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The evolution of COVID-19: A discontinuous approach

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The evolution of the COVID-19 disease is monitored on the basis of the daily number of infected patients and the daily number of deaths provided from national health agencies. The variation of such parameters with time parallels that described for the growth/decay of historic transportation systems revealing the appearance of discontinuities. The evolution of the pandemic disease is represented in terms of two nominally equivalent formulations: a logistic model with sharp changes in its rate parameters, and in topological terms resulting in 2nd order phase transitions in the infected patients/time space.

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1. Introduction

The mathematical modelling of the spread of a pandemic disease is crucial for its day-to-day appropriate surveillance and control measures and the prediction of the future behaviour. The rapid expansion of the COVID-19 has produced an unprecedented impact in all countries. The management of this disease, although facilitated by the rapid dissemination of data, is made difficult by the difficulty in applying control tests to the entire population and the non-uniformity of the criteria used by the different national health agencies to compute the infected people [1].

Various mathematical models have been used to describe the evolution of pandemic diseases [2]. This evolution is in general interpreted in terms of ‘smooth’ models based on the SIR (Susceptible-Infectious-Recovery) model introduced in 1927 by McKendrick and Kermack [3–5], logistic approximations [6,7] or transmission networks aimed to calculate the basic reproduction number by using the serial intervals and intrinsic growth rate [8,9].

These curves have in common with the different logistic models [10] their “smooth” character in general displaying a unique inflection point in the total number of infected persons vs. time curves. Examination of available data for the COVID-19 pandemic episode in successive stages [11–13] for different countries suggests, however, a more complex behaviour. This can be monitored using the time evolution of the daily number of infected persons, \(I_D(t)\), and deaths, \(D_D(t)\) for which reported data differ from the expectances from logistic-type modelling.

These variations are formally similar to those previously described [14,15] in the evolution of historical transportation systems based on topological [16] or logistic [17] approaches. The growth and decay of these systems can be described either in terms of topological phase transitions between small-worlds and fractal-type scaling and in terms of logistic growth/decay with sharp variations in the rate constants. The formal analogy between the discontinuities in the evolution of transportation systems and the COVID-19 suggests the possibility to describe the disease evolution in terms of discontinuous steps. The current report explores some implications of this possibility in regard to the management of the disease.

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2. Results and discussion

2.1. The continuous view of disease evolution

In the SIR model [3–5] to describe the time evolution of an epidemic disease, the population is divided into individuals susceptible \( S(t) \), infected \( I(t) \), and removed \( R(t) \) at the time \( t \) which are related with three rate laws of the form:

\[
\begin{align*}
\frac{dS(t)}{dt} &= -\beta S(t)I(t); \quad \frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t); \quad \frac{dR(t)}{dt} = \gamma I(t)
\end{align*}
\]

(1)

where \( \beta \) and \( \gamma \) are the rate constants associated, respectively, to the contact (susceptibility to disease) and removed (either dead or recovered) individuals [18]. To solve these equations, it is assumed that a removed individual cannot be infected again and that the size of the population remains equal to \( N \) individuals so that \( R(t) = N - S(t) - I(t) \) [19]. These equations have to be integrated taking a set of initial values \( S(0) = S_0, I(0) = I_0, \) and \( R(0) = R_0 \) [18]; a refinement consists of the consideration of time-dependent values of the rate constants \( \beta \) and \( \gamma \) [20]. The SIR set of equations can be simplified assuming that, in the initial stage of the disease, the number of removed individuals is considerably less than the number of infected ones and that these are clearly lower to the number of susceptible people. At the beginning of the disease propagation, this last essentially equals the total population \( N \). Then,

\[
I(t) \approx I_0 e^{\beta N t}; \quad I_0(t) = \frac{dI(t)}{dt} \approx I_0 \beta N e^{\beta t}
\]

(2)

where \( \alpha = \beta N \). In turn, the late period of decay can be symmetrically approximated by an equation of the type:

\[
I_D \approx \frac{dI(t)}{dt} \approx I_\ast \gamma e^{-\delta t}
\]

(3)

where \( I_\ast \) represents some threshold value of \( I_D(t) \) and \( \delta \) is the corresponding decay exponent.

The evolution of continuously growing but pressured systems can be described in terms of a logistic model. This was originally formulated by Verhulst [21] and has been extensively applied to describe human population evolution and a variety of biological and social systems [22]. In differential form, the Verhulst logistic equation can be expressed as:

\[
\frac{dI(t)}{dt} = kI(t) \left[ 1 - \left( \frac{I(t)}{I_{lim}} \right) \right]
\]

(4)

where \( I(t) \) represents the number of infected individuals tending to a limiting value \( I_{lim} \). Integration between the initial population \( I_0 \) and a limiting value (or carrying capacity), \( I_{lim} \), yields:

\[
I(t) = \frac{I_0 I_{lim}}{I_{lim} - I_0} e^{-kt} + I_0
\]

(5)

This equation predicts a s-shaped variation of \( I(t) \) on \( t \) with an inflection at the half of the carrying capacity, \( I_{lim}/2 \). According to Chen [23], the logistic curve can be divided into four parts, namely exponential growth, acceleration, deceleration, and logarithmic decay. The first derivative of this curve, equivalent to the number of patients by time unit (i.e. to the daily number of infected patients, \( I_0(t) \)) varies with time defining a fir tree-shaped curve, characterized by an acute maximum between monotonically growing and decaying branches [16].

To describe different biological and geographic systems, different modifications of Eq. (4) have been proposed. Much of these equations can be generalized as [24–26]:

\[
\frac{dI(t)}{dt} = kl(t)^a \left[ 1 - \left( \frac{I(t)}{I_{lim}} \right) \right]^c
\]

(6)

where \( a, b, c \), are exponents to be adjusted. This equation can be seen as a rate law for a growing system in which the individuals are submitted to a growing tendency, given by the term \( I(t)^a \), and a simultaneous decaying, given by the \( \left[ 1 - \left( I(t)/I_{lim} \right) \right]^c \) term.

Taking the classical form of the Verhulst equation (i.e., taking \( a = b = c = 1 \)), yields as limiting cases growing and decaying equations analogue to Eqs. (2) and (3) taking the corresponding integration limits. In the most simple case, the intermediate region can be modelled taking the Richards version of Eq. (4) [27] (corresponding to \( a = c = 1 \)) and assuming that \( I_0/I_{lim} << 1 \). The resulting equations are:

\[
I(t) \approx I_0 \left( 1 + bkt \right)^{1/b}; \quad I_0(t) = kl_0 \left( 1 + bkt \right)^{1+b/b}
\]

(7)

which corresponds to a potential rate law. This equation is formally equivalent to those which can be derived from transportation systems replacing the number of infected patients by the length of the transportation system and the time by population [15]. Conjointly considered, Eqs. (2), (3), and (7) suggest that we can approximate different stages in a logistic-type epidemic episode in terms of exponential growth and decay steps accompanying an intermediate potential step.
The above equations can also be treated in topological terms translating it into a geometrical approach taking a infected patients/time \((I(t))/t) space by analogy with the length of the transportation system/population geographical space \([14]\). Here, Eqs. (2) and (3) will be formally equivalent to a system displaying the small-worlds topology whereas Eq. (7) is formally equivalent to a transportation system with fractal growth \([14]\).

2.2. Analysis of COVID-19 data

We used the official data published by the European Centre for Disease Prevention and Control at 06th April, 07th May and 23th June 2020, provided by the national health agencies of different countries. Such data have several aspects to be underlined: (i) the criteria used to compute \(I_0(t)\) and \(D_0(t)\) were not uniform and even varied with time in each country; (ii) in several cases, re-normalizations were introduced by adding or subtracting a significant quantity of patients in a giving day (see Supplementary information, Figures S.1 and S.2). In spite of these serious limitations, available data permits to detect common tendencies for the different countries (vide infra). The criteria used for data processing were: (i) the times were individually computed for each country taken as \(t = 0\) the day at which the first positive COVID-19 case was detected in each country; (ii) the first case in each country was followed by several days with zero cases; the initial exponentially growing data were computed since there was a continuous detection of infected patients in each country; (iii) normalization data consisting of zero, large positive or negative cases introduced by the national health agencies were removed.

Figure S.1 illustrates the data corresponding to the time variation of the total number of infected people, \(I(t)\), for China. Such data define a s-shaped curve typically used to describe the progression of the disease. The variation of the daily number of infected persons, \(I_0(t)\), in South Korea and China can be seen in Figures 1a and 1b. In both cases, the data points can be fitted to an exponentially growing curve at the beginning of the disease (continuous lines) whereas, after reaching a maximum \(I_0\) value, the data points can be satisfactorily fitted to an exponential decay. The South Korea \(I_0(t)\) vs. time curve fits well with the expected behaviour for a logistic evolution of the disease, defining a fir-tree profile with a well-defined maximum with no other inflections \([17,23]\). In contrast, the Chinese data appear to define three branches characterized by: (i) apparently abrupt transitions occur between the different branches, and (ii) the data in the intermediate region (dotted line in Fig. 1b) do not accommodate to an exponential growth.

This last situation was found on analysing both \(I_0(t)\) and \(D_0(t)\) data for the different tested countries. This is illustrated in Fig. 2 for Italy and in Fig. 3 for Spain (see also Fig. S.2), in both cases using the data reported at 07th May 2020. Remarkably, all curves show the maximum expected for a logistic behaviour but the ascending and descending branches are not monotonically growing or decaying. The initial exponential growth leads to a sharp transition to a more or less long region of potential growth which ends abruptly when the exponential decay initiates. This intermediate region is characterized by linear variations of \(\ln I_0(t)\) and \(\ln D_0(t)\) with \(nt\), as predicted by Eq. (7) when \(bkt \gg 1\). This behaviour is formally analogue to that observed in the evolution of historic transportation systems \([14,15]\), summarized in Figure S.3 of Supplementary information.

Fig. 4 depicts the plots of \(\ln I_0(t)\) vs. \(\ln t\) for Italy and Spain. The slope of such representations, \(g = (1-b)/b\), is representative of the rate of propagation of the disease in this regime. Although there is relatively large dispersion in the day-to-day values of \(I_0(t)\), linear tendencies can be reasonably assumed, our data revealing a faster increase in the number of infected in Spain (slope 3.9) than in Italy (slope 1.7).

In several cases, the decay can be resolved into two (or more) exponential decays with an apparent discontinuity between them so that the overall both \(I_0(t)\) and \(D_0(t)\) vs. time data can be divided into (at least, vide infra) 3–5 regimes of propagation of the disease.

This behaviour is formally analogue to that described for the rise and fall of historical transportation systems \([14,15]\), one example of which is illustrated in Fig. S.3, where the time variation of the ratio between the total length (\(L\)) and the population (\(H\)) of the historical tram system of Valencia (Spain) is depicted. Clearly, the \(L/H\) ratio defines three regions in the diagram corresponding to a fast growing (blue line) a fast decaying (green line) and an intermediate non-exponential region.

This behaviour can be equivalently interpreted in terms of a logistic approximation, assuming that sharp modifications in the kinetic parameters occur, as studied by Ausloos \([16]\), and in terms of 2nd order phase transitions between two topologies, small-worlds and fractal \([14]\), following the formalism discussed by Csányi and Szendrói \([17]\). In its application to transportation systems, the small-worlds behaviour defines the exponential growth and decay branches whereas the fractal topology defines the behaviour of the intermediate region.

2.3. Comparative trial and outbreaks

COVID-19 data provided at 06th April 2020 were first treated. Fig. 5 compares the \(I_0(t)\) vs. time curves at 06th April 2020 of France, Germany, USA and United Kingdom. In all cases, the initial exponential growth was followed by a well-defined intermediate, potential region in the \(I_0(t)\) vs. time curve. Table 1 summarizes the data of the rate parameters for the exponential growth (Eq. (2)), potential growth (Eq. (7)) and exponential decay (Eq. (3)) for different countries using the above data \([11]\) for a complete set of statistical parameters, see Table S.1 in Supplementary information.

On comparing such data with those for China, Italy, South Korea and Spain (Fig. 1 and S.2 in Supplementary information), the most relevant comparative features can be summarized as: (a) the initial progression of the infection,
Fig. 1. Time variation of the daily number of COVID-19 infected persons in (a) South Korea and (b) China. The time is computed from the day where the first Chinese patient was identified. All COVID-19 data were taken from [10] (06th April 2020). The continuous lines correspond to exponential growth and decay lines and the dotted lines to the potential growth. The arrows mark the sharp transitions between different regimes.

Table 1
Summary of statistical parameters for the growing, decay and intermediate regions of the $I_d(t)$ vs. $t$ curves of the COVID-19 disease for different countries.

| Country | Growth exponent $\alpha$ (days$^{-1}$) (Eq. (2)) | Potential exponent $g$ (Eq. (7)) | Decay exponent $\delta$ (days$^{-1}$) (Eq. (3)) | Time interval (days)$^a$ | Time interval for curve fitting (days)$^b$ |
|---------|---------------------------------|---------------------------------|---------------------------------|----------------|----------------|
| China   | 0.45 ± 0.07                      | 4.2 ± 0.2                       | $-0.13 \pm 0.02$                | 101            | 83 ± 2         |
| S. Korea| 0.32 ± 0.06                      | Step non detected               | $-0.170 \pm 0.018$              | 80             | 49 ± 2         |
| Italy   | 0.240 ± 0.016                    | 1.7 ± 0.2                       | $-0.036 \pm 0.011$              | 100            | 75 ± 3         |
| Spain   | 0.329 ± 0.017                    | 3.9 ± 0.5                       | $-0.035 \pm 0.014$              | 99             | 46 ± 2         |
| France  | 0.247 ± 0.014                    | 5.8 ± 0.8                       | $-0.06 \pm 0.03$                | 106            | 72 ± 2         |
| Germany | 0.260 ± 0.019                    | 2.5 ± 0.7                       | $-0.05 \pm 0.02$                | 106            | 74 ± 2         |
| UK      | 0.207 ± 0.016                    | 3.2 ± 0.8                       | $(-0.0021)^c$                   | 116            | 83 ± 4         |
| USA     | 0.307 ± 0.012                    | 6.6 ± 0.5                       | $(-0.0075)^c$                   | 115            | 85 ± 4         |

$^a$The time intervals are computed taken as $t = 0$ the day at which the first positive COVID-19 case was detected in each country.

$^b$The time interval used for curve fitting was initiated at the time where continuous detection of infected cases was reported.

$^c$Data for the decay regime of UK and USA were taken at 23th June 2020 from [12]; such data exhibit large dispersion.

The growth stage, represented by the exponent in Eq. (2), was faster for China, followed by South Korea, Spain and USA; (b) the decay stage has been clearly attained solely by China, South Korea, Italy and Spain. The decay in the first two countries was clearly faster than that currently occurring in the second ones; (c) the potential region is that producing more significant
The previous three-step modelling of COVID-19 data has potential predictive value (vide infra). The projection of the decay curves for Italy and Spain using 06th April data (See Supplementary information, Figure S.4) are coincident with the data subsequently reported by the respective national health agencies at 07th May 2020 depicted in Figs. 2 and 3. It is pertinent to note that in several cases, the initial region of the decay branch of the $I_D(t)$ vs. $t$ and $D_D(t)$ vs. $t$ curves can also be reasonably fitted to a potential function (the decay analogue of Eq. (7)), but in all the studied cases, the exponential fit was better in terms of the regression coefficient.

Remarkably, 06th April data in suggest that France and Germany have initiated the decay while United Kingdom and USA remain within the ascending branch of the $I_D(t)$ vs. $t$ curve. These results were confirmed by 07th May and 23th June data, presented in Fig. 5 for France and Germany (see also Supplementary information, Figures S.5 and S.6) and Fig. 6 for United Kingdom and USA. Clearly, the French and German curves display marked exponential decays with $\delta$ exponents of $-0.061$ and $-0.050 \text{ days}^{-1}$, respectively, comparable to those determined (see Table 1) for Italy and Spain. In contrast, United Kingdom and USA curves exhibit large data dispersion in their third branch and clearly slow variation with $\delta$ exponents of $-0.0021$ and $-0.0075 \text{ days}^{-1}$, respectively. In brief, this means that the rate of decay of the disease is considerably lower in the case of these two last countries. The case of Brazil is depicted in Fig. 7. Unfortunately, the disease remains in the growing regime without reaching its maximum.

The current modelling also permits a prospective analysis of different situations, illustrated in Fig. 8a and Figures S.7 and S.8 (Supplementary information) on the basis of the Spanish data. The exponential decay calculated from 06th April data with an exponent ($\delta$) of $-0.035 \text{ days}^{-1}$ can be compared with the prediction for the hypothetical case where the exponent was increased to a value ($-0.100 \text{ days}^{-1}$) close to those of China and South Korea. These data do not permit a clear separation between an exponential decay and a potential-type decay whose theoretical predictions taking exponents differences, in terms of duration, and infection rate (given by the slope of the $\ln I_D(t)$ vs. $t$ representations) between countries, being particularly important in France, UK and USA.
Fig. 3. Time evolution of the COVID-19 disease in Spain expressed as (a) $I_D(t)$ vs. $t$ and (b) $D_D(t)$ vs. $t$ curves. The time is computed from the day where the first patient was identified. The lines represent the fit of different sets of data points to Eqs. (2) (exponential growth), (3) (exponential decay) and (5) (potential growth). 07th May 2020 data [11]. The arrows mark the transitions between different propagation regimes.

Fig. 4. Plots of $\ln I_D(t)$ vs. $\ln t$ for data points corresponding to the central region in the COVID-19 diagrams for Italy (squares) and Spain (solid squares) in Figs. 2a and 3a.
of the potential function in Eq. (7) of $-1.7$ and $-3.9$ adopted by symmetry with those in the growing periods (see Table 1), are shown in Figure S.7 of Supplementary information.

Interestingly, an early detection of outbreaks can be modelled. In Fig. 8a and S.8 (Supplementary information) we superimpose the Spanish exponential decay recorded at 06th April 2020 to hypothetic new pandemic growths at the 60th day. These are assumed to be exponential, the former (Fig. 5a) of three days of duration at the same rate that the original in Spain (characterized by an exponent of 0.33 days$^{-1}$), and the second (Fig. 5b) having a much lower expansion (exponent of 0.030 days$^{-1}$) but prolonged by ten days. In both cases, it is assumed that the new outbreak is followed by an exponential decay at the Spanish exponent of $-0.035$ days$^{-1}$.

These results provide opportunity for a fast detection of possible outbreaks. Interestingly, the profile of the $I_D(t)$ vs. $t$ plots is in agreement with those recorded in cases of recognized outbreaks, as is illustrated in Fig. 8. Fig. 8a depicts the $I_D(t)$ vs. $t$ plot simulating an outbreak occurring in Spain (from data reported at 06th April 2020, [11]) at the 60th day with an exponent of 0.030 days$^{-1}$ for ten days followed by an exponential decay with $\delta = -0.035$ days$^{-1}$, that obtained for the ‘ordinary’ Spanish decay curve. The profile of the $I_D(t)$ vs. $t$ curve is clearly similar with that corresponding to the outbreak(s) reported by Iran at 23th June 2020 [13], depicted in Fig. 8b.

This last case is a clear example of the discontinuous evolution of the disease. In fact, the initial growth appears to occur in two successive exponential waves (marked by grey arrows in Fig. 8b) and the subsequent decay curve is interrupted by two apparently successive outbreaks (marked by white arrows in Fig. 8b). These data are also illustrative of the importance of a uniform counting of patients. In cases where $I_D(t)$ show low dispersion, as is the case in Fig. 8b, the detection of outbreaks can be made in 3–5 days, but obviously, an early detection is much more difficult if large data dispersion masks the outbreak.
2.4. Discussion

The simplified treatment described here permits a rapid comparison of the data from different countries. This is particularly relevant because the strategies adopted against the disease are country-sensitive. However, two previous questions should be faced: (i) are the abrupt changes in the \( I_D(t) \) vs. time curves ‘true’ regime changes or merely mathematical artefacts of a continuous variation of the disease parameters?, and (ii) have the different steps any significance in relation to the mode of propagation of the disease?

The first question can be responded on comparing the data in Figs. 2, 3 and 5–8, where similar discontinuity features can be observed. In the logistic closure, these features can be interpreted as sharp transitions from one kinetic regime represented by Eq. (4), to one different, represented by Eq. (6), in line with the kinetic formulation of infective diseases [28]. For our purposes, the relevant point of emphasize is that the significant differences in the duration and ‘rate’ of the intermediate potential region, clearly suggest that the model of abrupt 2nd order phase changes cannot be considered as mathematical artefacts without physical (epidemiological) meaning. In this regard, a first aspect to note is that social systems evolving according to logistic curves can be modelled assuming that there are abrupt variations in the rate constant of the equation, thus introducing discontinuities, just breaking the fir tree-shaped form of the first derivative curve equivalent to our \( I_D(t) \) vs. \( t \) and \( D_D(t) \) vs. \( t \) ones [16,29].

The second aspect to underline is that, at least under several conditions, the logistic equations can also be interpreted in topological terms. In short, the idea is that the propagation of a disease has in common with the expansion of biological and social networks their step-by-step construction. Physical and social networks such as transportation systems can be described in terms of graph models involving a large number of nodes, links, etc. adopting a determined topological...
structure. For our purposes, the relevant points to emphasize are: (i) two basic types of topologies, small-worlds and fractals have been used to describe different networks [30–34]; (ii) there is a dichotomy between fractal and small-worlds topologies in real world networks [17]; (iii) under certain conditions, these topologies can be discriminated based on ‘gross’ parameters of the whole of geographic, biological, etc. systems [16].

As previously noted, the disease features can be 'geometrically' treated defining an infected patients/time space. Using this formalism, the exponential growing and decay regimes can be assigned to a small-worlds topology. The potential growth regime can be associated to fractal topology in this idealized space so that the intersections between the different regimes can be described as 2nd order phase changes in the idealized $I(t)/t$ space. Accordingly, the COVID-19 evolution can be formally (and equivalently) described in terms of logistic-type curves experiencing sharp disruptions [15] or as topological phase transitions [14] in the infected patients/time space.

In this context, the question to treat in the biomedical research is if the abrupt transitions observed in the COVID-19 pandemic event can reflect the changes in the topological mode of disease progression. This is in line with studies dealing with the application of statistical–mechanical analogies on the space propagation of diseases [35] and the small-worlds [36,37] and fractal [38] modelling of epidemic processes [20]. Under this view, the first step of exponential growth corresponds to a small-worlds type of close vicinity contact. The adoption of social separation protocols probably results in a change of the propagation mode, passing to a potential-type progression further passing to an exponential decay. These steps can in principle be approximated by Eqs. (2), (7), and (3), respectively, so that the $\alpha$, $g$, $\delta$, coefficients should be related to the connectivity or transmissibility of the disease. At the expense of the aforementioned biomedical research,
Fig. 8. \( I(t) \) vs. \( t \) graphs illustrating: (a) a simulated outbreak occurring in Spain as a sharp exponential growth (Eq. (2)) at the 60th day with an exponent of 0.030 days\(^{-1}\) for ten days followed by an exponential decay (Eq. (3)) at the Spanish exponent of −0.035 days\(^{-1}\), and (b) data for Iran, 23th June 2020 [12]. Grey squares: reported data; circles: theoretical infected patients. Grey arrows mark the initial one- or two-wave expansion of the disease and white arrows mark the outbreaks appearing in the decaying branch of the curves.

The data treatment described here can be seen as an analytical tool facilitating the evaluation of the progression of the disease, the effectiveness of the applied control measures, and the detection of outbreaks.

3. Conclusions

Analysis of available data on COVID-19 disease using daily infected patients and daily deaths for different countries suggests that there are more or less abrupt transitions in the time variation of these parameters. These transitions cannot be reconciled with a smooth logistic evolution of the pandemic disease characterized by a fir tree–shaped curve with a unique defined maximum without additional inflections. In contrast, COVID-19 data can in general be described in terms of an initial exponential growth followed by a potential one and subsequent one or more exponential decay steps separated by inflections or discontinuities.

This behaviour is formally equivalent to that observed in the rise and fall of historic transportation systems. This analogy suggests that the evolution of COVID-19 can be described on the basis of two formally equivalent interpretations: (i) as logistic curves displaying abrupt variations in the rate parameters, and (ii) in terms of topological phase transitions formally occurring in a infected patients/time space. The reported analysis permits to characterize significant differences in the evolution of the disease between different countries and detect, under favourable conditions, the appearance of outbreaks.

Obviously, there is a considerable effort of analysis to be made in order to elucidate the biomedical implications of these discontinuities. In spite of its simplicity, the current discontinuous approach can be viewed as a functional tool contributing to simplify this analysis.
CRediT authorship contribution statement

**Antonio Doménech-Carbó:** Conceptualization, Data processing, Writing. **Clara Doménech-Casasús:** Data processing, Writing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary material related to this article can be found online at https://doi.org/10.1016/j.physa.2021.125752.

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