A stretched logistic equation for pandemic spreading

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ABSTRACT

In this brief work we present a novel approach to the logistic dynamics of populations and epidemic spreading that can take into account of the complex nature of such a process in several real situations, where due to different agents the dynamics is no longer characterized by a single characteristic timescale, but conversely by a distribution of time scales, rendered via a time-dependent growth rate. In detail, a differential equation containing a power-law time dependent growth rate is proposed, whose solution, named *Stretched Logistic Function*, provides a modified version of the usual logistic function. The model equation is inspired by and applied to the recent spreading on COVID-19 disease in Italy, showing how the real dynamics of infection spreading is characterized by a time dependent dynamics. A speculative discussion of the Stretched Logistic Function in relation to diffusion processes is attempted.

1. Introduction

The pandemic outbreak of COVID-19, caused by the SARS-COV-2 virus, represents an epochal fact of our age, with all its consequences still unpredictable, in terms of social, economic and environmental effects. Studying the dynamics of its outbreak, with the hope to become able to make reliable predictions of its future evolution, has represented, and still represents, a powerful challenge for a huge interdisciplinary scientific community, ranging from Medicine to Social Sciences, from Epidemiology to Economy. That of Bio-Mathematics is a discipline of paramount importance in such a collective study, lavishing generously a fantastic mass of models mimicking the epidemic dynamics.

In this paper we propose a variant of the logistic dynamics/equation by considering *the dynamics of the total number of infected people* in the case of COVID-19 pandemic spreading in Italy. The aim of the study is to propose an ordinary differential equation (ODE) and its solution for the evolution of the total number of infected people N in the case of a time-dependent growth rate. The particular form of proposed ODE is then taken as a starting point for a future study, in which the microscopic dynamics of contagion will be investigated, in forthcoming publications.

The total number of infections N should solve an ODE coherent with the dynamical theory of the epidemic: it is of use to remind a class of "first principle" dynamical models of infection evolution, namely the *compartmental models* [1], with the typical subdivision of the whole population into S susceptible individuals, I infected ones, R recovered ones, and so on. The fundamental hypotheses on which such models are based are very simple, essentially a combination of rate equations with the *mass hypothesis*, according to which individuals of the different compartments may "interact" with all the units [2]. This gives rise to rather simple coupled ODEs, with at most quadratic non-linearities representing the encounter of susceptible and infected people, that gives rise to infection spreading [3].

If the "fundamental", space implicit, epidemic dynamics undergoes such a compartmental model, it is possible to show that the total number of infections N satisfies a *logistic ODE* [4–6], that is completely identical to that of a population growth according to Verhulst's theory [7]. Verhulst Equation, also referred to as *logistic equation*,

$$\frac{dN}{dt} = \hat{\rho} N \left(1 - \frac{N}{N_\infty} \right), \tag{1}$$

where $\hat{\rho}$ and N_∞ are assumed as constant. This ODE has been widely used and variously modified, in order to adapt it to the spreading of different diseases [8,9], included the COVID-19 case [10,11].

In [12] the logistic ODE is altered via powers of the N variable in the right hand side of (1), fitting the resulting solution with the COVID-19 outbreak data of China, Korea, Japan, Iran and Italy. In [13] this approach was discussed in terms of the topological properties of the distribution of infected persons, and of the "interpersonal contact network".

The original logistic Eq. (1) shows constant growth rate $\hat{\rho}$ and carrying capacity N_∞; in this study, the central result presented is that the growth rate of the logistic equation solved by the total number of infections depends on time as a decreasing power law:

$$\hat{\rho}(t) \propto \frac{1}{t^\beta} \ / \ \beta \in (0, 1). \tag{2}$$

This time-dependent growth-rate model is motivated by simple considerations on the time series $N(t)$ and $dN(t)/dt$ collected in Italy during the COVID-19 outbreak, and studying the evolution of the ratio

$$\hat{\rho}(t) \overset{\text{def}}{=} \frac{\frac{dN}{dt}(t)}{N(t)\left(1 - \frac{N(t)}{N_\infty}\right)} \tag{3}$$

against time.

Given the relationship (2), the problem is to explain this result from a "fundamental" point of view, i.e., from the point of view of the "microscopic picture" of contagion. The argument here is that the trend (2) may be justified in terms of the complexity of the underlying dynamical system: the latter results from the interplay of the inter-personal contact network, and the "external forcing" of the Government's lockdown measures. On the one hand, as power laws characterize many aspects of the topology of complex networks [14,15], one may expect that, suppressing the power-law distributed links of inter-personal relationships via lockdown measures, the "network diffusivity" of the spreading decreases with time as a power-law. On the other hand, a dynamical system theory justification of (2) is possible, interpreting the product $\hat{\rho}(t)N$ as the part of total infections able to spread the COVID-19 at time t, according to the probabilistic theory of systems with sticky domains in their phase space [16].

The paper is organized as follows.

In Section 2 the data set studied is presented, and a preanalysis of it is described: this pre-analysis is necessary to render experimentally sensible the data set, that depends strongly on the day-to-day variability of the population examined (different daily number of swabs). This variability is accurately removed, in order to work on more reliable time series. In this Section, the plot of (3) against time is presented, with the key result (2).

Section 3 is devoted to the presentation of the *stretched Logistic function*, i.e. the time behaviour best-fitting the time series of the total number of infected people, and the ODE satisfied by it, with time-varying growth rate. It is also shown how the best-fitting curve, analytically determined, satisfies an ODE involving a conformable fractional derivative.

Section 4 presents the proper analysis of the fit of the stretched logistic curve to the data, in which the excellent agreement is highlighted, and the artifacts of non-constant sampled population are indicated as a week-periodic component.

Last Section 5 is dedicated to the theoretical discussion about the possible justifications of the behaviour (2), while some future numerical analysis investigations, deepening the present study, are sketched.

2. Dataset and pre-analysis

The model proposed in this work is motivated by some consideration on the spreading of the COVID-19 pandemic in Italy. In detail, we start by considering the time series of the *total number of infected people*, from the daily numbers provided by *Dipartimento della Protezione Civile* (available on web for the period) from February 27, 2020 to June 3, 2020. We also considered the time series of the daily numbers of new infected people, $n(t)$, and of medical swabs, $s(t)$. Thus, the time series of the total number of infected people, $N(t)$, registered officially from the beginning of the
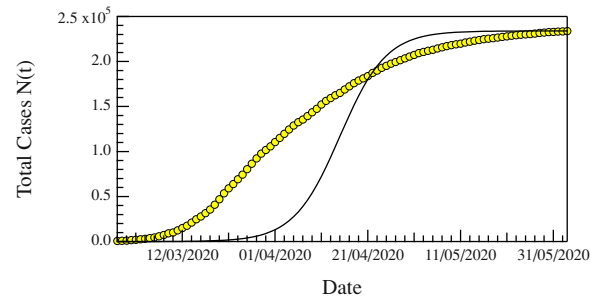

Fig. 1. The trend of the total number of infected people, $N(t)$, for the COVID-19 pandemic in Italy. The solid line is a best-fit using the logistic function [see Eq. (5)].

epidemic, is calculated as:

$$N(t) = \int_0^t dt' n(t'). \tag{4}$$

Fig. 1 reports the trend in time of the total amount of infected people, $N(t)$, in comparison with the expected trend according to the standard logistic function, i.e.,

$$N(t) = \frac{N_\infty}{1 + \left(\frac{N_\infty}{N_0} - 1\right)e^{-\rho t}}, \tag{5}$$

where $N_0 = N(0)$ is the initial value, N_∞ is the maximum value for $t \to \infty$, and ρ is the constant infection rate (the growth rate of the logistic ODE, satisfied by (5)).

The agreement between the actual trend and the logistic function is extremely poor, suggesting that the observed behavior does not follow the prediction of Verhulst's dynamics [7]. The observed trend seems to be a stretched version of the Logistic one.

Figs. 2 and 3 show the actual trend of the daily number of infected people, $n(t)$, and the corresponding daily number of medical swabs, $s(t)$. Apart from the average trend, we can observe a quasi-periodic oscillation both in $n(t)$ and $s(t)$ with a characteristic timescale of about 7 days. This is evident by applying an Empirical Mode Decomposition method [17,18] to both the time series but, in particular to the time series of the daily medical swabs, which clearly evidences how the short timescales are characterized by a periodicity of 7 days (see the inset of Fig. 3). A detailed discussion of this analysis is provided in the Appendix A. We remark that in the case of the daily medical swabs the ratio between the long term variability and the weekly one (as measured by the standard deviation of the fluctuating part) is approx 16%, i.e., a significant percentage. The emergence of a long-time trend and a characteristic timescale in the daily number of medical swabs suggests that some possible spurious effects could be contained in the signal of
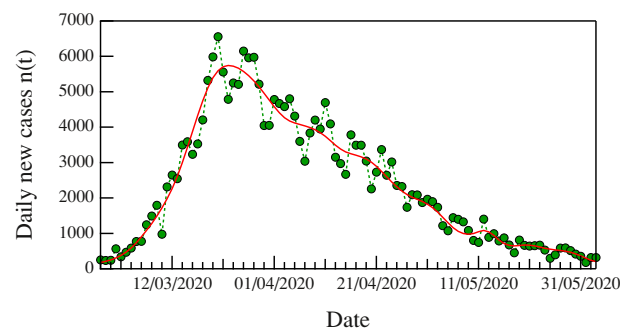

Fig. 2. The trend of the daily number of infected people, $n(t)$, for the COVID-19 pandemic in Italy. The solid line is the average trend, obtained by applying the EMD method (see Appendix A) and considering the IMFs whose characteristic timescale is longer than 1 week.
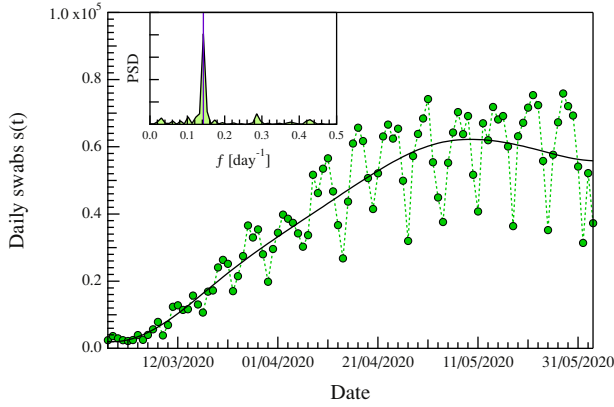
Fig. 3. The number of daily medical swabs, $s(t)$, as a function of time. The solid line is the average trend obtained by the EMD method (see Appendix A). The inset shows the PSD of the fluctuating part of the signal (i.e., the sum of the IMFs). A clear periodicity of 7 days (the vertical bar) is observed.

the daily number of infected people, and consequently in the time series of the total number of infected people, $N(t)$.

The behaviour of the daily medical swabs suggests that the time series of the total number of infected people could be not a reliable quantity to investigate the pandemic spreading in time. Indeed, the daily number of infected people, $n(t)$, is conditioned to the number of daily medical swabs, $s(t)$, i.e., $n(t) = n(t|s)$ where s is itself a function of time. In other words, the actual situation of monitoring pandemic spreading in time is different from what is generally done in a controlled laboratory experiment where the check is done over a quasi-constant number of individuals.

One possible way to overcome this problem it to consider a different time series, the time series of the daily infected people normalized to the number of daily medical swabs, i.e.,

$$n^*(t) = 100\frac{n(t)}{s(t)}, \tag{6}$$

and successively using this time series to define the corresponding *normalized total number of infected people, $N^*(t)$*, defined as

$$N^*(t) = \int_{t_0}^{t} n^*(t')dt'. \tag{7}$$

This new time series is thus no longer dependent on the number of daily medical swabs, being not-affected by spurious effects as the weekly modulation present in the time series of the daily medical swabs, $s(t)$, shown in Fig. 3. Indeed, $n^*(t) \equiv n(t|100)$, i.e., it is conditioned to a fixed number of medical swabs per day (taken as reference equal to 100), so that it refers to a similar condition experiment removing the high variability and periodic modulation of the medical swabs per day.

Fig. 4 shows the trend of the *normalized total number of infected people, $N^*(t)$*, in comparison with a logistic function. Again the agreement is very poor. The different trend of actual data in comparison with logistic behavior suggests that the rate ρ of pandemic spreading may acquire a dependence on time. Thus, to unveil if this is the case and what could be the functional form of the dependence on time of the rate ρ, we can try to evaluate it using the logistic equation,

$$\dot{N}(t) = \rho N(t)\left(1 - \frac{N(t)}{N_\infty}\right), \tag{8}$$

and defining a time-dependent rate $\rho(t)$ according to the following relation,

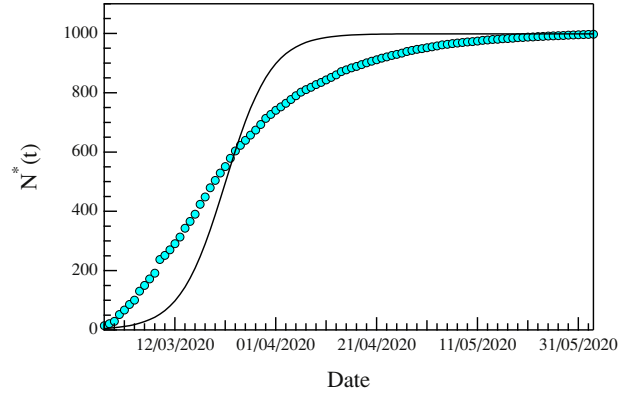$$\rho(t) = N_\infty \frac{\dot{N}(t)}{N(t)(N_\infty - N(t))}. \tag{9}$$

Fig. 4. The normalized total number of infected people, $N^*(t)$, as a function of time. The solid line is the expected trend using a Logistic function.

Fig. 5 shows the time dependence of the rate $\rho(t)$ as a function of time. To evaluate the quantity N_∞ we used the asymptotic value of $N^*(t)$, obtained by extrapolation from Fig. 4. The rate $\rho(t)$ shows a clear dependence on time and the functional form of this dependence seems to be a power-law, i.e.,

$$\rho(t) = \rho_0 t^{-\beta}, \tag{10}$$

where the exponent β is between 0 and 1.

On the basis of the above pre-analysis we may conjecture that the time dependence of $N^*(t)$ seems to be that of a logistic equation with a power-law time dependent rate. We will call this as *Stretched Logistic Equation* (SLE) and in the following Section 3 we will discuss the model emerging from this equation.

3. The stretched logistic model

The time dependence of the rate of pandemic spreading reported in Fig. 5 suggests that a more appropriate model for the evolution of the pandemic in Italy would be that of a Logistic equation where the contagion rate follows a power-law as those reported in Eq. (10). Thus, a best suitable modeling for the observed spreading of the pandemic contagion could be given by the following ODE:

$$\dot{N}^* = \hat{\rho}(t)\left(1 - \frac{N^*}{N_\infty}\right) \tag{11}$$

where the time dependent rate $\hat{\rho}(t)$ can be written

$$\hat{\rho}(t) = \frac{(1-\beta)\rho}{t^\beta} \tag{12}$$

being thus $\rho_0 = (1-\beta)\rho$. In conclusion, the ODE we claim to describe the pandemic spreading observed takes the form

$$\dot{N}^*(t) = \frac{(1-\beta)\rho}{t^\beta}\left(1 - \frac{N^*(t)}{N_\infty}\right). \tag{13}$$

In Eq. (13) the splitting $\rho_0 = (1-\beta)\rho$ is done in view of how the ODE will be solved: this integration may proceed rather easily via separation of variables (see Appendix B). The solution of Eq. (13) can be written as

$$N^*(t) = \frac{N_\infty}{1 + \left(\frac{N_\infty}{N_0} - 1\right)e^{-\rho t^{(1-\beta)}}}, \quad \beta \in (0,1), \tag{14}$$

where $N_0 = N^*(0)$. This equation defines a stretched expression of the classical logistic function, and thus we named is as *Stretched Logistic Function*.

It is possible to write the Eq. (11) using a different type of time-derivative, *the conformable fractional derivative* (CFD), introduced by
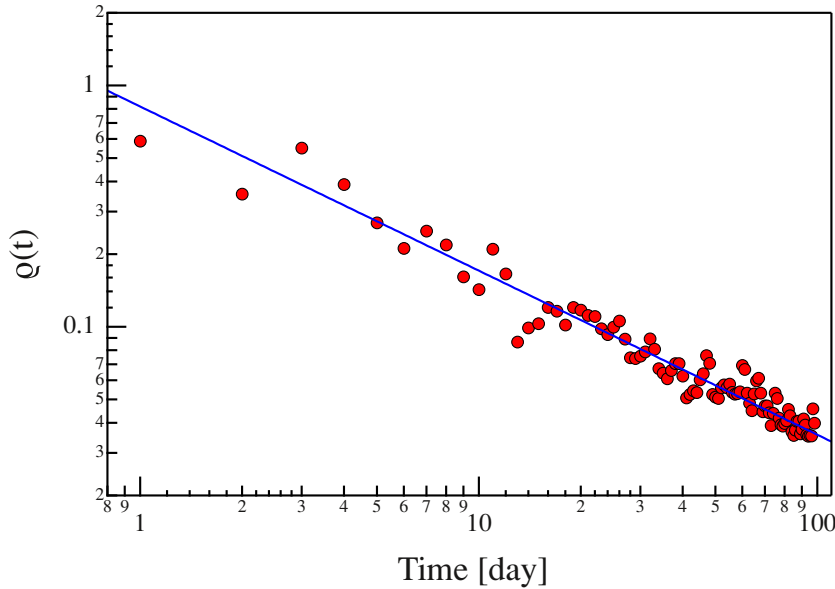
Fig. 5. The time dependence of the rate, $\rho(t)$, as obtained using Eq. (9). The solid line is a power-law characterized by an exponent $\beta = [0.67 \pm 0.04]$.

Khalil et al. [19] and defined as

$$T_\beta(\varphi)(t) \overset{def}{=} \lim_{\epsilon \to 0} \frac{\varphi(t + \epsilon t^\beta) - \varphi(t)}{\epsilon}, \quad \beta \in (0, 1], \ t \geq 0. \tag{15}$$

This CFD is a good tool to "reabsorb" the time dependence of $\hat\rho$ in Eq. (13): indeed, considering the definition (15), the authors of Ref[19]. show that, provided φ is differentiable, and its CFD exists, the latter is related to the first derivative of φ as

$$\exists \frac{d\varphi}{dt}(t), T_\beta(\varphi)(t) \ \Rightarrow \ T_\beta(\varphi)(t) = t^\beta \frac{d\varphi}{dt}(t). \tag{16}$$

This means that any differentiable function N satisfying (13) can be also stated to satisfy:

$$T_\beta N = (1 - \beta)\rho N\left(1 - \frac{N}{N_\infty}\right), \tag{17}$$

being T_β the linear operator defined in Eq. (15). Now, one may say that, within the interval $\mathcal{I} = (0, +\infty)$, the function $N^*(t)$ satisfies precisely the CFD Eq. (17), as it is differentiable in $\mathcal{I}$ and its first derivative satisfies, at each $t \in \mathcal{I}$, the ODE of Eq. (13).

About the CFD definition in Eq. (15) and its property in Eq. (16) on differentiable functions, some debate in the literature must be reported: the CFD is an operation presenting much more affinities with the ordinary first derivative than the other definitions of fractional derivatives, as the operator D_t^α defined in Ref. [20]: for instance, in [21] the CFD is proved to have all the "classical properties" that the integer order calculus attributes to differentiation. However, according to what proven in [22], the definition Eq. (15) introduces an operator that is basically a first order derivative with a local coefficients, because it shows, for instance, the Leibniz property [23]: no true difference exists between stating that N^* is a solution of the proper ODE of Eq. (13), and its CFD counterpart of Eq. (17), because all in all the operation T_β is a local linear differential operator, not adding, for instance, any "memory effect" to the dynamics of the phenomenon studied, as the "traditional" fractional differential operator D_t^α quoted before.

Although the approach in terms of CFD is analogous to the previous standard ODE with time-dependent parameters, it can better describe the temporal locality of the contagion spreading rate, providing a different framework to interpret the obtained results.

4. Analysis and results

We, now, move to the comparison between the SLF model and the actual data for the pandemic spreading of COVID-19 in Italy, as described using the normalized total number of infected people, $N^*(t)$.

Fig. 6 reports the nonlinear best fit of the normalized total number of infected people, $N^*(t)$, using the SLF of Eq. (14) in comparison with the standard logistic behavior. We also plot in the inset the deviation from the expected SLF, defined as $\Delta N^*(t) = N^*(t) - \tilde{N}^*(t)$, where $\tilde{N}^*(t)$ is the result of the fit. The agreement is excellent, supporting that a SLF can describe very well the behavior of the spreading of the COVID-19 in Italy. Furthermore, we get a value for the β exponent of the SLF $\beta = [0.63 \pm 0.03]$. This value is consistent with the exponent of the power-law of the time dependent rate $\hat\rho(t)$ reported in Fig. 5.

To better evaluate the agreement between the actual data of $N^*(t)$ and the proposed SLF model we perform a *Chi-squared test*. The test returns a value of $\chi^2 \sim 13$ against a critical value $\chi_c^2 \sim 120$ for a confidence limit of $\alpha_\chi = 0.05$, thus, confirming the validity of the fit. Indeed, we are 95% confident that data support our model.

As a final check of the agreement between the proposed model for COVID-19 spreading and actual data, we have plotted
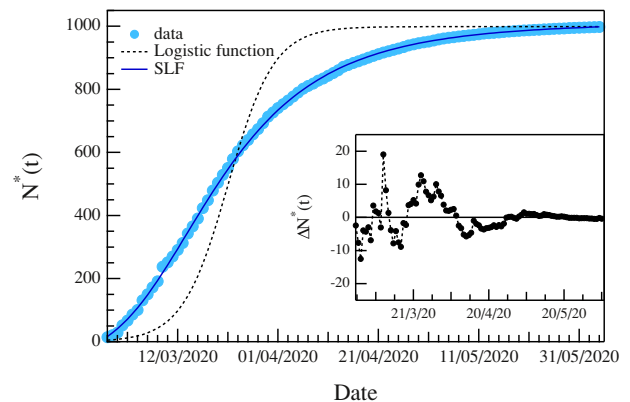

Fig. 6. The nonlinear best fit of the normalized total number of infected people, $N^*(t)$, using the SLF of Eq. (14). Dashed line is the logistic behavior reported in Fig. 4. The inset shows the deviation, $\Delta N^*(t)$, of actual data from SLF.
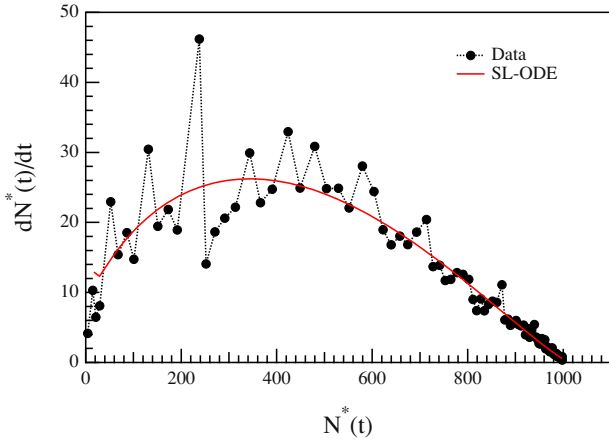
Fig. 7. Comparison between the daily dependence of $\dot{N}^*(t)$ on $N^*(t)$ and the expected one based on Eq. (13).

in Fig. 7 the comparison between the daily dependence of $\dot{N}^*(t) = dN^*(t)/dt$ on $N^*(t)$ and the expected one based on Eq. (13). The agreement in terms of mean trend is good, although large fluctuation are observed in the first period. In particular, the large fluctuation observed around $N^* \sim 220$ is due to a problem in the correct assignment of the daily value of new infected people, as reported by the official data of the *Dipartimento della Protezione Civile*.

Within the limits of our statistical analysis, according to which the SLF is the best fit of the normalized total amount of infected people dependence on time $N^*(t)$, the ODE of Eq. (13) describes correctly the dynamics of COVID-19 infection in Italy, once we have corrected the spurious effects due to the high daily variability of the number of medical swabs. We will now try to give an interpretation to this result in terms of inter-personal relationship network and Governmental measure effects.

5. Discussion and conclusions

Let us now discuss a possible interpretation of the results presented in the previous Section. The main result of our study is to have found that, when appropriately normalized, the number of total infected people $N^*(t)$ in Italy has undergone a modified logistic equation, *the Stretched Logistic Equation*, that is characterized by a time-dependent growth rate, which follows a power-law on time. This SLF can be also found as the solution of an equation involving a CFD, according to which the power-law dependence of the rate is the consequence of a local dependence on time of the derivative operator. Furthermore, the comparison between the model and the data is exceptionally excellent, supporting all the previous theoretical scenario.

Once the experimental curve $N^*(t)$ is shown to follow the dynamics in Eq. (13), one would like to give some explanation of "why" the time-dependence of the $\hat{\rho}(t)$ growth rate should be that in Eq. (12) or, put otherwise, guess what that expression suggests in terms of contagion dynamics.

Eq. (13) may be regarded as the balance, or competition, between two terms, a growth term $\left(\frac{dN}{dt}\right)_{\text{growth}}$ and a limiting term $\left(\frac{dN}{dt}\right)_{\text{lim}}$, such that:

$$\begin{cases} \dfrac{dN}{dt} = \left(\dfrac{dN}{dt}\right)_{\text{growth}} + \left(\dfrac{dN}{dt}\right)_{\text{lim}}, \\[2mm] \left(\dfrac{dN}{dt}\right)_{\text{growth}} = \dfrac{(1-\beta)r}{t^\beta}N, \\[2mm] \left(\dfrac{dN}{dt}\right)_{\text{lim}} = -\left(\dfrac{dN}{dt}\right)_{\text{growth}}\dfrac{N}{N_\infty}, \\[2mm] \beta \in (0,1). \end{cases} \tag{18}$$

The mathematical form of the accretion term may be interpreted in two ways, that should be proven to be equivalent in a future study of the microscopic mechanism of the COVID-19 spreading.

A first interpretation is that the N individuals infected-so-far at time t are all contributing to spreading the contagion, according to the *time dependent rate* $\hat{\rho}(t) = \frac{(1-\beta)\rho}{t^\beta}$, so that

$$\left(\frac{dN}{dt}\right)_{\text{growth}} = \frac{(1-\beta)\rho}{t^\beta} \cdot N. \tag{19}$$

This first interpretation, that is the simplest one, states that the contagion rate *pro capite* decreases with time as a negative power law $\mathbb{O}\left(t^{-\beta}\right)$, with $\beta \in (0,1)$. This rate decrease could be attributed to the efficiency of the lockdown measures taken by the Government, that are equivalent to a random suppression of inter-personal links in the network of social relationships and, hence, contagion events. This is a network theoretical interpretation, and points towards future studies of numerical experiments on networks.

The other explanation we suggest is that the form of $\left(\frac{dN}{dt}\right)_{\text{growth}}$ is just the product between the *constant rate* ρ and a *time decreasing portion* N_{act} of the infected-so-far population N, that is "active in spreading" the epidemic:

$$\left(\frac{dN}{dt}\right)_{\text{growth}} = \rho N_{\text{act}}, \quad \frac{N_{\text{act}}}{N} = \frac{1-\beta}{t^\beta}. \tag{20}$$

This interpretation argues about a shrink with time of the percent of infected people acting as spreaders, of course again as $\mathbb{O}\left(t^{-\beta}\right)$.

In order to explain such alternative interpretation, one may turn to the theory of *subdiffusive regime* of chaotic systems, as explained in [16]. Complex dynamical systems may be characterized by "sticky domains" in their phase space Γ, i.e. finite regions $\mathbb{B} \subset \Gamma$ within which the trajectory may remain for a certain *waiting time* Δt, and then suddenly exit. These waiting times are not uniquely determined for each domain $\mathbb{B}$, but may vary from trajectory to trajectory: in general, it is sensible to treat this exit process probabilistically, and it is possible to see that the probability that a trajectory leaves a domain $\mathbb{B}$ after a time Δt reads [24]:

$$p_{\mathbb{B}}(\Delta t) = \frac{A(\mathbb{B})}{(\Delta t)^{1+\beta(\mathbb{B})}}, \quad \beta(\mathbb{B}) \in (0,1), \quad \forall \mathbb{B}. \tag{21}$$

In Eq. (21) the scripts $A(\mathbb{B})$ and $\beta(\mathbb{B})$ mean that those numbers are domain-dependent.

It is possible to argue that the portion $\Pi_{\mathbb{B}}(t)$ of trajectories that have left $\mathbb{B}$ at a certain time t is given by the sum of all trajectories entering $\mathbb{B}$ at times $\tau \leq t$, each in the corresponding portion $p_{\mathbb{B}}(\Delta t) \equiv p_{\mathbb{B}}(t-\tau)$; so, according to Eq. (21), the total portion $\Pi_{\mathbb{B}}(t)$ reads:

$$\Pi_{\mathbb{B}}(t) = \int_{-\infty}^{t} p_{\mathbb{B}}(t-\tau)d\tau = \int_{-\infty}^{t} \frac{A(\mathbb{B})d\tau}{(t-\tau)^{1+\beta(\mathbb{B})}} = \frac{A(\mathbb{B})}{\beta(\mathbb{B})t^{\beta(\mathbb{B})}}. \tag{22}$$

The functional form $\Pi_{\mathbb{B}}(t) = \frac{A(\mathbb{B})}{\beta(\mathbb{B})t^{\beta(\mathbb{B})}}$, with $\beta(\mathbb{B}) \in (0,1)$, is precisely the same as the ratio $\frac{N_{\text{act}}}{N}$ in Eq. (20).

Now, we argue that, out of the total N people infected-so-far, at time t the fraction N_{act} spreading the COVID-19 amounts to

$$N_{\text{act}}(t) = \Pi_{\mathbb{B}_0}(t)N = \frac{A}{\beta t^\beta} \cdot N,$$

i.e., they are as many as those trajectories leaving *some suitable sticky domain* $\mathbb{B}_0$ of *some suitable complex system* describing the microscopic contagion dynamics. This would correspond to the fact that an exposed person, after incubating the illness and undergoing the lockdown, starts infecting other people with the same

tempo of the trajectory of a complex system leaving a sticky domain. We may imagine as some domain $\mathbb{B}_0$ the condition of *locked down, isolated infective people*: the portion of them who has left this condition at time t is calculated taking inspiration from Eq. (22) to write:

$$N_{\text{act}}(t) = \frac{\nu}{t^{\beta}} N, \quad \beta \in (0, 1). \tag{23}$$

The factor ν is some dimensionalization factor, with $[\nu] = t^{\beta}$ in order for Eq. (23) to be correct. Assuming that only N_{act} units take part to further spreading the contagion, and that the contagiousness of each of them is given by the basic rate ρ_0, so that $[\rho_0] = t^{-1}$, one may re-write Eq. (18) as:

$$\frac{dN}{dt} \stackrel{Eq.(23)}{=} \frac{\rho_0 \nu}{t^{\beta}} N \left(1 - \frac{N}{K}\right). \tag{24}$$

This is a time explicit ODE of the same form of Eq. (13), once the identification

$$\rho = \frac{\nu}{1 - \beta} \rho_0. \tag{25}$$

is done.

In conclusion, we have proposed a very simple upgrading of the logistic dynamics for a pandemic spreading (as the COVID-19 disease in Italy) which takes into account a power-law dependence on time of the infection growth-rate. This dependence can be the effect of at least two different mechanisms: a simple reduction of the inter-personal links, and/or the effect of isolation of infected people. Moreover, it is not excluded that the time-local dependence of the infection rate on t may represent an approximation of more complicated, non-time-local expressions, possibly leading to integro-differential equations [25].

Clearly, our results call for further analysis on both theoretical and numerical sides, not to mention the need to try the same analysis on the COVID-19 spreading in other Countries.

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.

Acknowledgements

Appendix A. Empirical Mode Decomposition of medical swabs

The Empirical Mode Decomposition (EMD), introduced by Huang et al. [17], is a fully data-adaptive analysis method capable of decomposing nonstationary and/or nonlinear signals into a finite set of oscillatory components, the *Intrinsic Mode Functions* (IMFs), without any *a priori* assumption, so to reduce mathematical hypotheses and artifacts. The EMD method, originally developed as a preconditioning for Hilbert transform, has become widely used to investigate signals coming from complex systems and nonstationary dynamics, being applied in several different frameworks, from space physics to geophysics [26–28], and so on.

The IMFs, into which a signal is decomposed via EMD, are oscillatory modes obtained via an iterative approach, named *sifting process* [17,18], and characterized by two main features:

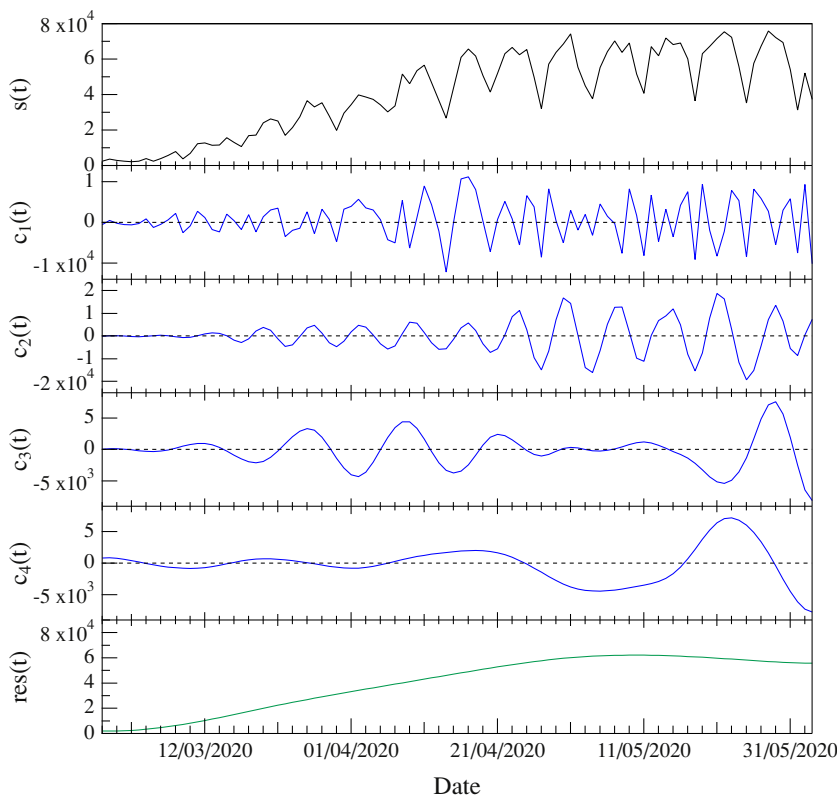- IMFs have an equal number of zero crossings and local extrema (or they differ at most by one);

Fig. A1. EMD of the daily medical swabs time series, $s(t)$. From top to bottom: the actual time series $s(t)$, the IMFs $c_k(t)$ with $k = 1, 2, .., 4$ and the residue $res(t)$. We may state that this $res(t)$ quantifies the policy to increase the number of swabs taken.

Table A1
Average periodicities and variances of the IMFs of daily medical swabs times series.

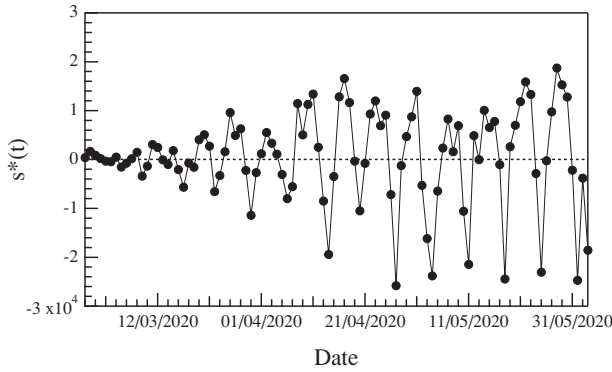| k	$\langle T_k \rangle$ (day)	σ_k^2
1	3.5 ± 1.0	2.5×10^7
2	7.0 ± 0.4	5.4×10^7
3	13 ± 2	0.7×10^7
4	28 ± 6	0.8×10^7

Fig. A2. EMD of the daily medical swabs time series, $s(t)$. From top to bottom: the actual time series $s(t)$, the IMFs $c_k(t)$ with $k = 1, 2, .., 4$ and the residue $res(t)$.

- the local average of the local maxima envelope must be equal to the absolute average value of the local minima one.

As a result of the EMD a signal $x(t)$ can be written as

$$x(t) = \sum_{k=1}^{n} c_k(t) + res(t), \tag{A.1}$$

where $c_k(t)$ are the IMFs and $res(t)$ is a monotonic function which represents the final residue of the decomposition. In other words, the method is a data-adaptive filter bank [29,30].

In our analysis we have applied EMD method to identify oscillatory modes in the medical swabs time series $s(t)$ in order to remove the long term trend before applying usual Fourier analysis.

Fig. A.1 shows the IMFs of $s(t)$ time series obtained by applying the EMD. The $s(t)$ time series has been decomposed into 4 IMFs $c_k(t)$, plus a residue $res(t)$. Each IMF is characterized by a characteristic mean oscillatory periodicity that can be evaluated by measuring the average time distance between two successive maxima and/or minima. To each of these oscillatory modes we can also assign a sort of energy by computing the corresponding variance σ_k^2.

Table A.1 reports the average periodicities $\langle T_k \rangle$ and the corresponding variances σ_k^2. A clear periodicity of ~ 7 days is present along with its harmonics and sub-harmonics confirming the emergence of this modulation in the medical checks.

Fig. A.2 reports the detrended time series $s^*(t)$ of the daily medical swabs used to compute the Power Spectral Density (PSD) reported in the inset of Fig. 3. The 7-day modulation of medical swabs is very evident especially from April 1, on.

Appendix B. Solution of the Stretched Logistic ODE

In this Appendix we report the solution of the stretched logistic ODE (13).

Let us write Eq. (13) in the following form,

$$\frac{dN}{N\left(1 - \frac{N}{N_\infty}\right)} = (1 - \beta)\rho t^{-\beta} dt, \tag{B.1}$$

and integrate it,

$$\int_{N_0}^{N(t)} \frac{d\nu}{\nu\left(1 - \frac{\nu}{N_\infty}\right)} = (1 - \beta)\rho \int_0^t \tau^{-\beta} d\tau. \tag{B.2}$$

The integral on left-hand side can be written also in the form,

$$\int_{N_0}^{N(t)} \frac{d\nu}{\nu\left(1 - \frac{\nu}{N_\infty}\right)} = \int_{N_0}^{N(t)} \left[\frac{A}{\nu} - \frac{B}{\nu\left(\frac{\nu}{N_\infty} - 1\right)} \right] d\nu \tag{B.3}$$

where the quantities A and B have to be computed by solving the identity

$$\frac{A}{\nu} - \frac{B}{\nu\left(\frac{\nu}{N_\infty} - 1\right)} = \frac{1}{\nu\left(1 - \frac{\nu}{N_\infty}\right)} \quad \forall \nu. \tag{B.4}$$

This identity returns

$$A = 1 \quad B = \frac{1}{N_\infty}. \tag{B.5}$$

Thus, by solving the integration of Eq. (B.2) after having applied the separation given in Eq. (B.3) one gets,

$$\ln\left(\frac{N(t)}{N_0}\right) - \ln\left(\frac{N(t) - N_\infty}{N_0 - N_\infty}\right) = \rho t^{1-\beta}, \tag{B.6}$$

that with simple algebraic manipulations returns

$$N(t) = \frac{N_\infty}{1 + \left(\frac{N_\infty}{N_0} - 1\right)e^{-\rho t^{1-\beta}}}. \tag{B.7}$$

This is exactly the expression given in Eq. (14). □

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