First-wave COVID-19 daily cases obey gamma law

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ABSTRACT

Modelling how a pandemic is spreading over time is a challenging issue. The new coronavirus disease called COVID-19 does not escape this rule as it has embraced over two hundred countries. As for previous pandemics, several studies have attempted to model the occurrence of cases caused by COVID-19. However, no study has succeeded in accurately modelling the impact of the infectious agent. Here we show that COVID-19 daily case distribution in humans obeys a Gamma law, which two new parameters can describe without any adjustment. Though the Gamma law has been exploited for nearly two centuries to describe the statistical distribution of spatial or temporal quantities, the goodness-of-fit rationale using two or three parameters has remained enigmatic. The new Gamma law approach we demonstrate here emerges from actual data and sheds light on the underlying mechanisms of the observed phenomenon. This finding has promising applicability in the epidemiological domain and in all disciplines involving branching systems, for which our Gamma law approach may bring a solution to hitherto unsolved problems.

1. Introduction

Since 2019, the coronavirus disease so-called COVID-19 caused by the infectious agent SARS-CoV-2 has contaminated more than three hundred million humans worldwide and killed more than five million of them. Modelling the spread of an infectious disease in general and, in particular, a viral disease is challenging to achieve. According to Neuberger et al. (Neuberger, Paul, Nizar, & Raoult, 2013), appropriate modelling oscillates between haphazard and hazard. The contamination dynamics of an infectious agent are typically studied using the mathematics of variable complexity. At the same time, the objective of model formulation and analysis may take roots in many different frameworks (Anderson & May 1991). Conceptual models are based on equations set a priori and parameters adjusted a posteriori, whether they apply to viruses in general (Graw & Perelson, 2016) or the specific case of COVID-19 (Lin et al., 2020). A variety of models have been proposed to date to analyze or predict the evolution of an epidemic. For instance, the Susceptible-Exposed-Infectious-Removed (SEIR) model has been widely used (Lin et al., 2020; Sanche et al., 2020). The Global Epidemic and Mobility (GLEAM) project proposes stochastic models of disease transmission based on real-world data on populations and human mobility to promote intervention strategies that minimize the impact of epidemics (Chinazzi et al., 2020). Using this framework, Balcan et al.
(Balcan et al., 2009) have decomposed the earth’s surface into Voronoi cells, which were centered on international airports, and shown multiscale mobility networks in the spreading of diseases.

Here we introduce a new approach based on statistical physics whose goal is to provide a general and robust model of the evolution over time of a natural phenomenon. Our approach is based on available data without any adjustment before or after the mathematics. Let us first consider that the COVID-19 virus spread describes a tree as follows (Cauchemez et al., 2011; Faye et al., 2015). In a first cascade, the first infected individual (patient $P_0$) contaminated on average $R$ patients $P_1$. The ratio or reproductive number $R$ is usually noted $R_0$ at the beginning of the epidemic. This has well been defined by Anderson et al. (Anderson et al., 2004), studied by Zhang et al. (Zhang et al., 2020) for the Diamond Princess cruise ship, and discussed by Thomson et al. (Thompson et al., 2020). In a second cascade, the $R$ patients $P_1$ contaminate $R^2$ patients $P_2$, and so on. This way, we get a propagation tree with $n$ cascades. Fig. 1 shows a simplified contamination tree. The line segment $P_0E_0$ represents the contagiousness duration of patient $P_0$, where points $P_0/E_0$ are the beginning/end, respectively. After time $l_1$ (line segment $P_0P_1$), the patient $P_0$ contaminates a first patient $P_1$. Then, after another value of $l_1$ (line segment $P_0P_0$), a second patient $P_1$ is contaminated and so on. In Fig. 1, the longest contamination chain has the length $L$ defined as in Equation (1).

$$L = l_1 + l_2 + l_3$$

where $l_1 = P_0P_1'; l_2 = P_1P_2'; l_3 = P_2P_3'$.

If the time taken by a patient $P_i$ to contaminate the $R_i+1$ patients $P_i+1$ was always the same, and if $R$ was constant, it would be easy to fix the number of cases at every moment of the epidemic corresponding to every end of $n$ cascades. This is unfortunately not the case. Thus, we note $l_i$ the length of the $i$th cascade as the time taken by a patient $P_{i-1}$ to contaminate one of the $R$ patients $P_i$, which time scale may vary (days, hours, etc.). Let us keep in mind that $l_i$ does not have the same value for all contaminated patients $P_i$. Consequently, the length of the contamination chain, which is the time between $P_0$ contamination and that of any of the patients $P_n$ in the $n$th cascade, can be expressed as the total length $L$ of $n$ components $l_i$ as in Equation (2).

$$L = \sum_{i=1}^{n} l_i$$

The $l_i$ components are the times spent in steps 1, 2, ..., $i$, ..., $n$ of the contamination chain. This time $l_i$ has been elsewhere called serial interval by Zhang et al. (Zhang et al., 2020). In the Supplementary Material S1 section, we demonstrate that the probability density function (PDF) of the variable $L$ can be expressed by a Gamma law as in Equation (3).

$$F(L) = \frac{1}{(2\hat{l})^{\frac{1}{2}} \Gamma(\frac{3}{2})} L^{\frac{3}{2}} e^{-\frac{3}{2\hat{l}}}$$

In Equation (3), $\hat{l}$ is the average length of components $l_i$; $\Gamma$ is the Gamma function of Euler; $L$ is the length of the contamination chain between patient $P_0$ and any of the contaminated patients; $n$ is the number of cascades required to pass

Fig. 1. Schema of COVID-19 contamination tree. Points $P/E$ represent the start/end, respectively, of the contagiousness duration of patient $P_0$, patient $P_1$ and so on.
from the patient $P_0$ to any of the patients $P_i$; $m$ is the average of contamination chain length with $m = \bar{L}$. Therefore, we get $\bar{L} = \frac{1}{m}$. Two new parameters, the number of cascades $n$ and the average length of the contamination chain component $\bar{L}$, add value to the traditional ones, the shape parameter $\alpha$ and the scale parameter $\beta$ of the Gamma law (Woo, 1999) of Equation (4).

$$F(L) = \left(\frac{1}{\beta}\right)^\alpha \frac{1}{\Gamma(\alpha)} L^{\alpha-1} e^{-\frac{L}{\beta}}$$

According to Lancaster (Lancaster, 1966), we owe the Gamma law to Laplace (Laplace, 1836). For 186 years, the Gamma law has used two (sometimes three) parameters, $\alpha$ and $\beta$, to model a phenomenon over time, which are not obviously meaningful even for the experts of the field. Here, we propose that our new parameters $n$ and $\bar{L}$ are likely to shed light on the underlying mechanisms of the studied phenomenon. In epidemiology, $n$ and $\bar{L}$ can be meaningful by representing the number of branches or cascades and the average length of a branch or cascade, respectively.

This article used our new Gamma law approach to elucidate how COVID-19 first-wave has spread in different countries. In three studies, we show that this approach best fits the pandemic’s natural course over time compared to other distributions.

2. Results

We develop the Methods in the Supplementary Material S2 section and show the results in Tables 1 and 2 and Figs. 2–4.

2.1. Study 1: entering the COVID-19 pandemic

In a first study, we examined COVID-19 case distribution in five countries: China, Germany, Austria, Israel, and New Zealand (see Table 1 lines 1–5 and Fig. 2).

We first selected China, where the epidemic presumably started in Wuhan, Hubei province. Let us decline the variables in Table 1, line 1. The rate of cases per mille residents for the whole country was 0.05%. The first-wave epidemic lasted 54 days and concerned 77,251 cases between January 22 and March 16, 2020. According to our Gamma approach (see Introduction section), the number $n$ of individuals between the zero case and any case was 17, and the average duration of contamination $\bar{L}$ between one individual and another was 1.3 days (see Table 1 line 1).

We plotted the same data in Fig. 2A, showing the histogram of probability density function (PDF) in frequency as a function of time in days. As one may observe, two raw aberrant values of 14,108 and 5090 cases on February 12th and 13th led to seven aberrant values in the 7-day moving average. These values rather than insincere might be inherent in the difficulty to count cases (and the necessity to catch up) in the early stage of the epidemic. Other countries have also exhibited in their count of cases catching-up values. For that reason, we decided to let the data as they are rather than correcting them. We plotted cases (and the necessity to catch up) in the early stage of the epidemic. Other countries have also exhibited in their count of cases catching-up values. For that reason, we decided to let the data as they are rather than correcting them. We plotted observed data against our Gamma approach and the Lognormal law as a control since the two laws have previously been used in concurrence (e.g., Cho, Bowman, & North, 2004). Notably, the Kolmogorov-Smirnov was calculated on the cumulative density functions (CDF) so that the P-value on the CDF may sometimes un

Table 1: For the COVID-19 first-wave in 2020 and for each country (CH, China; GE, Germany; AU, Austria; IS, Israel; NZ, New Zealand; BE, Belgium; SP, Spain; IT, Italy; FR, France; FI, Finland; CZ, Czechia; SL, Slovenia; LI, Lithuania; CR, Croatia; LA, Latvia), we report the rate of cases per mille residents (Case/pop), numbers of days, total number of cases, mean (in days) and variance $\sigma^2$ of the observed distribution of daily cases; $n$ (number) and $\bar{L}$ (in days) values of the Gamma distribution; peak values (in frequency) of the observed and Gamma distributions; and P values of the Kolmogorov-Smirnov test between the observed distribution and, respectively, Gamma (P1) and Lognormal (P2) distributions.

| Country | Case/Pop | Days | Cases | Mean | $\sigma^2$ | $n$ | $\bar{L}$ | Peak<sup>a</sup> | Peak<sup>b</sup> | P1 | P2 |
|---------|----------|------|-------|------|-----------|-----|----------|----------------|----------------|----|----|
| Study 1 |          |      |       |      |           |     |          |                |                |    |    |
| CH      | 0.05%    | 54   | 77,251| 21.6 | 56.2      | 17  | 1.3      | 0.060          | 0.056          | 0.735 | 0.572 |
| GE      | 2.24%    | 119  | 186,639| 56.7 | 346.0     | 19  | 3.1      | 0.031          | 0.022          | 0.984 | 0.460 |
| AU      | 1.76%    | 72   | 15,701| 35.0 | 125.4     | 20  | 1.8      | 0.048          | 0.037          | 0.874 | 0.607 |
| IS      | 1.76%    | 96   | 16,620| 54.8 | 158.1     | 38  | 1.4      | 0.037          | 0.032          | 0.042 | 0.018 |
| NZ      | 0.29%    | 75   | 1497  | 32.5 | 84.7      | 25  | 1.3      | 0.050          | 0.045          | 0.497 | 0.275 |
| Study 2 |          |      |       |      |           |     |          |                |                |    |    |
| BE      | 5.33%    | 122  | 61,272| 50.4 | 445.8     | 11  | 4.4      | 0.024          | 0.020          | 0.986 | 0.951 |
| SP      | 4.94%    | 85   | 234,188| 42.9 | 184.3     | 20  | 2.1      | 0.037          | 0.031          | 0.710 | 0.347 |
| IT      | 3.98%    | 132  | 240,325| 51.0 | 496.8     | 10  | 4.9      | 0.024          | 0.020          | 0.991 | 0.832 |
| FR      | 2.00%    | 100  | 135,114| 54.8 | 254.3     | 24  | 2.3      | 0.031          | 0.026          | 0.683 | 0.266 |
| FI      | 1.31%    | 133  | 7256  | 56.9 | 543.1     | 12  | 4.8      | 0.023          | 0.018          | 0.092 | 0.215 |
| CZ      | 0.76%    | 72   | 8160  | 37.3 | 188.8     | 15  | 2.5      | 0.032          | 0.031          | 0.959 | 0.749 |
| SL      | 0.70%    | 81   | 1467  | 29.3 | 197.8     | 9   | 3.4      | 0.033          | 0.032          | 0.681 | 0.020 |
| LI      | 0.58%    | 81   | 1619  | 32.5 | 337.9     | 6   | 5.2      | 0.033          | 0.025          | 0.976 | 0.681 |
| CR      | 0.55%    | 77   | 2193  | 41.8 | 174.2     | 20  | 2.1      | 0.034          | 0.032          | 0.393 | 0.290 |
| LA      | 0.56%    | 89   | 1072  | 37.9 | 410.4     | 7   | 5.4      | 0.030          | 0.023          | 0.853 | 0.282 |

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goodness of fit (Massey Jr., 2012), the Gamma curve led to a higher value than the Lognormal one. It also predicted a peak in the curve only three days earlier than observed.

In the first group, we added four countries where the public health policy has been strict in detecting and isolating cases, at least in the early stage of the pandemic: Germany (Laffet, Haboubi, Elkadri, Georges Nohra, & Rothan-Tondeur, 2021), Austria (Moshammer, Poteser, Lemmerer, Wallner, & Hutter, 2020), Israel (Yom-Tov, 2021), and New Zealand (Bandyopadhyay & Meltzer, 2020). We show the data in Table 1, lines 2—5 and Fig. 2B, where we sorted the countries by decreasing impact defined as the rate of cases per mille residents (reverse range = 2.24‰ ± 0.29‰).

Fig. 2B shows that, again, the Gamma distribution better fitted the Lognormal one as evidenced by a higher P-value for the four countries, should the observed curve be either smooth (Germany and Austria) or noisy (Israel and New Zealand). One may also see the precision of our Gamma approach in calculating the date of the peak value in case frequency: four days later between the theoretical and observed distributions for Germany, one day later for Austria, two days later for Israel, and two days earlier for New Zealand (see Fig. 2B).

Then, we observed the results in countries with a different public health policy, as the pandemic can end when the availability of susceptible individuals or the reproductive rate decreases (Cobey, 2020).

| Country | Gamma P1 | Gaussian P3 | Weibull P4 |
|---------|----------|-------------|------------|
| CH      | 0.735    | 0.572       | 0.735      |
| GE      | 0.984    | 0.063       | 0.367      |
| AU      | 0.874    | 0.874       | 0.959      |
| IS      | 0.042    | 0.955       | 0.090      |
| NZ      | 0.497    | 0.196       | 0.771      |

For the COVID-19 first-wave in 2020 and for each country (CH, China; GE, Germany; AU, Austria; IS, Israel; NZ, New Zealand; BE, Belgium; SP, Spain; IT, Italy; FR, France; FI, Finland; CZ, Czechia; SL, Slovenia; LI, Lithuania; CR, Croatia; LA, Latvia), we report the P values of the Kolmogorov-Smirnov test between the observed distribution and, respectively, Gamma (P1), Gaussian (P3) and Weibull (P4) distributions. The Lognormal distribution (P2) is not shown (see Table 1). Gray cells show the superiority of other than Gamma distributions.

Fig. 2B shows that, again, the Gamma distribution better fitted the Lognormal one as evidenced by a higher P-value for the four countries, should the observed curve be either smooth (Germany and Austria) or noisy (Israel and New Zealand). One may also see the precision of our Gamma approach in calculating the date of the peak value in case frequency: four days later between the theoretical and observed distributions for Germany, one day later for Austria, two days later for Israel, and two days earlier for New Zealand (see Fig. 2B).

Then, we observed the results in countries with a different public health policy, as the pandemic can end when the availability of susceptible individuals or the reproductive rate decreases (Cobey, 2020).

2.2. Study 2: Top ten most impacted countries by first-wave COVID-19 pandemic

In a second study, we examined COVID-19 case distribution in ten countries where the public health policy has been less strict than the ones above: Belgium, Spain, Italy, France, Finland, Czechia, Slovenia, Lithuania, Croatia, and Latvia. We show the data in Table 1, lines 6—15 and Fig. 3, where we also sorted countries by decreasing impact (reverse range = 5.33‰ ± 0.56‰).

For this second group of countries, the parameter n was 13 ± 6 (range = 6—24), and the parameter 7 was 3.7 ± 1.4 days (range = 2.1—5.4 days).

Fig. 3 shows that, again, the Gamma distribution offered a better fit than did the Lognormal distribution, as evidenced by a higher P-value for the ten countries, regardless of the shape of the observed curve. Again, our Gamma approach accurately
Fig. 2. Study 1. Histogram of probability density function (in frequency) of COVID-19 observed daily cases in (A) China (CH) and (B) Germany (GE), Austria (AU), Israel (IS), and New Zealand (NZ) using 7-day moving averages (solid line) and their theoretical fits by Gamma (solid-dotted line) and Lognormal (dotted line) distributions as a function of time (in days). P values are those of Kolmogorov-Smirnov tests between the observed distribution and each theoretical one. Tags indicate the corresponding dates of beginning, peaks of observed and Gamma distributions, and end in 2020.
Fig. 3. Study 2. Histogram of probability density function (in frequency) of COVID-19 observed daily cases in Belgium (BE), Spain (SP), Italy (IT), France (FR), Finland (FI), Czechia (CZ), Slovenia (SL), Lithuania (LI), Croatia (CR), and Latvia (LA). Other notations as in Fig. 2.
Fig. 4. **Study 3.** Histogram of probability density function (in frequency) of COVID-19 observed daily cases in Belgium (BE) and Italy (IT) using 7-day moving averages (solid line) and their theoretical fits by Gamma (solid-dotted line), Lognormal (dotted line), Gaussian (dashed line), and Weibull (dash-dotted line) distributions as a function of time (in days). Other notations as in Fig. 2.
calculated the peak value in daily case frequency: from a minimum difference between the observed distribution and the Gamma fit of two days for Lithuania to six days for France (see Fig. 3).

Finally, we compared the two groups of countries (Study 1 vs. Study 2). The between-group difference was different for parameter $I$ (Mann-Whitney $U$ test, $Z = -2.57$, $P < .05$), but not for parameter $n$ due to high variability ($Z = 1.96$, $P > .05$).

2.3. Study 3: Fine-tuning the comparison between gamma and other distributions

As one may argue that the Lognormal distribution is insufficient to demonstrate our Gamma approach’s superiority, we conducted another control using further distributions. While Poisson and Gumbel were excluded for theoretical reasons (see Discussion section), we challenged our Gamma approach with Gaussian and Weibull distributions.

Gaussian and Weibull distributions have frequently been used in medical studies (Collett, 2015). Furthermore, the Weibull distribution has recently been proposed to model the serial interval distribution in the COVID-19 pandemic (Adam et al., 2020). We can write the Weibull PDF as in Equation (5):

$$f(x) = \frac{a}{b} \left( \frac{x}{b} \right)^{a-1} \exp \left( -\left( \frac{x}{b} \right)^{a} \right)$$

where $a$ and $b$ are the shape and scale parameters, respectively.

The Weibull mean is $b \Gamma \left( 1 + \frac{1}{a} \right)$ where $\Gamma$ is the Euler gamma function. We manually set the shape parameter $a$ by trial and error, then $b$ is calculated from $a$. In our study, we obtained the best result when $a$ was set to 3 so that $b$ was 55.

Data for the fifteen countries of studies 1 and 2 are shown in Table 2 and for two countries in Fig. 4.

As shown in Table 2, our Gamma distribution offered a better fit and corresponding P-value than did other distributions in most, but not all, cases. Indeed, whereas Gamma distribution better fitted the observed curve compared to Lognormal distribution in 100% of the fifteen countries (see Table 1), the Gamma distribution better fitted the empirical distribution in 11/15 or 73% of countries when compared to the Gaussian one, and in 9/15 or 60% of countries when confronted to the Weibull one.

For clarity of display, Fig. 4 shows only two countries that the early stage of the pandemic dramatically hit: Belgium and Italy. As evidenced by P-values, the Gamma distribution better fitted the observed data than all other distributions in these two examples.

3. Discussion

The present study introduced a new view of the well-known Gamma law, in which we now set the parameters from a statistical-physics-based calculation. Using data from fifteen countries undergoing the COVID-19 pandemic, we showed the goodness-of-fit of the Gamma law compared to other distributions. The main findings were as follows. (1) In fifteen countries where the public health policy has been either rigorous or accommodating, our Gamma law approach better fitted the distribution of observed daily cases of COVID-19 than did another skewed distribution, the Lognormal law, in 100% of countries. (2) Using symmetrical (Gaussian) or other skewed (Weibull) distributions, our Gamma law approach better fitted the observed data in 73% of countries against the Gaussian law and 60% of countries against the Weibull one. (3) New Gamma distributions have been used in medical studies, should they have a positive skewness as Gamma or not (Collett, 2015). We could not use the Poisson distribution as its unique parameter $\lambda$ equals both the mean and the variance, which was not the case in our observed data. The Gumbel distribution exhibits a positive skewness, and its PDF is given by Equation (6):

$$F(x) = \exp \left( -\frac{x-m}{\beta} \right)$$

where $m$ is the mean of variable $x$ and $\beta$ a given parameter.

Though the Gumbel distribution is easy to use as it involves only one parameter, we abandoned it as no value of $\beta$ provided a satisfying result. The Lognormal distribution, another skewed distribution used elsewhere against Gamma distribution in meteorology or hydrology (Cho et al., 2004), was chosen as an excellent theoretical fit in our Study 1, though weaker than our Gamma approach. Study 3 introduced the Gaussian distribution as a possible control, and 4/15 countries showed that the observed data could fit a symmetrical distribution, consistent with previous studies (Adam, 2020; Ferguson et al., 2005; Ferguson et al., 2006). Ferguson et al. (Ferguson et al., 2006) modelled the mitigation of the influenza pandemic and ended up with a Gaussian distribution to describe the evolution of cases. Gaussian and Gamma plots can become similar when $n$ reaches a high value of 80 or more. More recently, studies have provided evidence that the Gamma law well describes experimental data though they did not offer, contrary to our present study, the theory demonstrating the relevance of the law (Li et al., 2020; Verity et al., 2020). Using the $\theta$-SEIHRD model to plan the need for beds, the study by Ivorra et al. (Ivorra, 2020)
Our second study gathered the ten most impacted countries following our criteria (see Supplementary Material section S2). The policy has presumably been more tolerant at the early pandemic stage. The results showed that our Gamma approach better fitted the observed than did the Lognormal law in 10/10 countries (Study 2), the Gaussian law in 7/10 countries (except Spain, Slovenia, and Croatia), and the Weibull one in 7/10 countries (except Spain, Czechia, and Croatia). We saw above that the new Gamma parameter $\tilde{I}$ was higher in Study 2 than in Study 1 (3.7 ± 1.4 against 1.8 ± 0.8 days, respectively). To clearly understand why a strict public health policy of detection-isolation decreases the parameter $\tilde{I}$, there is a need to come back to the contamination tree (see Introduction section and Fig. 1). Let us imagine that a country policy allows restricting to 1 the number of contaminated patients by a given individual. The consequence is that patient $P_3$ only contaminates patient $P_3$. Thus, the longest components $I_3 (P_3, P_2$ and $P_2, P_1$) are eliminated (see Fig. 1). The same occurs for successive patients (not shown in the figure) $P_4, P_5, P_6 (3 < i \leq n)$, thus reducing parameter $\tilde{I}$. As Maier and Brockmann (Maier & Brockmann, 2020) emphasized, each government strategy aiming at limiting the impact of the pandemic had a crucial role in the evolution of cases and deaths. This explains why the curve exhibited a sub-exponential start in China at the epidemic’s beginning. In contrast, we expected a faster exponential starting curve, as was the case in H1N1 in 2009 (de Picoli Junior et al., 2011) or Ebola in 2014 (Hunt, 2014). Similarly, Flaxman et al. (Flaxman et al., 2020) have explored the critical role of non-pharmaceutical interventions in eleven European countries and shown that national lockdowns and closure of schools indeed reduced the spread of COVID-19. Consequently, any time delay in such interventions yields a PDF with a faster initial phase than expected by the Gamma law. For instance, this was the case in our study for Spain and Italy (see Fig. 3). Our demonstration and findings, together with the explanation of previous intuitive or qualitative studies (Giordano et al., 2020; Iovra et al., 2020; Q. Li et al., 2020; Sanchez et al., 2020; Verity et al., 2020), evidence that the temporal distribution of cases follows a Gamma law, which we defined here in extenso. Results also validate the general hypothesis according to which the distribution laws of all $I_i$ are identical thus yielding Equation (3). More recently, Oliu-Barton et al. (Oliu-Barton et al., 2021) compared anti-COVID-19 measures of two groups of countries of the Organisation for Economic Co-operation and Development (OECD) depending on whether they chose a strategy of SARS-CoV-2 elimination or mitigation. In countries of their first group (gathering Australia, Island, Japan, New Zealand, and South Korea), the number of deaths was 25 times weaker than that of countries of their second group (Austria, Belgium, Canada, Chile, Colombia, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Israel, Italy, Latvia, Lithuania, Luxembourg, Mexico, Netherlands, Norway, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden, Switzerland, Turkey, the UK, and the USA). Though their study did not mention the SI, we reexamined our data using their classification and our selection criteria (see Supplementary Material section S2). Only one country (New Zealand) remained in our first group, while ten countries made up the second group (Austria, Belgium, Czechia, Finland, France, Germany, Israel, Italy, Slovenia, Spain). Consistent with our initial classification, our Gamma $\tilde{I}$ value was 1.3 days in only New Zealand vs. 3.1 days in the new group of 10 countries. In other words, an elimination strategy of
SARS-CoV-2 may yield a lower $\bar{I}$ than does a mitigation strategy. The influence of public health policy on parameter $n$ is more challenging to demonstrate. Only a stringent policy may limit the number of cascades in the contamination chain and finally stop the epidemic. This is what we observe in China, a large and high populated country, where the number of cascades might be potentially enormous if one waits the pandemic to vanish itself. However, parameter $n$ is only 17 in China, the lowest of our first group, probably due to the rigorous policy of isolation (complete lockdown). In our Study 2, low values of $n$ could be observed, which always concerned small and low populated countries where the patient reservoir is limited. Our assumption is corroborated by the observation that the pandemic can end when the availability of susceptible individuals decreases (Cobey, 2020). In summary, we suggest that parameters $n$ and $\bar{I}$ are influenced by each country’s national public health policy, though differently. Parameter $\bar{I}$ is lowered as soon as the country takes efficient measures of detection-isolation, whereas parameter $n$ may only be influenced by a full and rigid lockdown.

To conclude, as COVID-19 spread draws a contamination tree, it is virtually possible to apply our Gamma law approach to any problem involving a branching system. Nature offers many branching systems: rivers, trees and plants, aerial branching system, underground roots, corals and lichens, phylogenetic trees in genetics, family tree structure in demography, dendritic growth of crystals. Further applications may concern biology and physiology: blood networks, lung networks, neural networks, etc. Thus, our Gamma law approach offers promising directions to inspire future scientists in various disciplines involving branching systems.

**Author contributions**

JD and OAC conceived the study and wrote the manuscript.
JD developed the mathematical theory and algorithm.
OAC made the coding.

**Data availability statement**

Data are fully and freely available at https://www.worldometers.info/coronavirus/.

**Declaration of competing interest**

The authors declare no conflict of interest.

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None.

**Appendix A. Supplementary data**

Supplementary data to this article can be found online at https://doi.org/10.1016/j.idm.2022.02.004.

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