



Power-law growth of the COVID-19 fatality incidents in Europe

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ABSTRACT

We report on the dynamic scaling of the diffusion growth phase of the COVID-19 epidemic in Europe. During this initial diffusion stage, the European countries implemented unprecedented mitigation policies to delay and suppress the disease contagion, although not in a uniform way or timing. Despite this diversity, we find that the reported fatality cases grow following a power law in all European countries we studied. The difference among countries is the value of the power-law exponent $3.5 < \alpha < 8.0$. This common attribute can prove a practical diagnostic tool, allowing reasonable predictions for the growth rate from very early data at a country level. We propose a model for the disease-causing interactions, based on a mechanism of human decisions and risk taking in interpersonal associations. The model describes the observed statistical distribution and contributes to the discussion on basic assumptions for homogeneous mixing or for a network perspective in epidemiological studies of COVID-19.

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1. Introduction

The combination of a long incubation period of a disease and the absence of effective pharmaceutical prevention treatment may result in fast population infection. This is the case of COVID-19, which became a pandemic that weighted on the national health systems worldwide. The transmission dynamics of coronavirus variants are subject of continuous investigation (Lauer et al., 2020; Wang et al., 2020). Under these circumstances, statistical analysis may serve to evaluate measures aiming to delay or reduce the contagion and guide the related state policies (Peng et al., 2020). Mathematical modeling may also play a role in deciding which measures curb the spreading, by providing simulations of the diffusion process and forecasting its inflection point and ending time (Roda et al., 2020; Li, Yang, Dang, Meng et al., 2020; Roosa, Lee, Luo et al., 2020; Ebrahim and Memish, 2020; Chatterjee, Chatterjee, Kumar, & Shankar, 2020; Lin et al., 2020; Wu et al., 2020). In this framework, our work contributes with statistical analysis and a new model for the growth epidemic phase that is based on interpersonal social associations and deviates from the homogeneous mixing model approach.

The proliferation of state measures poses difficulties on modeling. Certain measures that were applied to delay the contagion are of proven efficacy, like the isolation of infection cases and contact tracking (Hellewell et al., 2020). In addition, in

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order to suppress the propagation, the European countries proceeded by restricting mass gatherings and implementing partial lockdown measures. Greece is one of the countries that acted immediately. Schools were closed before any fatality incident was recorded in the country. Within twelve days that followed, most businesses and markets also closed and a mandated quarantine at home was reinforced. Other countries like the United Kingdom did not take such measures immediately, letting the disease spread among less vulnerable people like the younger individuals, hoping for a gradual herd immunization of the whole population (Kwok et al., 2020). Most European countries preferred to be in the middle of the two extremes, applying a lockdown when the COVID-19 cases had risen substantially. It remains an open question how these diverse policies are reflected on the sigmoid curve of the disease diffusion, in each country.

Our work addresses this issue and finds that, despite the diversity, there exist common features in the statistical distribution of the growth phase, among all countries. In particular, we demonstrate the following: *i*) The fatality cases increase following a power law at a national level. The difference between countries is in the value of the exponent, in the range $3.5 < \alpha < 8.0$. To the best of our knowledge, such feature has not been pointed out in the literature. *ii*) The power law dynamics persist over several orders of magnitude in fatality cases, i.e., from a few incidents to thousands. Over this range, an exponential increase cannot provide a reasonable fit for the growth data. *iii*) Systematic deviations appear 15–20 days after the implementation of the mandatory lockdown in the country. *iv*) We propose a model that provides a robust approximation of the observed statistical behavior, which considers the dynamics of the social face-to-face contacts that perpetuate contagion.

2. Data analysis

There are several parameters of the disease diffusion that one may examine, such as the daily increase of the confirmed cases, the daily active cases or the fatalities. Some of them, however, are measured using very different recording protocols across Europe, which is hard to interpret at today's early stage of the pandemic. Especially the cases of infected people are grossly underreported in certain countries (Roda et al., 2020). Due to lack of extensive testing across the population, the reported cases may not include people who have no symptoms or contacts with a medical unit. Therefore, we primarily focus on the statistics of the fatality cases, which are more reliable. In this work we analyze Worldometer's COVID-19 data till April 8, 2020, that are available online (Worldometer, 2020).

Based on current estimates, COVID-19 follows a course of ~14 days from the first symptom to death (Wang et al., 2020), with an infection-fatality ratio IFR that varies in different countries 0.3–1% (WHO, 2020) and is estimated from meta-analysis of research data at 0.68% (Meyerowitz-Katz and Merone, 2020). This means that, at the time fatality cases appear, the penetration of the infection is already substantial. Tracking the contacts of infected people eventually reveals cases from an unknown source of contagion. The spread of the infection therefore starts from uncertain routes, and the beginning of the contagion is difficult to pinpoint. For practical purposes, in this work we estimate the “first day” ($t = 0$) of the contagion from the fatality records. Without loss of generality, we assume that the contagion in each country started $t_0 = 14$ days before three fatal cases ($n = 3$) be recorded. We will show below that this assumption is consistent with observed data (in Fig. 3). In any case, a different assumption that alters t_0 by a few days would not change qualitatively the main results of this work.

Fig. 1 displays various ways to present the fatality cases for the case of Spain, one of the first hard hit countries in Europe. In particular, we show the cumulative number $n(t)$ as a function of time t in a linear, semi-log and double-logarithmic plot. The vertical dashed line passes through $n = 3$, which occurred in March 5. It is clear that the best fit for the growth of the fatality data is provided by a straight line in the double-logarithmic plot, suggesting $n(t) \propto (t - t_0)^\alpha$, with exponent $\alpha = 7.7 \pm 0.2$ in the case of Spain.

A deviation from the straight line in Fig. 1c appears at large values of n at $t > 40$, indicating the time that the fatality rate slows down. However, on March 13 (or $t = 22$), the Spanish authorities had imposed a lockdown to restrain face-to-face social contacts (Mitjà et al., 2020). The intervening period is in reasonable agreement with the 14-day cycle of COVID-19, and provides strong evidence that this policy is the cause of the fatality rate decrease. In general, we expect changes in the management of the epidemic to have an effect on fatal incidents with a 14-day delay. On the other hand, changes in the medical treatment of the disease have the potential to be almost immediately effective.

In Fig. 2 we show the data from several European countries with a large number of fatality cases. We observe that the dominant behavior above $n > 3$ can be described by a power-law increase of the cumulative fatality cases. In most countries, the exponent is in the range $6.5 < \alpha < 7.0$. The highest value of α we find for Spain $\alpha = 7.7$ (in Fig. 1) and the lowest for Greece $\alpha = 3.6$. The absolute value of α is relatively sensitive to the definition of the axis origin t_0 but the trend among countries and the existence of the power law growth are fairly robust. A systematic deviation from power law at large values of $n(t)$ is evident only in the case of Italy, at $t > 45$. Similar to Spain, such deviation appeared 15–20 days after the government imposed (on March 9) a nationwide lockdown. In fact, Italy and Spain were the first countries in Europe to implement a nationwide mandatory lockdown. This suggests that the power law in the data range in Figs. 1 and 2 corresponds to people infected *before* the enforcement of general restrictions on personal activities and direct contacts.

Finally, we juxtapose the observed statistics of the fatality incidents to those of the reported COVID-19 infected cases, for the same period (Worldometer, 2020). Although the recording practices of infected individuals vary across Europe, there are certain semi-quantitative results about the power law diffusion that can be deduced.

In Fig. 3, the double logarithmic plot shows the confirmed case data $N_c(t)$ that are shifted parallel to the x-axis, so that the onset of both the recorded cases and the removed individuals occur approximately at the same x-axis intercept. The horizontal shift Δ depends on the testing practices in each country: The time $t_0 - \Delta$ corresponds to the average tracking period

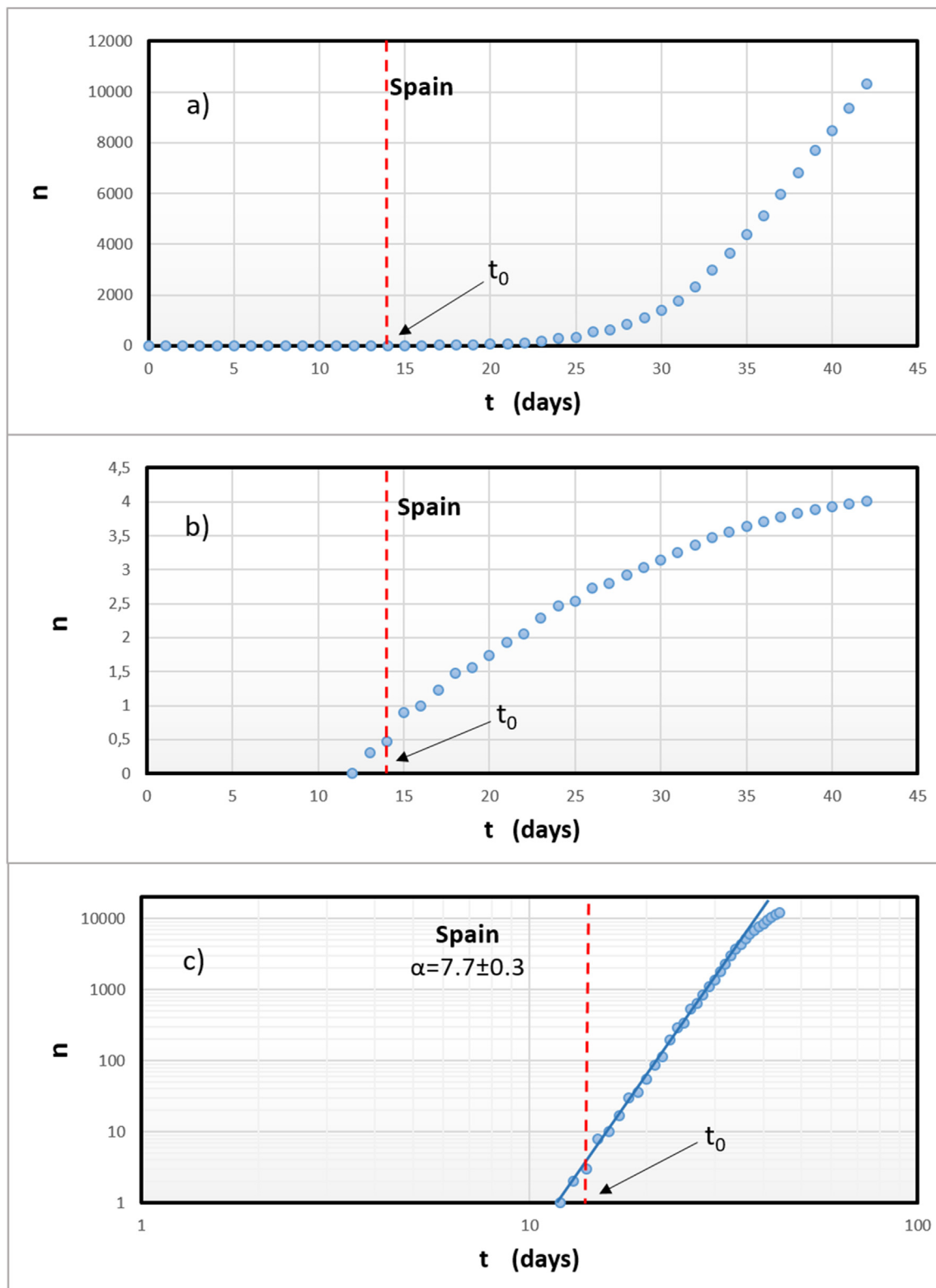


Fig. 1. The number of fatality cases $n(t)$ from COVID-19 in Spain. The onset of the contagion is assumed to be $t_0 = 14$ days before the first three incidents are recorded (see text). a) Plot with linear axes $n(t)$ versus time. b) The plot $\log(n)$ vs time cannot be fitted to a straight line, indicating that an exponential curve cannot describe data throughout the depicted range. c) Plot with both n and t in logarithms, which is fitted by a straight line ($R^2 = 99.8\%$), suggesting a power law $n \propto (t - t_0)^{7.7}$ in the region $3 < n(t) < 7000$.

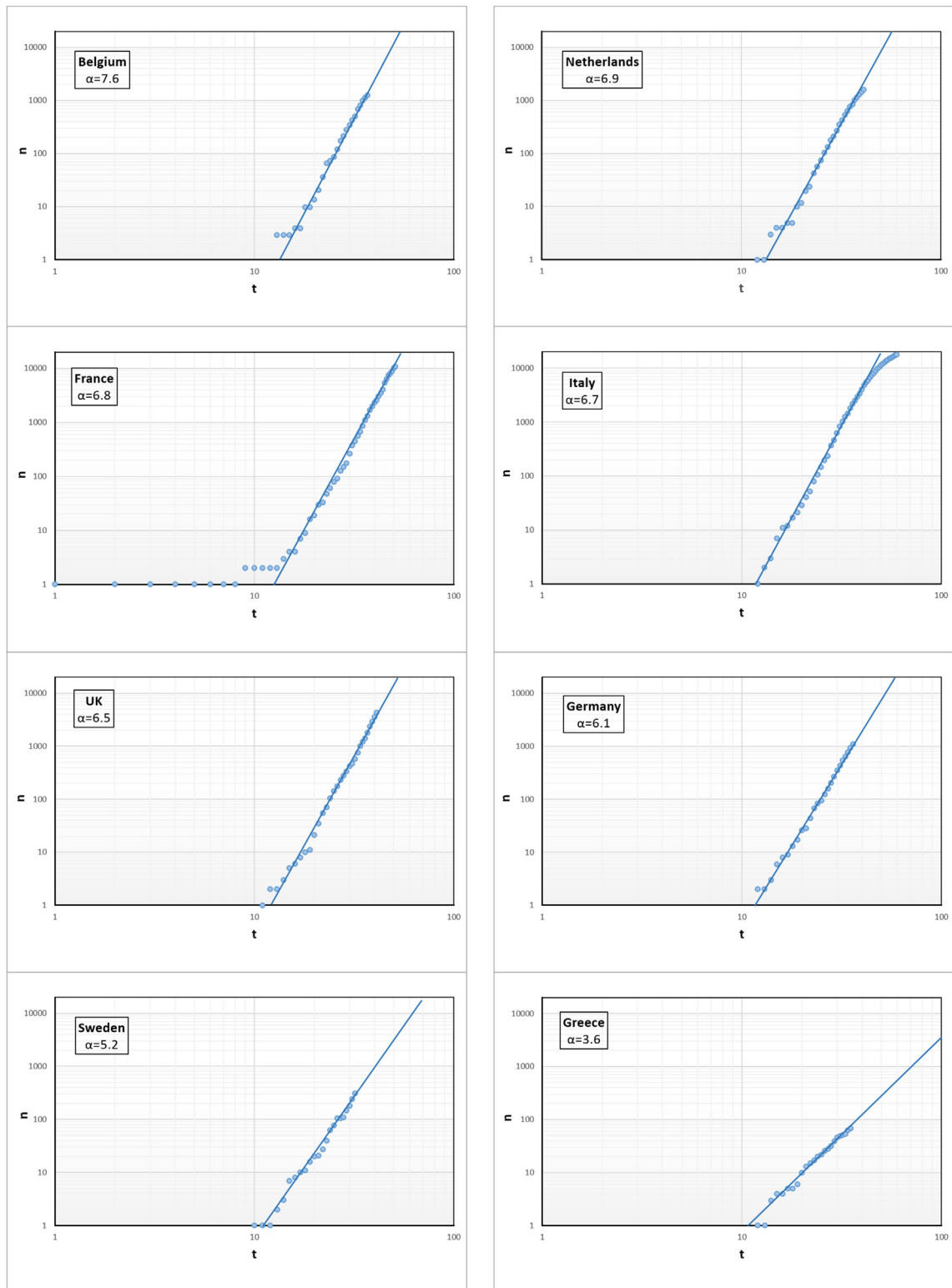


Fig. 2. Plots of the fatality record $\log n$ vs. $\log t$ for eight European countries. We kept the same scale in the corresponding axes to aid a visual comparison. The solid lines represent fits to a power-law with typical $R^2 = 99.7\text{--}99.9\%$, for $n > 3$.

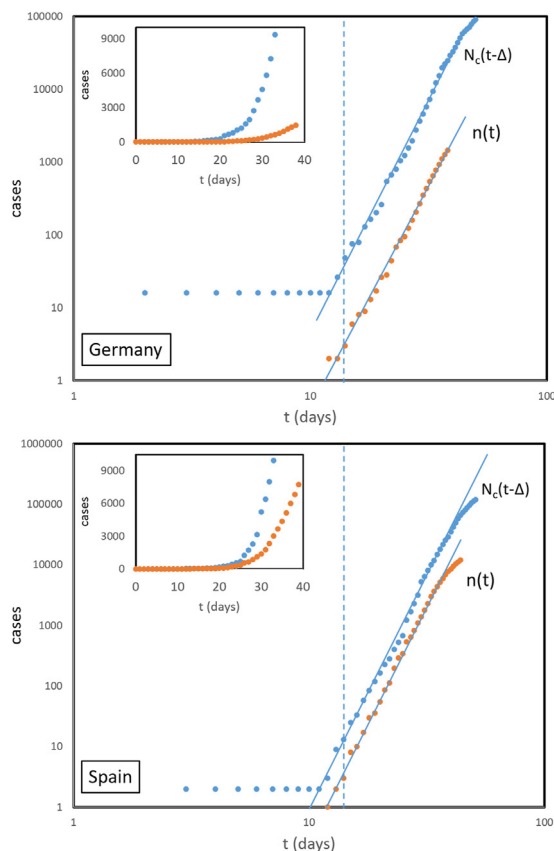


Fig. 3. Comparison of the confirmed infected cases (blue) to the fatality cases (brown). *Inset:* Plot of the data in linear axes. *Main graph:* In a double-logarithmic plot, the onset of the fatality cases $n(t)$ coincides with the onset of the confirmed cases $N_c(t-\Delta)$, shifted by $\Delta = 13$ days in Germany and $\Delta = 7$ days in Spain. The functional dependence of both growth curves in each country is fitted with the same power law (in Germany $\alpha = 6.1 \pm 0.3$ and in Spain $\alpha = 7.6 \pm 0.3$), with $R^2 = 99.6\%$.

before an infected individual is recorded as a confirmed case. Shown in Fig. 3 are Germany and Spain with $\Delta = 13$ and $\Delta = 7$, respectively, while all other cases we studied cluster in the intermediate range $10 = \Delta \leq 7$.

With the onset of the $N_c(t)$ and $n(t)$ data set at t_0 , we observe that the recorded cases increase approximately parallel to the fatality cases in the graph. This means that $N_c(t - \Delta) = C n(t)$, with the proportionality constant C depending on the country. From Fig. 3 we derive $C \approx 15$ for Germany and $C \approx 3$ for Spain. All other European States we studied give intermediate values for C .

The variation of the parameters Δ and C can be attributed to the difference in the recording practices of infected individuals across Europe. We expect countries like Germany, which implements a large scale testing procedure across the general population, to record a higher percentage of the infected individuals (i.e., with larger C and with Δ approaching t_0). On the other extreme, Spain was one of the first European countries hit by the pandemic, so that the contact tracking may not have been fully implemented during the initial diffusion phase. It is thus not surprising that the percentage of confirmed cases is smaller, with the infected individuals recorded several days after their exposure to the virus (small C and Δ).

Given that the IFR for COVID-19 is as small as 0.3–1% (WHO, 2020) suggesting that $C \geq 100$, the confirmed cases are much less than the actual infected individuals. However, the functional dependence $N_c(t - \Delta) = C n(t)$ persists for all the countries we studied, despite the variation in Δ and C . It is then reasonable to assume that this relation holds not only for the confirmed cases, but also for all infected individuals since their first day of symptoms, so that $N(t - t_0) \propto n(t)$ or, by changing variables, $n(t + t_0) \propto N(t)$.

A power law increase of the *infected cases* is also corroborated by recent studies in mainland China (Maler and Brockmann, 2020). However, such sub-exponential dependence has been attributed to population-wide isolation measures and quarantine of symptomatic individuals. In contrast, the European data analyzed in this report refer to people infected before the implementation of a national lockdown. This suggests that a power law growth could be a more general feature of COVID-19 diffusion dynamics. In the next section, we address the issue for both infected and fatality cases with a model.

2.1. The model

As shown in Figs. 1–3, the existence of a power-law growth holds for a variety of countries with different age distribution, immunization characteristics, community practices, political and economic environment. The underlying diffusion mechanism should then reflect a general population characteristic and *be independent of the details* of the aforementioned parameters. On the other hand, the diffusion mechanism should relate to the face-to-face contacts, which are the main cause for the COVID-19 spread. We propose a simplified model for the occurrence of these contacts and thus for the probability a healthy individual to get infected.

In each community, a person associates to others by habit, need or tradition, participating in certain social networks (ex, professional, educational, family, friendship networks) or appearing in communal and religious gathering places. Therefore, personal contacts strongly depend on a general framework that is particular to the country of residence, at the time we consider. When the COVID-19 appeared in China and till the first fatality incidents in each European country, such framework remained practically unaltered, poised though with the awareness for the infection and the suggestions of the medical personnel and the state. As noted in the previous section, the fatality cases in Figs. 1 and 2 up to the flattening of the curve correspond to people infected during this particular period, before the implementation of mandatory restrictions or a national lockdown.

For a three-week period prior to the onset of fatality cases in the country, people acted in a way that actually perpetuated the COVID-19 contagion. Aware of the risk involved, an individual might have reservations to engage in direct personal contacts with other people. There are instances that he/she would be able to postpone direct contacts repeatedly. However, there is a fatigue growing slowly: As such instances accumulate and time progresses, he/she becomes more prone to succumb, especially in this period of voluntary and not mandatory restrictions. That way, the probability an individual meets someone face-to-face and gets infected increases, depending recursively on the history of such incidents.

We can formally depict this recursive time dependence. Assume $\lambda(t)$ is the probability that a healthy individual gets infected between time t and $t + dt$. We write

$$\lambda(t) = \frac{\alpha}{t} \int_0^t \lambda(t') dt' \quad (1)$$

with $t = 0$ the initial value of time in this process. Eq. (1) is our model equation. It proposes a “memory effect”: The probability $\lambda(t)$ that a person gets infected (by direct contact) depends on the average of all past values of λ , multiplied by a parameter α . Values of $\alpha > 1$ intensify past experience and urges a person to overcome his reservations and proceed to face-to-face contact. Values $\alpha < 1$ mean that such feelings from past experience are suppressed, $\lambda(t)$ decreases and the contagion is eventually diminished.

As noted, the parameter α has both social and personal characteristics. For simplicity though, we assume that it depends most prominently on the national framework that creates the need for individual actions, so that it is approximately constant for the whole susceptible population. Solving Eq. (1) and setting the starting date of the memory effect at $t_0 = 0$ (i.e., when the first infected cases were recorded in the country), we get:

$$\lambda(t) = \left(\frac{t}{\tau}\right)^{\alpha-1} \quad (2)$$

We have assumed that λ is a probability function and therefore $0 < \lambda < 1$. Then, the parameter τ introduced in Eq. (2) should be larger than all values of t that are relative to our problem. It has physical meaning of the upper limit in time, where the “memory effect” presumed in our model is valid.

We now construct a model equation for the initial growth phase we study. In all our data, the fatalities number a few thousand incidents. Given the estimated IFR for COVID-19 (Meyerowitz-Katz, Merone, 2020), we expect that the corresponding infected cases are two orders of magnitude higher. This estimation corresponds to much larger values from the recorded data, but is still much smaller from the total susceptible population in a country of a few million inhabitants. Thus, the growth phase of the epidemic in our model is in the limit $n \ll N \ll N^*$ where n denotes the fatality cases, N the infected cases and N^* an estimation of the total susceptible population. In this limit, the susceptible individuals at time t are $N^* - N(t)$ approximately, each one with probability $\lambda(t)$ to be infected. We write

$$\frac{dN}{dt} = \lambda (N^* - N) \quad (3)$$

We substitute $\lambda(t)$ and solve the differential equation to find

$$N(t) = N^* \left(1 - e^{-\left(\frac{t}{\tau}\right)^\alpha} \right) \quad (4)$$

The expression (4) has the form of the 2-parameter Weibull cumulative probability distribution, with shape parameter $\alpha > 0$. Specifically for $\alpha > 2$, as is the case of our data where $3.5 < \alpha < 8.0$, the expression (4) takes the form of a sigmoid curve, with inflexion point $\sim \tau$. Then, our considerations in Eq. (2) that our model is restricted to $t < \tau$ are self-consistent and with our assumption $N \ll N^*$ for constructing Eq. (3). In this limit, after rewriting the Weibull expression (4) as

$$\ln \left(1 - \frac{N}{N^*} \right) = - \frac{\left(\frac{t}{\tau}\right)^\alpha}{\alpha} \quad (5)$$

we use $\ln \left(1 - \frac{N}{N^*} \right) \approx - \frac{N}{N^*}$ and the curve (4) is reduced to a simple power law $N(t) \propto t^\alpha$.

Following our discussion of Fig. 3, the fatality incidents relate to the infected cases by $n(t + t_0) \propto N(t)$, appearing $t_0 \approx 14$ days after infection. Thus, finally, in the limit $n \ll N \ll N^*$ the model predicts:

$$n(t + t_0) \propto N(t) \propto t^\alpha \quad (6)$$

This is the power law that fits all our data up to the inflection point of the curve. The parameter t_0 is an adjustable parameter of the fit (it corresponds to the onset of the growth curves in Figs. 1–3). The upper bound of the validity of the fit is another adjustable parameter, as it occurs for reasons external to the model assumptions, such as the implementation of a mandatory lockdown. Such measure restricts people's direct contacts abruptly, in a way not predicted by the assumptions for our model Eq. (1). Within the range of its validity, the model provides a robust approximation of the power-law dynamics of the growth diffusion phase. It also introduces the notion of a memory effect for interpersonal associations, as a key concept for understanding the mechanism that underlies the observed diffusion distribution of the COVID-19 epidemic.

3. Discussion

We have showed that a single parameter α , in the range $3.5 < \alpha < 8.0$, describes the growth of the COVID-19 of the fatality cases at a national level in Europe. A distinction between an emergence diffusion phase, with slow case increase, and a growth phase with exponential increase, is not a good approximation of the process, as is shown in Fig. 1b. The diffusion grows in a single phase, where the fatality data can be reasonably well fitted to a single power law with exponent α , from the first few cases to thousands.

This observation can prove a practical diagnostic tool. A straight line data fit in the double logarithmic plot (such as in Figs. 2 and 3) can be used as a useful tool for reasonable predictions on a power law growth from very early data. As is discussed above, such tool might be valid for both fatality and infected cases, although analysis of the latter should proceed with caution, due to differences in the testing practices for COVID-19 across Europe.

The exponent α in the model is a measure of the complexity of interpersonal associations that clearly depend on the restrictions on social distancing taken by the government. Therefore, α provides the means to evaluate the effectiveness of such measures not only among different countries, but also at different time windows in the same country, as, for instance, at different COVID-19 waves.

The model equation that fits the data has an intuitive physical meaning. Given the form of λ , the diffusion Eq. (3) can take the form

$$\frac{dN}{dt} \propto N^{1-\frac{1}{\alpha}} (N^* - N) \quad (7)$$

so that the power law (Eq. (6)) is still a solution, in the limit $n \ll N \ll N^*$. The exponent is $1 - 1/\alpha < 1$, for all our fitted data sets. The expression (7) differs from the logistic diffusion model (or in fact from any homogeneous mixing model like the SIR or SEIR), as the rate dN/dt is not linear in N . It depends on the term $N^{1-\frac{1}{\alpha}} < N$ that increases at a slower rate than N , especially for countries with small α . That is, a susceptible individual is not at risk from anyone infected in the country, but from a subset of N , apparently those who are closer. This feels intuitively correct. The concept of infection from neighboring individuals might be easier to incorporate within the methodologies of network-based models (Bansal et al., 2007). It is also expected to give rise to a spatial heterogeneity in the disease spread. In fact, such heterogeneity has been seen in epidemiological patterns at different length scales and is correlated to a truncated power-law distribution of infected cases (Blasius, 2020). However, it remains an open issue how Eq. (7), which is validated by our observations at a country level, can be associated with a fractal spatial disease distribution, which is implied in that work (Blasius, 2020). We currently work on this research direction,

investigating the relationship between diffusion growth and spatial heterogeneity, by incorporating our model assumptions to percolation analysis, using computer simulations.

It is common practice in the field of Social Network Analysis to describe the diffusion of infection, of information or of technologies, using the same diffusion and epidemiological models. In this context, the model Eq. (1) is not new in the literature. It has been proposed as a general model for the process and the timing of decision making, in various human activities (Vazquez, 2007). As a basis of a diffusion process, it has been already successful to describe the spread of ICT mobile technologies worldwide (Xenikos, 2011). It may be that the memory effect, as a mechanism of human decisions and risk taking in interpersonal associations, lies in the core of diverse diffusion processes, as is proposed in this work for the COVID-19 epidemic.

In conclusion, our work showed that, despite the diversity of mitigation policies during the growth diffusion phase across Europe, the fatality cases initially increase following a power law at a national level. A similar power law is consistent with the growth of the recorded infected cases. The difference among the European countries is in the value of the exponent in the range $3.5 < \alpha < 8.0$. The observed statistical distribution is described by a model for a mechanism of timing in human decisions and interpersonal associations, suggesting a deviation from the homogeneous mixing assumption in epidemiological model analyses.

Declaration of competing interest

The authors D. G. Xenikos and A. Asimakopoulos of the manuscript “Power-law growth of the COVID-19 fatality incidents in Europe” claim no conflict of interest.

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