RESEARCH ARTICLE

The COVID-19 Omicron Wave in the Framework of a New Mathematical Modeling in Few European Countries and the Right Time for Lifting Restrictions

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Abstract

Objectives: The COVID-19 Omicron wave in Romania, Bulgaria and Germany is considered in retrospective till begin of March 2022. The aim is to describe both country specific features and common trends related the same underlying pathogen as well as to compare shortly the results and derived parameters to those from a similar application to few strongly affected countries in the beginning of 2022: the USA, the UK and France.

Methods: The main novelty of the approach used to describe the Pandemic is the dynamical tracking of successive generations of infected people instead of treating in time the evolution of few large compartments within which the total population is partitioned.

Results: The daily observed new infection cases are described over a large time scale in a reasonable way after normalization and the derived model parameters in all cases are consistent. The position of the calculated Pandemic peaks in time in Romania and Bulgaria indicates a transition from the second to the third generation of infected people while in the larger countries the transition is from the third to the fourth generation.

Conclusions: The rapidly acquired temporary immunity and vaccination effects reinforced the expectation of eventually control/stop the COVID-19 Pandemic soon. However, lifting restrictions should have been done carefully and country specifically, and of course at the right time. Later developments after March 2022 have shown that the expectations were too optimistic and Omicron waves generated by another virus sub-variants did complicate the situation.

Key Words: *Linear differential equations; Precise solutions; Modeling of epidemics; Epidemics peaks; Omicron wave*

1. Introduction

In the beginning of 2022, the importance of the COVID-19 Pandemic's issue does not need any argumentation [1]. Since the first signals for the seriousness of that Pandemic worldwide in the beginning of 2020 [2], much has been learned about the SARS-CoV-2 virus itself, though this process is not finished because new virus variants/mutations appear with time, with different properties, including much increased contagiousness in some cases. This is the case with the Omicron variant identified in late November 2021 [3]. The present work is concerned with some mathematical aspects of addressing and modeling the Omicron-stage of the Pandemic which is now dominating or will be soon dominating in most countries of the world [4]. However, one should never forget that dealing with the development of Epidemics is a multidisciplinary subject. Epidemiologists, specialists in infections, virologists, medics with different specializations, pharmaceutics, immunologists, molecular biologists etc. naturally participate by addressing the issues relevant to them. Thus, the modeling remains just a more or less reliable quest for mathematical apparatus able for short and/or long-term forecasting. In this way, it is possible to address more efficiently the issue of the health, social and economic price that societies must pay to stop/control the Pandemic.

In particular, when in the beginning of March 2022, the Omicron wave has reached in many countries its maximum and decreasing trends are observed, the question of lifting different restrictions arises again. This time, there are objective and real preconditions which are met, and which make reasonable such a program of "return to the normal". However, this general trend cannot be a basis for automatism in dealing with the problem, within about the same nature and tempo of lifting restrictions everywhere. On the contrary, this should be done by considering the specific features of the situation at every place (country or even region, maybe). The present work illustrates that latter need by showing the necessity of more precise modeling and observed effects of (fortunately small) changes in the decreasing trends, which are obviously related to lifting restrictions, in few European countries. The concrete cases investigated are the developments related to the Omicron wave in Romania, Bulgaria and Germany in the period 30.11.2021 (shortly after the first identification of that variant) till beginning of March 2022. Thereby, some text and illustrations from two previous publications of ours [5,6] are widely used for support.

2. The Method Employed for the Calculations

The possibility of describing an Epidemics over the full-time range of its duration is very suitable indeed. However, this may be difficult for cases where an Epidemics can become endemic, pathogens undergo evolution or immunity (acquired by recovering from illness or given by vaccination) has a limited duration. To solve such problems, if possible, a class of involved Epidemics models, based so far mainly on reference [7], were developed and applied, also including many additional features and attempts to take into account more complex effects that originally done in [7]. Since their basic idea is to partition the population into compartments (groups), these models are commonly denoted as "compartmental" ones. Following the logic of the infection propagation, transition rates describe the probability for individuals to move from one compartment to another. Thus, within the simplest version of the model considered, namely the so-called SIR model, there exist three compartments consisting of the people susceptible to infection (S), the infected people (I) and the number of recovered people (R). The number of people in each of them is a function of the time t. Other variants upgrading SIR contain more compartments including people with other, different

status in the propagation of the infection and the corresponding transition rates. Thereby, in some cases immunity with limited duration is also considered. This seems to be the case of the Covid-19 Pandemic, at least for a part of the population.

Before addressing the issue of the model employed in the present work, we shortly present some details on previously developed models for modeling Epidemics with the aim to ensure a basis for comparison of all these approaches in the context of advantages and disadvantages. The dynamics of the SIR model is governed by two transition rates. The first one, also logically, is related to the transition rate from the compartment of the susceptible people to the one of the infected people ($S \to I$). It is usually denoted by β and represents the product of the the average number of contacts per person per unit time and the probability for disease transmission in a contact between an infected individual and a susceptible one. Thus, the infection spreading transition rate is evaluated as $\beta I/N$ where I/N is the fraction of contacts involving an infected individual for the group I and N is the total population (i.e sum all compartments). The $I \to R$ transition rate is denoted by γ end represents the inverse of the mean duration of the infection τ_R or mean time needed for recovery (i.e., $\gamma = 1/\tau_R$. The assumptiom that the distribution of the time spent in the infected state (a random variable) is an exponential distribution leads to the possibility to formulate mathematically the problem without the so-called vital dynamics (births and deaths, also the demography) as:

$$\frac{dS(t)}{dt} = -\frac{\beta I(t)S(t)}{N}$$
$$\frac{dI(t)}{dt} = \frac{\beta I(t)S(t)}{N} - \gamma I(t) \qquad [1]$$
$$\frac{RI(t)}{dt} = \gamma I(t)$$

where $N = S(I) + I(t) + R(t) = const$. This system of non-linear differential equations can be solved with respect to $S(t)$:

$$S(t) = S(0)e^{-R_0(R(t)-R(0))/N} \qquad [2]$$

Further, the dynamics of the Epidemics within the model depends strongly on the so-called basic reproduction number R_0,

$$R_0 = \frac{\beta}{\gamma} \qquad [3]$$

An epidemic outbreak occurs if $R_0 > 1$ since then $dI(0)/dt > 0$. In the opposite case of $R_0 < 1$, $dI(0)/dt < 0$, and an epidemic outbreak is not observed. Later, R_0 (also in the context of its practical determination for a given infection disease) will be discussed. In 2014, Harko et al. found an exact analytical solution of the SIR model [8]. In the context of the COVID-19 Pandemic case, however, the SIR model cannot predict the late future developments because it is not clear at all how long the resistance to new infection (acquired immunity) of the once recovered people will last as well as because the appearance of new variants of the virus is not considered. Further developments within the SIR (e.g., SIR with vital dynamics or demography) and beyond have been developed and applied:

- A model called **SIS** is used when any lasting immunity is not observed, for example cold and influenza. Here, the differential equations include only the I and S compartments, which permanently "communicate" with each other.

- The **MSIR** model includes a maternally derived immunity compartment (M) for the newborn whose immunity lasts some time.

- The **SEIR** model is used in the case of infectious diseases with long incubation period with absent infectiousness. The corresponding compartment is the one of the exposed (E).

Similarly, other models as the **SEIS** with no acquired immunity, the **MSEIR** with some passive immunity and a latency, the **MSEIRS** with temporary immunity in the R-compartment leading again to a R → S transition.

By this short recapitulation of SIR-like models it becomes evident that only the MSEIRS model could in principle describe the dynamics of COVID-19 by implementing second-infection rate for recovered people after some not very well-defined time, individual for everyone. However, effects of vaccination (with again unclear how long-lasting resistance at present) and age-structure dependencies have to be considered. Additional complexity is added by eventual vector transmission (e.g., infections resulting from viruses on open public surfaces). Options to try to solve these problems by modifying the transition rates between compartments in simple models as the one which is used in the present work have been discussed. Season dependences have also to be considered and reflected in the S→I transition rate which thus depends on time and has some period T ($\beta(t)=\beta(t + T)$). An illustration of such an approach can be found in reference [9] (see also the papers quoted therein) where the authors utilize statistical analysis of data and mixing of sinusoidal epidemic waves of season character.

In addition, they are a multitude of works dedicated to the issue of Epidemics which are not based on SIR-like models and ideas but still are keeping a relation to them. Apart the purely numerical approaches (for details see e.g., reference [10]) based on calculation of a mean growth rate, one can enumerate,

- Applications of the **Science of networks** [11].

- **Complexity Science** where complex systems are better described when introducing feedback loops, instabilities, and cascade effects [12] (these cascades may be associated with the infection spreading).

- Unification of the above in **Studies of Epidemics in complex networks** [13].

- **Statistical Physics in Epidemiology**, namely in investigating the impact of vaccination [14]. Such studies focus on the roles of individual behavior and heterogeneous contact patterns.

The considerations made so far of the achievements in the field of modeling and predicting the development of Epidemics, it becomes clear that a new approach should present features which improve the treatment of some aspects of the Pandemic spreading and even better, if

possible, provide new tools for the description of this complicated and complex process. An important fact is that till now the dynamics of the Epidemic process was described mainly as transitions between several large compartments of the population (the SIR models), without considering the sequence of "human to human to human to..." contacts i.e., without detailed tracking of the different generations of infected people. Recently, we published [5] a new and simple method for describing Epidemics including consecutive ways where this problem was solved. In this method, a decomposition of the group (compartment) of infected people into the different generations of infected individuals appearing in the chain of the "human to human to human to..." transmission is employed. These generations are tracked as well as the whole process of the infection propagation and this represents the most important novelty of the model. Such tracking is not possible within the SIR-like models as already mentioned. When successive generations are considered, it is easier to take into account changes in R_0 occurring during the Epidemics due e.g., to changes in social behavior caused by decisions of sanitary authorities (confinement, deconfinement, reconfinement,...), season-dependent changes, appearance of new virus variants with different contagiousness than the initial one, etc. This is also a new feature. Some additional newly open possibilities for studying the spread of the Epidemics process as e.g., associating the start of the impact of new virus variants with a particular moment in time are also available. While the above new features may be presented as components of the model which make it superior in the corresponding concrete aspects to previous models in the field, this does not mean, of course, a superiority in all aspects. For example, within the model used in the present work the very simple compartmentalization into only two groups of infected and recovered people does not reflect the very complex structure of the general population. Another limitation is the approximation of the existence of an inexhaustible reservoir of susceptible to infection which is not valid in all possible cases and at all time-stages of the Pandemic. Therefore, it might be better to make the statement that the present work is only a useful and necessary complement to this type of study.

As already mentioned, within the model [5] the first of group (or compartment) of infected people is decomposed into different generations of infected individuals appearing successively. The other main structure are the generations of recovered people who leave the corresponding generation of infected individuals after some interval of time needed for recovery (see below). In the model, linear differential equations are solved [5] while e.g., the SIR-like models require the solving of non-linear differential equations. The processes of infection spread, and recovery are governed by two transition rates, λ_R (rate of recovery) and λ_C (rate of infection or spreading rate). The rates are assumed to be constant in time when a single Epidemics wave is described. Here, one comes to one of the limitations of the model, namely that the infection spread, and recovering are supposed to occur while obeying statistical laws, within large enough population which provides an inexhaustible source of susceptible people. In the same way, the time for recovery can be treated as a random variable deciding the "fate" of each infected individual among all of them. Similar to most of the models describing Epidemics, the distribution of the recovery times used represents an exponential distribution with mean recovery rate $\lambda_R = 1/\tau_R$ (with τ_R being the mean time needed for recovery). Concerning the rate λ_C of the infection spreading, it is also considered to remain constant for a given Epidemics wave. However, it may be very largely influenced by measures as confinement, reduction of social contacts, reconfinement, lifting restrictions, appearance of new virus variants etc. and then another consecutive wave has to be included in the considerations as done e.g., in [5]. Studies of these effects are presented in references [15-17] and references therein.

As already mentioned in Section 1, the Omicron variant of SARS-CoV-2 is characterized by higher contagiousness than the other dominant previous variants (in different time periods), the δ-one "possessing" the previous record. Although in some countries mixing of the δ and Omicron waves is observed by mid January 2022, in others a very strong effect of increase of the daily new cases indicates the forthcoming dominance of Omicron. The very simple mathematics in Zhang et al., 2022 [5] opens the possibility to forecast the development of Epidemics in time for different infection and recovery rates. This is quite relevant for getting a fast idea for cases related to the appearance of strongly contagious infection pathogens as Omicron and the considerations in that model which is used in the present work are not limited to the time of the Epidemics outbreak. The main point is, as it is in many scientific disciplines, that when one factor dominates all other factors which influence somehow a phenomenon, scientists consider such a case as a testing ground for checking a particular model and simultaneously learn more about the overwhelmingly dominant factor. Simply, the picture at an early stage is quite pure and not obscured by later developments which are likely to occur because of some desynchronizations in the otherwise globalized world.

The relevant data sets of points for Romania, Bulgaria and Germany were taken from the site [18] and is displayed in Figures 1-3 with open diamonds. As matter of fact the site http://www.ourworldindata.org/ provides valuable research and data on 297 topics (by 27.05.2023) in order to help solving global problems. The data points for the three countries considered here cover the time range from 30.11.2021 to about 05.03.2022. As discussed in Zhang et al., 2022 [5], the total population is, of course, not tested every new day. Also, the number of people tested fluctuates each day, sometimes (e.g., on weekends) drastically. A more realistic picture may be obtained using data rolled (smoothed) on the basis of the 7 or 14 days numbers. It is much better to perform a normalization of the above raw data for following better in time and compare the absolute number of new daily cases of infections for the same constant fraction of the total population. There are factors, however, which may bias the normalization as e.g., possible concentration of tests in regions of the country with higher number of new cases or within clusters of enhanced transmission, several tests for one individual in the period considered, the very nature and sensitivity of the tests as diagnostic tools etc., and these factors may vary with time. The explicit use of the normalization discussed above is another novelty in our approach to describe/reproduce the new infection cases per day.

The fitting procedure to reproduce the normalized data is described in detail in [5]. The best results obtained are presented in Figures 1-3 with a continuous line. The parameters derived are also indicated. Before discussing the results, we remind the basic features of the new, tracking method employed. The first step is the determination of the functions $i_n(t)$ which represent the number of infected individuals in the different generations enumerated by n. The logic is borrowed from the description of the time evolution of the population of excited states in nuclear, atomic, and molecular physics which are interconnected by transitions (mainly electromagnetic, photons and γ-quanta). The main difference with the case discussed in the present work (and in [5]) is that while in the analog situations many levels with very different deexciting transition probabilities each are under consideration, here one has successive generations of infected individuals each one populated by the previous generation with probability per unit time (rate) λ_C and undergoing recovery with the rate λ_R. Hence a modification of the formalism is needed [5]. Namely, the first generation (the so-called zero patients) $i_1(t)$ simply obeys a differential equation similar to the radioactivity decay law of

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Rutherford-Soddy:

$$\frac{di_1(t)}{dt} = -\lambda_R i_1(t) \qquad [4]$$

with the solution $i_1(t) = \lambda_R i_1(0) e^{-\lambda_R t}$. For the next generations, the linear differential equation for the derivative of $i_n(t)$ contains on the r.h.s. the decrease of $i_n(t)$ and the increase due to infections from the previous generation i_{n-1}, always with the same rates i.e.,

$$\frac{di_n(t)}{dt} = -\lambda_R i_n(t) + \lambda_C i_{n-1}(t) \qquad [5]$$

The general solution (result) for the nth generation obtained as explained in [5] reads:

$$i_n(t) = \frac{\lambda_C^{n-1} i_1(0) t^{n-1} e^{-\lambda_R t}}{(n-1)!} \qquad [6]$$

The total number of infected people as function of time is given by the sum over the different generations:

$$i(t) = \sum_{k=1,2,\ldots N_{max}} \frac{\left(\frac{\lambda_C}{\lambda_R}\right)^{k-1} n_1(0) x^{k-1} e^{-x}}{(k-1)!} \qquad [7]$$

where N_{max} is the last generation appreciably reached at time t and $x = \lambda_R t$.

The expression resembles a sum of Poisson distributions weighted by the factors $\left(\frac{\lambda_C}{\lambda_R}\right)^{k-1}$ and overall scaled by the factor $i_1(0)$. This formulation may not be fully correct from a mathematical point of view when taking into account the discrete character of the Poisson distribution and the resemblance is rather formal. The quantity defined as $R_0 = \lambda_C / \lambda_R$ is the so-called basic reproductive number in the framework of the present model [5]. This reproductive number though widely used is somewhat model-dependent as discussed in detail in [19-22]. Roughly, this is the number of people who will be infected by one contagious individual up to the moment when this individual completely recovers from the infection. It is easy to see the complexity of R_0 by considering the fact that the infection spread depends not only on the transmission probability but also on the frequency of contacts etc. The quantity R_0 is thoroughly discussed in [5] (starting around Equation 15 in Section 2 of [5] and later, when the results in Table 1 there are discussed). Whatever it is, Equation 6 can be rewritten as,

$$i_n(t) = (R_0)^{n-1} \frac{i_1(0)(\lambda_R t)^{n-1} e^{-\lambda_R t}}{(n-1)!} \qquad [8]$$

It is to be noted that in the formalism presented the dependence on R_0 is very strong, changes with the generation number n and is different from that in the other models designed so far to describe Epidemics in time. A more careful examination allows to conclude that the peak (maximal) value of $i_{N_{max}}(t)$ dominates the sum of all generations of infected people $i(t)$ up to N_{max}. The only maximum of $i_n(t)$ occurs at,

$$t_{max} = (n-1)/\lambda_R = (n-1)\tau_R \qquad [9]$$

If one considers $i_n(t)$ as a distribution over time, its expectation (mean) value M1= $n\tau_R$ lies on the time axis later (by τ_R) than the maximum of $i_n(t)$. The expected time range of the epidemics depends on τ_R and n, and increases with n, of course.

Table 1: *Summary of parameters derived by fitting the data on the new daily infection cases for the countries considered in the present work. The initial date of the Omicron wave, which is treated as an adjustable parameter, is displayed in the second column. The next three columns present the parameters of the wave used to calculate the different generations of infected people $i_n(t)$ (λ_C, $i_1(0)$ and λ_R) which best the data. All rates are in days^{-1}. The mean recovery time τ_R is shown in column 6 (in days). The next column 7 present the time t_{max} (in days) when the calculated maximum of the Omicron peak is found. The corresponding generation number "n" and the basic reproductive number R_0 are displayed in columns 8 and 9, respectively.*

Country	0-start day	λ_C	$i_1(0)$	λ_R	τ_R	t_{max}	Number n	R_0
USA	25	6.57	2	0.116	8.6	47	4	57
	25.12.2021					16.01.2022		
UK	19	7.29	1	0.1865	5.4	34	4	39
	19.12.2021					03.01.2022		
France	32	5.87	1	0.095	10.5	62	4	62
	05.01.2022					30.01.2022		
Romania	49	6.7	3	0.098	10	70	3	68
	18.01.2022					08.02.2022		
Bulgaria	37	5.41	1	0.082	12.2	61	3	66
	06.01.2022					29.01.2022		
Germany	45	4.96	1	0.104	10	64	4	48
	14.01.2022					02.02.2022		

The most often used data for monitoring Epidemics consists of the sequence of newly infected people per day normally established by tests. It can be calculated as,

$$C(t) = \lambda_C \sum_{n=2}^{K_{max}} i_{n-1}(t) \qquad [10]$$

The upper limit K_{max} of the generation numbers depends on the Epidemics status at time t. When a particular data set is considered K_{max} is treated as a fitting parameter ensuring the best description as explained in [5]. By trying to reproduce the normalized data on the new cases per day, the function $C(t)$ was used to fit the data in Figures 1-3 for the specified cases.
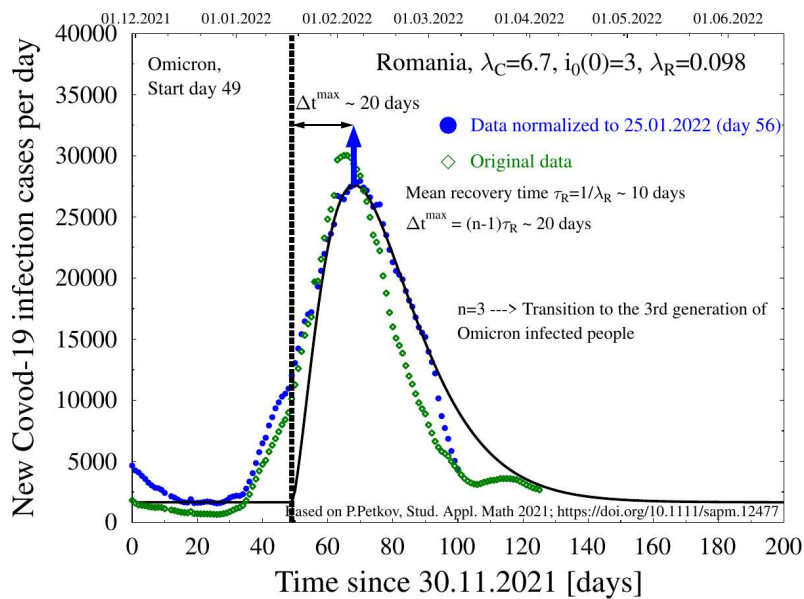
Figure 1: *The Omicron wave of the COVID-19 Pandemic in Romania. All data were taken from the site [18]. The original raw data on the newly registered cases per day and the corresponding normalized data points are represented by open diamonds and filled circles, respectively. The plateau-like part of the data before the effect of increase is considered as a constant (averaged) background and reflecting the previous stage of the Pandemic. The calculations (fits) according to Equation 10 are represented by a continuous line. A maximum of the peak is predicted about February 4th. The derived parameters are also indicated. The infection and recovery rates are in $days^{-1}$.*
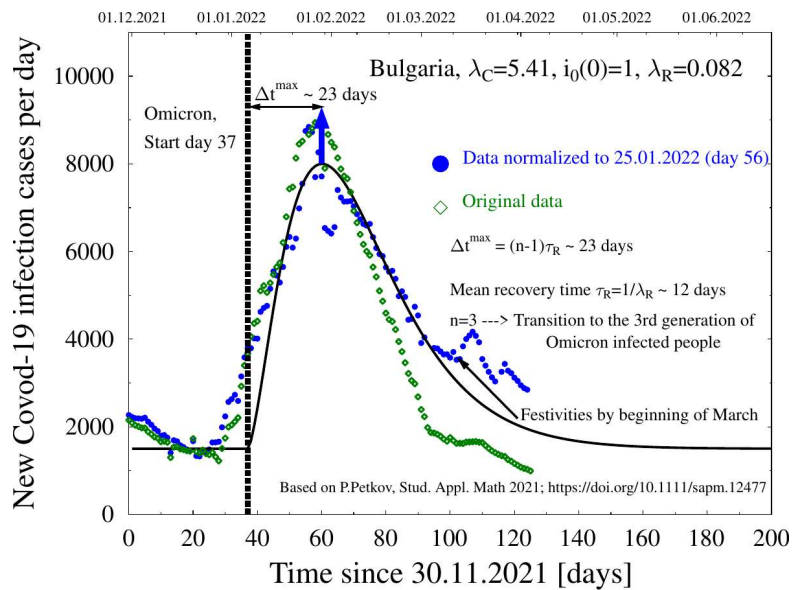

Figure 2: *The same as in Figure 1 but for Bulgaria. Here, the maximum of the peak is predicted about January 29th.*
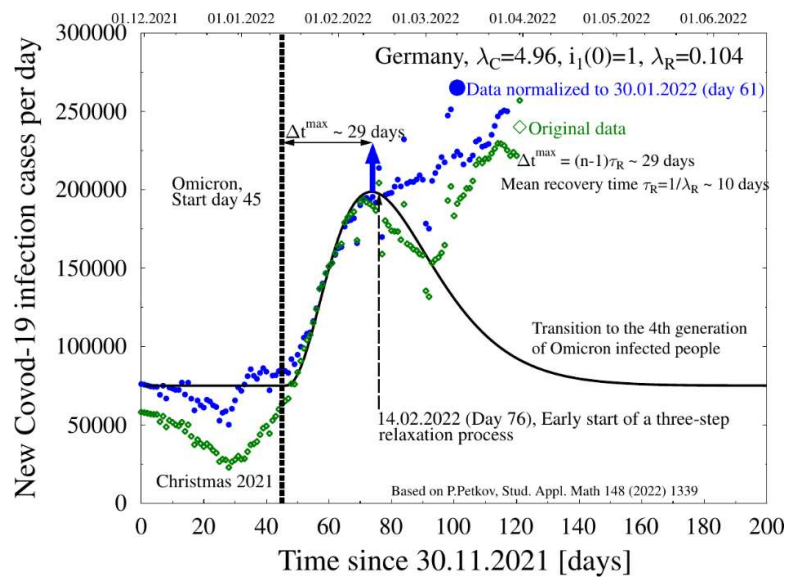
Figure 3: *The same as in Figure 1 but for Germany. Here, the maximum of the peak is predicted about February 12th. A vertical line indicates the date 14.02.2022 when a three-step relaxing restriction did start and a few days later the expected decreasing trend was suddenly transformed into an opposite, increasing one.*

3. Discussion of the Results for the Daily New Cases of Infections

The data points in Figures 1-3 display a quite complicated behavior with time, especially for the normalized points in the beginning of December 2021 and for the raw data by beginning of January. The simplest version of the model presented in [5], i.e., without considering consecutive waves and infected people entering the investigated system from outside, cannot describe all the data set. Therefore, we decided to take into account the contribution of the Pandemic before Omicron by subtracting a constant background determined by averaging over a subset of points with similar behavior with time. In this way, in the beginning of January 2022 an effect of increase is definitely observed. However, a purer Omicron effect is observed later, preceded by a period where there is some mixed role of earlier variants (δ on top, of course) and the incoming Omicron wave. Thus, the time position of the start of the latter wave was treated as an adjustable parameter allowing a reproduction of the fast increase accompanied by a change of the slope of splines passing through a set of successive data points toward higher value. After that, calculations using Equation 10 were performed in order to reproduce the data. In the next sections, we consider specifically the data for the three countries considered.

3.1. Romania

All data are normalized to the point at 25.01.2022 (both earlier or later registered). At this date, 77161 tests were performed in Romania [18]. The expected peak position of the fitted curve is about February 4th (day 66). This corresponds roughly to 21 days after the "start" of the Omicron wave and according to the relation Δt_{max}=(n-1) τ_R (Equation 9), with τ_R=1/$\lambda_R \approx 11$ days, indicates n=3 i.e. this is the moment when the third generation of infected people is dominant. But one should not forget that this generation provokes infections in the 4th

generation and without some other effects on the Pandemic's development one should arrive to even higher numbers. This does not happen and will be discussed a bit later below. Also, far beyond the maximum the raw data indicates a much faster decrease of the new infection case per day than the calculated curve and the normalized points. This deviation deserves attention when a program for gradually lifting the restrictions has to be made.

3.2. Bulgaria

The analysis presented in Figure 2 is similar to the analysis for Romania in Figure 1, with small differences in the derived parameters. The normalization is made with respect to the data point at 25.01.2022 when 30627 test were performed. A somewhat unexpected is the behavior of the normalized point in the vicinity of the maximum which displays large fluctuations. This is due to irregularities in the otherwise smooth behavior of the number of tests per day according to the site [18]. Namely, the four points around February 1st which drop down are characterized by number of tests around 40000, i.e., are larger by minimum 15% than the neighboring ones, although also obtained by a 7-day rolled procedure. The opposite effect is observed a bit earlier, just before the maximum of the calculated curve. It should be noticed that the latter is very close to the position of the maximum indicated by the raw data as well as the normalized points lie in a nearly perfect way on the calculated curve on the decreasing side. They were not used for fitting. The raw data also indicates here a much faster decrease.

3.3. Germany

The analysis presented in Figure 3 is in general similar to what has been shown in Figures 1 and 2 for Romania and Bulgaria, respectively. However, there are features and differences in the derived parameters which need some comments. First, the countries under comparison are very different with Germany on the single one side, indeed. For example, the population of Germany is much larger (about 80 million) against about 6 million for Bulgaria and 19 million for Bulgaria, the infection rate λ_c=4.96 days^{-1} is the smallest, the actual generation of infected people is the n=4 one. The normalization in Figure 3 for Germany was made with respect to the data point at 30.01.2022 when 364841 tests were performed. The most significant and may be important effect is the tendency for increase shortly after the maximum on February 12th. In Figure 3 a vertical line indicates the date 14.02.2022 when a three-step relaxing restriction did start and a few days later the expected decreasing trend was suddenly transformed into an opposite, increasing one. Another difference is the drop of the new daily infection cases around Christmas 2021 which cannot be completely corrected even by the normalization on a day per day basis. This may be an indication that for the specific case of Germany the proposed way of normalization is biased by some factors which remain to be investigated. Also, large fluctuations in the behavior of the normalized points are observed in the vicinity of the maximum. Different from the case of Bulgaria (Figure 2), they cannot be associated with deviations from the smooth behavior of the time evolution of the number of tests per day. In this way, the behavior of the data in Figure 3 appears as the most complicated one among the considered in this work. It may also suggest that the process of lifting restrictions began a bit too early. An investigation of the effects of vaccination level and acquired temporary immunity, which are discussed below for some other countries, may clarify the situation.

3.4. Comparison with data from other countries

The parameters of the fitted curves in Figures 1-3 require some comments. First of all, the infection rates $\lambda_C = 5 \div 6.2$ days^{-1} are very large. They can be compared to the value of 0.71 days^{-1} derived in [5] for the first wave in the USA and Europe in spring of 2020 related to the original Wuhan virus. In Table 3 of reference [5], the rates of transmission are compared in relative units with respect to contagiousness (i.e., for the Wuhan virus one has 1.0, for $\alpha : 1.4 \div 1.9$, for $\delta: \geq 3$). In addition, in calculations according to the model of [5] the ratio $R_0 = \lambda_C / \lambda_R$ participates with ever increasing effect, at the power of $(n-1)$ for every next generation number n. Therefore, is no wonder that the Omicron wave becomes so fast the dominant one (in the period discussed). For larger τ_R (smaller λ_R) the effect is complementary enhanced. For comparison, we present in Figure 4 data for three other countries where the Omicron wave had a strong effect on the Pandemic in the beginning of 2022: the USA, the UK and France. The figure is taken from the investigation performed in [6] and modified for the present work by adding more data points closer to present. The reproduction of the data by the calculations in Figure 4 is reasonable in the region of increase and in the vicinity of the maximum in all three cases. The role of the normalization is also clearly seen, and in the cases of the UK and France is quite dramatic. There are indications that the decreasing part of the data after the peak maximum can be also well described after normalization by the calculations (as it is clearly seen in the cases of the UK and France). After the maxima, the raw data for the USA and France decrease much faster than the calculated curves. This difference is related to a gradual decrease of the daily tests once the peak value has been reached. In general, after the maximum only a decrease may be expected in principle. However, a realistic estimate of its actual speed and state (i.e., when a sufficiently low level will be reached) is of importance for the control of the Pandemic and eventually lifting restrictions, for example. This is strongly suggested by the development in the UK after the initialization of such lifting measures about 21.01.2022 (Figure 4B). Large fluctuations of the new infection cases per day are observed both in raw and normalized data although on average the decreasing trend is conserved and that lifting of restrictions finally seem to be made not too early. It has also to be mentioned that the Omicron wave has started a bit earlier in the UK. In the case of the Omicron wave, the evolution downwards is related to the existence of a very large fraction of the population possessing protection against Covid-19 due to vaccination and natural (temporary) immunity acquired after recovery from being infected. The case of the USA (Figure 4A) probably is a very good illustration of these circumstances with both raw and even normalized data lying below the calculated curve after mid-February. The role of the acquired immunity within the Omicron wave is supported by estimates that in 3-4 months about the same number of people are (or will be) infected as in the nearly 2 previous years of the Pandemic. The UK was the first country where such effects have been discussed and intentions of lifting gradually all restriction measures were declared, soon followed by others.

The fitted infection rates λ_C in Romania, Bulgaria and Germany are compatible within the range of values derived for the USA, the UK and France. The adjustable "start days" of the first group of countries are about 20 days later than those of the second group (except for France to some extent). It may seem unexpected, but from the present perspective lifting restrictions in Romania and Bulgaria looks much more timely and reasonably than in the case of Germany and to some extent in France. In this context, the example, and the experience of the development in the UK may be very useful. It is not our intention to formulate rules for lifting restrictions, but a criterion on how much the data and fits are above the acceptable "background" at a given planned time may be also useful. Thereby, mathematical modeling

has still to be employed along other guiding lines of social, health and economics character, in general.
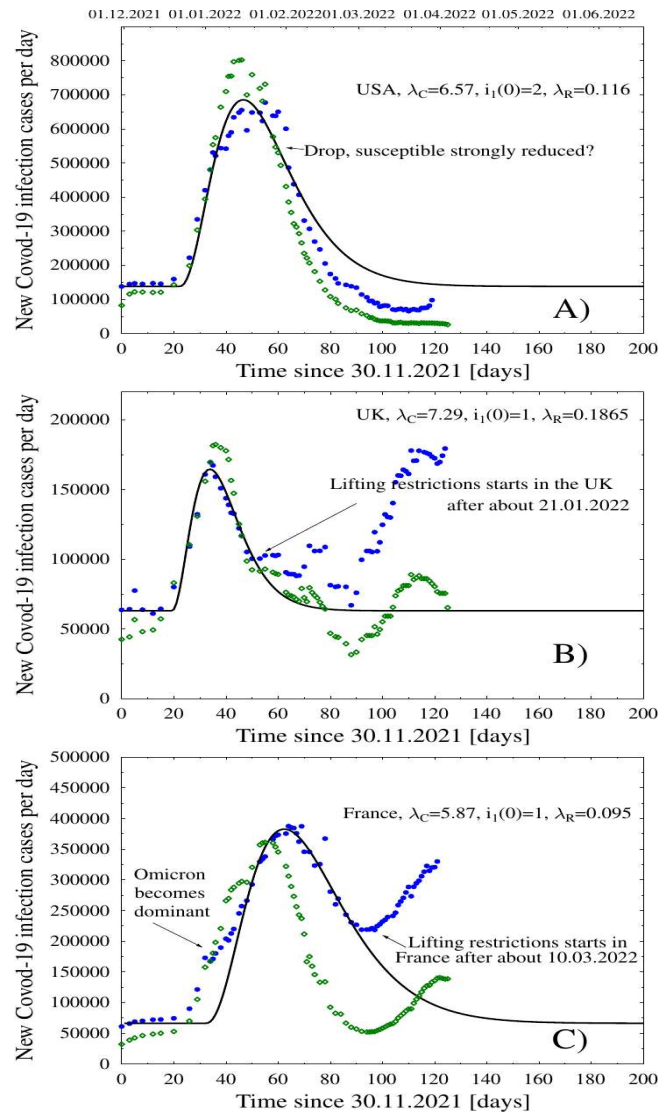

Figure 4: *Part A (top): The Omicron wave of the COVID-19 Pandemics in the USA illustrated by the normalized newly registered cases per day and the original raw data (without normalization) are represented by filled circles and open diamonds, respectively. All data, including the number of tests per day used for a normalization (correction), were taken from the site [18]. The plateau-like part of the data before the effect of increase is considered as a constant (averaged) background which reflects the previous stage of the Pandemic related developments to future. The most successful calculation (fit) according to Equation 10 is represented by a continuous line. The derived parameters are also indicated, with the infection and recovery rates in days^{-1}. The effect of normalization is clearly seen and is rather large. An inspection of the data on the number of tests done daily shows a non-interrupted reduction trend after reaching the maximum which correlates partly with the very fast decrease of the raw new daily cases. A reduction of the latter cases is predicted also by the calculation, but it has a much slower character. Parts B, C: The same as in part A, but for the UK and France, respectively. For discussion of specific features seen in each of the three panels (some of them shortly indicated in the figure).*

4. Conclusion

The COVID-19 Omicron wave in Romania, Bulgaria, and Germany till begin of March 2022 is considered within a new approach [5] for modeling Epidemics and a short comparison is made of similar application to few strongly affected countries in the beginning of 2022: the USA, the UK and France. Because of the much larger contagiousness of Omicron, its wave starts to dominate the Pandemic at some time moment, after which the simplest version of the model [5] is employed (without consecutive waves and incoming infected from outside the system). The daily observed new infection cases are described in a reasonable way after normalization. The position of the calculated Pandemic peaks in time in Romania and Bulgaria indicates a transition from the second to the third generation of infected people. For comparison, in the USA, UK and France the transition is from the third to the fourth generation. The parameters derived by reproducing the data in the three countries considered are consistent with those derived earlier for the USA, the UK and France (i.e., infection and recovery rates). Due to the high contagiousness of Omicron, a large part of the population goes through a contact with the virus in a relatively small period of time (3-4 months), and the resulting number of infected people is comparable with the cumulative effect of nearly two years of since the start of the Pandemic. Therefore, some temporary acquired immunity seemed to be realized. Adding the very serious effects of vaccination, a general hope appeared that controlling/stopping the COVID-19 Pandemic would be realistic soon. However, lifting restrictions should have been done carefully and country specific, and at the right time, as illustrated by the examples of the UK and Germany and to some extent in France. Indications that the load on the health systems was weaker in the late stage of the Omicron wave though the number of new cases remained relatively high has also encouraged a faster but gradual lifting. Later developments after March 2022 have shown, however, that the above expectations were too optimistic and Omicron waves generated by another virus sub-variants did complicate the situation.

The present work represents only a mathematical modeling of the Pandemic and does not deal with any other aspect of health, social or economic character as well as throwing away any possibility for unexpected developments. Though during the finalization of the present work in May 2023, the WHO declared [23] that the COVID-19 pandemic "is now an established and ongoing health issue which no longer constitutes a public health emergency of international concern".

Institutional Review Board Statement

This study was performed in a private company operated by the author.

Data Availability Statement

The data used in the study are public, taken from https://ourworldindata.org/coronavirus-testing. The implemented software can be provided by the author at request.

Acknowledgments

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