I_c with Covid-19

In a recent work, we modeled the evolution of the cumulative number of infected people I_c in 15 countries with the sigmoid Boltzmann equation (SBE), evolving as a function of time, t. The SBE equation deals with the switching of numbers, I_c , from an initial state, I_i , to a final state, I_{max} , through the transition, t_p . At this point, we can consider that the transition, t_p , corresponds to what is called the pandemic peak.

$$I_{c} = I_{c,\max} \left[1 + \left(\frac{I_{i} - I_{c,\max}}{I_{\max}} \right) \times \left\{ 1 + \exp\left(t - t_{p}\right) / \Delta t \right\}^{-1} \right]$$
(5)

Knowing that at least one person is infected therefore $I_i = 1$ and taking into account that the maximum number of infected people, I_{max} , takes huge values, so $I_{max} >>> I_i$, the Eq. (5) becomes:

$$I_{c} = I_{c,\max} \left[1 - \left\{ 1 + \exp\left(t - t_{p}\right) / \Delta t \right\}^{-1} \right]$$
(6)

On a logarithmic scale, the sigmoid equation becomes:

$$\log I_c = \log I_{c,\max} \left[1 + \left(\frac{\log I_i - \log I_{c,\max}}{\log I_{c,\max}} \right) \times \left\{ 1 + \exp\left(t - t_p\right) / \Delta t \right\}^{-1} \right]$$
(7)

Considering that at least one person is infected, so $I_i = 1$, the Eq. (7) becomes:

$$\log I_c = \log I_{c,\max} \left[1 - \left\{ 1 + \exp\left(t - t_p\right) / \Delta t \right\}^{-1} \right]$$
(8)

For the spread of the pandemic in a given population, the Boltzmann equation (SBE) allows us to derive important parameters describing the spread of the virus. The most important parameters are the time interval, Δt , the percolation time, t_p , and the maximum number of infected persons, $I_{c, \max}$:

• The pandemic percolation time t_p

This is the transition point corresponding to the pandemic percolation threshold. At this time, the number of infected people rises drastically until the day with the maximum propagation speed. After that time the speed of virus spread decreases and the number of infected cases per day begins to decrease. It represents the pandemic peak

• Maximum number of infected persons *I*_{c, max}

It is a cumulative number of infected people signaling the stabilization of the epidemic crisis in a population. The real maximum number of people infected is in the vicinity of this number.

• The time constant Δt

It is called the time constant. It characterizes the rise of the exponential part (gradually or abrupt). Generally, the epidemic state stabilizes when the number of infected cases N reaches almost the maximum number of infected cases $I = 0.99I_{c, \text{max}}$ which corresponds to maximum time, t_{max} of pandemic spread:

Considering Eq. (6), the t_{max} value can be calculated from the following equation:

$$t_{\max} = 2.19\Delta t + t_p \tag{9}$$

So, we can estimate the time necessary for the stabilization of the epidemic state of each country t_{max} from Eq. (9). From an epidemiological point of view, the Δt value must necessarily depend on the effectiveness of the precautionary and preventive measures taken by the authorities of each country.

2.2.4 The characteristic contamination frequency

For reverse micelles systems, the energy required to make two micelles appear and activate the exchange of charges between them is called the activation energy of percolation. This energy constitutes a barrier to be crossed for this energy constitutes a barrier to be crossed to put two micelles in contact and trigger the exchange of charges. It takes the form of the famous empirical law of Arrhenius [13]:

$$\sigma = A \exp\left(-E_p/RT\right) \tag{10}$$

Where σ is the electrical conductivity of the micelles. *R* is the universal constant of ideal gases. *T* is the temperature. *A* is a pre-exponential factor having the same unit as σ . Typically, the refinement of Arrhenius law was effected by the Eyring transition state theory [17, 18], where the pre-exponential factor *A* is shown as the entropic factor of the transition state. In this theory the transition kinetic constant *k* is correlated with temperature by law analogous to that of Arrhenius:

$$k = A \exp\left(-\Delta H/RT\right) \tag{11}$$

$$k = \frac{K_B T}{h} \exp\left(-\Delta S/R\right) \exp\left(-\Delta H/RT\right)$$
(12)

Where k is kinetic constant, ΔS and ΔH are the transition state entropy and enthalpy, K_B is the Boltzmann constant and h is the Planck constant. In another report [18], the pre-exponential factor A was also correlated to motion, rate, disorder, speed ... of particles. Tian Hao [6] considers that the movement of infected individuals and individuals exposed to contamination is analogous to that of the movement of particles in various systems such as granular systems, colloidal systems ... He suggests that the equations of conductivity and viscosity are also applicable in the description of the viruses spread. In his work, he asserts that Eyring Rate Process Theory and Free Volume Concept [6, 14] are applicable on the movement of individuals carrying viruses which means that the more the infected and exposed individuals have the more free volume to move, the higher the probability of transmission.

So, for the virus spread, Arrhenius law can be applied to the cumulative number of infected cases *I* as follows:

$$I = A_c \exp\left(-t_C/t\right) \tag{13}$$

Having the dimension of time, t_C is equivalent to the Arrhenius temperature $\frac{E_a}{R}$ [18], A_c is a pre-exponential factor considered as the contamination frequency factor and t is the number of days. The contamination frequency A_c can be determined from the slope of the linear portion of the curve:

$$\ln I = \ln A_C - \frac{t_C}{t} \tag{14}$$

2.2.5 Scaling laws and critical exponents

We have mentioned before that the rationalization of the experimental results resulted in two theoretical approaches discussing the state of a system during the percolation phenomenon. A static model which suggests that at the time of percolation, the charge carriers merge with their neighbors, thus establishing a network of connected particles exchanging charges. Besides, a dynamic model whose particles carrying the charges are in permanent collision, merge randomly at the percolation threshold, and exchange the charges. The scheme depicted in **Figure 3** simplifies the difference between the two percolation models.

Theoretically, scale laws have been established to identify the predominant model for a given system. These laws are explained by two equations, which are applied only around the percolation point. For electrical percolation in reverse micelles systems, induced by temperature variation, these equations take the following forms:

$$\sigma = \beta (T_p - T)^{-s}, T \prec T_p \tag{15}$$

$$\sigma = \gamma (\mathbf{T} - T_p)^{t_s}, T \succ T_p \tag{16}$$

Where β and γ are free parameters. *S* and t_s are called the critical exponents. These two laws are valid near to the temperature of the percolation, T_p . Critical exponent values exhibit the difference between static percolation and dynamic percolation [13]. In fact, in the case of static percolation, the predicted theoretical values of critical exponents were found to be $t_s = 1.6$ and s = 0.7. Divergence of these values was used to be the proof of dynamic percolation.

In the case of the propagation of Covid-19, these two equations apply to the vicinity of the peak pandemic as follows:

$$I = \beta (t_p - t)^{-s}, t \prec t_p \tag{17}$$

$$I = \gamma \left(t - t_p \right)^{t_s}, t > t_p \tag{18}$$



Figure 3. Schematic representation of the two percolation models.

From an epidemiological point of view, the static percolation model corresponds to the formation of geolocated chains of transmission of the virus [15]. However, the dynamic model reflects randomly distributed chains of transmissions in space.

2.2.6 Speed of the pandemic spread

Typically, to detect the percolation threshold (temperature, volume fraction ...), a differential method is used [9, 13]. The method consists of determining the maximum of the curve $\partial\sigma/\partial T$ versus the temperature (volume fraction...). This curve measures the speed of the variation of electrical conductivity as temperature varies.

Similarly, we can consider that the differential, $\partial I_c/\partial t$, measures the speed of propagation of the contamination V_p (and therefore of the virus) as a function of time. Thus, the maximum speed corresponds to the maximum curve $\partial I_c/\partial t$ versus time (Days).

$$V_p = \frac{\partial I_c}{\partial t} \tag{19}$$

3. Application to the cases of China, Tunisia, France, Italy and Germany

Using data provided by Johns Hopkins university resource center [19] on the number of infected cases in 5 countries (China, France, Germany, Italy and Tunisia) during 6 months of the virus spread since the day of the first case detection of until June 30.

3.1 The cumulative number of people infected I_c

We plotted in **Figure 4** the variation of the cumulative number of infected people in each country versus the number of days since the first detected case. The existence of 3 stages can be discerned: a first phase, where the number of cases varies gradually over time. A second phase in which the number of cases



Figure 4.

Variation of the cumulative number of confirmed case I_c versus days since first case t. The red line (-----) represents the sigmoid Boltzmann equation fit (SBE).

	$N_{ m max}$	t_p	Δt	t_{\max}	R^2	
China	82011.460	18	4.944	28.827	0.993	
Italy	227262.403	63	11.227	87.587	0.929	
France	154264.941	75	10.901	98.873	0.993	
Germany	184037.613	71	10.184	93.302	0.994	
Tunisia	1142.577	32	12.184	58.682	0.994	

Table 2.

Fit parameters of number of infected cases I_c (cumulative) with the SBE equation, for the different countries studied.

unexpectedly rises very quickly and a third phase in which the rate of increase in the number of cases is stabilized overtime. We have therefore adjusted all these curves with the sigmoid Boltzmann equation (SBE) (Eq. (6)). The results are listed in **Table 2**. The fit results can therefore be interpreted with respect to the evolution of the epidemic situation as follows:

• China

The number of infected cases reaches maximum of around 82011.46. The rise to this maximum lasts approximately 28 days. The transition point to a stable state is marked around day 18 (pandemic peak) since the first case detected.

• Tunisia

The number of infected cases reaches maximum of around 1142.57. The rise to this maximum lasts for approximately 58 days. The transition point to a stable state is marked around day 32 (approximately 1 month) (pandemic peak) since the first case detected.

• Italy

The number of infected cases reaches maximum of around 227262.40. The rise to this maximum lasts for approximately 87.58 days. The transition point to a stable state is marked around day 63 (approximately 2 months) (pandemic peak) since the first case detected.

• Germany

The number of infected cases reaches maximum of around 227262.40. The rise to this maximum lasts approximately 93.302 days. The transition point to a stable state is marked at day 71 (approximately 2.5 months) (pandemic peak) since the first case detected.

• France

The number of infected cases reaches maximum of around 154264.94. The rise to this maximum lasts approximately 98.873 days. The transition point to a stable state is marked around day 75 (pandemic peak) since the first case detected.

3.2 The contamination frequency A_c

By plotting the Arrhenius curve Ln(I) versus $\frac{1}{t}$ (**Figure 5**), we have calculated the contamination frequency, A_c , from the intercept of its linear portion. The results for



Figure 5. Arrhenius plot of the number of cumulative infected persons Iversus days.

the 5 studied countries are listed in **Table 3**. The low values observed for China and Tunisia reflect a reduction in the contamination frequency in these two countries. This can be attributed to the anticipation of the authorities of these two countries for reducing the mobility of people by imposing general confinement very early. However, the huge values observed for the 3 European countries reflect a very high contamination frequency. This can be explained by a delay in taking decisions relating to the restriction of people's movement.

3.3 The dynamic behavior of virus spread during the critical period

The determination of the critical exponents (Eqs. (17) and (18)) before (s) and after (t_s) the percolation point informed us about the percolation model which dominated the spread of the virus in each country. The results reported in **Table 3** show values have largely deviated from theoretical values. This represents a very strong tendency toward the dynamic model for all countries. This reveals that the chains of covid-19 virus transmission are randomly distributed in space and the contamination is dispersed in all regions. However, this general trend does not prevent us from observing deviations toward the static model, especially before the pandemic peak (s value), for Tunisia and China.

COUNTRY	S	$\Delta = (S - S_{th}) $	t_s	$\Delta = (t_s - t_{th}) $	A_c
TUNISIA	0.160	0.54	0.037	1.563	2416.317
CHINA	0.170	0.53	0.035	1.565	85819.368
GERMANY	0.123	0.577	0.053	1.547	2.532.10 ⁸
FRANCE	0.121	0.579	0.051	1.549	2.532.10 ⁸
ITALY	0.076	0.624	0.042	1.558	1.436.10 ⁷

 Table 3.

 The critical exponents and contamination frequency for the 5 studied country.

3.4 Speed of the pandemic spread

In the first section of this article, we stated that the differential $\frac{\partial I}{\partial t}$ estimation of the variation rate in the number of people infected I as a function of the change in the number of days t since the first case is, therefore, the speed of the pandemic spread V_p (Eq. (19)). For the 5 studied countries, we measured this differential. The results were reported in **Figure 6**. As we can see, the speeds of the virus spread in the different countries gradually increase over time until they reach a maximum value $V_{p \max}$, then they start to decrease. It is crucial to note that the dates corresponding to the maximum speeds reached coincide with the dates recorded as pandemic peaks $t_p(\frac{t}{t_p} = 1)$ that have been determined by the Boltzmann sigmoid equation (SBE).

Furthermore, we can also notice that the speeds achieved take on considerable values except for Tunisia ($V_{p \max} \approx 55$ cases per day), a country which Covid-19 did not greatly affect.

To assess the speed of propagation between the studied countries, we also have adjusted our findings by estimating the root mean square speed of propagation V_{PRMS} for each country:

$$V_{PRMS} = \sqrt{\frac{\sum_{i} V_{pi}^2}{n}}$$
(20)

Where V_{pi} the spread speed for day *i* and *n* is the number of days since the first case. In **Figure 7**, we have depicted the variation of the root mean square speed of Covid-19 in the studied 5 countries. As reported, the highest V_{PRMS} was recorded for Italy exceeding the speed of $V_{PRMS} = 2000$ cases/day. However, the lowest one was recorded for Tunisia with a value that does not exceed $V_{PRMS} = 19$ cases/day.



Figure 6. Speed of the pandemic spread V_p versus $\frac{t}{t_n}$ for the 5 studied countries.



Figure 7. The root mean square speed of propagation V_{PRMS} since the first case until 30 June, for the 5 studied country.

4. Conclusions

We analyzed epidemic data on the cumulative number of cases infected with covid-19 in 5 countries affected differently by the pandemic. The data describe the state of the virus spread during more than 6 months of its appearance (appeared at the beginning in China (December 2019)). This analysis was consisted of the application of the percolation theory on the evolution of the cumulative number of people infected I_c in each country. Based on an analogy between the spread of Covid-19 in a population and the electrical percolation of reverse micelles, we introduced the covid-19 pandemic percolation. First, adjusting the data using the Boltzmann sigmoid equation (SBE) made it possible to derive important parameters related to the spread of the pandemic: The first represents the cumulative number of people infected $I_{c, \max}$, from which the epidemic state in each country begins to stabilize. The second is the pandemic peak time t_p (threshold of pandemic percolation), this is a critical day corresponding to the transformation of the epidemic situation from serious to stable state. The third is a time interval Δt that we have called the time constant. This constant represents the momentum of exponential pandemic progression in each country. It allowed us to estimate the time necessary $t_{\rm max}$ for the stabilization of the epidemic state in each country. Comparing the value of this constant in each country makes it possible to assess the effectiveness of the preventive measures taken by the authorities.

By applying the Arrhenius law on the cumulative number of cases in each country, we introduced a characteristic contamination factor this rate measures the frequency of interpersonal contact in each country. This permits us to compare contamination frequency following the traffic restriction measures taken by each country (border closure, general confinement, geo-located confinement, etc.). The application of scale laws at the vicinity of the percolation threshold t_p has shown a total predominance of the dynamic percolation model of contamination. This predominance has been interpreted by the existence of transmission chains of the virus randomly distributed in each country (and not local chains).

Finally, the determination of the propagation speed V_p of covid-19 in each country showed that the maximum propagation speed was recorded during the pandemic peak t_p (previously determined by SBE equation). Moreover, the calculation of the quadratic mean root square speed of propagation V_{PRMS} allowed us to compare the evolution of the speed in each country.

Finally, all of the results show that Tunisia and China have implemented the most effective strategies to combat the first wave of Covid-19. Indeed, Tunisia's authorities have opted for general containment (lockdown) throughout the country since the second week after the first confirmed case of Covid-19 was discovered. According to our findings, this strategy significantly reduced the frequency of contact between individuals carrying the virus, as well as the speed of covid-19 propagation over the next three months. As a result, the total number of cases infected with covid-19 remained very low. This clearly demonstrates the effectiveness of this strategy in combating the pandemic. In addition, the second country which showed low propagation indicators (contact frequency, speed of propagation, total number of infected people) is China. This is due to China's adoption of a strategy known as targeted containment. That is, the confinement was limited to the city of Wuhan (the site of the virus's appearance). Such a strategy has clearly demonstrated its effectiveness by significantly slowing propagation. However, the three European countries (Italy, France, and Germany) experienced relatively high propagation rates as well as a high number of covid-19 cases. These outcomes are the result of the authorities' failure to implement general containment procedures on the right time.

This further proves that the most effective strategy to bypass the spread of covid-19 is either general containment or targeted containment.

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Conflict of interest

The authors declare that they have no competing interests.

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