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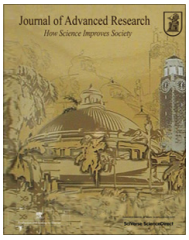

ORIGINAL ARTICLE

Numerical study for multi-strain tuberculosis (TB) model of variable-order fractional derivatives

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ABSTRACT

In this paper, we presented a novel multi-strain TB model of variable-order fractional derivatives, which incorporates three strains: drug-sensitive, emerging multi-drug resistant (MDR) and extensively drug-resistant (XDR), as an extension for multi-strain TB model of nonlinear ordinary differential equations which developed in 2014 by Arino and Soliman [1]. Numerical simulations for this variable-order fractional model are the main aim of this work, where the variable-order fractional derivative is defined in the sense of Grünwald–Letnikov definition. Two numerical methods are presented for this model, the standard finite difference method (SFDM) and nonstandard finite difference method (NSFDM). Numerical comparison between SFDM and NSFDM is presented. It is concluded that, NSFDM preserves the positivity of the solutions and numerically stable in large regions than SFDM.

Introduction

Variable-order fractional calculus (i.e., the fractional differentiation and integration of variable order) is the generalization of classical calculus and fractional calculus, which were invented by Newton and Leibnitz hundreds of years ago. Now the study on it becomes a hot pot in recent ten years [2–7]. It has turned out that many problems in physics, biology, engineering, and finance can be described excellently by models using mathematical tools from variable-order fractional calculus, such as mechanical applications [2], diffusion process [5], multifractional Gaussian noise [8], and FIR filters [9]. For more details, see [7,10] and references therein. Understanding the transmission characteristics of infectious diseases in communities, regions and countries can lead to better approaches to decrease the transmission of these diseases [11]. Variable-order fractional derivative is good at depicting the memory property which changes with time or spatial location [3,5].

TB is growing more resistant to treatment worldwide according to study released in August 2012 in the journal Lancet, a finding that suggests the potentially fatal disease is becoming more difficult and costly to treat [12]. In this article we focused our attention in Egypt.

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We consider in this work a model developed by Arino and Soliman for TB [1]. The model incorporates three strains, drug-sensitive, MDR and XDR. Several papers considered modeling TB such as [13,14], but the model we consider here includes several factors of spreading TB such as the fast infection, the exogenous reinfection and secondary infection along with the resistance factor. The main aim of this paper was to study numerically the multi-strain TB model of variable-order fractional derivatives which incorporates three strains: drug-sensitive, MDR and XDR. We develop a special class of numerical method, known as NSFDM for solving this model. This technique, developed by Mickens (1980) [15–23] has brought a creation of new numerical schemes preserving the physical properties, especially the stability properties of equilibria, of the approximated system. Numerical comparison between NSFDM and SFDM is presented. When the secondary infection generated by an infected individual exceeds the unity, there are no analytical results proved for the model, such as the existence and stability of the endemic equilibrium (EE). In this case we use the developed NSFD numerical scheme to approximate the endemic solution numerically and investigate its stability. Furthermore, with the help of the NSFDM, we answer the following question: Given the data provided by the World Health Organization (2012) on the current parameters corresponding to the propagation of the TB in Egypt, what would be the required rate of treatment to achieve in order to control the disease? The proposed method showed its superiority in preserving the positivity (compared to the numerical standard method considered in this work) of the state variables of the systems under study. This is an essential requirement when simulating systems especially those arising in biology. This paper is organized as follows: In Section 'Mathematical model', Mathematical model is presented. Preliminaries and notations on variable-order fractional differential equations are given, in Section 'Preliminaries and notations'. Equilibrium points and their asymptotic stability are presented in Section 'Variable-order fractional derivatives for multi-strain TB model'. Variable-order fractional derivatives for the multi-strain TB model are presented; moreover, the construction of the proposed nonstandard numerical scheme is carried out in Section 'Equilibrium points and their asymptotic stability'. In Section 'Numerical results and simulations', Numerical results and simulation are discussed. Finally, in Section 'Conclusions' we presented the conclusions.

Mathematical model

The multistrain TB-model given in [1] can be formulated as follows:

$$S' = b - dS - \beta_s \frac{SI_s}{N} - \beta_m \frac{SI_m}{N} - \beta_x \frac{SI_x}{N}, \tag{1}$$

$$L_s' = \lambda_s\beta_s \frac{SI_s}{N} + \sigma_s\lambda_s\beta_s \frac{RI_s}{N} + \gamma_s I_s - \alpha_{ss}\beta_s \frac{L_sI_s}{N} - \alpha_{sm}\beta_m \frac{L_sI_m}{N} - \alpha_{sx}\beta_x \frac{L_sI_x}{N} - (d+\varepsilon_s+t_{1s})L_s, \tag{2}$$

$$L_m' = \lambda_m\beta_m \frac{SI_m}{N} + \sigma_m\lambda_m\beta_m \frac{RI_m}{N} + \gamma_m I_m + \alpha_{sm}\beta_m\lambda_m \frac{L_sI_m}{N} + (1-P_1)t_{1s}L_s + (1-P_2)t_{2s}I_s - \alpha_{mm}\beta_m \frac{L_mI_m}{N} - \alpha_{mx}\beta_x \frac{L_mI_x}{N} - (d+\varepsilon_m)L_m, \tag{3}$$

$$L_x' = \lambda_x\beta_x \frac{SI_x}{N} + \sigma_x\lambda_x\beta_x \frac{RI_x}{N} + \gamma_x I_x + \alpha_{sx}\beta_x\lambda_x \frac{L_sI_x}{N} + \alpha_{mx}\beta_x\lambda_x \frac{L_mI_x}{N} + (1-P_3)t_{2m}I_m - \alpha_{xx}\beta_x \frac{L_xI_x}{N} - (d+\varepsilon_x)L_x, \tag{4}$$

$$I_s' = \alpha_{ss}\beta_s \frac{L_sI_s}{N} + (1-\lambda_s)\beta_s\left(\frac{SI_s}{N} + \sigma_s\frac{RI_s}{N}\right) + \varepsilon_s L_s - (d+\delta_s+t_{2s}+\gamma_s)I_s, \tag{5}$$

$$I_m' = \alpha_{mm}\beta_m \frac{L_mI_m}{N} + (1-\lambda_m)\beta_m\left(\frac{SI_m}{N} + \sigma_m\frac{RI_m}{N} + \alpha_{sm}\frac{L_sI_m}{N}\right) + \varepsilon_m L_m - (d+\delta_m+t_{2m}+\gamma_m)I_m, \tag{6}$$

$$I_x' = \alpha_{xx}\beta_x \frac{L_xI_x}{N} + (1-\lambda_x)\beta_x \times \left(\frac{SI_x}{N} + \sigma_x\frac{RI_x}{N} + \alpha_{sx}\frac{L_sI_x}{N} + \alpha_{mx}\frac{L_mI_x}{N}\right) + \varepsilon_x L_x - (d+\delta_x+t_{2x}+\gamma_x)I_x, \tag{7}$$

$$R' = P_1t_{1s}L_s + P_2t_{2s}I_s + P_3t_{2m}I_m + t_{2x}I_x - \sigma_s\beta_s\frac{RI_s}{N} - \sigma_m\beta_m\frac{RI_m}{N} - \sigma_x\beta_x\frac{RI_x}{N} - dR. \tag{8}$$

All variables in above system and their definition are in Table 1. Also, all parameters and their interpretation are in Table 2.

The basic reproduction number $\boldsymbol{R_0}$

The basic reproduction number R_0 for system (1)–(8) is given by [1]

$$R_0 = \max(R_{0s}, R_{0m}, R_{0x}), \tag{9}$$

where

$$R_{0s} = \frac{\beta_s(\varepsilon_s + (1-\lambda_s)(d+t_{1s}))}{(\varepsilon_s+d+t_{1s})(t_{2s}+\delta_s+d) + \gamma_s(t_{1s}+d)},$$

Table 1 All variables of the system (1)–(8) and their interpretation.

Variable	Definition
$S(t)$	The susceptible population individuals who have never encountered TB
$L_s(t)$	The individuals infected with the drug-sensitive TB strain but who are in a latent stage, i.e., who are neither showing symptoms nor infecting others
$L_m(t)$	Individuals latently infected with MDR-TB
$L_x(t)$	Individuals latently infected with XDR-TB
$I_s(t)$	Individuals infected with the drug-sensitive TB strain who are infectious to others (and most likely, showing symptoms as well)
$I_m(t)$	Those individuals who are infectious with the MDR-TB strain
$I_x(t)$	Individuals who infectious with the XDR-TB strain
$R(t)$	Those individuals for whom treatment was successful
$N(t)$	The total population $N = S + L_s + L_m + L_x + I_s + I_m + I_x + R$