Report

Infection Wave Dynamics

Hannah Dopmeyer

2804615

392185 Bioinformatics and Data Science in Pandemics

Summer Semester 2021

Bielefeld University

Bielefeld, August 27, 2021

Contents

1 Introduction and Problem Definition

Since 1.5 years the COVID-19 pandemic is dominating everybody's life. ON August 02, 2021 almost 200 Million people have been infected with the new Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2 virus). The understanding and modeling as well as the prediction of case numbers is crucial to deal with the pandemic. Suitable data to use include the number of infected persons, which are tested positive (as daily new cases or accumulated) or the number of deaths related to COVID-19.

In this report, a phenomenological approach is presented, in which the accumulated case numbers are compared with the Gompertz function. The Gompertz function is fitted to the data and predictions up to the next five days are made. The main source is the paper "Empirical model for short-time prediction of COVID-19 spreading" published in PLOS Computational Biology in December 2020 [1]. It is written by five authors coming from the disciplines of Medicine, Biology and Physics. The overall goals are to model the cumulative cases of infected individuals, to predict short-time behavior and also be able to make statements about the long-time behavior. One motivation is to use these results to predict short-term hospital and intensive-care units, which are one limiting factor of the health system.

One difficulty for modeling and predicting COVID-19 cases is the unknown mechanism of the pandemic. In particular the widespread global governmental control measures are in that form unique and weaken the use of classical epidemiological models. The required assumption for those models (see Section 2) are simply not fulfilled for the COVID-19 pandemic. If the models would be used for the COVID-19 setting the results would have no meaningful interpretation in terms of infection dynamics. However, it could be the case, that the actual fitting of the COVID-19 data would work with respect to these models. But in that case the mechanism of the models do not play any role and it is only a phenomenological analysis. Motivated by that limitation of the classical models, a phenomenological approach is chosen from the beginning: The idea is to not assume anything about the spreading-mechanism of the SARS-CoV-2 virus, but only work with the pure (cumulative) case numbers. As candidates for the fitting function a standard logarithmic function and the Gompertz function are chosen. The logarithmic function is often used for disease simulations (it is in fact the resulting function for cumulative case numbers based on the SIR-model, see Section 2). The Gompertz function was proposed for life contingencies but also has applications for the number of tumors, number of bugs in a software and particle multiplicities at high energies [3]. Motivated by the daily new cases, the Gompertz function was chosen as the function to work with.

2 Methods

In this section, a classical approach to infection wave dynamics is presented. It is explained why this method does not work for the situation of COVID-19. Afterwards a phenomenological approach and the Gompertz function are studied. Lastly the explicit use of this to model and predict the cumulative number of COVID-19 cases is given.

2.1 Classical Approach

One classical approach to model infection wave dynamics is the SIR model, in which S stands for susceptible, I for infectious and R for recovered individuals of a population. If a susceptible and an infectious individual meet, the infectious one transmits the disease to the susceptible with a probability γ. After some time the infectious individual turns into a recovered one [1].

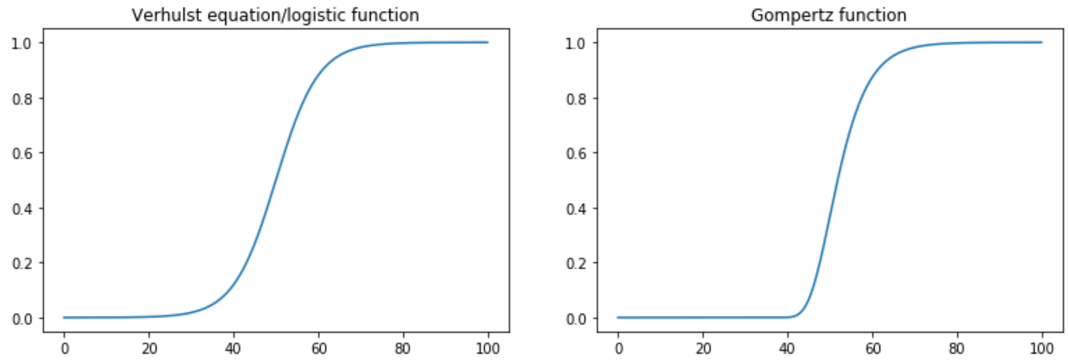
This interacting particle approach is very common in modeling various interactions in populations, such as predator-prey interactions (predator is searching for prey, predator kills the prey, predator eats the prey, predator is saturated, predator gets hungry again) but also for processes such as giving birth dying or internal ranking fights. The broad concept is the same as the molecular equations in chemistry.

The SIR model has been used for real-life epidemics, as the Ebola epidemic in 1995 and 2003 and the SARS I epidemic in 2003. However, with the fraction of susceptible individuals in the population and the assumed steady movement as the two key drivers, it does not fit to the situation of the COVID-19 pandemic. As studied in [2], the driving factors for the COVID-19 pandemic are the governmental control measures, such as social distancing, closing of schools and educational systems or travel restrictions. These large-scale measures are unique for the current pandemic and weaken the use of classic epidemiological models. Apart from this new factor, there is another difference between the assumption of the SIR model and COVID-19 epidemic: According to the SIR-model, the spreading of a disease only ends, if a certain herd immunity,due to previous infection, is reached. In contrast, herd immunity (in that sense) is aimed for the COVID-19 pandemic. In early stages the aim was to reduce the number of infectious individuals and in the long-term the desired immunity is, for the majority of people, achieved by vaccination and only for a smaller fraction due to a previous infection [1].

2.2 Phenomenological Approach

To make statements and predictions for the behavior of the infection waves, the known, classic models cannot automatically be used. The possibilities are now to either:

- understand the underlying mechanism on how the governmental measures influence the transmission and update the existing models



(a) Verhulst equation **(b)** Gompertz function

Figure 1: The graph of the Verhulst and the Gompertz function.

or

- do not predict the behavior using a model, but rather a phenomenological approach.

The first choice requires a deep understanding of the pandemic and the effects of the control measures; a understanding, which is at the current time not existing. The second approach does not need any assumptions or knowledge of the underlying behavior and focuses only the (case or death) numbers. Here, a method based on the second idea is presented.

The general setting is the following:

i) Use of a phenomenological approach for the cumulative cases of infected individuals.

ii) Comparing the case numbers with a suitable function on the interval $[t_0, t]$.

iii) Make predictions about the case number for the time $t + \Delta t$.

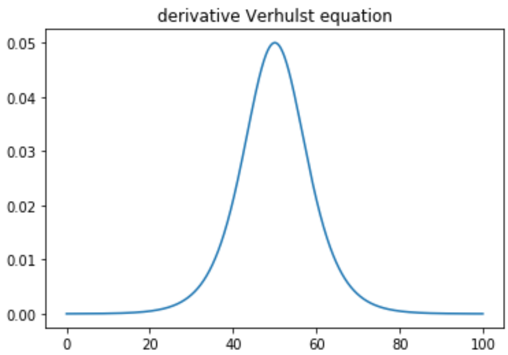
Candidates for that function are the Verhulst equation, also called the logistic function, and the Gompertz function. Their graphs are shown in Figure 1.

The main difference between the two functions is the saturation of the growing factor. Apart from that the functions look very similar and could potentially represent the number of cumulative COVID-19 cases. Let $N(t)$ be the number of cumulative cases described by the two functions. Then the growing factor as the change in time is exactly the derivative

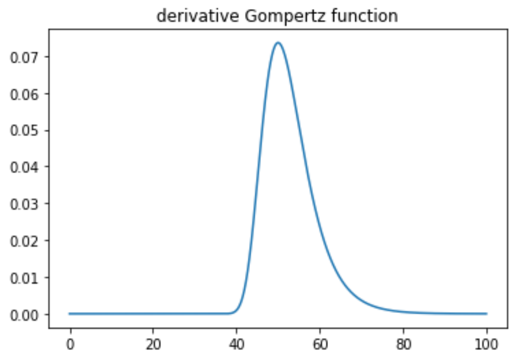
$$\frac{dN(t)}{dt}. \tag{1}$$

In the COVID-19 setting, the growing factor as the change in time is interpreted as the daily number of new cases. Therefore, as a second step, the respective derivatives and those daily new cases are compared, see Figure 2.

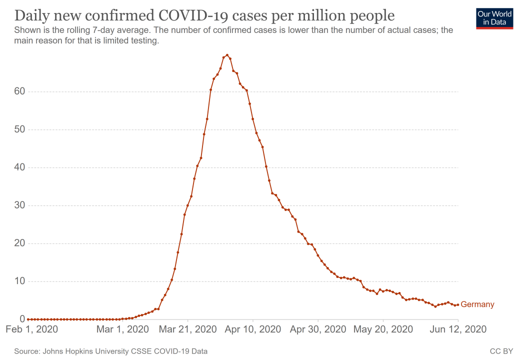
The daily new cases are better described by the derivative of the Gompertz function, which motivates the overall comparison with the Gompertz function, rather than the



(a) Derivative of the Verhulst function



(b) Derivative of the Gompertz function.



(c) Daily new COVID-19 cases in the interval from 02.02.2020 until 12.06.2020 in Germany. Source: [4]

Figure 2: Derivative of the Verhulst and Gompertz function and the daily new COVID-19 cases.

logistic function. Even if the comparison between the derivative of the Gompertz function and the daily new cases is convincing, the main analysis is done by using the original Gompertz function together with the accumulated case numbers.

2.3 The Gompertz Function

Now some mathematical details about the Gompertz function are explained, to better understand its behavior and its differences to other functions, such as the logistic one. For a detailed study, see [3] The following ingredients and notations are needed:

- The observation period in which the Gompertz function is fitted to the accumulated case numbers is set to $[0, t]$ (so $t_0 = 0$).
- $N(t)$ denotes the number of cumulative cases at time t and solves two ordinary differential equations, namely

  i)
  $$\frac{dN(t)}{dt} = \mu(t)N(t) \quad \text{exponential groth of } N(t) \tag{2}$$

  ii)
  $$\frac{d\mu(t)}{dt} = -a\mu(t) \quad \text{exponential decay of } \mu(t) \tag{3}$$

  leading to the solution

  $$N(t) = \exp\left(-\frac{1}{a} \cdot \exp(-at)\right). \tag{4}$$

- K denotes the final number of cases and N_0 the initial number of cases at $t = 0$.

By standard reformulation the Gompertz function is given by

$$N(t) = K \cdot \exp\left(-\ln\left(\frac{K}{N_0}\right)\exp(-at)\right). \tag{5}$$

The interpretation of this equation is as follows:

- K (final case number) and N_0 (initial case number) as introduced above.
- The function $\mu(t)$ as the infection probability per infected people, see [3].
- The parameter a as the level of the governmental restrictions, see [1].

The use of the expression $\ln\left(\frac{K}{N_0}\right)$ in (5) seems surprising at this point, but is a valid reformulation of the form in (4) with the included parameters K and N_0. The reason for exactly this expression is, that key properties of the Gompertz function will explicitly depend on $\ln\left(\frac{K}{N_0}\right)$, which justifies (5).

In [3] the function $\mu(t)$ (denoted by $k(t)$ in [3]) is interpreted as the infection probability per infected people. The reason for its exponential decay is mostly, that it is a good fit to the COVID-19 cases (which is not evident at this point, but will be clear later on, see Section 3).

Assuming those fitting properties, [3] provides one possible explanation for the exponential decay, see Chapter 4 "Mechanism of appearance of the Gompertz function" in [3]. The starting point is, that the characteristic behavior of the Gompertz function with a fast increase and an exponential decrease is well-known for many physical processes. A detailed analysis is given for the number of π and Δ particles produced in the nucleus-nucleus (Au + Au) collision at an incident energy of 1 GeV/nucleon, which is indeed described by the Gompertz function. The main idea is now to link this process to the COVID-19 dynamics, as they are both transport processes. For this we have

- The Δ particles represent Coronavirus carrier as infected, but not yet positive tested persons (might or might not be tested positive later) and π particles represent positive tested persons (= COVID-19 cases).
- In early stages of the pandemic the number of carries N^{Δ} increases exponentially.
- With ongoing time the carriers either develop symptoms and are tested positive (transmission from Δ to π particles) or recover and do not transmit the disease any longer, leading to a slower decrease then increase.
- The number of carriers N^{Δ} is roughly proportional to the derivative $\frac{dN^{\pi}}{dt}$ interpreted as the daily new COVID-19 cases.

Note that the exponential decay of the growing factor $\mu(t)$ was one feature of the Gompertz function, which was not shared by others, as seen above. The logarithmic function for example has a linear saturation of this factor (in comparison to the exponential decay here). This difference is really determined by the parameter a, which could be interpreted as the level of the governmental restrictions (see [1]).

With that explored form different quantities can be computed. Interesting examples are the behavior for small and large t, the peak of daily new cases t_p or the time to arrive at 90% of the total cases K, denoted by t_{90}. More precisely:

$$N(t) \approx N_0 \cdot \exp(\mu_0 t) \quad \text{for small } t, \text{ with } \quad \mu_0 = a \cdot \ln\left(\frac{K}{N_0}\right), \tag{6}$$

so the Gompertz functions behaves as an exponentially growing function with growing parameter $\mu_0 = a\ln(\frac{K}{N_0})$ and

$$N(t) \approx K \quad \text{for large } t, \tag{7}$$

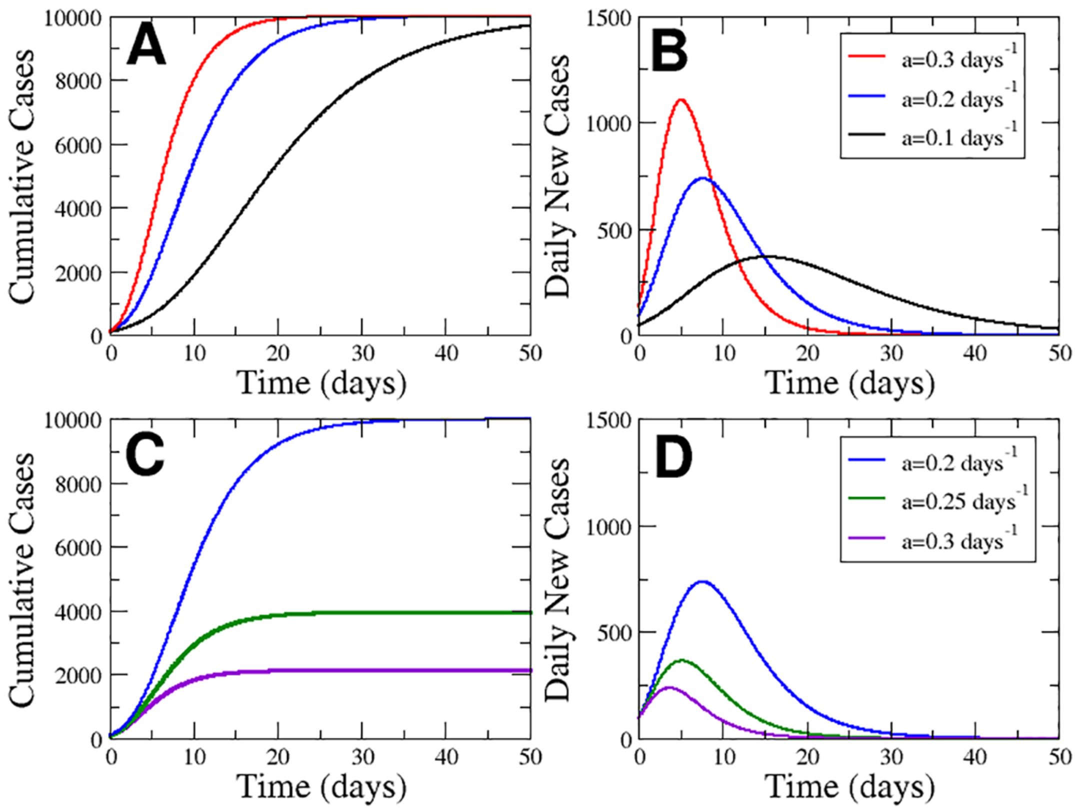


Figure 3: Properties of the Gompertz function. In A and B the parameter K as the total number of cases is kept constant and a varies. In C and D the initial growing factor μ_0 is constant and a varies. Th figures A and C show the original Gompertz function $N(t)$, which models the cumulative cases. Figures B and D represent the derivative $N'(t)$ of the Gompertz function, which corresponds to the daily new cases. Source: [1]

which is inline with the introduction of the parameter K. The above defined quantities t_p and t_{90} are explicitly given by

$$t_p = \frac{1}{a} \ln\left(\ln\left(\frac{K}{N_0}\right)\right) = \frac{1}{a} \ln\left(\frac{\mu_0}{a}\right), \tag{8}$$

and

$$t_{90} = -\frac{1}{a} \ln\left(\frac{\ln(0.9)}{\ln\left(\frac{K}{N_0}\right)}\right), \tag{9}$$

with μ_0 as above. Both times and the initial behavior directly depend on a, so this factor is really an important one for the Gompertz function. Remember that the parameter a was also the one, which represents the desired saturation of the growing factor.

This properties and the dependencies on a and K are visualized in Figure 3.

In A and B of Figure 3 the total number of cases $K = 10^4$ is kept constant and a is varied. An increase in a leads to a decrease of t_{90}, t_p and an increase of the initial growing factor μ_0. If μ_0 is kept constant and a is varied, an increase in a leads to a decrease in K (see C and D of Figure 3).

2.4 Explicit Use

The parameters a and K of the Gompertz function are fitted to number of cumulative infected and positive tested COVID-19 cases by applying the minimum least squared error method. Bases on that fitting the short-term predictions (up to five days after the observation period) are made. The fitting is performed using Matlab and the data is taken from the European Center for Disease Prevention and Control. The analysis is first done for Chinese regions, in which the pandemic was relatively far developed. Afterwards several European countries were considered. The fitting can be evaluated with the statistical parameter R^2, which is obtained by fitting procedure and by comparing the actual cases to the predicted ones.

3 Results and Evaluation

First, a short summary of the results for the Chinese regions is provided and then the fitting for the European countries is studied. The corresponding error evaluation is given and the use use of filters is discussed. The section closes with long-term estimated and the current state of the pandemic.

3.1 Chinese Regions

The fitting to the data of the Chinese regions yielded sufficiently good results, with R^2 close to 1 for the cumulative cases and up to 0.94 for the induced daily new cases (so comparing the fitted function to the cumulative cases to the data of daily new cases). These results strengthen the idea, that the Gompertz function is a convenient function to model the pandemic for regions, which are close to saturation. For a first impression what the results look like, see Figure 4 in which fitting was performed for the regions Hubei, Guangdong and Henan. The values for K, a and the obtained R^2 are shown, both for the cumulative and the daily new cases of infected persons.

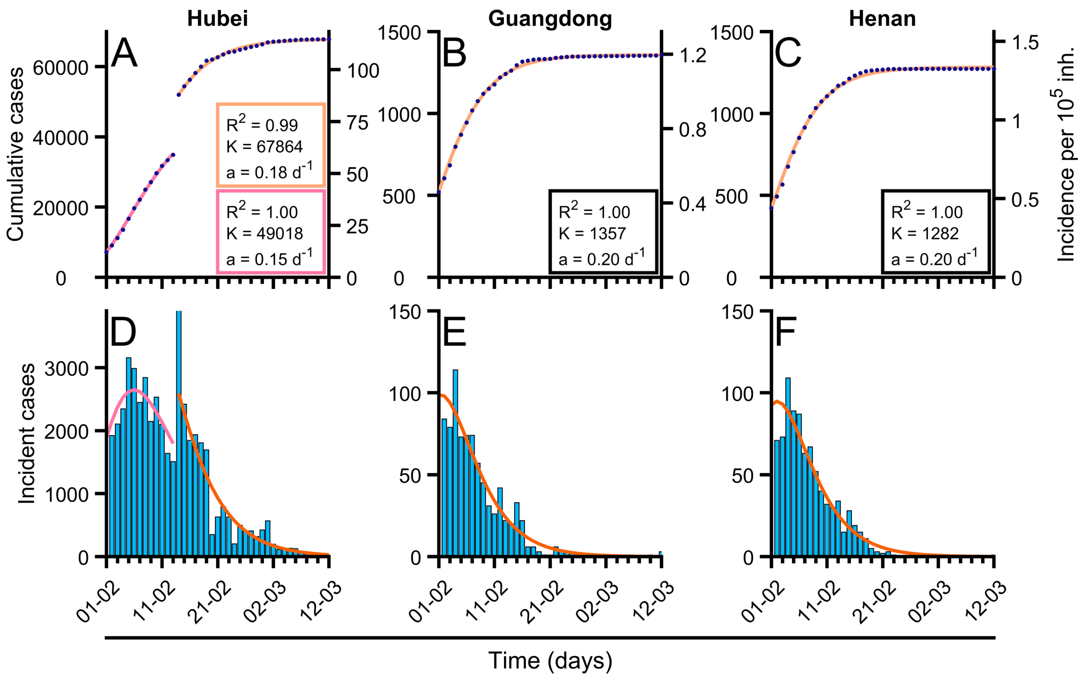


Figure 4: Fitting of the Gompertz function to the cumulative cases in the Chinese region Hubei (A), Guangdong (B) and Henan (C) with the resulting values for R^2, K and a. The derivative of the fitted Gompertz function together with the daily new cases is shown in Subfigures D, E, F. The discontinuity in the Hubei is caused by a change in the protocol for reporting cases. Source: [1]

As a second step the fitted parameters were used to predict the number of cumulative cases for the future. At three times of the pandemic the cumulative cases (blue dots) were

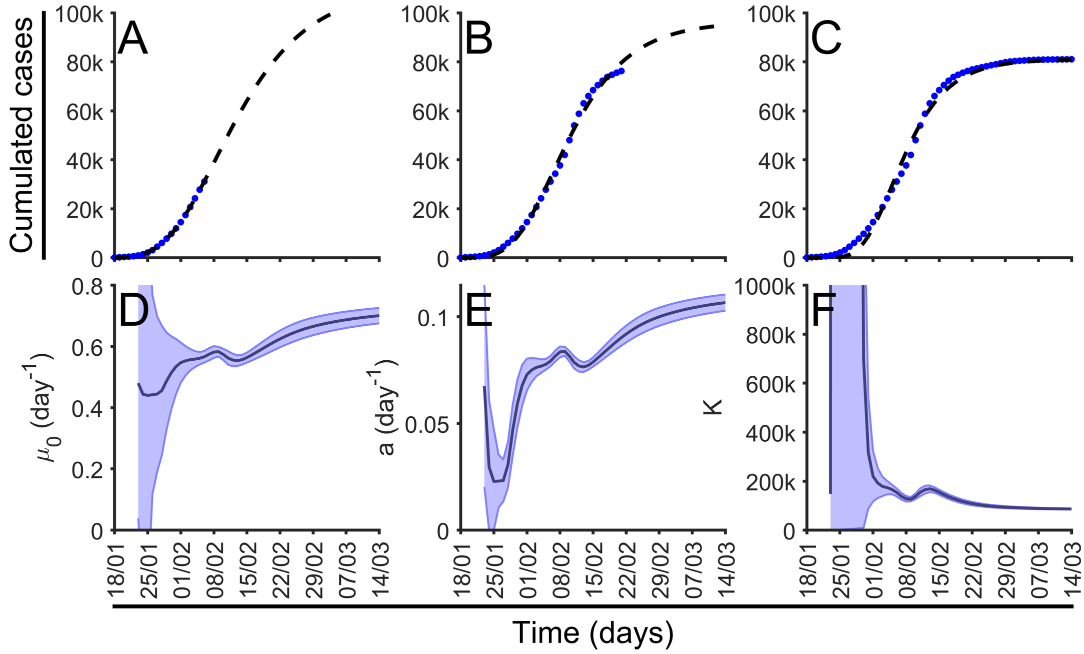


Figure 5: In Subfigures A, B and C the accumulated case numbers (blue dots) are evaluated at three different stages of the pandemic, with A as the earliest time (initial growth) and C as the latest (close to saturation). First the Gompertz function was fitted to the past (the known blue dots) and then the future development was predicted (back dashed line). The Subfigures D, E and F show the dynamical fitting of the parameters μ_0, a and K respectively. Every day, those parameters, together with a 99% confidence interval were computed. Source: [1]

used to model and predict the number of cumulative cases (A,B,C respectively). With ongoing time, the results got more accurate. In addition, a "dynamical fitting" for the parameters μ_0, a and K was performed. Every day the 99% confidence interval and the point estimate were depicted. With ongoing time the confidence interval shrunk.

3.2 European Regions

The researchers analyzed the cumulative cases in different European countries. The setting was as follows:

- A minimum of 100 confirmed cumulative cases was required to start the analysis. By this the initial spread of the pandemic was excluded.
- Only the last 15 days were considered. This is motivated by the effect of the governmental control measures, which can in short time lead to another behavior.

Their analysis then consisted of two parts:

i) At the end of the observation period, the Gompertz function (orange line) is fitted to the cumulative case numbers (blue dots) based on the last 15 days.

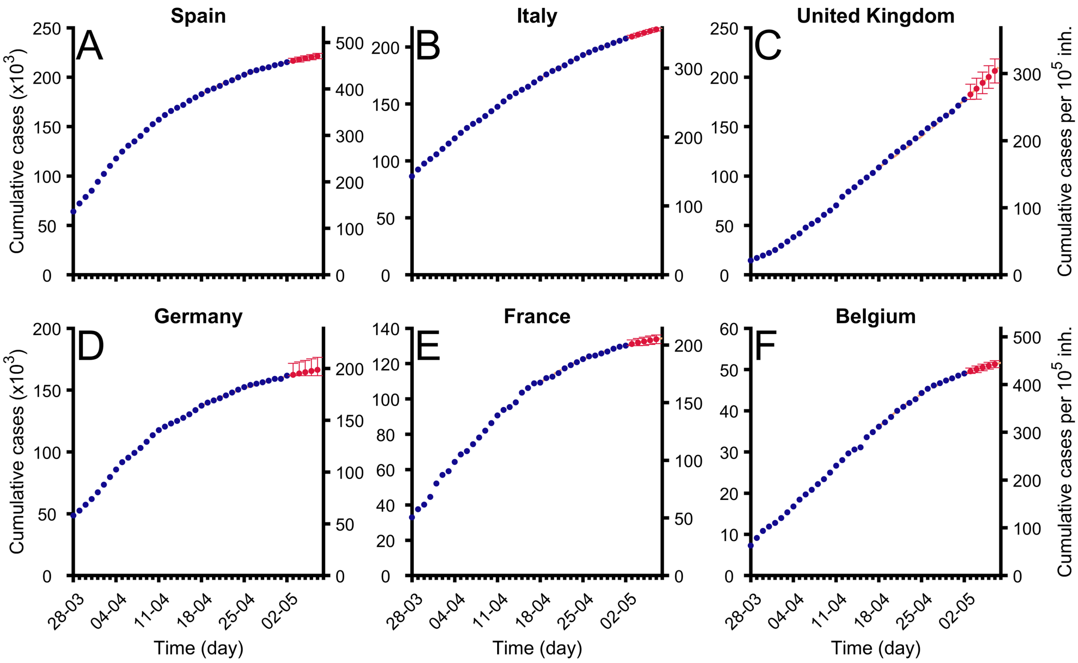


Figure 6: Fitting of the Gompertz function to the cumulative case numbers for different European countries. Blue dots represent cumulative cases, the (thin) orange line stands for the fitting of the Gompertz function using the 15 last data points. Red dots are used for the prediction for the next one to five days and red bars indicate the confidence interval. Source: [1]

ii) Predictions for the next five days and the corresponding 99% confidence intervals (red points and red lines) are made based on the previous fitting.

The results for both steps of the analysis are shown in Figure 6. In comparison to the Chinese regions the derivative of the fitted Gompertz function is not compared to the daily new cases here. The fitting and prediction only uses the cumulative cases.

3.2.1 Error Evaluation

The predicted cases were compared to the actual number of cases. An example is given in the Table 1 of the appendix. At the 29.04.2020 the accumulated cases of the last 15 days were considered to predict the cumulative cases for the next day (30.04.2020) third next day (02.05.2020) and fifth next day (04.05.2020). For each day one prediction and the 99% confidence interval were given. Also the final case number K was forecast. During the next five days the actual number of cumulative cases were monitored and included in the table. An interesting example is the prediction for the UK, where the predictions were too low compared to the actual case numbers.

Based on the comparison of the predicted and observed data some error evaluation is made. In Figure 7 the relative error of the prediction with respect to the real data is

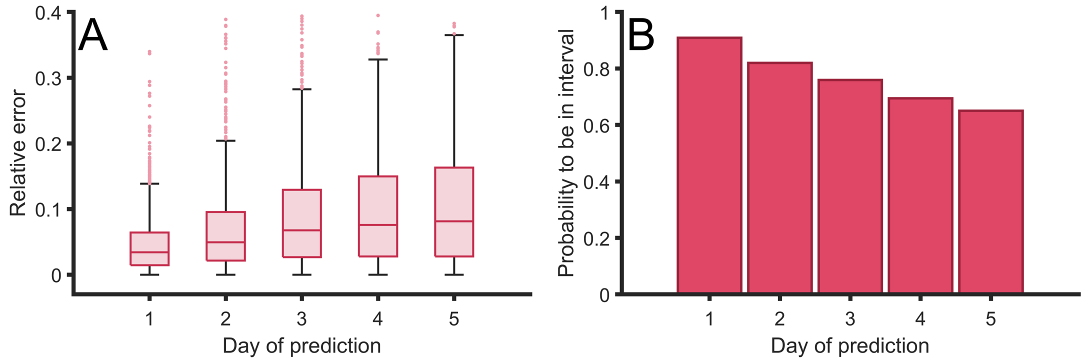


Figure 7: Error evaluation with A as the relative error of the predictions with respect to the day of prediction and B as the probability to be in the prognosticated confidence interval. Source: [1]

given as well as the probability for the real data to lie within the 99% confidence interval. Unsurprisingly the relative error is increasing as the day of prediction increases, while the probability to lie in the confidence interval is decreasing with increasing day of prediction.

3.2.2 Filters

To further improve the results different filters were considered. Instead of the uniform weight of the 15 data points three other methods were compared, namely

i) A linear increase in weight.

ii) A parabolic increase in weight.

iii) An added relevance (with a factor of 100) to the last three data points.

The same analysis as described above (fitting the Gompertz function to the last 15 points-including the filters- and then prediction for the next five days and error evaluation) is performed, see Figure 8. For the probability to lie in the 99% confidence interval one has to be careful about the comparability, the larger the interval the higher the probability to be hit. For that reason two different confidence intervals are considered: Light colors represent the relative confidence interval with respect to each filters (possibly varying in size), and dark color stands for comparing a fixed interval (that for the uniform weight of all 15 data points).

The best results were obtained by using the third filters, i.e. adding relevance to the last three data points. Interestingly, added relevance to only the last two or one data points was less precise.

3.2.3 Long-term Prediction

As for the Chinese regions a dynamical fitting is performed for the parameters K, t_p and t_{90}. Those values and the 99% confidence intervals are daily predicted and shown in Figure

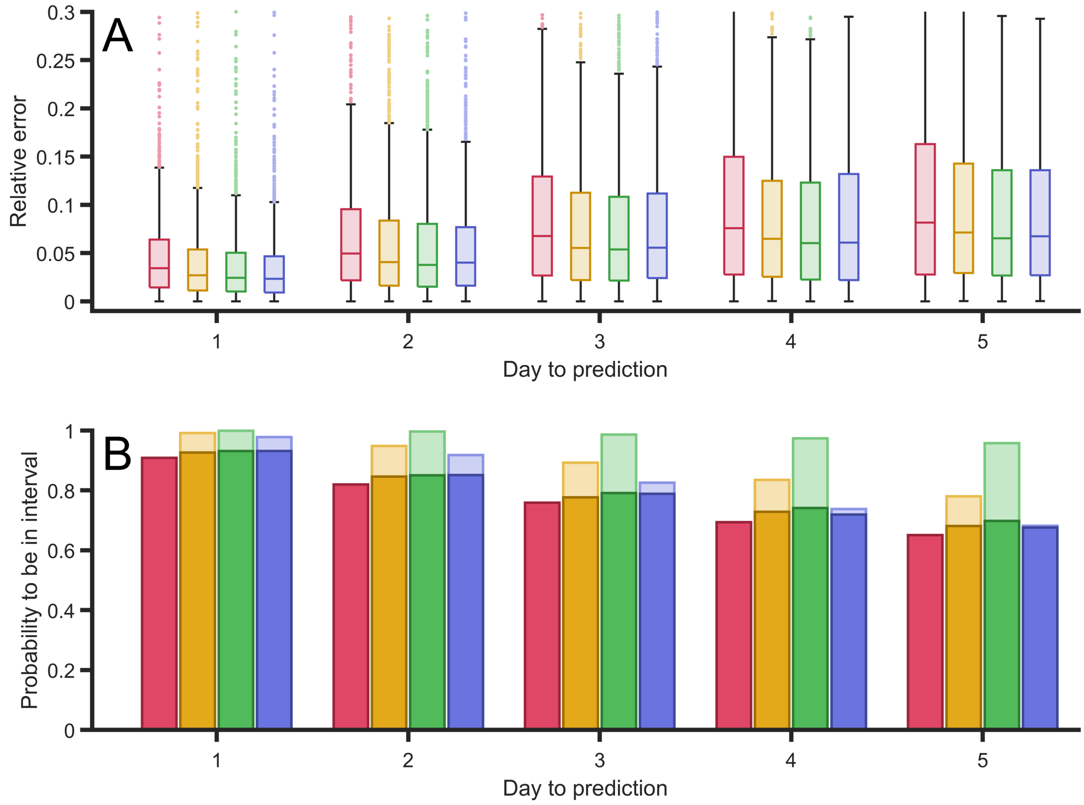


Figure 8: Error evaluation in the sense of the relative error (A) and the probability to be in the confidence interval (B) using different filters. Red reflects the uniform weight on all 15 data points, yellow for a linear increase in weight, green for a parabolic increase in weight and blue for a extra relevance of the last three data points. The light and dark shades in Subfigure B are used for the variable confidence interval size (light) and fixed confidence interval (dark). Source: [1]

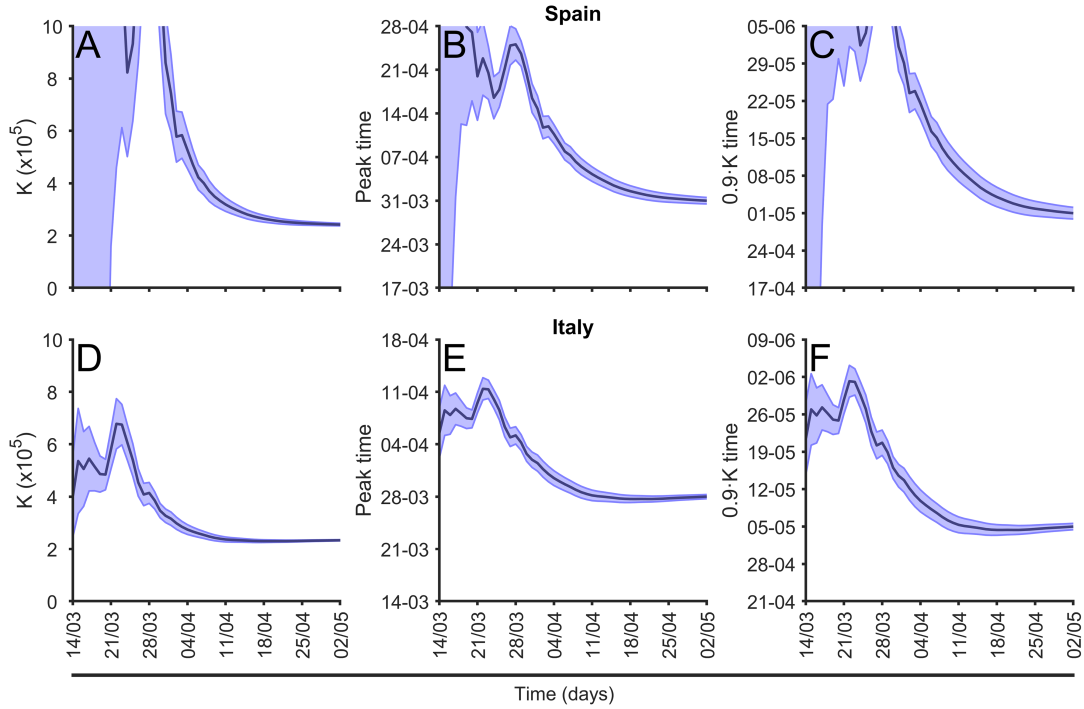


Figure 9: Dynamical fitting for the parameters K, t_p and t_{90} for the countries Spain (A, B. C) and Italy (D, E, F). The black line stands for the predicted value of the parameters and the blue area for the corresponding confidence interval. Source: [1]

9.

Over time the confidence intervals shrink and seem to converge to a stable estimate for all three parameters. The differences between the predictions for Spain and Italy are due to the different stages of the pandemic. In Italy the pandemic was already further developed and the behavior more accurate to predict, while the pandemic's behavior was rather unknown in Spain.

3.2.4 State of the Pandemic

As a last analysis the state of the pandemic for different countries in Europe was studied. For this, the time t_p of the new cases peak and the time t_{90} were estimated (along with the corresponding error bars obtained by the fitting). The results are visualized in part A of Figure 10. It can be seen that the state of the pandemic varies, even between neighboring countries. For example Norway is close to its prognosticated peak of new cases and also has a relatively early date for reaching the 90% of total cases. Its neighbor country Sweden has one of the latest prognosticated time t_p and the time t_{90} could not even be included to the time-scale.

In figure B the reported cases per 100.000 citizens is shown and compared to the predicted final incidence. In this representation the relative extent of the COVID-19 pan-

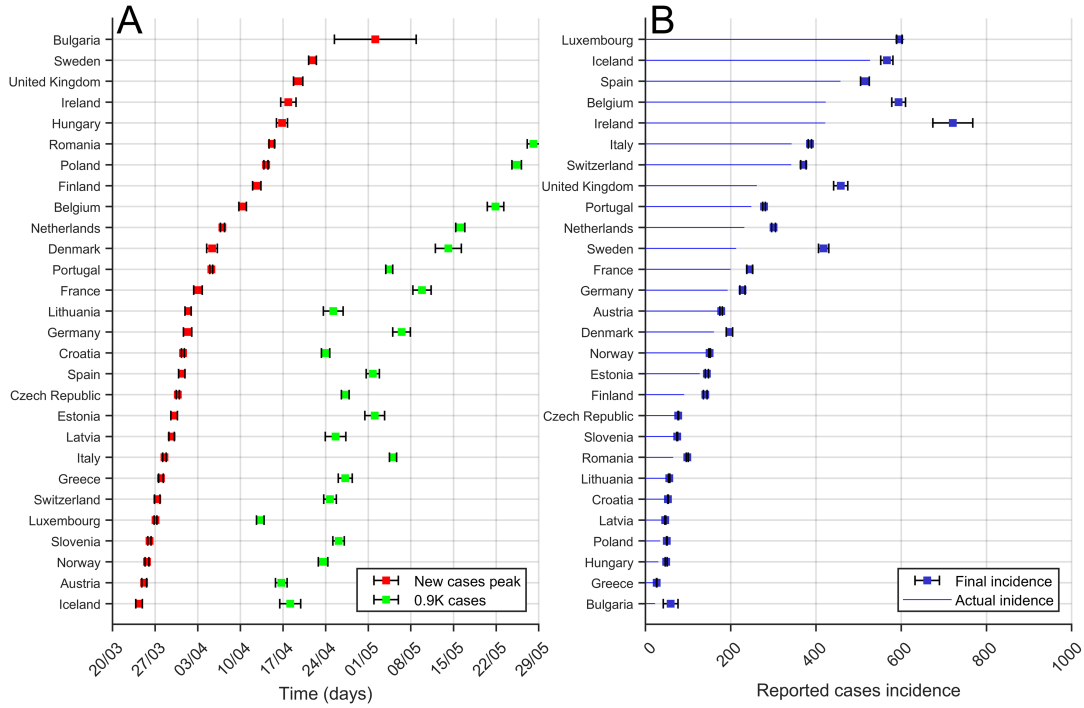


Figure 10: State of the pandemic with Subfigure A showing the prognosticated time t_p and t_{90}, along with the error bars and Subfigure B the predicted final incidence K (blue dot) together with the actual incidence (blue line). Source: [1]

demic can be seen. Luxembourg has the highest incidence per citizen (with the predicted incidence being almost identical to the actual incidence) and Bulgaria the lowest incidence (and a high uncertainty).

4 Discussion and Outlook

The use of the Gompertz function to model the observed number of cumulative COVID-19 cases and to predict the cumulative COVID-19 for the next five days cases in several regions with respect to the used data worked sufficiently well. The fitting parameter R^2 is close to 1, indicating a very good approximation of the COVID-10 cases by the Gompertz-function. The predictions were shown to be correct in 90% of the cases (meaning the actual case number lies with 90% in the predicted confidence interval). The COVID-19 dynamics and in particular the effects of governmental control measures are understood too little to work with the classical infection dynamics models. Instead a reasonably motivated phenomenological approach was performed. The underlying behavior, especially the exponential decay of the growing factor, of the Gompertz function seemed to work well for the effects of the governmental control measures. By fitting the parameters μ_0, a and K to the last 15 data points reliable predictions can be made for the next five days. The probability for the actual case incidence to lie in the computed confidence interval is up to 90% for the first day, see Figure 7. These results can be improved by choosing a filter, which gives additional weight to the last three data points. Using a dynamical fitting (daily fitting of the parameters and confidence intervals) the predictions symmetrically converged. To sum up, the Gompertz function worked fine to model and predict (short- and long-term) the cumulative COVID-19 cases with the regarded data sets.

However, the infection wave dynamics changed massively since the paper was published. As an impression the cumulative cases for COVID-19 and the daily new cases up to June 2021 were given in Figure 11 and Figure 12 respectively.

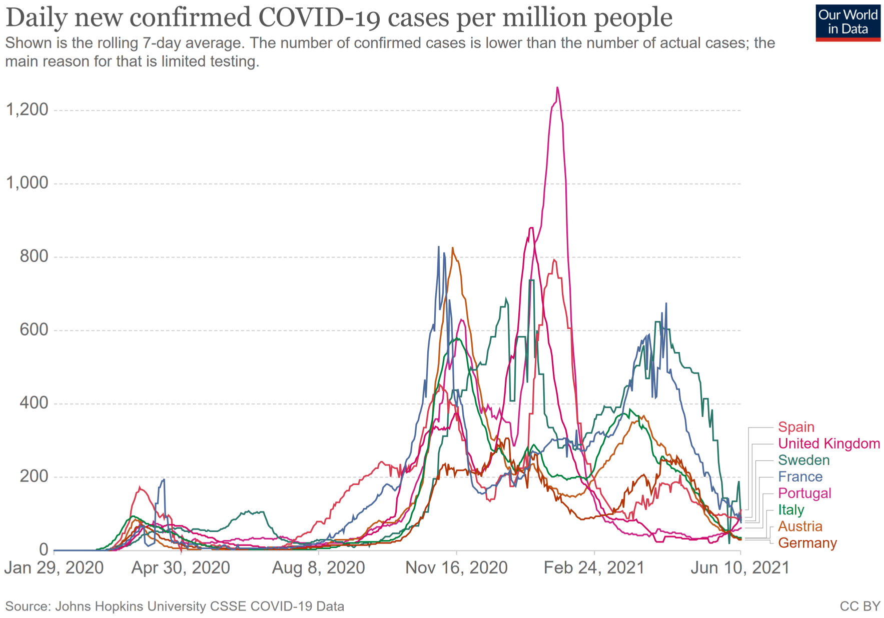


Figure 12: Daily new confirmed COVID-19 cases per million people for different countries in Europe from January 2020 until June 2021. Source: [4]

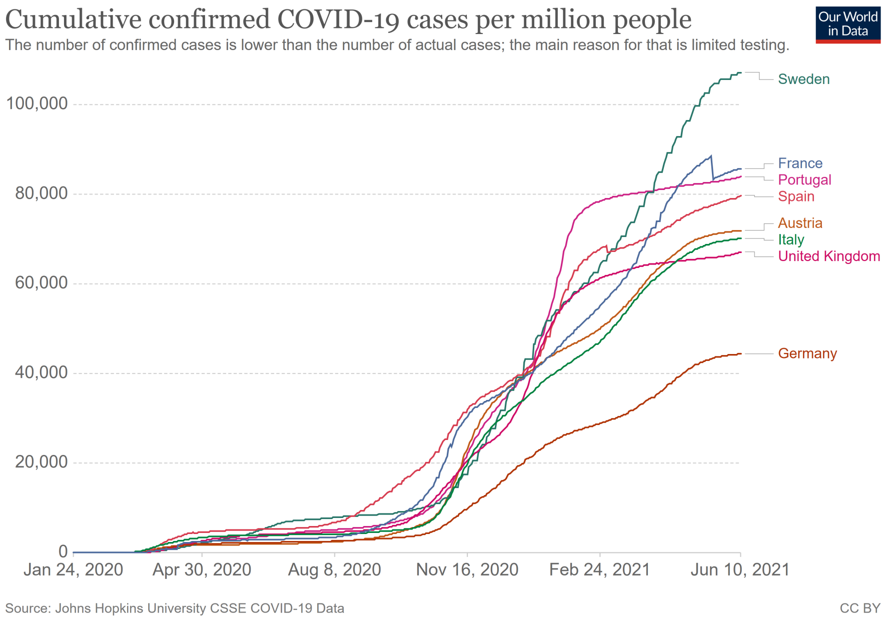


Figure 11: Cumulative confirmed COVID-19 cases per million people for different countries in Europe from January 2020 until June 2021. Source: [4]

The data used in the paper [1] is from spring 2020 (received 08.05.2020). Comparing the data from spring 2020 with today, the case numbers since November 2020 are clearly dominating the pandemic. The robust prediction for the parameters t_p, t_{90} and K all turned out to be wrong (predicted K for Germany = 200.000, while current (08/2021) cumulative case number greater than 3.780.000!) As such the obtained results and used methods cannot be transferred to later stages of the pandemic with higher numbers of cases.

Not only the case numbers increased after the paper was published, but also new drivers for the pandemic arose: On one hand the vaccination and on the other hand the new mutations. Both are crucial and need to be considered when modeling and predicting aspects of the COVID-19 pandemic. One change is the method could also be to work with the COVID-19 deaths, since those numbers are not depended on test-strategies and might be more robust to use. However, also with varying test-strategies (or counting strategies) the Gompertz-function is still of use, see 4 in which such a change in counting was performed. In that case the fitting was split into two parts, with sufficiently good results for both intervals. Even with a change in the test or counting strategy the underlying behavior is well described by the Gompertz function (for intervals of the same strategy). The Gompertz-function is sclaed differently in the intervals, but the characteristic behavior remains the same.

The Gompertz function might still work for the complex case with mutations and vaccination (since it did not depend on any assumptions or underlying mechanisms), but a new analysis is definitely needed.

A Appendix

Table 1: Prognosticated (at 29.04.2020) and actual case numbers for the dates 30.04.2020, 02.05.2020, 04.05.2020, source: [1]

Countries	Cases	April 30		May 2	
		Prediction	Reported	Prediction	Reported
Spain	213942	215365 [213942-220067]	**215183**	217465 [213942-222263]	**217804**
Italy	201505	203403 [201505-206418]	**203591**	206856 [203761-209951]	**207428**
United Kingdom	161145	165268 [162977-167560]	**165221**	172953 [170582 -175324]	177454
Germany	157641	158753 [157641-160596]	**159119**	160718 [158837-162598]	**161703**
France	126835	127941 [126835-130010]	**128442**	129882 [127761-132004]	**130185**
Belgium	49227	49698 [49227-51501]	**49741**	50616 [49227-52459]	**50565**
Netherlands	38416	38889 [38416-41086]	**38802**	39462 [38416-41696]	**39791**
Switzerland	29181	29279 [29181-29545]	**29324**	29433 [29181-29703]	**29622**
Portugal	24324	24654 [24324-25941]	**24692**	25113 [24324-26427]	**25351**
Ireland	19877	20253 [19877-21523]	**20253**	20791 [19877-22087]	**20833**

Countries	Cases	May 4		Parameter K	
		Prediction	Reported		
Spain	213942	219240 [214283-224197]	**219205**	239508	
Italy	201505	209946 [206707-213185]	**210717**	232434	
United Kingdom	161145	180122 [177596-182648]	186599	318644	
Germany	157641	162370 [160428-164311]	**163175**	194071	
France	126835	131599 [129385-133812]	**131287**	163290	
Belgium	49227	51399 [49488-53309]	**50990**	67095	
Netherlands	38416	39918 [38416-42206]	**40571**	52600	
Switzerland	29181	29554 [29278-29830]	**29822**	32352	
Portugal	24324	25497 [24324-26855]	**25524**	28376	
Ireland	19877	21232 [19896-22569]	**21506**	39108	

https://doi.org/10.1371/journal.pcbi.1008431.t001

B References

[1] Catalã, M. ; Alonso, S. ; Alvarez-Lacalle, E. ; Lãşpez, D. ; Cardona, P.-J. ; Prats, C. : Empirical model for short-time prediction of COVID-19 spreading. In: *PLOS Computational Biology* (2020). https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1008431#pcbi.1008431.ref004

[2] Kucharski, A. J. ; Russell, T. W. ; Diamond, C. ; Liu, Y. ; Edmunds, J. ; Funk, S. ; Eggo, R. M.: Early dynamics of transmission and control of COVID-19: A mathematical modelling study. In: *The lancet* (2020). https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30144-4/fulltext

[3] Ohnishi, A. ; Namekawa, Y. ; Fukui, T. : Universality in COVID-19 spread in view of the Gompertz function. In: *Progress of Theoretical and Experimental Physics* 2020 (2020), 10, Nr. 12. http://dx.doi.org/10.1093/ptep/ptaa148. – DOI 10.1093/ptep/ptaa148. – ISSN 2050–3911. – 123J01

[4] Our World in Data: *Coronavirus Pandemic (COVID-19)*. https://ourworldindata.org/coronavirus#coronavirus-country-profiles, . – Accessed: 2020-06-10