Superspreaders and lockdown timing explain the power law dynamics of COVID-19

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Abstract

Infectious disease outbreaks are expected to grow exponentially in time, when left unchecked. Measures such as lockdown and social distancing can drastically alter the growth dynamics of the outbreak. Indeed the 2019-2020 COVID-19 outbreak is characterized by a power law growth 1. Strikingly however, the power law exponent is different across countries 2. Here I illustrate the relationship between these two extreme scenarios, exponential and power law growth, based on the impact of superspreaders and lockdown strategies to contain the outbreak. The theory predicts an inverse relationship between the power law exponent and the speed of the lockdown that is validated by the observed COVID-19 data across different countries.

Research from the late 90s and the 2000s uncovered the heterogeneity of social connectivity patterns, causing deviations from common expectations 3-6. Superspreaders are the manifestation of this heterogeneity in the contest of infectious disease outbreaks: most infected individuals infect a few other individuals (secondary cases), but a few infected superspreaders generate a large number of secondary cases 7. This was already observed in the 2002-2004 severe acute respiratory syndrome (SARS) outbreak as well as the 2012 Middle East respiratory syndrome (MERS) outbreak, and it has recently been reported for the ongoing COVID-19 outbreak 8-10.

In earlier work I investigated the influence of superspreaders on infectious disease outbreaks 11. These analyses showed that superspreaders can lead to a new type of infectious disease dynamics that is better described by a power law rather than the canonical exponential growth. To understand how that happens let us have a look at the two trees of disease transmission in Fig. 1A and B. In Fig. 1A most individuals transmit the disease approximately to the same number of other individuals, and the chain of transmissions extends in this manner over several generations. The dynamics of the number of new cases \( n(t) \) at a given time \( t \) in this case described by the exponential law 11

\[
n(t) = N_0 R_0 \sum_{d=1}^{D} R^{d-1} \frac{1}{\tau} \frac{1}{(d-1)!} \left( \frac{\tau}{\tau} \right)^{d-1} e^{-\frac{t}{\tau}}
\]

Here \( N_0 \) represents the number of patients zero. \( N_0 = 1 \) for the country where the outbreak originated, but it can be larger than 1 in countries where multiple infected cases arrive and start a new outbreak. \( R_0 \) is the average number of secondary cases generated by a patient zero, \( R \) is the average number of secondary cases generated by infected individuals other than patient zero and \( R_0 R^{d-1} \) is the number of new cases at generation \( d \) of the outbreak. \( D \) is the final generation, when the outbreak ends due to natural extinction or interventions strategies. The remaining part of equation (1) translates generations into infection times. It is basically the time interval distribution of a chain of \( d \) disease transmission events, where \( T \) is the average time from being infected to disease transmission.

When \( D \) is very large, equation (1) represents the Taylor expansion of the exponential
If $R > 1$ then the outbreak grows exponentially over time, else if $R > 1$ the outbreak decays exponentially. This is the canonical expectation of infectious disease dynamics. In this scenario the key quantity is the reproductive number $R$ and interventions strategies are focused on bringing it below 1.

However, there are a number of assumptions behind equation (2) that make it inadequate to model all infectious diseases outbreaks. First, we have just assumed that $D$ is large, i.e. that the free spreading of the disease goes over several generations. That would typically be true for infectious diseases with mild symptoms such as the common cold, but it is not the case for COVID-19. The mortality and hospitalization rate of COVID-19 infections have led governments to impose strict lockdown measures. As a consequence, the tree of disease transmission is truncated after a few generations, as shown in Fig. 1B.

Second, the distinction between patient zero and the other infected individuals needs a deeper analysis. The disease spreading introduces a bias towards individuals with larger daily person-to-person proximity contacts. For example, if the disease is transmitted via the daily proximity patterns between individuals and each individual is in contact with others at a rate $\Lambda$, then

$$R = \frac{E(\Lambda^2)}{E(\Lambda)^2}$$

where $E()$ denotes the expectation based on the distribution of $\Lambda_i$ in the population. If $\Lambda_i$ exhibits small variations around its expected value then $R \approx R_0$. However, the existence of superspreaders tell us that there are a few individuals with very large $\Lambda_i$. In reality $E(\Lambda^2) \gg E(\Lambda)^2$, implying that $R \gg R_0$. 

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**Figure 1.** Causal tree of disease transmission of an infectious disease outbreak. A) Typical topology leading to an exponential growth. B) Typical topology leading to a power law growth.
When these two elements are taken into consideration, a small number of generations $D$ and the existence of superspreaders, then equation (1) is better approximated by

$$n(t) \approx N_0 R_0 R^{D-1} \frac{1}{T} \frac{1}{(d-1)!} \left(\frac{t}{T}\right)^{D-1} e^{-\frac{t}{\tau}}$$

Equation (4) makes a testable prediction, that the exponent of the power law growth, $n(t) \sim t^\alpha$, depends on $D$,

$$\alpha = D - 1$$

In the COVID-19 context, the number $D$ of generations, or rounds of unhindered spread, in a population is determined the time between contact with patients zero and a lockdown measure imposed. Therefore $D$ can be estimated as the number generations of disease transmission from patient zero to the implementation of lockdown,

$$D \approx \frac{t_{\text{lockdown}} - t_{\text{first case}}}{T}$$

where $t_{\text{lockdown}}$ is the time when the lockdown was implemented and $t_{\text{first case}}$ is the time when the first case was reported. $T$, as before, is the average time
from being infected to disease transmission. Combining equations (5) and (6) then yields
\[
\alpha = \frac{t_{\text{lockdown}} - t_{\text{first case}}}{T} - 1
\]

To test the equation above I collected data for the power law exponents and the date of first confirmed case (World Health Organization, WHO) associated with the COVID-19 outbreak in several countries. To test equation (7), \(T\) was estimated as the COVID-19 incubation time, which is approximately 5 days \(^{13}\). I have also assumed that most countries (China excluded) implemented lockdown measures around March 20\(^{th}\) (79 days from Jan 1\(^{st}\)) \(^{14}\). Based on these parameter estimates we obtain the values predicted by equation (7) are in very good agreement with the data in Fig. 2.

In conclusion, the power law dynamics of the COVID-19 outbreak and the relationship between the power law exponent and the time interval between first case and lockdown, are a validation of the new power law of infectious disease spreading \(^{11}\). Again this study also underscores the crucial importance of early lockdown timing in the control of an infectious disease in a population with superspreaders.

**Methods**

The mathematical formulation leading to equation (1) was reported in Ref. \(^{11}\).

The time of first confirmed case were retrieved from the WHO website at https://covid19.who.int/. Except for China, that was assumed as 8\(^{th}\) of December, when the first suspected case in Wuhan was reported having symptoms of coronavirus.

The time of lockdown was assumed to be the 20\(^{th}\) of March for all countries but China, as reported in Ref \(^{14}\) and available at https://www.politico.eu/article/europes-coronavirus-lockdown-measures-compared/. For China we assumed the 1\(^{st}\) of January, when the Wuhan market was closed.

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**Authors' contributions**

AV conceived the project and wrote the manuscript.

**Competing interests**

The authors declare no competing interests.