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On Analysis of Development of an Infectious Disease in the Development of an Organism

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Abstract

In this paper, we investigate the development of an infectious disease in a population of organisms using a mathematical model described by a system of Ordinary Differential Equations (ODEs) with time-varying parameters. The incorporation of time-dependent parameters enables the model to capture variations in epidemic conditions and disease transmission during different stages of an outbreak, providing a more realistic representation of epidemic dynamics than models with constant coefficients. An analytical solution of the proposed model is obtained using the Method of Functional Corrections (MFC), which provides an efficient framework for analyzing nonlinear epidemic systems without relying on numerical approximations. The analytical expressions derived from the proposed approach provide insight into the influence of model parameters on disease progression and facilitate the qualitative assessment of epidemic behavior under varying conditions. The obtained results demonstrate that the proposed analytical framework can effectively describe the temporal evolution of infectious diseases while preserving the mathematical structure of the original model. Owing to its flexibility and analytical nature, the proposed approach can serve as a useful tool for investigating infectious disease dynamics and may provide theoretical support for future studies in epidemiological modeling and health informatics.

Keywords: Development of an infectious disease, Model of process, Analytical approach for analysis.

1 | Introduction

Infectious diseases remain one of the most important threats to global public health because of their rapid transmission, high morbidity and mortality rates, and substantial socioeconomic consequences. During the last decade, recurrent outbreaks of emerging and re-emerging infectious diseases have demonstrated the

necessity of developing reliable mathematical tools capable of describing epidemic dynamics and supporting public health decision-making. The COVID-19 pandemic, together with recent outbreaks of influenza, dengue fever, monkeypox, and other infectious diseases, has further emphasized the importance of mathematical epidemiology as an essential component of disease surveillance, prediction, and control [1–3]. Consequently, mathematical models have become indispensable instruments for understanding transmission mechanisms, evaluating intervention strategies, and supporting evidence-based health policies.

Ordinary Differential Equation (ODE) models constitute one of the most widely used approaches for describing infectious disease transmission because of their mathematical tractability and biological interpretability. Since the pioneering work of compartmental epidemic models, numerous extensions have been proposed to investigate disease spread under different epidemiological assumptions. These models allow researchers to estimate epidemic thresholds, evaluate disease persistence, investigate equilibrium behavior, and assess the influence of epidemiological parameters on disease dynamics. Owing to their flexibility and relatively simple mathematical structure, compartmental models continue to play a central role in modern epidemiological research [4–6].

Although classical epidemic models have achieved remarkable success, many of them assume that transmission, recovery, or removal rates remain constant throughout the epidemic process. Such an assumption is often unrealistic because disease transmission is influenced by multiple time-dependent factors, including behavioral changes, governmental interventions, seasonal variations, vaccination campaigns, environmental conditions, and pathogen evolution. Consequently, epidemic parameters may vary significantly during different stages of an outbreak, leading to dynamic transmission patterns that cannot be adequately represented by constant-coefficient models. Recent studies have therefore focused on incorporating time-varying parameters into compartmental epidemic models to improve their ability to represent real epidemic processes and to provide more accurate descriptions of disease evolution [7–10]. These investigations have shown that introducing temporal variability into epidemiological parameters substantially enhances the capability of mathematical models to describe multiple epidemic waves and changing transmission conditions.

Despite the significant progress achieved in mathematical epidemiology, obtaining analytical solutions for nonlinear epidemic models remains a challenging problem. Most epidemic models are governed by nonlinear systems of ODEs whose exact solutions are generally unavailable. Consequently, researchers have employed various numerical techniques, including finite difference methods, Runge–Kutta algorithms, predictor–corrector schemes, and finite element approaches, to approximate the solutions of nonlinear epidemic systems [11–13]. Although these numerical methods provide satisfactory approximations, they often require repeated computations under different parameter settings and may offer limited theoretical insight into the intrinsic behavior of the epidemic process.

To overcome these limitations, considerable attention has recently been directed toward semi-analytical and analytical methods capable of producing explicit approximate solutions for nonlinear differential equations. Among these approaches, the Homotopy Perturbation Method (HPM), Adomian Decomposition Method (ADM), Variational Iteration Method (VIM), Differential Transform Method (DTM), and Optimal Auxiliary Function Method (OAFM) have been successfully applied to a wide range of nonlinear engineering and biological problems [14–18]. These methods combine relatively simple computational procedures with satisfactory convergence properties, making them attractive alternatives to purely numerical techniques.

Various semi-analytical methods, including the ADM, VIM, HPM, and the Method of Functional Corrections (MFC), have been successfully applied to nonlinear differential equations arising in biological and epidemiological systems [18–21]. These approaches provide analytical approximations while reducing the computational burden associated with repeated numerical simulations.

Although analytical methods have been widely employed in mathematical biology, relatively few studies have investigated epidemic models incorporating time-varying parameters using the MFC. Most existing studies either consider autonomous epidemic systems with constant coefficients or emphasize numerical simulations

without providing analytical approximations of the epidemic trajectories [7], [8]. As epidemic transmission rates, recovery rates, and intervention effects naturally evolve over time, there remains a need for analytical techniques capable of addressing nonlinear epidemic systems with temporally varying coefficients.

Motivated by these observations, this paper investigates the development of an infectious disease in a population of organisms using a system of nonlinear ODEs with time-dependent parameters. The proposed mathematical formulation preserves the flexibility required to describe changing epidemic conditions while remaining suitable for analytical investigation. The MFC is employed to derive analytical approximations of the solution, allowing the temporal evolution of the epidemic to be investigated without relying exclusively on numerical procedures.

The main contribution of this work lies in the analytical treatment of a generalized epidemic model with time-varying parameters using the MFC. The proposed methodology provides an efficient framework for investigating nonlinear epidemic dynamics, improves the analytical understanding of parameter-dependent disease evolution, and offers a theoretical basis for future developments in mathematical epidemiology and health informatics.

2 | Method of Solution

In this section we consider the following model based on solution of the following system of ODEs:

$$\begin{cases} \frac{dS(t)}{dt} = \gamma(t) - \beta(t)S(t)[I(t) - U(t)] - \mu(t)S(t), \\ \frac{dI(t)}{dt} = \beta(t)S(t-\tau)[I(t-\tau) - U(t-\tau)] - [v_1(t) + v_2(t) + \mu(t)]I(t), \\ \frac{dR(t)}{dt} = v_1(t)I(t) - [\eta(t) + \mu(t)]R(t), \\ \frac{dU(t)}{dt} = v_2(t)I(t) - [\eta(t) + \mu(t)]U(t), \end{cases} \quad (1)$$

where $S(t)$ is the number of organisms susceptible to infection; $I(t)$ is the number of asymptotically infected organisms; $R(t)$ is the number of infected organisms with associated symptoms; $U(t)$ is the number of infected organisms with relevant symptoms but not reported; t is the current time; τ is the delay; $\gamma(t)$, $\beta(t)$, $\eta(t)$, $\mu(t)$, $v_1(t)$ are the parameters of the system. Initial conditions for the functions $S(t)$, $I(t)$, $R(t)$ and $U(t)$ could be written as:

$$S(0)=S_0, I(0)=I_0, R(0)=R_0, U(0)=U_0. \quad (2)$$

We solved the system of *Equations (1)* by the method of averaging of functional corrections [6], [7]. In the framework of the considered method we replace the required functions on their not yet known average values α_1 in right sides of the *Equations (1)*. Next integration of the obtained relations on time leads to the following relations to determine the first-order approximations of the required functions in the following form:

$$\begin{aligned} S_1(t) &= \int_0^t \gamma(\theta) d\theta - \alpha_{IS} (\alpha_{II} - \alpha_{IU}) \int_0^t \beta(\theta) d\theta - \alpha_{IS} \int_0^t \mu(\theta) d\theta + S_0, \\ I_1(t) &= \alpha_{IS} (\alpha_{II} - \alpha_{IU}) \int_0^t \beta(\theta) d\theta - \alpha_{II} \int_0^t [v_1(\theta) + v_2(\theta) + \mu(\theta)] d\theta + I_0, \\ R_1(t) &= \alpha_{II} \int_0^t v_1(\theta) d\theta - \alpha_{IR} \int_0^t [\eta(\theta) + \mu(\theta)] d\theta + R_0, \end{aligned} \quad (3)$$

$$U_1(t) = \alpha_{1I} \int_0^t v_2(\theta) d\theta - \alpha_{1U} \int_0^t [\eta(\theta) + \mu(\theta)] d\theta + U_0. \quad (3)$$

Not yet known average values were determined by the following standard relation [6], [7]:

$$\alpha_{1p} = \frac{1}{\Theta} \int_0^\Theta \rho_1(t) dt. \quad (4)$$

Substitution of *Relations (3)* into *Relation (4)* and solution of obtained equations gives a possibility to obtain relations for the required average values:

$$\begin{aligned} \alpha_{1S} &= \frac{\frac{1}{\Theta} \int_0^\Theta (\Theta - t) \gamma(t) dt + S_0}{\frac{1}{\Theta} \int_0^\Theta (\Theta - t) \beta(t) dt + \frac{1}{\Theta} \int_0^\Theta (\Theta - t) \mu(t) dt}, \\ \alpha_{1I} &= \frac{I_0}{\frac{1}{\Theta} \int_0^\Theta (\Theta - t) \beta(t) dt + \frac{1}{\Theta} \int_0^\Theta (\Theta - t) [v_1(t) + v_2(t) + \mu(t)] dt}, \\ \alpha_{1R} &= \frac{R_0 + \frac{1}{\Theta} \int_0^\Theta (\Theta - t) v_1(t) dt}{\frac{1}{\Theta} \int_0^\Theta (\Theta - t) [\eta(t) + \mu(t)] dt}, \quad \alpha_{1U} = \frac{U_0 + \frac{1}{\Theta} \int_0^\Theta (\Theta - t) v_2(t) dt}{\frac{1}{\Theta} \int_0^\Theta (\Theta - t) [\eta(t) + \mu(t)] dt}. \end{aligned} \quad (5)$$

The second-order approximations were determined by replacement by required functions on the following sum $\rho(t) \rightarrow \alpha_2 + \rho_1(t)$ in the right sides of *Eq. (1)*. The replacement and integration of the obtained relations on time gives a possibility to obtain the second-order approximations of the required functions in the following form:

$$\left\{ \begin{aligned} S_2(t) &= \int_0^t \gamma(\theta) d\theta - \int_0^t \beta(\theta) [\alpha_{2S} + S_1(\theta)] [\alpha_{2I} + I_1(\theta) - \alpha_{2U} - U_1(\theta)] d\theta - \\ &\quad \int_0^t \mu(\theta) [\alpha_{2S} + S_1(\theta)] d\theta + S_0, \\ I_2(t) &= \int_0^t \beta(\theta) [\alpha_{2S} + S_1(\theta - \tau)] [\alpha_{2I} + I_1(\theta - \tau) - \alpha_{2U} - U_1(\theta - \tau)] d\theta - \\ &\quad \int_0^t [v_1(\theta) + v_2(\theta) + \mu(\theta)] [\alpha_{2I} + I_1(\theta)] d\theta + I_0, \\ R_2(t) &= \int_0^t v_1(\theta) [\alpha_{2I} + I_1(\theta)] d\theta - \int_0^t [\eta(\theta) + \mu(\theta)] [\alpha_{2R} + R_1(\theta)] d\theta + R_0, \\ U_2(t) &= \int_0^t v_2(\theta) [\alpha_{2I} + I_1(\theta)] d\theta - \int_0^t [\eta(\theta) + \mu(\theta)] [\alpha_{2U} + U_1(\theta)] d\theta + U_0. \end{aligned} \right. \quad (6)$$

Average values of the second-order approximations of the required functions were determined by the following standard relations [22], [23]:

$$\alpha_{2p} = \frac{1}{\Theta} \int_0^\Theta [\rho_2(t) - \rho_1(t)] dt. \quad (7)$$

Substitution of *Relation (6)* into *Relation (7)* and solution of the obtained equations gives a possibility to obtain relations for the required average values:

$$\begin{aligned}
 \alpha_{2S} &= \left[\int_0^{\Theta} (\Theta - t) \beta(t) S_1(t) [I_1(t) - U_1(t)] dt + \int_0^{\Theta} (\Theta - t) \mu(t) S_1(t) dt - \alpha_{IS} (\alpha_{II} - \alpha_{IU}) \times \right. \\
 &\quad \left. \frac{1}{\Theta} \int_0^{\Theta} (\Theta - t) \beta(t) dt - \alpha_{IS} \int_0^{\Theta} (\Theta - t) \mu(t) dt \right] \left[\int_0^{\Theta} (\Theta - t) \mu(t) dt \right]^{-1}, \\
 \alpha_{2I} &= \left\{ \int_0^{\Theta} (\Theta - t) \beta(t) S_1(t - \tau) [I_1(t - \tau) - U_1(t - \tau)] dt + \int_0^{\Theta} (\Theta - t) [v_1(t) + v_2(t) + \mu(t)] \times \right. \\
 &\quad \left. I_1(t) dt - \int_0^{\Theta} (\Theta - t) \beta(t) S_1(t) [I_1(t) - U_1(t)] dt \right\} \left\{ \int_0^{\Theta} (\Theta - t) \beta(t) [I_1(t) - U_1(t)] dt + \right. \\
 &\quad \left. \int_0^{\Theta} (\Theta - t) \beta(t) S_1(t - \tau) [\alpha_{2I} + I_1(t - \tau) - \alpha_{2U} - U_1(t - \tau)] dt \right\}^{-1}, \tag{8} \\
 \alpha_{R2} &= \left\{ \int_0^{\Theta} (\Theta - t) v_1(t) I_1(t) dt - \int_0^{\Theta} (\Theta - t) [\eta(t) + \mu(t)] R_1(t) dt \right\} \left\{ \int_0^{\Theta} (\Theta - t) v_1(t) dt - \right. \\
 &\quad \left. \int_0^{\Theta} (\Theta - t) [\eta(t) + \mu(t)] dt \right\}, \\
 \alpha_{U2} &= \left\{ \int_0^{\Theta} (\Theta - t) v_2(t) I_1(t) dt - \int_0^{\Theta} (\Theta - t) [\eta(t) + \mu(t)] U_1(t) dt \right\} \left\{ \int_0^{\Theta} (\Theta - t) v_2(t) dt - \right. \\
 &\quad \left. \int_0^{\Theta} (\Theta - t) [\eta(t) + \mu(t)] dt + \int_0^{\Theta} (\Theta - t) v_2(t) dt + \int_0^{\Theta} (\Theta - t) [\eta(t) + \mu(t)] dt \right\}^{-1}.
 \end{aligned}$$

Functions $S(t)$, $I(t)$, $R(t)$ and $U(t)$ were analyzed analytically by using the second-order approximations in the framework of method of averaging of function corrections. The approximation is usually enough good approximation for to make qualitative analysis and to obtain some quantitative results. All obtained results have been checked by comparison with results of numerical simulations.

3 | Discussion

In this section we analyzed changing in time of the functions $S(t)$, $I(t)$, $R(t)$ and $U(t)$. The figure below shows typical dependencies of the considered numbers of organisms. Changing of values of parameters of the considered model leads to appropriate changes of the considered functions. These relationships show that epidemics can occur and then end due to anti-epidemic measures or the extinction of a population of organisms. Solid lines are results of analytical calculations. Dashed lines are results of numerical calculations (explicit difference scheme). Points are experimental results from Ref. [24]. Choosing of parameters of the considered process gives a possibility to control on the process.

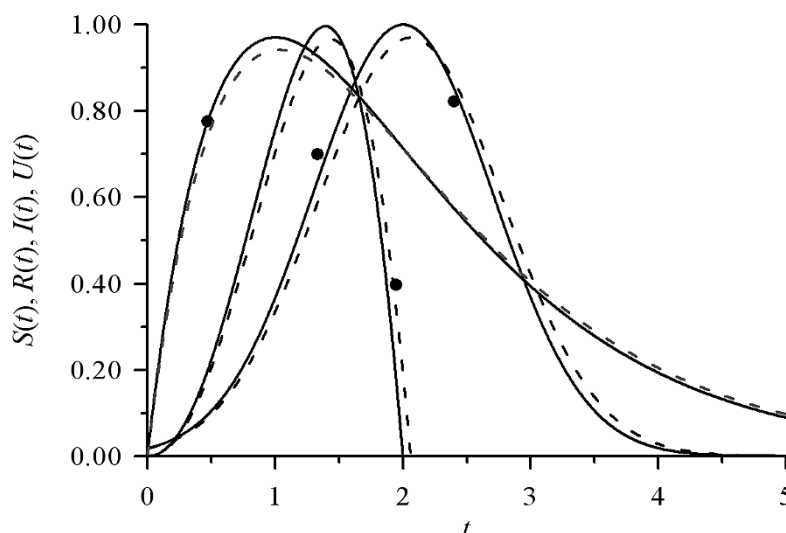


Fig. 1. Typical dependences on time of quantities of organisms. Solid lines are results of analytical calculations. Dashed lines are results of numerical calculations (explicit difference scheme). Points are experimental results from Ref. [24].

4 | Conclusion

In this study, an analytical investigation of the development of an infectious disease in a population of organisms has been presented using a mathematical model described by a system of ODEs with time-varying parameters. The proposed model provides a mathematical framework for predicting the temporal evolution of infectious diseases under varying epidemic conditions. The incorporation of time-dependent parameters enables the model to capture variations in the pace of epidemic development, providing a more realistic representation of disease transmission than conventional models with constant coefficients.

The MFC was employed to derive analytical approximations of the nonlinear epidemic system. The obtained analytical expressions provide valuable qualitative insight into disease evolution and facilitate interpretation of the influence of epidemiological parameters on epidemic dynamics. Unlike purely numerical approaches, the proposed analytical methodology preserves the mathematical structure of the original model while providing an efficient analytical framework for investigating nonlinear epidemic systems.

The present study demonstrates that the proposed analytical approach is suitable for analyzing epidemic models with time-varying parameters and may serve as a theoretical basis for future developments in mathematical epidemiology and health informatics. Future work may extend the proposed model by incorporating additional epidemiological compartments, vaccination strategies, stochastic effects, or real epidemiological data to further improve its applicability in disease surveillance and public health decision-making.

In summary, the main achievements of this study can be highlighted as follows. The development of an infectious disease in a population of organisms was analytically investigated using a mathematical model formulated as a system of ODEs with time-varying parameters. A mathematical model for predicting the temporal evolution of the infectious disease was considered, and an analytical approach based on the MFC was employed to investigate the proposed model. Furthermore, the proposed formulation accounts for variations in the pace of epidemic development through time-dependent parameters, allowing changes in epidemic conditions to be incorporated into the analytical framework.

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Data Availability

All data are included in the text.

Conflicts of Interest

The authors declare no conflict of interest.

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