Mathematical Modelling of an Epidemic Based on Covid-19 Spread Functions

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Abstract

The study of the mechanisms of epidemic spread is an important way of controlling the disease. Reducing damage from a coronavirus epidemic is linked to the use of methods and tools for mathematical modelling of Covid-19 spread. Epidemic wave representations are used to characterize the spread of Covid-19, which is highly visual and informative. However, this "wave" representation places increased demands on Covid-19 spread models.

For mathematical modelling of the spread of the Covid-19 epidemic, is considered the application of specific Covid-19 propagation functions, based on constrained growth functions. The Covid-19 spread functions show high accuracy in approximating statistical data, which demonstrates the good adequacy of these functions in principle. Application of the Covid-19 propagation functions makes it possible to quantitatively describe the basic concepts of the epidemic and conduct a comparative parametric analysis of the epidemic's spread and predict the development of the epidemic. Comparison of parameter values makes it possible to identify differences in indicators and growth rates, based on which the results of epidemic control can be assessed.

Keywords 1

Covid-19 spread functions, approximation of Covid-19 statistical evidence, parametric analysis

1. Introduction

Mathematical modelling of epidemic spread makes an important contribution to disease control. Modelling the mechanisms of epidemic spread and predicting its evolution can significantly reduce the damage caused by a pandemic [1-5]. Quantitative model simulations can provide comparative analysis and predictive modelling of temporal descriptions of key epidemic categories such as the number of people who became ill, recovered and died [6-9]. Covid-19 propagation models are therefore subject to increasing demands, not only for consistency with statistical data but also for the adequacy and accuracy of the underlying concept descriptions.

As we know from [10-11], the SIR model developed by Kermack and McKendrick in 1927-1933 is widely used to describe epidemics, which is based on a scheme of epidemic transition of basic variables from one category to another. The variables used as basic variables are those that denote the number of individuals: those susceptible (*S*) become infected (*I*), then recover (*R*). The SIR model is represented by a system of 1st order coupled differential equations that describe the time dependence of the underlying concepts, where the coupling is given by conditions that stipulate the sum of the variables and their derivatives.

Models which implement the concept of epidemic transition have gained wide popularity and development, so the SIR class of models today also contains varieties: SIRS, SEIR, SIS, MSEIR, etc. However, the experience of applying SIR class models for mathematical modelling of Covid-19 spread [10, 12-15] has shown insufficient consistency of the calculations of basic variables with statistical data.

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The desk review [15] noted that “An attempt to apply these models (SIR class) to the case of a coronavirus pandemic in Ukraine showed that they fail when heterogeneous populations, different routes of transmission and the presence of randomization factors are present”. Therefore, the project team concluded that any projections derived for Ukraine, with its characteristic heterogeneity, using SIR models and their derivatives cannot be considered correct and certain coincidences of projected data may have a random nature. Therefore, the team of the “FORSAIT COVID-19” project applied a group of methods of different nature and class to conduct a series of studies of the coronavirus propagation process in Ukraine, based on the consideration that if the results obtained using different methods are close, the plausibility of the studies is increased.

Thus, the problem with mathematical modelling of the spread of Covid-19 is the lack of adequacy of SIR models, preventing the accuracy of description, analysis and prediction. The fundamental shortcoming of SIR models, in our opinion, is that in the epidemic transition concept, the dynamics of the main variables (ill I, recovered S) are defined through the concept of “contact”, which is defined by the product of the variables. This representation of the interaction of variables severely limits the modelling capability of the epidemic. The lack of accuracy of SIR models necessitates new approaches for mathematical modelling of Covid-19 spread. New approaches that can improve the adequacy consist of having models of the underlying concepts formed as independent constructs.

The nature of the statistics of the Covid-19 coronavirus epidemic shows that they are highly like logistic functions. Therefore, we note the application of logistic functions to approximate a piece of given statistical information. A mathematical model of the spread of the Covid-19 coronavirus epidemic is considered in [16], which uses a simplified logistic model of the form describing the growth in the number of cases. However, the application of this logistic equation has shown that this model is of low accuracy. To improve the accuracy, it is suggested that the study range should be divided into regions with partial logistic functions, which cause significant computational difficulties.

In the article [17], the authors note: “Having realised the complexity of the forecasting task, the authors decided to restrict themselves to the simplest logistic model”. The low accuracy of the calculation results obtained in [16, 17] can be attributed to the fact that simplified representations of logistics models were used for modelling.

The article [18] considers the wave structure of an epidemic, which is represented by a set of elementary epidemic flows (waves) shifted along the time axis and differing in parameter values. A constrained growth function based on a generalized logistic model with extended description capabilities due to additional conditions were used for mathematical modelling of Covid-19 propagation. Based on this model, an analytical description of the epidemic in the form of a complex flow of epidemic events was obtained, which can be seen as a solution to an approximation problem for a piece of given statistical information. However, the content of the article is limited to the approximation task for statistical information describing the flow of events. Since the generalized logistic model in mathematical modelling of epidemic event fluxes has shown increased adequacy and a high degree of compliance of the calculations with the original statistical data, it seems appropriate to apply this model to modelling epidemic propagation functions.

This article aims to develop mathematical models of epidemics in the form of basic event propagation functions for key epidemic concepts based on a generalised logistic function and to use these models for analysis and forecasting.

2. Mathematical models of epidemic spread

2.1. Non-linear differential equations of epidemic spread

Review the following basic concepts of the Covid-19 epidemic. Statistics use the following basic categories to refer to the spread of an epidemic:

1. The number of individuals who became ill (infected).
2. The number of individuals who died (deaths).

The statistics by category are set on an accumulative basis, where intermediate totals are used to show the total amount of data as it grows over time. By modelling Covid-19 prevalence statistics using regression relationships, we obtain a representation of the epidemic prevalence functions, which have the following properties

- the functions are monotonically increasing;
- the growth of the functions is limited to a certain value (threshold, plateau) to which the function tends asymptotically.

Thus, the epidemic spread functions are S-shaped logistic curves. Therefore, to describe the epidemic spread functions, we will use the constrained growth functions that have proved themselves in conflict interaction models [18-21]. In general, constrained growth functions are defined in algorithmic form as solutions to a 2-nd order nonlinear differential equation [18, 19]:

- for the number of infected individuals $x(t)$

$$a_2 x(t)\frac{d^2x(t)}{dt^2} + (1 + a_1 x(t))\frac{dx(t)}{dt} + (a_0 x(t) - \varphi)x(t) = 0; \tag{1a}$$

- for the number of fatal cases $y(t)$

$$b_2 y(t)\frac{d^2y(t)}{dt^2} + (1 + b_1 y(t))\frac{dy(t)}{dt} + (b_0 y(t) - \phi)y(t) = 0, \tag{1b}$$

where $x(t)$, $y(t)$ are epidemic variables; φ, ϕ – growth rates;$\{a_2; a_1; a_0\}$, $\{b_2; b_1; b_0\}$ – phenomenological coefficients, which are treated as epidemic parameters.

Since the epidemic spread functions are monotonically increasing, to represent them we restrict ourselves to a 1st order nonlinear differential equation at $a_2 \approx 0$, $b_2 \approx 0$:

- for infected individuals

$$\frac{dx(t)}{dt} + \frac{a_0 x(t) - \varphi}{1 + a_1 x(t)} x(t) = 0; \tag{2a}$$

- for fatal cases

$$\frac{dy(t)}{dt} + \frac{b_0 y(t) - \phi}{1 + b_1 y(t)} y(t) = 0, \tag{2b}$$

Equations (2a) and (2b) can be considered as a generalised representation of the Verhulst logistic equation [22-25], to which equations (2a) and (2b) can be reduced with the parameters $a_1 = 1$ and $b_2 = 1$.

2.2. Functions of the spread of the Covid-19 epidemic

Solutions to equations (2a) and (2b) specify the epidemic spread functions in the form of constrained growth functions, which are used to describe the spread of Covid-19. The epidemic propagation functions $x(t) = f(t, \varphi, a_0, a_1)$, $y(t) = f(t, \phi, b_0, b_1)$ have two equilibrium states:

1. Initial equilibrium – unstable, $x(0)$ when $t = 0$;
2. Final equilibrium – stable, $X(t) \to X$ when $t \to \infty$.

A characteristic element of the epidemic propagation functions are expressions for the equivalent growth rate coefficients:

- for infected individuals

$$\tilde{\varphi}(t) = \frac{\varphi - a_0 x(t)}{1 + a_1 x(t)}; \tag{3a}$$

- for fatal cases

$$\tilde{\phi}(t) = \frac{\phi - b_0 y(t)}{1 + b_1 y(t)}; \tag{3b}$$

Expressions (3a) and (3b) for equivalent growth rates describe an important property of epidemic spread functions, namely that equivalent growth rates are not a constant but a function of primary variables.

The epidemic spread functions vary over a range bounded by equilibrium states. A final steady-state equilibrium corresponds to the conditions that the derivatives $\frac{dx(t)}{dt} \approx 0$, $\frac{dy(t)}{dt} \approx 0$ and expressions for the coefficients of the equivalent growth rates $\tilde{\varphi} \approx 0$ and $\tilde{\phi} \approx 0$, are zero.

An important characteristic of epidemic spread functions is the plateau (the upper limit of the constrained growth function) – the threshold value towards which the constrained growth function tends to move in a finite steady-state equilibrium. To determine the plateau of the epidemic's spread function, we formulate equations corresponding to the zero values of the equivalent growth rate

- for infected individuals

$$a_0 X - \varphi = 0; \tag{4a}$$

- for fatal cases

$$b_0 Y - \phi = 0. \tag{4b}$$

where X, Y – plateau values.

Plateau values are defined as solutions to equations (4a) and (4b):

- for infected individuals

$$X = \frac{\varphi}{a_0}; \tag{5a}$$

- for fatal cases

$$Y = \frac{\phi}{b_0}. \tag{5b}$$

The plateau of the epidemic spread functions is characterized by the ratio of the growth rate to the phenomenological coefficient.

Note that the equivalent growth rate of infected individuals (3a) varies in the range from the exponential growth rate of $\tilde{\varphi}(0) = \varphi$, when $t = 0$, to zero $\tilde{\varphi}(0)_{t\to\infty} \approx 0$ when $t \to \infty$. Correspondingly, the equivalent growth rate of lethal cases (3b) varies in the range from the exponential growth rate value of $\tilde{\phi}(0) = \phi$, when $t = 0$, to zero $\tilde{\phi}(0)_{t\to\infty} \approx 0$ when $t \to \infty$.

2.3. Discrete Covid-19 spreading function

Let us use the Covid-19 spreading function representations as to the solutions to equations (2) for a discrete-time as our computational expressions:

- for infected individuals

$$x_{k+1} = (1 + \tilde{\varphi}(x_k))x_k; \tag{6a}$$

where $\tilde{\varphi}(x_k) = \frac{\varphi - a_0 x_k}{1 + a_1 x_k}$ – equivalent growth rate coefficient.

- for fatal cases

$$y_{k+1} = \left(1 + \tilde{\phi}(y_k)\right) y_k \tag{6b}$$

where $\tilde{\phi}(y_k) = \frac{\phi - b_0 y_k}{1 + b_1 y_k}$ – the equivalent rate of increase in fatalities.

The equivalent growth rate of infected cases $\tilde{\varphi}_k(x_k)$ varies in the range from $\tilde{\varphi}_k(0) = \varphi$, $k = 0$ to zero $\tilde{\varphi}_k(x_k) = 0$, $k \to \infty$. Correspondingly, the equivalent growth rate of lethal cases $\tilde{\phi}_k(y_k)$ varies in the range from $\tilde{\phi}_k(0) = \phi$, $k = 0$, to zero $\tilde{\phi}_k(y_k) = 0$, $k \to \infty$.

3. Calculations of Covid-19 spreading functions for different countries

3.1. Approximation of Covid-19 distribution statistics in different countries

Equations (6a) and (6b) were used to approximate the statistical data for the spread of Covid-19 in different countries. Actual data from the first wave of Covid-19 spread in the first half of 2020, which has no epidemic prehistory, are used as input data.

The countries selected for the calculation of the Covid-19 spreading functions are Ukraine [26], Italy [27], Spain [28] and France [29]. The definition of Covid-19 propagation functions consists in selecting parameters for expressions (6a)–(6b):

- φ, a_1, a_0 – for the propagation function of infected individuals;
- ϕ, b_1, b_0 – for the distribution function of lethal cases.

Using the values of the parameters were calculated the integral indices of X and Y – the plateau of Covid-19 spread functions, which is estimated in persons. For an overall assessment of the spread of the epidemic, the relative indicator was used $W = \frac{Y}{X}$.

To estimate the approximation error were used the relative mean absolute error – MAPE, which calculated according to the formula

$$\delta x = \frac{1}{N}\sum_{N} |\bar{x}_k - x_k| / \bar{x}_k,$$

where $\bar{x}_k$ – statistical data values.

For the selected countries, the MAPE values show a reasonably high approximation accuracy (Table 1).

Table 1

Approximation accuracy

Function type	Parameter	Country			
		Ukraine	Italy	Spain	France
ill	δx	3,0%	2,4%,	1,6 %	1,4 %
deceased	δy	7,0 %	4,6 %	2,2%	2,0%

Ukraine [26] (Figures 1 and 2) and Italy [27] (Figure 3) are chosen as examples to show how the calculated Covid-19 spread functions correspond to statistical data.

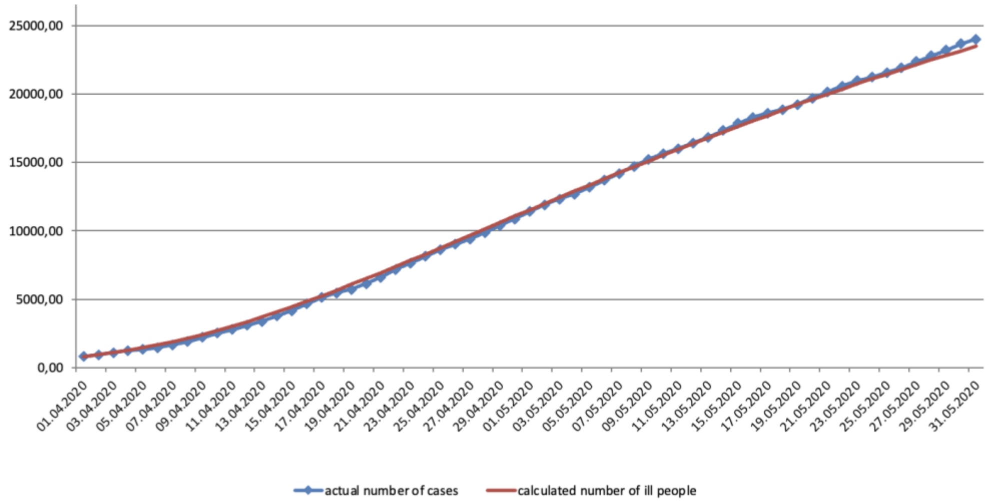

Figure 1: Compliance of the estimated values of Covid-19 infection spread functions with statistical data for Ukraine for April and May 2020

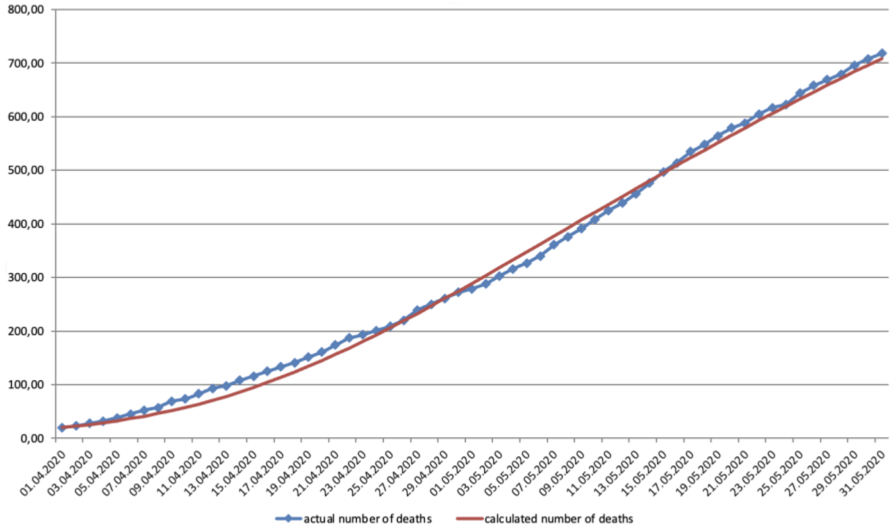

Figure 2: Compliance of the estimated Covid-19 fatality distribution functions to the statistical data for Ukraine for April and May 2020

Figures 1 and 2 clearly show a reasonably good correlation between the calculated and actual data, where the MAPE does not exceed 3% and 7%.

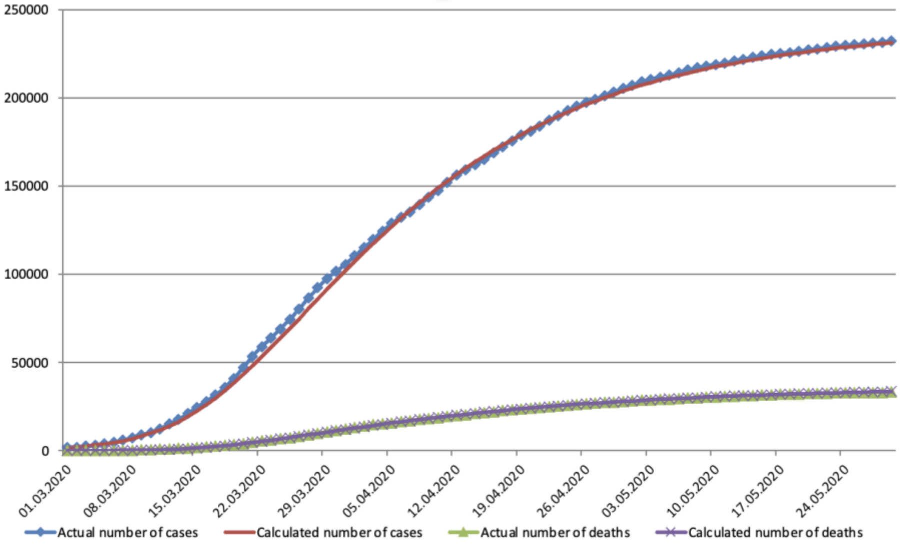

Figure 3: Compliance of the estimated Covid-19 spread functions with the statistics for Italy for March, April, and May 2020

Figure 3 clearly shows a reasonably good correlation between the calculated and actual data, where the MAPE does not exceed 3% and 5%.

A comparison of the calculated Covid-19 spread functions for different countries is shown in Figure 4.

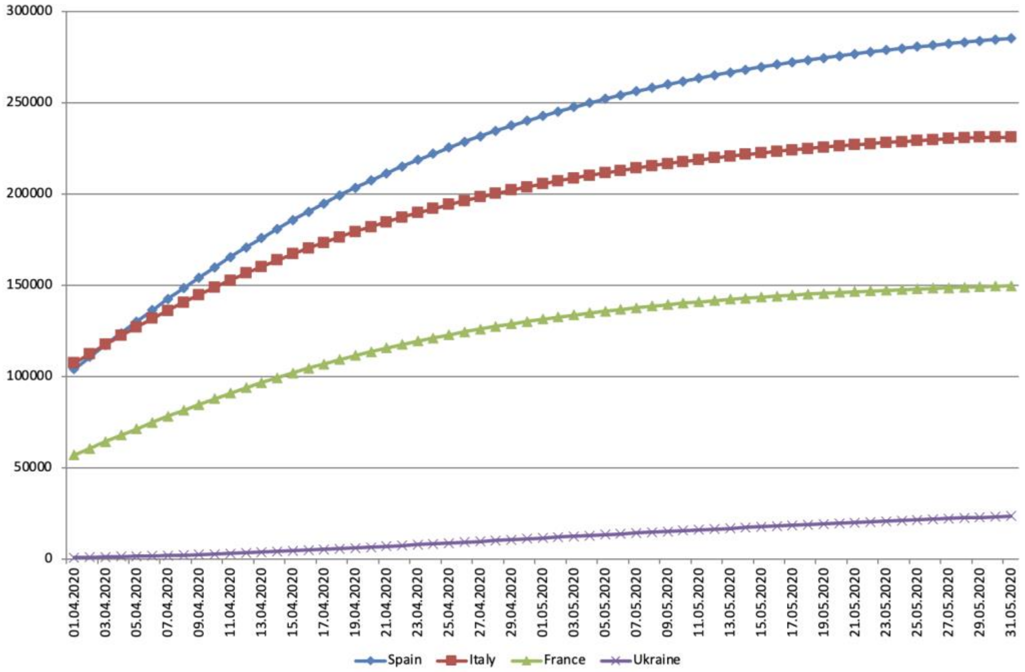

Figure 4: Comparison of estimated Covid-19 distribution functions for different countries for April and May 2020

Analysis of the results shows that the number of Covid-19 cases for Italy, France and Spain has almost reached a plateau, with values around the same level. Ukraine has passed the inflexion point of the Covid-19 prevalence curve and is halfway to the plateau. The number of Covid-19 cases in Ukraine is markedly lower than in the other countries examined

The curves of the Covid-19 spread functions are smooth and monotonic, which, assuming unchanged parameter values, allows them to be used for forecasts with a high degree of confidence.

3.2. Parametric analysis of Covid-19 spreading functions

The Covid-19 spreading functions in the different case studies share a common, universal mathematical design and differ in parameter values, which allows for a comparative parametric analysis of the spread of Covid-19. The parameter values for comparative analysis of the spread of Covid-19 in different countries are shown in Table 2.

Table 2

Parameter values for analysis

Function type	Parameter	Country			
		Ukraine	Italy	Spain	France
ill	X	42 000	240 000	250 000	200 000
	φ	0,2	0,235	0,25	0,2
	$a_1 \cdot 10^6$	230	16	15	17
	$a_0 \cdot 10^6$	4,76	1,00	1,00	1,00
deceased	Y	1400	36 500	36 000	50 000
	ϕ	0,15	0,34	0,34	0,47
	$b_1 \cdot 10^6$	4600	220	220	220
	$b_0 \cdot 10^6$	105	9,32	9,32	9,32
	$W = \frac{Y}{X}$	**0,03**	**0,15**	**0,14**	**0,25**

For Covid-19 cases:

- The values of the incidence rates φ are in the range $\varphi \in \{0{,}2; 0{,}25\}$ and differ insignificantly. The growth rate of the epidemic in these countries is about the same.
- For Italy, France and Spain, the phenomenological coefficients a_1 are in the range of $a_1 \cdot 10^{-6} \in \{15; 17\}$, $a_0 \approx 10^{-6}$ and differ slightly. In Ukraine, the coefficient $a_1 \approx 230 \cdot 10^{-6}$ is about 15 times larger than in the other countries. Given that the coefficient a_1 describes the inhibition effect of the Covid-19 spread, it can be concluded that Ukraine has a high resistance to the epidemic.
  For Ukraine, the coefficient values $a_0 \approx 4{,}76 \cdot 10^{-6}$ are almost 5 times higher than in the other countries. Given that $X = \frac{\varphi}{a_0}$, the consequence is that the threshold (plateau) X of the incidence curve decreases by a factor of almost 5 compared to other countries.

For Covid-19 lethal cases:

- The values of the indicators for the growth of the deceased ϕ, are in the range of $\phi \in \{0{,}15; 0{,}47\}$ and vary considerably. The value for Ukraine is three times lower than that for France.
- the values of the phenomenological coefficients for Italy, Spain and France are approximately the same $b_1 \approx 220 \cdot 10^{-6}$, $b_0 \approx 9{,}32 \cdot 10^{-6}$. For Ukraine, the value of the phenomenological coefficient $b_1 \approx 4600 \cdot 10^{-6}$ is 20 times higher than in the other countries, which indicates a high resistance to lethal cases;
- for Ukraine the coefficient value $b_0 \approx 105 \cdot 10^{-6}$ is 10 times those of other countries. Given that $Y = \frac{\phi}{b_0}$, the consequence is that the threshold (plateau) Y of the morbidity curve has been reduced by a factor of almost 20 compared to other countries.

The integral characteristic of an epidemic, defined as the ratio of deaths to cases $W = \frac{Y}{X}$, is several times smaller than in other countries.

As the values of the indicators can be linked primarily to prevention, sanitation, and treatment interventions, they can be used to assess the results of controlling the epidemic in different countries. The strategy for controlling the epidemic in terms of Covid-19 spread models is generic and consists of lowering the threshold (plateau) of the disease as much as possible (model parameters X, Y). This requires:

1. Decreasing the epidemic's growth rate (model parameters φ, ϕ).

2. Increasing resistance to the virus (model parameters a_1, b_1).
3. Reducing the range of the community of people accessible to infection (increase model parameters a_0, b_0).

Interpretation of these formal requirements is followed by known protective actions.

4. Conclusions

The epidemic spread models considered are fundamentally different from SIR models in the following respects:

- SIR class models investigate the behaviour of epidemic categories depending on the interaction between them, which is consistent with the principles of system dynamics. Representing SIR models as a coupled set of differential category equations limits the accuracy of the calculations.
- The epidemic spreading model examines the behaviour of epidemic categories as decentralised agents and how this behaviour determines the behaviour of the system, so the model is based on an unrelated set of differential category equations. This approach is consistent with agent-based modelling methodology, which has greater descriptive power than SIR models but requires a more detailed description of the epidemic categories. Agent-based models use a dynamic system representation in which the details of the descriptions are provided by feedbacks

The application of Covid-19 propagation functions based on the generalised logistic function shows a high approximation accuracy of the statistical data, which demonstrates the good adequacy of these functions. This correspondence with the original evidence suggests that the main problem of mathematical modelling of Covid-19 propagation, which boils down to the adequacy of epidemic models, can be solved by applying Covid-19 spreading models and functions.

The application of Covid-19 propagation functions makes it possible not only to quantitatively describe the basic concepts of the epidemic but also to construct a reliable forecast, provided that the parameters are constant. An even more important, in our opinion, the consequence of the application of Covid-19 propagation functions is a comparative parametric analysis of specific epidemic spread functions. Comparison of parameter values can reveal differences in growth rates and phenomenological coefficients, from which conclusions can be drawn about different processes of epidemic behaviour in different regions and countries. By linking these processes to prevention, sanitation and treatment interventions, differences in the results of the epidemic can be identified, analysed and good practices can be disseminated. In general, the application of Covid-19 spread functions can help to reduce the harm caused by a pandemic.

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