

A life circle of the COVID-19 progression in a given region

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Method Article

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Abstract

The Verhulst equation with variable parameters is applied to identify the features of disease spread within the framework of the general balance 'expended-reached' factors. The mathematical model of this balance facilitates revealing the growth features that cannot be identified by the SIR-like models. The proposed approach reconstructs actual object behaviour without any additional information on its features. Postulating the functional properties of the required values is not performed. The observations are processed under the condition that the reconstruction should ensure the small residual between the sample and the model-calculated state function.

Idea

The Verhulst equation with variable parameters is applied to identify the features of disease spread within the framework of the general balance 'expended-reached' factors. The mathematical model of this balance facilitates revealing the growth features that cannot be identified by the SIR-like models. The proposed approach reconstructs actual object behaviour without any additional information on its features. Postulating the functional properties of the required values is not performed. The observations are processed under the condition that the reconstruction should ensure the small residual between the sample and the model-calculated state function.

Object

A reconstruction of the COVID-19 evolutionary patterns by the Verhulst equation aims to determine the disease features based on a generalized model in the sense of the balance 'expended - reached'. The features of the COVID-19 progression in Germany, Switzerland, Sweden, and Brazil are studied. Their coronavirus cases demonstrate the different dynamics of the diseases. The purpose is to determine the general properties of the COVID-19 progression.

The identification of growth features is reduced to the reconstruction of the two model variable parameters using the sample of coronavirus cases. The character of the sought functions directly expresses what is occurring during the growth process. The results reflect the seven phases of the COVID-19 progression.

Methods

The developed approach is based on solutions to inverse problems, which should identify various representations of unknown parameters of a mathematical model and do so *in a series*. *Sequential solutions to inverse problems* ensure the identifiability of desired parameters that belong to an invariant family. *The locally sequential refinement* restricts local spikes *additionally to the general regularization* under a scheme of separate matching with observations. In total, relaxation of a solution eliminates disturbances at individual points during a complicated function approximation. A simulation with inverse

problems is applied to refine the known features of population dynamics. The desired parameters are reconstructed in the absence of information about their functional type and the presence of a sample whose size is smaller than the number of unknowns. The reconstruction shows that the parameters of the Verhulst equation should be introduced as *oscillatory functions*. The results emphasize the Verhulst equation's character as a generalized and fruitful model for an object growth simulation.

Results

From a biological viewpoint, the obtained results demonstrate that the Verhulst equation reflects the oscillatory paradigm of biological objects. The oscillation nature of the parameters of the Verhulst equation expresses the fundamental characteristic of chemical kinetics. The mechanisms, models, and phenomena that cause oscillations in biological and chemical systems are described in many studies. Nowadays, a review of the most typical oscillation phenomena in biological systems is proposed by Janson N.B. in "Nonlinear dynamics of biological systems. Contemporary Phys. 2012;53(2):137–168". The dynamics of disease spread generally corresponds to the homeodynamics paradigm.

The reconstructed oscillations of disease dynamics have analogues in physical chemistry, biochemistry, and epidemiology. The principle of biological oscillations has previously been mathematically described by Chester M. in "A fundamental principle governing populations. Acta Biotheoretica. 2012;60:289–302". The reconstructions confirm the opposition principle. In addition to the proposed *differential equation governing population dynamics* by Chester M., the Verhulst equation expresses an object's growth when, generally, an object's kinetic energy is transformed into its potential energy. *The renewal potential* can be introduced to reflect the spread dynamics. Together with *the favorability function* (see Chester M.), they cover general aspects of the interaction of the complex system 'object – environment'.

The well-known reduction of the SIR model to the Verhulst equation enhances the generalized nature of the Verhulst equation. The reduction means that the Verhulst equation is not a particular case of the simplest processes of the object change but is related and reflects the fundamental features of its growth. The systematic changes of the S-shaped curve convexity–concavity are essentially oscillations that lead to non-unique inflection points. Processing of experimental data demonstrates that the slowly oscillated growth process is characterized by high-amplitude oscillations of the growth rate and intensely varied object adaptation.

Smoothing of most inflection points leads to the loss of essential information about the phenomenon in question. The superposition of the growth process as the sum of partial solutions to the Verhulst equation with constant parameters, derived from the study by Pearl R. (see, "The curve of population growth. Proc. American Philos. Soc. 1924;63(1):10–17"), which is very popular in mathematical biology, cannot provide a complete representation of the object behaviour.

From an epidemiological point of view, the application of the Verhulst equation has shown that it gives *an accurate representation of the actual state* of the disease progression in a given region. The results reflect the peculiarities of the disease spread in a region of any level (e.g., a district, a city, a region, a

country), the tendency of the disease to spread, and the effectiveness of antiviral measures after the COVID-19 outbreak. The application of the Verhulst equation does not exclude the use of other models and supplements the results received through them. The information obtained by the Verhulst equation, despite its non-medical nature, is of paramount practical importance for *monitoring and controlling a current situation with the spread of the disease in a region*. A deeper understanding of the disease progression requires identifying the mechanisms for the different phases.

The approach development highlighted novel features of the growth process. The results refine and emphasize the significance of the Verhulst equation as the generalized model of object growth. The variable parameters of the Verhulst equation express the fundamental regularities of the system 'object – environment'. The behaviour of the reconstructed parameters is clearly interpretable and sufficiently informative to reflect the features of the process dynamics. They reveal the detailed characteristics of the object's interactions and its adaptation to the environment, including the different types of oscillations when the object is changed. The life cycle of the COVID-19 progression was revealed. The general solution to the Verhulst equation with variable parameters was determined.

From the mathematical viewpoint, the significance of the proposed processing is that the approach based on *an approximation of a given discrete set by a function satisfying a given phenomenological model*. Interpretation of experimental data applied directly to the explicit parameters of the adequate model without introducing assumed functional properties. The approximant of the sought quantities was not chosen as a function of a predefined behaviour. Its functional character was determined by the condition of satisfying the relevant phenomenological law. The model adequation governs observation fitting. The character of the approximant was reconstructed according to the stable and best sample approximation. The reconstruction does not require introducing the type of approximant, but requires a large number of approximation nodes. The reconstruction method accounts for the numerical features of the ill-posed formulation. By this means, *the obtained solution exhibits the object properties directly from experimental data processing* without postulation of the nature of the sought quantities and further estimation postprocessing. The analogues of such representations are MRT and CT diagnostics.

For a complete description of the approach and the COVID-19 spread features, see DOI: 10.1080/17415977.2021.1948025

Figures

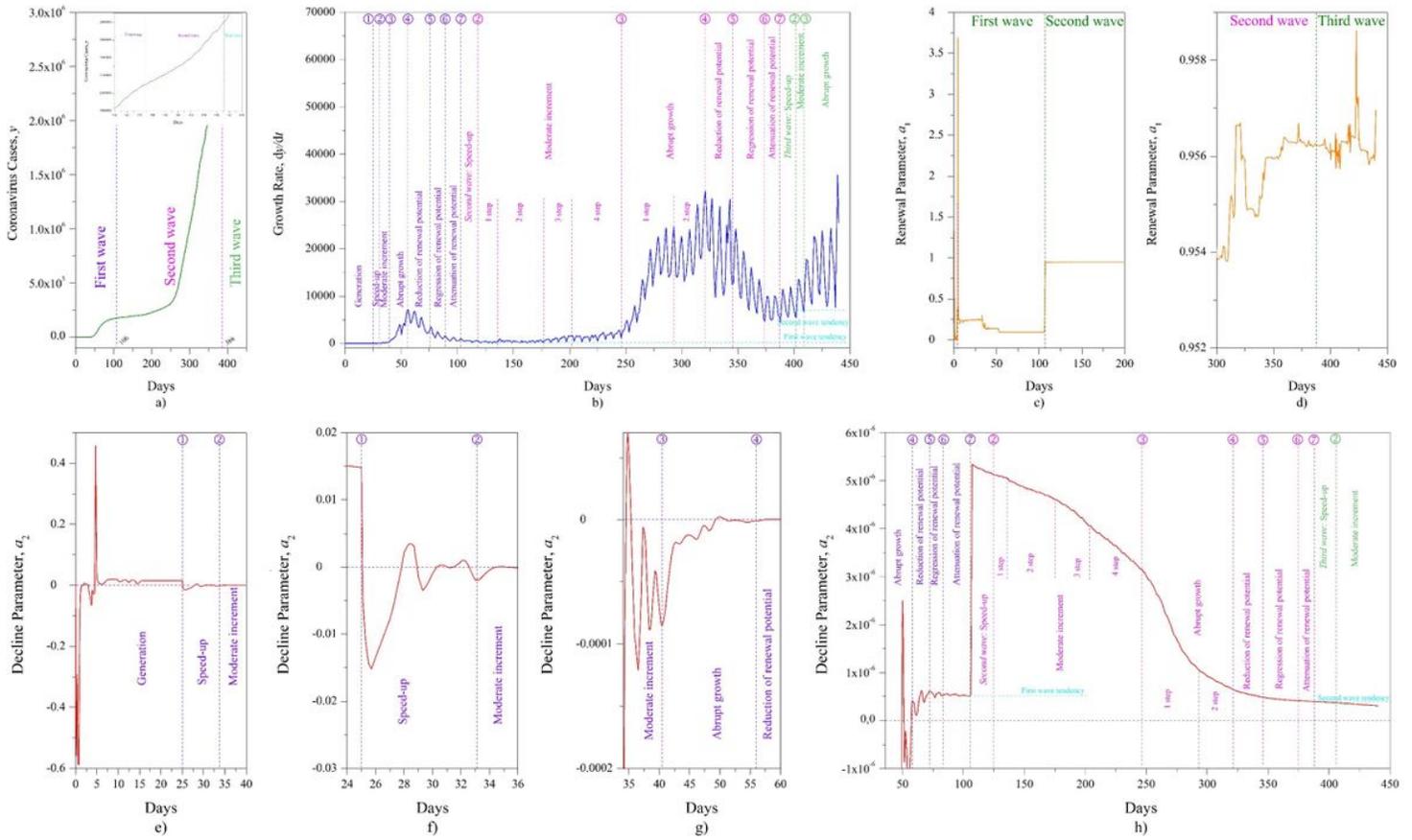


Figure 1

The patterns of the COVID-19 spread in Germany (the symbols 1–7 mark the moments of the dynamics changes).

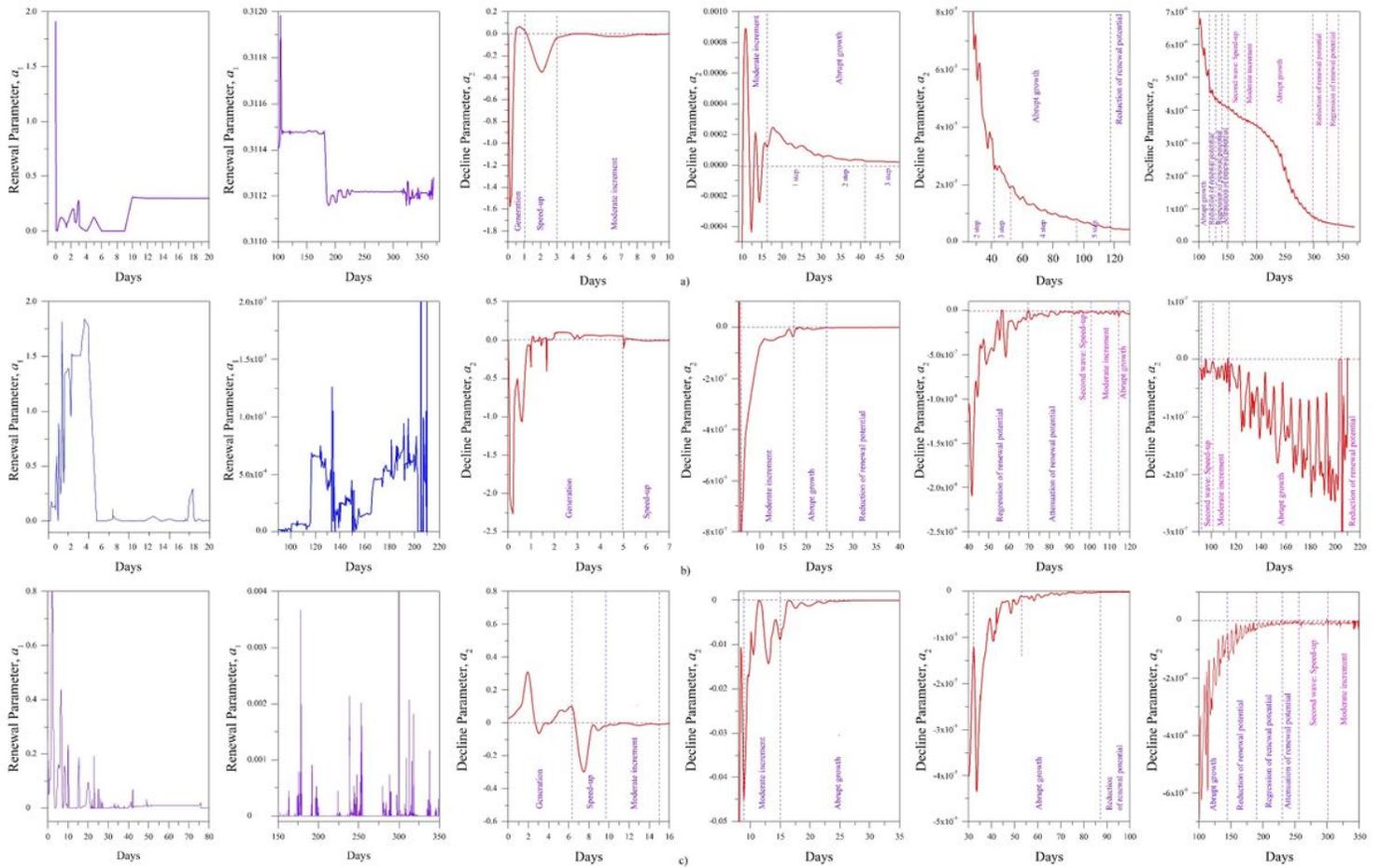


Figure 2

The parameters reconstruction for the different countries: a) Sweden; b) Switzerland; c) Brazil