

The SARS-CoV-2 Pandemic – a Dissipative Process and its Attractor - Interpretation of Observed Data

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Summary

The pandemic is assumed to be a dissipative process. Therefore, the daily incidences of infected persons is transformed by taking their logarithm. First, the time evolution of the SARS-CoV-2 pandemic in Germany is investigated. The resulting graph can be sub-divided into several distinct sections. Each of which is characterized by a regression line described by means of the parameter point (a, b) . Thereafter, the database is extended to 12 countries in order to have at our disposal enough points. The spatial distribution of the points is discussed in detail resulting in the identification of an attractor. Thereby an improved understanding of the course of the pandemic may be garnered.

Key words: SARS-CoV-2 pandemic, dissipating process, incidence rate, mortality rate, attractor, quadratic iterator

1 Introduction

The SARS-CoV-2 pandemic has acquired, in an extremely short time, a significant importance for science and for the public life in general. The present paper deals with the investigation of observed data for that pandemic from a mathematical viewpoint.

The basic idea is to treat the pandemic as a *dissipating process*. Typical of such processes is, on the one side, feeding and, on the other side, run-off. In the case of SARS-CoV-2 this means infection and course of the disease, respectively. The existence of exponential laws is a well known characteristic of dissipating processes.

Up to now, a large amount of basic scientific literature has been accumulated dealing with dissipating processes. We pick out mainly Falconer (1990), Kortus (2020), and Peitgen et al (1994). Neunhöfer & Hemmann (2005) discussed a similar investigation applied to earthquake swarms in the Vogtland (Germany) and in Western Bohemia (Czech Republic) region. That investigation deals with the exponential law between the frequency and the magnitude of earthquakes, which is well known in seismology since Gutenberg (1956). Neunhöfer (2020) already dealt with the SARS-CoV-2 pandemic, however, the present paper generalises the course of the pandemic such that at any time an exponential character exist no matter if the incidences rise or drop or remain constant.

The data used of this study include the daily incidence of infections and the daily incidence of died persons. The data sources are Radtke (2020/21) for Germany and ESDC (2020) for the other countries taken into consideration. The quality of the data is quite good, but they are significantly biased with a weekly period. Biases of more then 50 percent are reduced by a rough procedure of now-casting. Nevertheless, the strength of the weekly periodic bias can not be overlooked as shown later in Fig. 1.

2 Time course of the pandemic

Let n be the daily incidence of SARS-CoV-2 infections which should be described as an exponential process n in time t :

$$n = \exp(a+b \cdot t). \quad (1)$$

b may be positive or negative depending on whether the rate of incidence is increasing or decreasing.

(1) is characterized by the parameter point (a, b) . After taking the logarithm of both sides, it follows

$$n' = a+b \cdot t. \quad (2)$$

The exponential curve of n versus t changes into a line of n' versus t . Both formulas are characterised by the same point (a, b) which can be calculated from (2) by linear regression. Taking the logarithm is accompanied by warping which should be approximately corrected as discussed by Neunhöfer (2020).

The data of the pandemic are available in a sampled manner. Let \mathbf{N} be the set of all investigated data. \mathbf{N} consists of a number of subsets N_i , $i=1, 2, \dots, 12$. Each of them holds for a the state i . The separation according to different states takes account the existence of different infection rates r induced by different habits of the population and different reaction of the administration to the pandemic. Each subset consists of n_j , $j = 1, 2, \dots, t_i$ values. Let n_1 be the incidence at the day when the pandemic began in the state i , and t_i the length of the data subset in that state. In particular, there holds $t_i = 460$ for Germany and $276 < t_i < 300$ for the other states.

Fig. 1 displays the course of the SARS-CoV-2 pandemic in Germany from its onset on 2020, 27th February, until the end of our investigations about 15 months later. The data set is drawn using two different scales: above, n in the Euclidean scale and, below, n' in the semi-log scale. Each of them offer a special view on the course of the pandemic.

Top, the general course of the daily infections of the regarded part of the pandemic is depicted as a bar graph. It illustrates well the existence of three waves of the pandemic, the maximum incidence of the waves which occurred at the end of March, 2020, at mid-December, 2020, and at the mid-April, 2021, respectively. Furthermore, a strong weekly bias of the data of approximately 25% of the particular data level becomes obvious.

In contrast, the lower part of Fig. 1 is better adapted for a changing exponential process and discloses more details of the progress of the pandemic. The change to the semi-logarithmic plot proved to be favourable, if only because the weekly bias reduces significantly. The most important result is that the whole course naturally partitions into a number of discrete sections. Most of them indicates an individual *sub-process* characterized by a point (a, b) which holds during a limited period. Each sub-process can turn after a relatively short transmission into the successive one. Therefore, the pandemic in Germany consists

of 14 sub-processes. A change to the following sub-process can be both an intrinsic feature of the pandemic or a change in the population's behaviour. In fact, the behaviour can occasionally vary as a consequence of administrative orders. When the incidence level is relatively low, so-called *superspreadings* (ss) can be identified. These are relative high incidences observed during a very short time in a closely refined area.

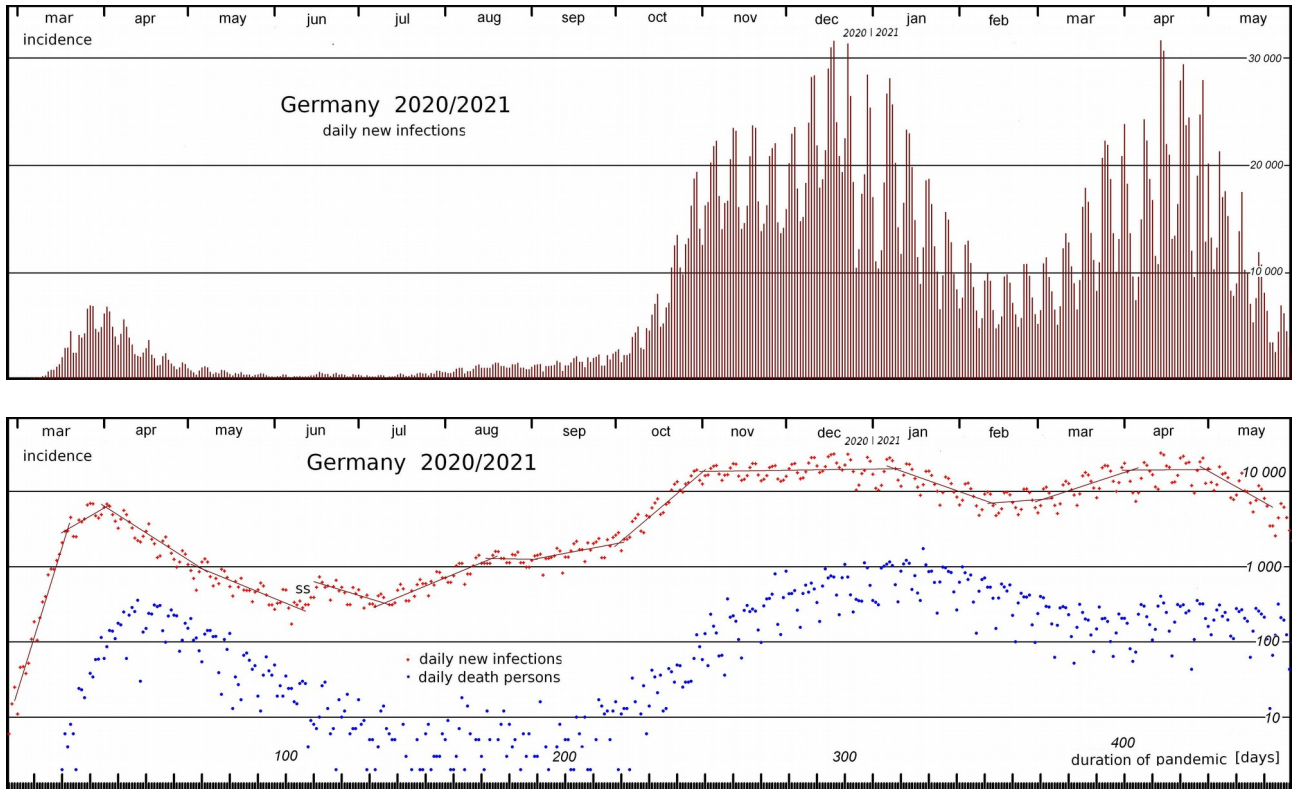


Fig. 1: Daily incidence of SARS-CoV-2 infections in Germany during the first 15 months of the pandemic. In the upper part, the incidence is drawn in the Euclidean scale, in the lower part in the semi-log scale. The time is indicated both calendrically (on top) or related to the beginning of the pandemic in Germany (bottom).

In addition to the incidence of infections, the mortality m of infected persons is an important feature of the impact of the pandemic on public health. The number of death persons per day is shown in the lower part of Fig. 1 (blue points). Compared to the infection rate, the bias is higher and the course is reasonably well correlated to it, but with a time delay and at a lower level.

3 The empiric attractor

This chapter benefits from utilising the semi-logarithmic space. It characterises the performance of the pandemic no longer by the incidences, but by the points (a, b) . \mathbf{P} is the set of all investigated points consisting of 12 subsets P which can be attributed to one state. Unfortunately, the volume of P is much smaller than the volume of N . Under the implicit presupposition that the pandemic has common features in different countries, data from a number of countries may be combined to a common database. In addition to Germany, the European countries Belgium, Czech Republic, France, Great Britain, Italy, Netherlands,

Poland, Spain, and Sweden as well as the Asian countries Japan, and South Korea are included. To make their observations comparable n should be substituted by the incidence density per one million inhabitants d . Furthermore, the d -axis in Figures 2 and 3 is rescaled as if d is a seven-days incidence density.

Following Neunhöfer & Hemmann (2005), Fig. 2 shows how the points of all sub-processes of \mathbf{P} are distributed over the plane b versus d . It is assumed that b is distributed symmetrically to zero, so that $|b|$ is plotted. The d -axis is set to be logarithmic.

All observed points are within the grey shaded area S_0 . It is considered as an approximation of an attractor applicable for the investigated pandemic and the regarded countries. The upper threshold of S_0 inclines for the most part continuously. By the fact, the exponential rise of the incidences according to (1) is slightly subdued. Due to our assumption from above, the lower threshold is $b = 0$.

To demonstrate how different \mathbf{P} can be distributed across S_0 , three sets from \mathbf{P} are marked with colour: first, violet indicates the Japanese data, being typical for a relative weak performance of the pandemic; second, blue indicates the German data, being typical for a relatively moderate performance; and third, green indicates the Netherlands data, being typical for a relative high performance. Even though they partly overlap each other they don't match each other and they vary more widely with respect to d than to b .

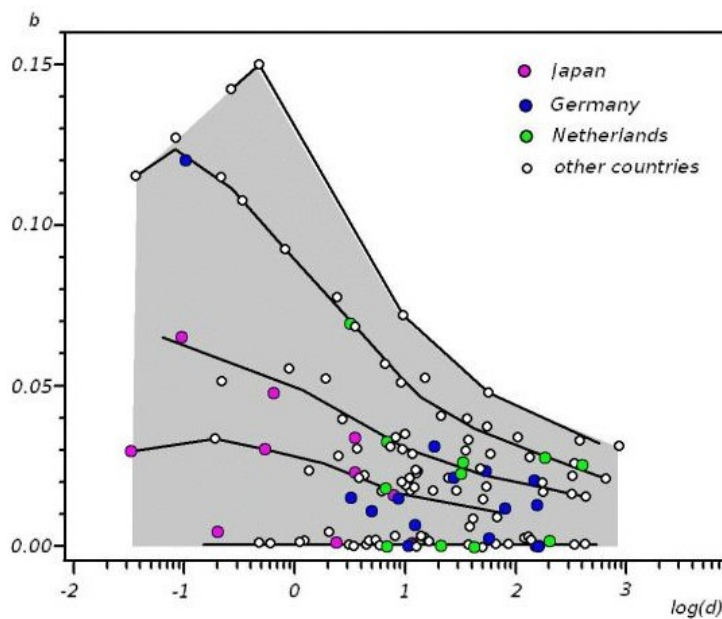


Fig. 2: Distribution of the calculated points of \mathbf{P} over the plane b versus d . The subsets of three countries are highlighted in a different colour. The shaded area is the approximation of an attractor S_0 .

A rough impression of how the points p are distributed over S_0 suggests that they are not distributed randomly and empty areas seem to exist. That's particularly evident in the left part of S_0 and around the lower threshold. However, this impression is not so clear in the rest of S_0 due to both the data inaccuracy and the shape of S_0 .

Fig. 3 will help us to recognize details of the p distribution. At first, there are points displayed as a modified circle. They form the left and the left hand part of the upper threshold of S_0 . These points belong to the initial phase of the pandemic in each country and disclose the pure intrinsic properties of the pandemic. Any other point is influenced by public

measures against the pandemic.

The range $\log(d) > 0$ contains the majority of the points. It is considered as having the best potential to achieve acceptable statistical results. In Fig. 3a, each point of S_0 has been marked with a colour which helps us to discriminate between five groups. A rough smoothing within each group yields the approximate branches

$$b = f_\mu(d), \mu = 0, 1, 2, 3, 4. \quad (3)$$

They are components of the attractor \mathbf{S} of the pandemic whereby each branch represents a distinct performance of the pandemic. The performance can be up or down depending on whether the sign of the observed b is positive or negative. Moreover, there is an indication that for a distinct value of d the distance between adjacent lines is approximately constant.

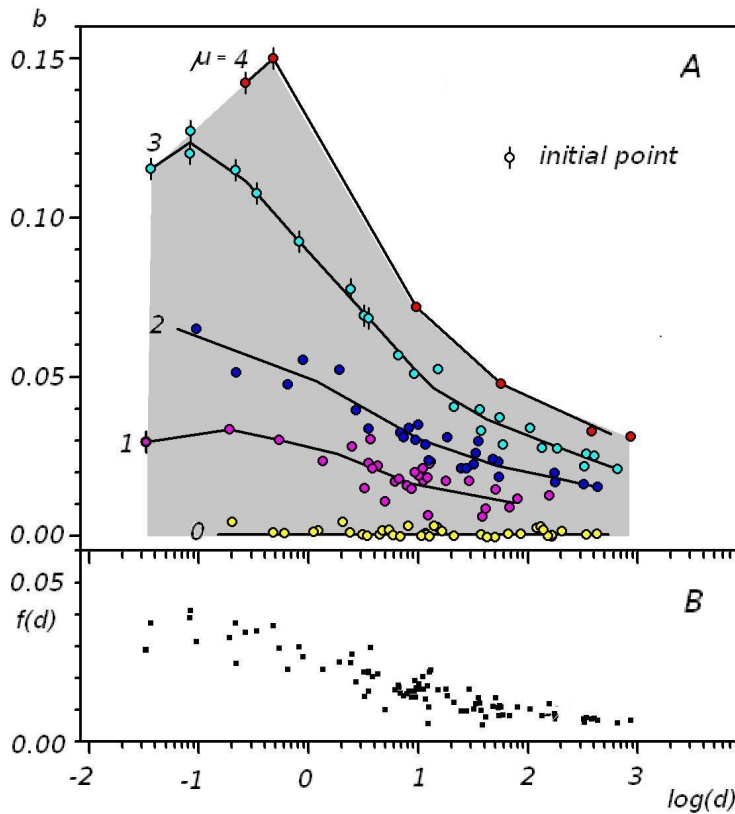


Fig. 3 A: The points within attractor S_0 are divided into five bands differentiated by colour. Within each band the points are roughly smoothed to an approximate curve each of which has been assigned a value μ .

Fig. 3 B: Result of the calculation of the approximated final attractor $\mathbf{S} f(d)$.

Consequently, it holds.

$$b = \mu \cdot f(d). \quad (4)$$

This equation can be considered as model of the SARS-CoV-2 pandemic. μ specifies the current stage or performance of the pandemic.

By applying b/μ , $\mu \neq 0$, each point (d, b) estimates one value of $f(d)$. The result for the whole data set is depicted in Fig. 3B. The distribution of all points approaches well a curve

$f(d)$ which can be regarded as the attractor \mathbf{S} of the data set.

The state of the pandemic at any particular time can be characterized completely by four elements: the infection rate n , the sign of b , the performance parameter μ , and the attractor \mathbf{S} .

With that result the investigation could end here, however, it may be useful to add some interpretation to the result.

4 *Interpretation*

It was shown in section 1 that b keeps constant over a certain period of the pandemic. Applying the model (4) such behaviour holds only if it is restricted to $\mu = 0$, which means, to the SARS-CoV-2 pandemic with constant incidence. Such contradiction between live and modelling Kortus (2020) has already noticed in connection with modelling other natural processes. He proposed as a reasonable explanation the additional existence of a memory or synonymously a hysteresis.

The regularity of b according to model (4) leads to the question: Does the pandemic behave like the quadratic iterator $x \rightarrow \lambda \cdot x \cdot (1-x)$ with λ as parameter? That iterator is well known as an archetypal example of one-dimensional dynamical processes, and it is characterised by the existence of systematic bifurcations or period doubling. The answer should be 'yes'. Then, μ may be *related to* λ and counts the number of the bifurcation the iterator is currently generating.

The combination of the SARS-CoV-2 virus and human population results in the outbreak of the SARS-CoV-2 pandemic. The attractor \mathbf{S} may be a mathematical model and describes how its progression can run. Only near the onset the pandemic reflects the unaffected or intrinsic human vulnerability to the virus. Thereafter, its progression is beneficially affected by the advice of virologists and government officials. The SARS-CoV-2 pandemic started in the countries considered here with different initial values μ : mostly, nine times, with 3, twice with 4, and once with 1. The general human vulnerability to SARS-CoV-2 may be assumed to be constant, therefore differences of μ in the initial stage of the pandemic must refer to local causes, e.g. different habits and lifestyle.

The pandemic as a whole can be completely characterized by four *fundamental parameters*:

1. The attractor \mathbf{S} as the invariant empiric model of the pandemic.
2. The daily infection rate n per one million inhabitants subjected to infection.
3. The exponent b of the exponential process. The sign of b , positive or negative, indicates whether the process is in an increasing or decreasing stage.
4. The parameter μ , $-4 \leq \mu \leq 4$, *an integer number*, which characterises the *performance* of the pandemic. It results from d and b while d is a suitably normalized value of n . The value zero of μ suggests a sideways performance and the other values, in ascending order, a weak, moderate, strong, and very strong

performance, respectively.

It is well known, that the great majority of individuals after a healed SARS-CoV-2 infection or a vaccination are for a certain time immunity to the virus. The data set used here comes from a period over which the share of healed persons was small enough to be negligible, and the opportunity of a vaccination didn't exist. At a later stage of the pandemic the number of convalescents or vaccinated persons increased remarkably and must be taken into consideration by subtracting them from the population figure in case the procedures described in chapter 3 are extended to a longer period.

To understand the impact of the pandemic on the public life the fundamental parameters of the pandemic must be supplemented by a number of *specific parameters*. The following two examples deal with consequences on the state-run health care system.

1. The *hospitalisation rate* h of corona-infected persons is

$$h(t)=n(t-\tau(t)). \quad (5)$$

$\tau(t)$ is the delay function the hospitalisation rate follows the infection rate. It can vary slowly with time and is to be determined statistically.

2. The *mortality* $m(t)$ due to the SARS-CoV-2 pandemic is drawn in Fig. 1 by blue points. It is related to n according to

$$m(t)=n(t-\kappa(t)). \quad (6)$$

$\kappa(t) > \tau(t)$ is the delay the mortality follows the infection rate and should be determined and handled similar to $\tau(t)$.

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