A universal generic description of the dynamics of the current COVID-19 pandemic

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Based on the analysis of the empirical data for the number of infections in more than 20 countries we propose here a hitherto unknown universal model for the spreading of the COVID-19 pandemic that depends not on time, but on the number of infections itself. This change of the independent variable overcomes the crucial issue of analyzing very different countries worldwide within one mathematical framework with similar parameters. This was previously impossible leading to individual description for every country. Our model allows describing the pandemic including its endpoint surprisingly good and giving a figure of merit for the success of the measures to fight the pandemic.

The continued pandemic caused by the SARS-CoV-2 puts enormous pressure on every aspect of society worldwide. From a scientific viewpoint, the fundamental challenge is to simulate the evolution of this pandemic based on limited, mostly empirical data. These simulations are quintessential on multiple levels: (a) to predict the time frame and overall number of infections, (b) to correspondingly prepare the medical and economic infrastructure, (c) to enact mitigative measures to “flatten the curve”, and (d) to learn from this dynamic for future pandemics.

Quite generally, there are two strategies to model pandemics. The “micro”- method would be to follow the fate of each member of the population modelling, its contacts and its infection happenings to microscopically model the pandemic in the way of a “Maxwell Demon”. Like in thermodynamics, this is not possible due to the lack of sufficient information. Therefore, in the other strategy, only average “macroscopic” aspects are taken into account. Most models are based on the so-called SIR model or extensions from it \cite{1-9} and depend on time as the independent variable. These models use multiple parameters like basic reproduction number
\( R_0 \) [2,8,10], average times of infection and recovery, and rates for mitigation measures (see e.g. [10]) to be fit to data. All these parameters are macroscopic averages thought to characterize a pandemic. As a consequence every country which has become a hotspot for the pandemic had to be treated individually with hugely varying conclusions (see e.g. [10-26]). This in turn has led to very different approaches to tackle the crisis even in geographically and culturally close countries. Furthermore, the rather abstract nature of the parameters of these models has provoked a lack of public insight undermining the authority of governments worldwide in this time of crisis. A serious problem of this approach, which has been overlooked in the current discussion and might explain the large sensitivity on the free parameters in these models, is that it suffers from chaotic behavior [27] making it difficult to grasp any generic behavior of the pandemic.

At first glance, using time as an independent variable seems to be natural, but it comes at a cost. Completely decoupled from the actual infectiousness of the virus or explicit measures taken by the government, the dynamics on a time scale get affected by many specifics of a region, like standard mobility – both the capability to travel as well as the actually performed travel – or culturally common group sizes and regular distances. If, in general, travel or meetings occur at all within the incubation time, one would expect that a similar fraction of the people get infected by the virus, independent of how frequent these meetings or travels are. Yet, it will naturally happen on different time scales, changing the fit parameters without any new insight on the disease. Furthermore, in all models a pandemic ends at infinite time, not allowing for a mathematically rigorous definition of the endpoint. Hence, we are suspicious whether time really is a good variable to study the generic laws of a pandemic.

Inspired by the Gompertz model [3, 7, 28] which allows a description of a pandemic irrespective of time, here we take a quite different approach by looking at the new infections as a function of totally infected people. By the above logic, the mentioned virus-independent variations in every country should be irrelevant, creating a much reduced complexity to analyze. Due to the extreme travel restrictions imposed worldwide, most countries have effectively removed travel across its borders. This isolation yields the unique advantage of having almost perfectly closed systems with fixed population numbers and supplies a huge number of experimental realizations of the pandemic. By analyzing the empirical data from countries with sufficient resources to give somewhat reliable infection numbers, we have been able to extract a simple generic law for the general dynamics of the pandemic. This law describes the increase of the doubling time \( D \) as a function not of time, but of the total number
of infections. The law depends, besides on the doubling time $D_0$ at the beginning of the pandemic characterizing the initial spread of the infection, on two more parameters: a proportionality constant $\rho$ coined “mitigation factor” that describes an exponential growth of $D$, and the end point of the pandemic $N_{\text{finit}}$, both crucially depending only on the enclosed population. Other parameters assumed to be relevant like the population density show surprisingly little relevance in this model.

Based on this very simple model we show that all centers of outbreak follow this law. Furthermore, it allows us to identify different waves in specific countries as well as the onset and easing of measures, evaluate the usefulness of certain measures, and, most important, provide a criterion for when the epidemic ends. All of this allows drawing very general conclusions on how the pandemic evolves in different countries, how to act now, when a new wave of outbreaks hits or a new pandemic arises.

**Results**

Provided that the fraction $\nu$ of infected persons $N$ is much smaller than total population $N_0$ (which for the current pandemic is the case), a pandemic with exponential growth can be described by the simple differential equation [2,3,7,25]

$$N_0 \frac{d\nu}{dt} = \Gamma \cdot \nu N_0,$$  \hspace{1cm}  (1.1)$$

where $\Gamma$ denotes the growth constant which is related to the doubling time $D$ by $\Gamma = \ln(2)/D$. Usually $\Gamma$ is assumed to be constant and to obtain the full dynamics of the pandemic one extends the simple equation (1.1) either into a set of non-linear coupled differential equations using a so called SIR model (or extensions), see e.g. [3,10]. The other possibility is to assume $\Gamma$ to be time dependent as in the Gompertz model where one assumes $\Gamma = \Gamma_0 \exp(-rt)$ [3]. Integration of Eq. (1.1) then leads directly to the Gompertz function $N(t) = N_{\text{finit}} \exp(-\Gamma/r \exp(-rt))$ with $N_{\text{finit}}$ the maximum number of infected persons, i.e. the endpoint of the pandemic. This model has been used, e.g., to analyze the COVID-19 pandemic in Germany [28] and Iran [29].

For the Gompertz model it is well known [3] that Eq. (1.1) can be cast into a form which completely eliminates time

$$\frac{1}{N} \frac{dN}{dt} = r \ln \left( \frac{N_{\text{finit}}}{N} \right),$$ \hspace{1cm}  (1.2)$$
removing in the process also $\Gamma_0$ from the equation.

Since the left hand side is nothing else than $\ln(2)/D$ one can empirically test the validity of the Gompertz model if the doubling times as function of $N$ follow

$$D(N) = \frac{\ln(2)}{\ln(N_{\text{final}} / N)}$$

(1.3)

Obviously, one can characterize with such a graphical representation, which we will call a “Gompertz plot”, the generic dynamics of a pandemic independent from any modelling assumptions. For a first test we choose four countries (or states) with a wide spread in population numbers namely the state of Hamburg (HH) in Germany, Switzerland (CH), the Netherlands (NL), and Italy (I). In all countries we can expect the data to be reliable. The infection data were taken from sources [30,31]. Given a time series of infection data

$$\{t_i, N_i; \quad i = 1\ldots M\},$$

an estimate for $D(t)$ can be calculated by

$$D(t_i) \approx (N_{i+1} - N_i) / [N_i \cdot (t_{i+1} - t_i)].$$

As shown in Fig. 1a, for all four cases the dependence of $\log(D)$ on $N$ seems to follow the Gompertz relation (1.3) as shown by the full lines with the same color as the dots, and also the infection numbers themselves are well reproduced (Fig. 2b). However, a closer look reveals some systematic deviations. So are both the initial overshoot and the following undershoot not present in the data. Rather, they seem to follow a strictly linear dependence in the first stage of the pandemic (phase 1, exponential dependence of $D$ on $N$). Also in the final phase 2 the super-exponential increase diverges to fast resulting in endpoints of the pandemic which are below the already reached infection numbers. So one needs a more flexible description, as is provided by the following “ansatz” for the growth constant $\Gamma$

$$\Gamma(vN_0) = \frac{\ln(2)}{D_0} \exp(-\rho_0 \cdot vN_0) / f(vN_0).$$

(1.4)

The constant $\rho_0$ will be designated as the “mitigation factor” as it reflects the effectiveness of mitigation measures and $D_0$ the initial doubling time. The function $f(N)$ describes a super-exponential growth of $D$ and can be assumed as\(^1\)

$$f(N) = 1 + \frac{1}{25} \tan^2 \left( \pi \frac{N}{2N_{\text{final}}} \right).$$

(1.5)

\(^1\) This function has been chosen because it describes the empirical data rather well.
As seen by the full black lines in Fig. 1a, with an appropriate choice of $D_0$, $\rho_0$ and $N_{\text{finit}}$ Eq. (1.4) with (1.5) give an almost quantitative description of the empirical data.

The results for the parameters that generate the black lines in Fig. 1a are given in Table 1. One expects $D_0$ to be almost constant, $\rho_0$ and $N_{\text{finit}}$ are expected to depend on the number of inhabitants of the country chosen, which were taken from [32], and indeed this is the case.

For a straightforward solution of Eq. (1.1) (together with Eq. (1.4)) with a differential equation solver we need to specify only the number of infections $N_{\text{start}}$ at a certain date $t_{\text{start}}$ where we set the origin of time to the 1st March 2020, and used the parameters $D_0$, $\rho_0$ and $N_{\text{finit}}$ from table 1. The results are shown in Fig. 1b. As obvious from the plots in Fig. 1B, the empirical data are extremely well described by our model (black lines). Exemplarily, the time dependence of the doubling time is shown for Switzerland (blue circles and lines). In the first days of the pandemic the doubling times are almost constant (with some statistical jitter due to the small numbers) leading to the exponential growth of the infection number. Then the measures used by all countries to control the epidemic begin to work and the doubling times increase. In the Gompertz model this increase is linear on a logarithmic scale. For later times the empirical data clearly deviate from this dependence, which our model is able to describe. Note the quite substantial non-linearity, despite the simple laws given by Eqs. (1.1) and (1.4).

The mitigation factors show a pronounced dependence on the number of inhabitants with the product $N_0 \cdot \rho_0$ being almost constant (see Table 1) suggesting a relation of the form

$$\rho = a \cdot N_0^b \cdot \rho_0$$  \hspace{1cm} (1.6)

Even more astonishing is the last entry of Table 1 that gives the product of the mitigation factor and the end number of infections turns out to be almost constant. This means that the end of the pandemic is closely related to the exponential increase of doubling times with the infection numbers suggesting a relation

$$N_{\text{finit}} = c \cdot \rho^d$$  \hspace{1cm} (1.7)

To check whether these relations are indeed a generic behavior of the pandemic, we applied our model to a large number of other countries, i.e. Austria (AU), France (F), United Kingdom (UK), Spain (E), Sweden (S), Denmark (DK), Hungary (H), Czechia (CZ), Belgium (B), Ireland (IR), Iceland (IS), Russia (RU), South Korea (SK), New Zealand (NZ), United
States of America (US), Brazil (BR), India (IN), and also to several states of Germany like Bavaria (Bay), North Rhine-Westphalia (NRW) and Mecklenburg-Western Pomerania (MV). In our analysis we also included Africa (AFR) to see whether here the pandemic follows similar laws. For all cases the detailed fits of the doubling times and the solutions of Eq. (1.1) are plotted in Fig. S2 to S8 (see SOM). The parameters of the fits and the number of inhabitants in each country or province can be found in Table S1. One should note that most of the countries follow the regular behavior shown in Fig. 1: an exponential increase of the doubling time followed by a super-exponential growth. However, there are some exceptions. In case of CZ the super-exponential growth is completely missing up to now. In some other cases (S, US, RU, IN, BR, AFR) we clearly see two phases of the pandemic with different mitigation factors, but no super-exponential growth period. For two cases DK and SK we see a complex multi-phase behavior with a super-exponential growth at the end. However, as shown by the fits in Figs. S6F, S7 and S8 the pandemic can still be described also in these cases by our ansatz, but with a multi-mode behavior where

\[
\Gamma(vN_0) = \sum_i \Gamma_{0i} \exp(-\rho_{0i} \cdot vN_0) \Theta(v_{bi} - v)\Theta(v - v_{ei}) \big/ f_i(vN_0),
\]

(1.8)

with \( \Theta(x) \) being the Heaviside step function and \( v_{bi}, v_{ei} \) denoting begin and end of the \( i^{th} \) period of the pandemic, respectively. In other words, our model clearly detects different phases of the pandemic, which, as will be discussed below, are related to onset and loosening of measures in the respective regions. All these cases will be indicated with blue color in Fig. 2 where part a shows the results for the mitigation factor plotted against the number of inhabitants, while part b shows the end points of the pandemic in each country vs. the mitigation factor. The initial doubling times are plotted in Fig. S1.

**Discussion**

In Fig. 2a the mitigation factors fall into two groups (denoted by full and open red triangles), which behave quite similar with respect to the population numbers only differing in the absolute magnitude of \( \rho \) by a factor of 8.6. The “irregular” cases either switch between these groups (as DK or BR) or stay in the same group (as RU, US, or IN). The full and dashed lines are the result of a logarithmic regression of Eq. (1.6) giving the following parameters:

\[
an = 1003 \pm 246 (\text{with } a = 117 \pm 30 \text{ for the dashed line}) \text{ and } b = -1.06 \pm 0.07.
\]

In Fig. 2b the countries with regular behavior are given by the full triangles obviously following very good our ansatz Eq. (1.7), the regression giving \( c = 0.460 \pm 0.054 \) and \( d = -1.050 \pm 0.013 \).
open blue triangles denote those countries which are still in the exponential growth regime, whereby the endpoints calculated with Eq. (1.7) have been used as ordinates. In case of Sweden and Czechia (full blue triangles) this was not possible as the actual numbers of infections are higher than the expected endpoints. This indicates a difference in the pandemic control (“Swedish model”). This seems also to be the case for South Korea (green triangle) due to the complex multi-phase behavior that can be traced back to the different stages of the pandemic.

The combination of Eq. (1.6) and (1.7) shows that the maximum number of infections and the number of inhabitants of a country is closely correlated, provided that the country uses the standard measures of border control and social distancing. We can therefore define as figure of merit for the effectiveness of pandemic control the ratio

\[ M = \frac{\frac{a d}{c} N_{\text{pop}}^{b-d}}{N_{\text{finit}}}, \]  

(1.9)

which is plotted in Fig. 3. Obviously, countries with \( M >> 1 \) have done an excellent job in controlling the pandemic, those with \( M < 1 \) have failed in this respect. Comparing with Fig. 2a we can state that countries with high mitigation factor (near the dashed line) have a very large \( M \), while countries with mitigation factor below the full line in Fig. 2a show a worse performance in the pandemic.

Our model predicts that the main factor that determines the pandemic is the number of inhabitants in each country. However, one expects that also the density of population has some influence. That such effects are indeed influencing the mitigation factor can be seen by a comparison of MV with HH (see table S1) which have almost the same population with a ratio of 35 in population density, but the mitigation factors differ by a factor of 6.5. Therefore this must be of minor importance (see also Fig. S9).

Finally, we shortly discuss the problem of correct infection numbers which is inherent in all modelling studies. Increasing the number of infections by \( \varepsilon \), the daily doubling time is not altered, only the mitigation factor is reduced by \( 1/(1+\varepsilon) \). This means that countries like India would move towards the regular behavior (full line in Fig. 2a). The important relation between the endpoint and mitigation factor (Fig. 2b) is not changed at all. This means that our model is quite robust against uncertainties in the exact number of infections.
What is most important for the community is that our model can be applied easily to the world as a whole. This is shown in Fig. 4, where the Gompertz plot shows that the pandemic is still in phase 1, with the endpoint still too far to be detectable. However, from the mitigation factor and relation (1.7) one can estimate that in the end about 90-100 Millions of people will be infected.

In conclusion, we have shown that the current COVID-19 pandemic follows generic laws that can be described by three parameters, the initial doubling time $D_0$, the mitigation factor $\rho$, and the endpoint of the pandemic $N_{\text{fin}}$. We find the initial doubling time to be almost the same for all countries investigated, the mitigation factor and the endpoint, however, depending mainly on the number of inhabitants of the area that is closed during the pandemic, and which is mostly identical with the population of a certain country. Therefore, our model allows the qualitative prediction of the pandemic for any country only from the number of inhabitants. Furthermore, by calculating the figure of merit $M$ (Eq. (1.9)) one can assess the success of the measures taken to reduce the pandemic. Finally, we stress that we only considered the number of infections. Whether the death toll also can be described by a similar generic law is under study.

**Methods**

We used for our analysis of the pandemic the numbers provided by the daily list of the “worldometer” organization [30] and the German newspaper “Die Morgenpost” [31]. All data used can be found in the Supplementary Materials. The mitigation factor $\rho$ and the endpoint of the pandemic were obtained by a least square fitting of the logarithm of the doubling times to Eq. (1.4) using standard statistical methods. The same has been done with the regression of Eqs. (1.6) and (1.7) to obtain the parameters $a, b, c$, and $d$. As differential equation solver we used the routines from MATHCAD15 [32], an example can be found in the supplementary material.
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Supplementary Material
Figures S1-S9
Tables S1
Data file Data_corona1.xls
Program file Italy_cor.pdf
| Country      | Inhabitants in millions $N_0$ | $D_0[d]$       | $10^4 \cdot \rho_0$ | $N_{\text{finit}}$ | $10^{-3} \cdot N_0 \cdot \rho_0$ | $N_{\text{finit}} \cdot \rho_0$ |
|--------------|-------------------------------|----------------|---------------------|--------------------|----------------------------------|----------------------------------|
| Hamburg (HH) | 1.82                          | 2.07±0.11      | 6.73±0.20           | 5300±75           | 1.226±0.036                     | 3.57±0.12                        |
| Switzerland (CH) | 8.65                      | 2.02±0.11      | 1.12±0.03           | 32000±150         | 0.97±0.03                      | 3.47±0.11                        |
| Netherland s (NL) | 17.13                  | 3.22±0.11      | 0.655±0.107         | 49000±200         | 1.122±0.029                    | 3.21±0.08                        |
| Italy (I)    | 60.46                         | 3.02±0.07      | 0.142±0.002         | (2.51±0.02) × 10^4 | 0.861±0.012                   | 3.57±0.06                        |

**Table 1.** Model parameters for the four countries as obtained from the fits in Fig. 1A. The second column gives the number of inhabitants in 2020, the third the initial doubling time, the fourth the mitigation factor, and the fifth the number of infected people at the end of the pandemic. The sixth and seventh column give the products of mitigation factor with the population number and with the number of infected people at the end of the pandemic.
Fig. 1. a) Daily doubling times as calculated from the number of infections vs. number of infected persons for three countries: HH Hamburg (red), CH Switzerland (blue), NL Netherlands (blue), I Italy (green). The data show clearly a two-phase behavior, first an exponential increase (full lines) followed by a super-exponential behavior (dashed lines), the divergence of which denotes the endpoint of the pandemic in each country.
b) Time dependence of infected persons. Dots: empirical data, lines: results obtained from solving Eq. (1.1) and (1.4) using the parameters from Table 1. The open blue triangles and the blue full line denote the dependence of doubling time on time for the Netherlands (right ordinate)
Fig. 2. Part a: Mitigation factors \( \rho \) vs. the number of inhabitants for various countries. The red triangles are those countries (first group) which have been included in the logarithmic regression with Eq. (1.6) giving the full line, the open triangles are the countries of group 2 which give in the regression the dashed line.

Part b: Endpoints of the pandemic vs. the mitigation factor. The full red triangles denote countries with a clear transition into a super-exponential increase of the doubling times (phase 2), which have been included into a logarithmic regression with Eq. (1.7). The open triangles denote countries which are still in phase 1. The expected endpoints are calculated using Eq. (1.7). The full blue triangles indicate countries which either show a complex dynamic as South Korea or that the endpoint calculated with Eq. (1.7) is smaller than the actual infection number indicating that our model is not applicable (see discussion for Sweden). The full list of countries and abbreviations is given in Table S1.
Fig. 3: Figure of merit $M$ (see Eq. (1.9)) for the countries investigated. The full line indicates $M = 1$, the dashed lines give the standard deviation of $M$ from the statistical errors in the parameters a, b, c and d.
Fig. 4: Analysis of the world-wide COVID-19 pandemic with our generic model. The panel shows the time dependence of the infection numbers, red triangles are the empirical data, the full red line give the result of our model using $N_{\text{init}} = 95$ million. The green dots gives the doubling times with the green lines showing the result of the calculation. The inset shows the “Gompertz” plot of the doubling time $D$ vs. infection numbers. It clearly reveals that the pandemic is still in phase 1.
Table S1.
Parameters for all countries investigated. The second column gives the shortcuts used in Fig.2 and 3, the third column the number of inhabitants taken from (7). The fourth columns gives the initial doubling time, the fifth the mitigation factor and the sixth the product of the mitigation factor with the number of inhabitants.
Fig. S1.
The initial doubling times vs. population numbers for the countries shown in Fig. 2. The symbols have the same meaning as in Fig. 2a. The red line gives the average value of $D_0 = 2.5\,d$. 
Fig. S2. Left side: Daily doubling times as calculated from the number of infections vs. number of infected persons for the indicated countries. Blue triangles: data used to fit the growth factor (red lines), red triangles: data use to fit the superexponential growth (blue lines). Right side: Time dependence of infected persons. Blue and red dots: empirical data, lines: results obtained from solving Eq. (1.1) and (1.4) using the parameters from Table S1. The green points denote the daily doubling times, the full green lines denote the fit results including phase 2, dashed line is without phase 2.
Fig. S3: same as Fig. S2
Fig. S4: Same as Fig. S2.
Fig. S5: Same as Fig. S2.
**Fig. S6:** Same as Fig. S2.
Fig. S7: Same as Fig. S2.
**Fig. S8:** Same as Fig. S2.
Influence of Population density

Fig. S9

Effect of the population density on the growth factor. Plotted is the ratio of growth factors for a pair of countries with approximately the same number of inhabitants vs. the ratio of their population densities. The red squares give the ratio of growth factors multiplied by the ratio of population numbers to correct for that influence, the red circles are obtained by multiplying with a correction factor $\gamma$ which indicate differences in the social distancing. Values are UK/F=0.55, DK/NZ=1.29 and US/BR=0.83 (a value<1 means that the first country of the pair has better control over the pandemic). The full line is the function $0.79/x^{2.2}$ with x the ratio of densities. The diagram clearly shows that there is indeed a influence of the population density on the pandemic, but since it depends only on the square root it is of minor importance.
