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# APPROXIMATE SOLUTION OF A NONLINEAR FRACTIONAL-ORDER HIV MODEL USING HOMOTOPY ANALYSIS METHOD

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**Abstract.** In the present paper, we propose and analyze a nonlinear fractional-order SEIR (susceptible-exposed-infected-recovered) epidemic model to transmit HIV. The fixed points of the model and their stability results are obtained. Using the fractional derivatives, we relied on the Caputo fractional derivative. Further, we employed the homotopy analysis method (HAM) to get an approximate solution of the dynamic fractional derivatives of the model. The purpose of using HAM as a solution technique is its reliability, easy to handle, that utilizes a simple process to adjust and control the convergence region of the obtained infinite series solution. It uses an auxiliary parameter and allows to obtain a one-parametric family of explicit series solutions. Firstly, several $\hbar$-curves are plotted to demonstrate the regions of convergence, then the residual and square residual errors are obtained for different values of these regions. In the end, numerical solutions are presented for various iterations to show the accuracy of the HAM. Besides, the convergence theorem of HAM is also proved. The obtained results show the effectiveness and strength of the applied HAM on the proposed fractional-order SEIR model. Also, from the sensitivity analysis results, it is seen that the parameters $\mu$ and $\sigma$ are more sensitive than $\epsilon$ and $\rho$ in disease transmission.

**Key words.** SEIR epidemic model, Caputo fractional derivative, Homotopy analysis method, Stability analysis, Basic reproduction number $\mathfrak{R}_0$.

## 1. Introduction

The increased logicality of modern computer capability has enhanced the prospect of mathematical modeling extraordinarily makes it possible to study very complex systems in a better way. Epidemiology in medicine deals with infectious and non-infectious diseases for their incidence, distribution, and possible control, and other factors relating to health. Initially, the branch was limited to infectious diseases, but nowadays, it finds applications to other diseases. HIV is the virus that causes destruction of the immune system by lowering down the $CD4^+$ T-cells that fight infection and makes the person host for many diseases that causes death. HIV has become the first global pandemic incurable due to the nonavailability of possible vaccines and is one of the major public health problems in the world today [1, 2, 3]. HIV will not survive outside the body, so the infection cannot be transmitted through daily activities like hugging an infected person, greeting by shaking hands, or kissing. This disease is transmitted via contaminated body fluids, including blood, semen, and vaginal secretions and through sexual intercourse (anal, vaginal, or oral) or by the use of the same needles among drug addicts [4, 5, 6, 7, 8, 9, 10]. Thus, HIV has very different characteristics. It is important to refine the basic ideas and extend the available literature models for a better understanding of this virus.

Infectious disease modeling has become an area of much attentiveness in recent years. Such accomplishments are useful to biomedical scientists for the prevention

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and control of disease outbreaks. In recent years, many fractional-order epidemic models have been proposed to describe the dynamics of various infectious diseases. Kumar and Kumar [11] introduced a fractional-order SIR model with a constant vaccination rate. By their analysis, they have shown that the model has two equilibria, namely disease-free equilibrium and the endemic equilibrium. They have analyzed their model for local stability. Obtained results showed the effectiveness and reliability of their applied method through the numerical procedure. Wiah et al. [12] developed a fractional SIRC model, in which they presented a detailed analysis of the two existing equilibrium points. Firstly, they have shown the positive solution of their model in fractional order. They used the multi-step generalized differential transform method to obtain the approximate numerical solution. Finally, they compared their numerical results with a nonstandard numerical method and fourth-order Runge-Kutta method for accuracy. Kheiri and Jafari [13] formulated a multi-patch HIV/AIDS epidemic model with fractional order derivative to investigate the effect of human movement on the spread of HIV/AIDS among patches. They derived the basic reproduction number $\mathfrak{R}_0$ and proved that if $\mathfrak{R}_0 < 1$, the disease-free equilibrium (DFE) is locally and globally asymptotically stable. In the case of $\mathfrak{R}_0 > 1$, they obtained sufficient conditions under which the endemic equilibrium is unique and globally asymptotically stable. They also formulated a fractional optimal control problem, in which the state and co-state equations were given in terms of the left fractional derivatives. The necessary conditions for fractional optimal control of the disease were obtained. Their numerical results show that implementing all the control efforts decreases HIV-infected and AIDS people in both patches significantly. Silva and Torres [14], in their paper, proposed and studied the local and uniform stability of a fractional HIV/AIDS model. They also carried out numerical simulations to illustrate their theoretical results. Naik et al. [15] proposed and analyzed a nonlinear fractional-order epidemic model for HIV transmission with two infectious stages. In their study, they took the Caputo type fractional derivative and generalized Adams-Bashforth-Moulton method for the numerical solution of the model. They also determined the model equilibria and studied their stability results. They also formulated a fractional optimality condition for their proposed model. The effectiveness of the used control strategies is shown through numerical simulations, which suggested the adopted control measures efficiently increase the life cycle of the HIV patients.

Recently, Ali et al. [16], in their manuscript, proposed a SIATR compartmental model for HIV/AIDS epidemics under fractal-fractional-order derivative. They constructed the existence theory utilizing Schaefer- and Banach-type fixed point theorems to solve their considered model. Besides, Ulam-Hyers and generalized Ulam-Hyers stability conditions via nonlinear functional analysis were established. A fractional Adams-Bashforth method based on two-step Lagrange polynomial is employed for numerical simulation of the considered model. They tested their simulated results for various fractal-fractional orders on some existing real data of disease spread in South Africa and shows that the values of compartments SIAT decrease as the treatment starts. Tamilalagan et al. [17] proposed an article in which they extended a classical HIV infection model to the fractional-order case under the influence of antibody and cytotoxic T-Lymphocyte (CTL) immune responses. They studied the effectiveness of antiretroviral therapy drugs, namely, protease inhibitors and reverse transcriptase, in suppressing HIV infection. They first discussed the dynamical behavior of their model through stationary states' linear stability and then figured out the stable regions of the infectious and infection-free steady states.