Homotopy Decomposition Analysis of a Tuberculosis Model

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Abstract: Homotopy Decomposition Method (HDM) is used to analyze both integer and non-integer systems of nonlinear differential equations describing tuberculosis dynamics. We use numerical examples to illustrate the technique and perform some simulations. In particular we show that the approximate solutions are continuous functions of the non-integer order derivative.
[Oukouomi Noutchie, SC. **Homotopy Decomposition Analysis of a Tuberculosis Model**. *Life Sci J* 2013;10(3):459-465] (ISSN:1097-8135). http://www.lifesciencesite.com. 67

Keywords: Nonlinear differential equations; tuberculosis model; fractional order derivative; homotopy decomposition method.

1. Introduction

Tuberculosis Tuberculosis (TB), one of the widest spread infectious diseases, is the leading cause of death due to a single infectious agent among adults in the world. According to the World Health Organization, one third of the world's population is infected with Mycobacterium tuberculosis (M. tuberculosis), leading to between two and three millions death each year. Factors that affect transmission of M. tuberculosis include the number, viability, and virulence of organisms within sputum droplet nuclei, and most importantly, time spent in close contact with an infectious person [1–8].
Tuberculosis is dependent on nonlinear contact processes that are determined by population size and density, as well as other factors. Demographic characteristics of a population, therefore, play a significant role in the development and progression of a TB epidemic. Mathematical models can provide a useful tool to analyze the spread and control of infectious diseases [1]. Mathematical models for tuberculosis are especially useful tools in assessing the epidemiological consequences of medical or behavioral interventions (which may cause many direct and indirect effects) because they contain explicit mechanisms that link individuals with a population-level outcome such as incidence or prevalence. Different mathematical models for tuberculosis have been formulated and studied (see e.g. [1–8] and references therein).

Based on epidemiological status, the population is divided into three classes: susceptible, latently infected (exposed) and infectious with the number in each class denoted by S, E and , I respectively. The model is represented by the transfer diagram in Fig. 1. All recruitment is into the susceptible class, and occurs at a constant rate Λ. The rate constant for non-disease elated death is μ, thus $1/\mu$ is the average lifetime. A fraction p of the newly infected individuals is assumed to undergo fast progression directly to the infectious class, while the remainder are latently infected and enter the latent class. Once latently infected with M. tuberculosis, an individual will remain so for life unless reactivation occurs. To account for treatments, we define $r_1 E$ as the fraction of latently infected individuals receiving effective chemoprophylaxis, and r_2 as the rate of effective per capita therapy. We assume that chemoprophylaxis of latently infected individuals reduces their reactivation at a constant rate r_1 and that the initiation of therapeutics immediately removes individuals from active status and places them into a latent state. The time before latently infected individuals who did not receive effective chemoprophylaxis become infectious is assumed to satisfy an exponential distribution, with mean waiting time $1/k$. Thus, individuals leave the class E to the class I at a constant rate $k(1-r_1)$. Also, after receiving a therapeutic treatment, individuals leave the class I to E at rate r_2.
Infectious have an additional death rate due to the disease with rate constant $d > \mu \geq 0$.

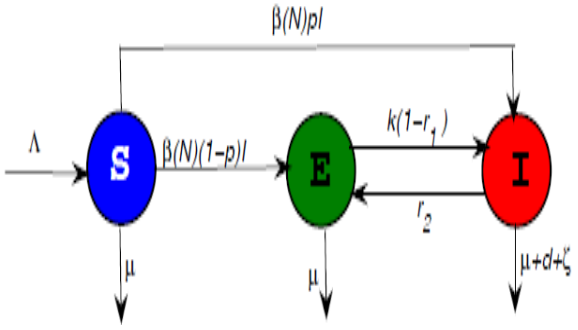

Figure. 1 Flow diagram.

We assume that the emigration only affects the class of infectious I so that the fraction δI of infectious leave the class I without receiving a therapy treatment for many reasons such as poverty, mentality, etc. Since TB latent individuals are not capable of transmitting the disease, we assume that a susceptible individual may become infected only through contacts with infectious. In each unit time, a susceptible individual has an average $\beta(N)I$ contacts that would be suffice to transmit the infection where $N = S + E + I$ is the total population size. Thus, the rate at which susceptible are infected is $\beta(N)SI$

This leads to the following system of differential equations for the rate change with respect to time of the numbers of susceptible, latently infected and infectious individuals: (1)

$$\begin{cases} \dfrac{dS(t)}{dt} = \Lambda - \beta(N)SI - \mu S, \\ \dfrac{dE(t)}{dt} = \beta(N)(1-p)SI + r_2 I - [\mu + k(1-r_1)]E, \\ \dfrac{dI(t)}{dt} = \beta(N)pSI + k(1-r_1)E - (\mu + d + \zeta + r_2)I. \end{cases}$$

Parameters Λ, μ, d, k, r_1 and r_2 are assumed to be positive and all other parameters are non-negative nonnegative with $p \in [0,1]$.

The purpose of this paper is to derive approximate analytical solutions for the standard form as well as the fractional version of equation (1) using the homotopy decomposition method (HDM). The paper is structured as follows: In Section 2, we present the basic idea of the homotopy decomposition method for solving partial differential equations. We present the application of the HDM for system Tuberculosis disease population dynamics modelling Section 3. In Section 4, we present the application of the HDM for system of fractional tuberculosis disease population dynamics model. The conclusions are then given in the final Section 5.

2. Preliminaries about Homotopy Decomposition Method [2]

To demonstrate the elementary notion of this technique we consider a universal nonlinear non-homogeneous partial differential equation with initial conditions of the following form [9-10]. (2)

$$\frac{\partial^m U(x,t)}{\partial t^m} = L\big(U(x,t)\big) + N\big(U(x,t)\big) + f(x,t), \quad m = 1,2,3\ldots$$

Focusing on the primary condition

$$\frac{\partial^i U(x,0)}{\partial t^i} = y_i(x), \qquad \frac{\partial^{m-1} U(x,0)}{\partial t^{m-1}} = 0, \qquad i = 0,1,2\ldots m-2$$

m is the order of the derivative where f is a identified function, N is the common nonlinear differential operator and L denotes a linear differential operator and m is the order of the derivative. The procedure first stage here is to apply the inverse operator $\frac{\partial^m}{\partial t^m}$ of on both sides of equation (2) to obtain

(3)

$$U(x,t) = \sum_{k=0}^{m-1} \frac{t^k}{k!} \frac{d^k u(x,0)}{dt^k} + \int_0^t \int_0^{t_1} \cdots \int_0^{t_{m-1}} L\big(U(x,\tau)\big) + N\big(U(x,\tau)\big) + f(x,\tau)\, d\tau \ldots dt$$

The multi-integral in Eq (3) can be transformed to.

(4)

$$\int_0^t \int_0^{t_1} .. \int_0^{t_{m-1}} L(U(x,\tau)) + N(U(x,\tau)) + f(x,\tau) d\tau .. dt$$

$$= \frac{1}{(m-1)!} \int_0^t (t-\tau)^{m-1} L(U(x,\tau)) + N(U(x,\tau)) + f(x,\tau) d\tau$$

so that equation (3) can be reformulated as

(5)

$$U(x,t) = \sum_{k=0}^{m-1} \frac{t^k}{k!} y_i(x) + \frac{1}{(m-1)!} \int_0^t (t-\tau)^{m-1} L(U(x,\tau)) + N(U(x,\tau)) + f(x,\tau) d\tau.$$

Using the Homotopy scheme, the solution of the above integral equation is given in series form as:

(6)

$$U(x,t,p) = \sum_{n=0}^{\infty} p^n U_n(x,t)$$

$$U(x,t) = \lim_{p \to 1} U(x,t,p)$$

and the nonlinear term can be decomposed as

(7)

$$NU(r,t) = \sum_{n=1}^{\infty} p^n \mathcal{H}_n(U)$$

where $p \epsilon (0, 1]$ is an implanting parameter. $\mathcal{H}_n(U)$ is the polynomials that can be engendered by

(8)

$$\mathcal{H}_n(U_0, \cdots\cdots, U_n) = \frac{1}{n!} \frac{\partial^n}{\partial p^n} \left[N\left(\sum_{j=0}^{n} p^j U_j(x,t) \right) \right], n = 0,1,2 \cdots\cdots$$

The homotopy decomposition method is obtained by the combination of decomposition method with Abel integral and is given by

(9)

$$\sum_{n=0}^{\infty} p^n U_n(x,t) = T(x,t) + p \frac{1}{(m-1)!} \int_0^t (t-\tau)^{m-1} \left[f(x,\tau) + L\left(\sum_{n=0}^{\infty} p^n U_n(x,\tau) \right) + \sum_{n=0}^{\infty} p^n \mathcal{H}_n(U) \right] d\tau$$

With

(10)

$$T(x,t) = \sum_{k=0}^{m-1} \frac{t^k}{k!} y_i(x)$$

Relating the terms of same powers of p, gives solutions of various orders. The initial guess of the approximation is $T(x,t)$ this is actually the Taylor series of the exact solution of order m.Note that this initial guess insures the uniqueness of the series decompositions [9-10].

3. Application of the HDM to the evolution model

In this section we employ this method for deriving the set of the mathematical equations describing the tuberculosis disease population dynamics model.

Resulting from the steps involved in the HDM method, we reach at the following integral equations:

$$p^0 : S_0(t) = S(0)$$

$$p^0 : E_0(t) = E(0)$$

(11)

$$p^0 : I_0(t) = I(0)$$

$$p^1 : S_1(t) = \int_0^t (\Lambda - \beta(N) S_0 I_0(\tau) - \mu S_0(\tau)) d\tau \ , \ S_1(0) = 0.$$

$$p^1 : E_1(t) = \int_0^t (\beta(N)(1-p) S_0 I_0(\tau) + r_2 I_0(\tau) - [\mu + k(1-r_1) E_0(\tau)]) d\tau, \ E_1(0) = 0.$$

$$p^1 : I_1(t) = \int_0^t (\beta(N) p S_0 I_0(\tau) + k(1-r_1) E_0(\tau) - (\mu + d + \zeta + r_2) I_0(\tau)) d\tau, \ I_1(0) = 0.$$

$$\vdots$$

$$p^n: S_n(t) = \int_0^t \left(\Lambda - \beta(N) \sum_{j=0}^{n-1} I_j S_{n-j-1}(\tau) - \mu \sum_{j=0}^{n-1} S_{n-j-1}(\tau) \right) d\tau \,, S_{n-1}(0) = 0.$$

$$p^n: E_n(t) = \int_0^t \left(\beta(N)(1-p) \sum_{j=0}^{n-1} I_j S_{n-j-1}(\tau) + r_2 I_{n-1}(\tau) - [\mu + k(1 - r_1) E_{n-1}(\tau)] \right) d\tau, \; E_n(0) = 0$$

$$p^n: I_n(t) = \int_0^t \left(\beta(N) p \sum_{j=0}^{n-1} I_j S_{n-j-1}(\tau) + k(1-r_1) E_{n-1}(\tau) - (\mu + d + \zeta + r_2) I_{n-1}(\tau) \right) d\tau, \; I_n(0) = 0.$$

Integrating the above, we obtain the following components:

$$S_0(t) = S(0) \;\; ; \quad E_0(t) = E(0) \;\; ;$$

$$I_0(t) = I(0) \qquad (12)$$

$$S_1(t) = (\Lambda - \beta(N) S_0 I_0 - \mu S_0) t$$

$$E_1(t) = (\beta(N)(1-p) S_0 I_0 + r_2 I_0 - [\mu + k(1-r_1) E_0]) t$$

$$I_1(t) = (\beta(N) p S_0 I_0 + k(1-r_1) E_0 - (\mu + d + \zeta + r_2) I_0) t.$$

For simplicity let us put:

$$a_0 = (\Lambda - \beta(N) S_0 I_0 - \mu S_0)$$

$$b_0 = (\beta(N)(1-p) S_0 I_0 + r_2 I_0 - [\mu + k(1-r_1) E_0])$$

$$c_0 = (\beta(N) p S_0 I_0 + k(1-r_1) E_0 - (\mu + d + \zeta + r_2) I_0)$$

.

Integrating $S_1(t)$, $E_1(t)$ and $I_1(t)$, we obtain

$$S_2(t) = \frac{t^2}{2} a_1$$

$$E_2(t) = \frac{t^2}{2} b_1 \qquad (13)$$

$$I_2(t) = c_1 \frac{t^2}{2}$$

where a_1, b_1, and c_1 are linear combinations of a_0, b_0 and c_1.

In general we obtain the following recursive formulas

$$S_n(t) = \frac{t^n}{n!} a_n,$$

$$I_{Ln}(t) = \frac{t^n}{n!} b_n,$$

$$I_{An}(t) = c_n \frac{t^n}{n!},$$

where a_n, b_n and c_n depend on the fixed set of empirical parameters. It therefore follows that the approximate solution of the system (1) is given as: (14)

$$\begin{cases} S_N(t) = \sum_{n=0}^{N} \frac{t^n}{n!} a_n \\ I_{LN}(t) = \sum_{n=0}^{N} \frac{t^n}{n!} b_n \\ I_{AN}(t) = \sum_{n=0}^{N} \frac{t^n}{n!} c_n \end{cases}$$

If for instant one suppose that, the initial number of susceptible individual in the location $S(0) = 96$ thousands; the initial number of TB exposed people $E(0) = 3$ thousands; the initial number of TB actively infected people $I(0) = 1$ thousand; the constant recruitment rate among the susceptible population $\Lambda = 0.25$; the natural death rate $\mu = 0.1$. Then the following approximate solution is obtained as result of first 8 terms of the series decomposition: (16)

$$S(t) = 96 - 11.2162t + 62.1069t^2 - 29.5924t^3 - 149.2t^4 + 48.3455t^5 - 20.6378t^6 + 15.5857t^7 + \cdots$$

$$I_I(t) = 3 + 36.8527t - 62.9161t^2 - 797.302t^3 + 151.174t^4 - 48.8926t^5 + 20.7629t^6 - 15.6036t^7 + \cdots$$

$$I_A(t) = 1 - 0.706394t + 0.252053t^2 - 0.252832t^3 - 1.96203t^4 + 0.573666t^5 - 0.131459t^6 + 0.0190148t^7 + \cdots$$

If in addition we assume that no new person migrates or is born in this area, we obtain the following figures. The approximate solutions of the main problem are depicted in Figure 1, Figure 2 and Figure 3 respectively.

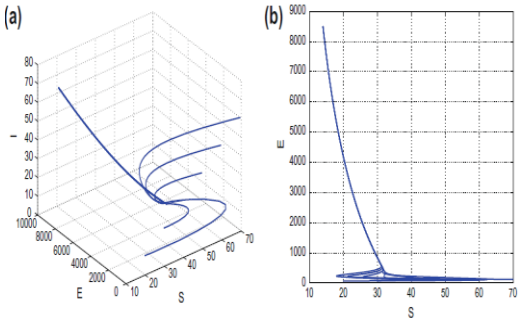

Figure. 2 Trajectories of the model and its plane figure. [1]

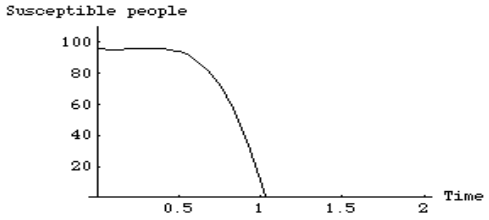

Figure. 3 Approximate solution for susceptibles in the location [2].

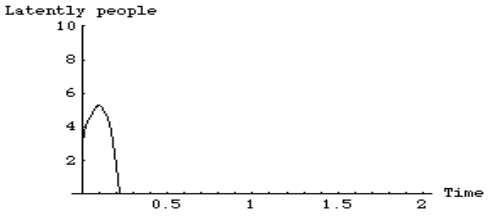

Figure. 4 Approximate solution for the exposed population [2]

Figure 2-4 show that, if there is migration or new born in the location of interest, the number of susceptible people will vanish as time goes, because of the natural death rate and due to TB. Note that any person that is latently infected is removed from the set of susceptible. Figure 3 indicates that, the number of people that are latently infected will increase up to a certain time and then vanish as time goes. This number will increase because, the number of number of susceptible people, will become latently infected since some are not vaccinated against the TB and finally will vanish due to. Figure 4 indicates that, the number of TB actively infected people will also vanish because of the natural death rate and the death due to TB.

4. Application of HDM to the fractional version of the evolution model

Fractional calculus has been used to model physical and engineering processes, which are found to be best described by fractional differential equations. It is worth nothing that the standard mathematical models of integer-order derivatives, including nonlinear models, do not work adequately in many cases. groundwater problem and so on (see [14-21])

4.1 Approximate solution of fractional version

The system of equations under investigation here is given below as: (20)

$$\begin{cases} \dfrac{d^{\mu}S(t)}{dt^{\mu}} = \Lambda - \beta(N)SI - \mu S, & 0 < \mu \le 1 \\ \dfrac{d^{\eta}E(t)}{dt^{\eta}} = \beta(N)(1-p)SI + r_2 I - [\mu + k(1-r_1)]E, & 0 < \eta \le 1 \\ \dfrac{d^{\upsilon}I(t)}{dt^{\upsilon}} = \beta(N)pSI + k(1-r_1)E - (\mu + d + \zeta + r_2)I, & 0 < \upsilon \le 1. \end{cases}$$

Following the discussion presented earlier, we arrive at the following equations (21)

$$p^0 : S_0(t) = S(0)$$

$$p^0 : E_0(t) = E(0)$$

$$p^0 : I_0(t) = I(0)$$

$$\vdots$$

$$p^1 : S_1(t) = \frac{1}{\Gamma(\mu)}\int_0^t (t-\tau)^{\mu-1}(\Lambda - \beta(N)S_0 I_0(\tau) - \mu S_0(\tau))d\tau, \quad S_1(0) = 0$$

$$p^1 : E_1(t) = \frac{1}{\Gamma(\eta)}\int_0^t (t-\tau)^{\eta-1}(\beta(N)(1-p)S_0 I_0(\tau) + r_2 I_0(\tau) - [\mu + k(1-r_1)E_0(\tau)])\,d\tau,$$

$$E_1(0) = 0$$

$$p^1: I_1(t) = \frac{1}{\Gamma(\upsilon)}\int_0^t (t-\tau)^{\upsilon-1}(\beta(N)pS_0I_0(\tau) + k(1-r_1)E_0(\tau) - (\mu+d+\zeta+r_2)I_0(\tau))\,d\tau,\ I_1(0) = 0$$

$$p^n: S_n(t) = \frac{1}{\Gamma(\mu)}\int_0^t (t-\tau)^{\mu-1}\left(\Lambda - \beta(N)\sum_{j=0}^{n-1} I_j S_{n-j-1}(\tau) - \mu\sum_{j=0}^{n-1} S_{n-j-1}(\tau)\right)d\tau\ , S_{n-1}(0) = 0$$

$$p^n: E_n(t) = \frac{1}{\Gamma(\eta)}\int_0^t (t-\tau)^{\eta-1}\left(\beta(N)(1-p)\sum_{j=0}^{n-1} I_j S_{n-j-1}(\tau) + r_2 I_{n-1}(\tau) - [\mu + k(1 - r_1)E_{n-1}(\tau)]\right)d\tau,\ E_{n-1}(0) = 0,$$

$$p^n: I_n(t) = \frac{1}{\Gamma(\upsilon)}\int_0^t (t-\tau)^{\upsilon-1}\left(\beta(N)p\sum_{j=0}^{n-1} I_j S_{n-j-1}(\tau) + k(1-r_1)E_{n-1}(\tau) - (\mu+d+\zeta+r_2)I_{n-1}(\tau)\right)d\tau,\ I_{n-1}(0) = 0.$$

Integrating the above, we obtain the following components:

$$S_0(t) = S(0)\ ;\quad E_0(t) = E(0)\ ;\quad I_0(t) = I(0) \qquad (23)$$

;

$$S_1(t) = -\frac{19.25}{\Gamma(1+\mu)}\ ;\quad I_{L1}(t) = \frac{39.54t^{\eta}}{\Gamma(1+\eta)}, I_{A1}(t) = -\frac{0.868}{\Gamma(1+\upsilon)}$$

$$S_2(t) = t^{\mu}\left(\frac{31.566}{\Gamma(1+\eta+\mu)} + \frac{4.86525t^{\mu}}{\Gamma(1+2\mu)} + \frac{29.546t^{\upsilon}}{\Gamma(1+\upsilon+\mu)}\right)$$

$$I_{L2}(t) = -t^{\eta}\left(\frac{31.598t^{\eta}}{\Gamma(1+2\eta)} + \frac{4.869t^{\mu}}{\Gamma(1+\eta+\mu)} + \frac{31.865t^{\upsilon}}{\Gamma(1+\upsilon+\mu)}\right)$$

$$I_{A2}(t) = t^{\upsilon}\left(\frac{0.398547t^{\eta}}{\Gamma(1+\eta+\upsilon)} - \frac{0.0101387t^{\mu}}{\Gamma(1+\upsilon+\mu)} + \frac{0.625684t^{\upsilon}}{\Gamma(1+2\upsilon)}\right)$$

$$S_3(t) = t^{\mu}\left(-\frac{3.58846t^{\mu+\upsilon}\Gamma(1+\mu+\upsilon)}{\Gamma(1+\mu)\Gamma(1+\upsilon)\Gamma(1+2\mu+\upsilon)} - \frac{0.388522t^{2\eta}}{\Gamma(1+2\eta+\upsilon)} - \frac{19.7583t^{\eta+\mu}}{\Gamma(1+\eta+2\mu)} - \frac{1.98509t^{2\mu}}{\Gamma(1+3\mu)} - \frac{39.4319t^{\eta+\upsilon}}{\Gamma(1+\mu+\upsilon+\eta)} - \frac{13.836t^{\mu+\upsilon}}{\Gamma(1+2\mu+\upsilon)} - \frac{26.0895t^{2\upsilon}}{\Gamma(1+\mu+2\upsilon)}\right)$$

$$I_{L3}(t) = t^{\eta}\left(-\frac{1157.5t^{2\eta}}{\Gamma(1+3\eta)} - \frac{189.513t^{\eta+\mu}}{\Gamma(1+2\eta+\mu)} + \frac{1.75158t^{2\mu}}{\Gamma(1+\eta+2\mu)} - \frac{1277.59t^{\eta+}}{\Gamma(1+2\eta+\upsilon)} + \frac{19.1633t^{\mu+\upsilon}}{\Gamma(1+\eta+\mu+\upsilon)} + \frac{7.2421t^{\mu+\upsilon}\Gamma(1+\mu+\upsilon)}{\Gamma(1+\mu)\Gamma(1+\upsilon)\Gamma(1+\eta+\mu+\upsilon)}\right)$$

$$I_{A3}(t) = t^{\upsilon}\left(\frac{0.22636699t^{\mu+\upsilon}\Gamma(1+\mu+\upsilon)}{\Gamma(1+\mu)\Gamma(1+\upsilon)\Gamma(1+2\upsilon+\mu)} - \frac{0.318522t^{2\eta}}{\Gamma(1+2\eta+\upsilon)} - \frac{0.0872046t^{\eta+\mu}}{\Gamma(1+\eta+2\mu)} + \frac{0.00739513t^{2\mu}}{\Gamma(1+3\mu)} - \frac{0.758873t^{\eta+\upsilon}}{\Gamma(1+\mu+2\upsilon)} + \frac{0.0885603t^{\mu+\upsilon}}{\Gamma(1+\mu+2\upsilon)} - \frac{0.28306t^{2\upsilon}}{\Gamma(1+3\upsilon)}\right)$$

The remaining terms can be obtained in the same manner. But here only few terms of the series solutions are considered and the asymptotic solution is given as: (24)

$$S(t) = S_0(t) + S_1(t) + S_2(t) + S_3(t) + \cdots$$
$$I_L(t) = I_{L0}(t) + I_{L1}(x,t) + I_{L2}(x,t) + I_{L3}(x,t) + \cdots$$
$$I_A(t) = I_{A0}(t) + I_{A1}(x,t) + I_{A2}(x,t) + I_{A3}(x,t) + \cdots$$

The following figures show the simulated solutions for different values of the fractional order derivatives. The approximate solutions of the main problem are depicted in Figure 5, Figure 6 Figure 7 respectively.

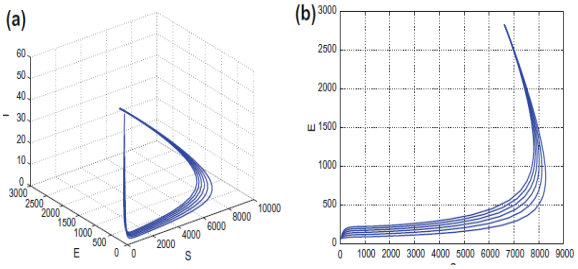

Figure. 5 Trajectories of the fractional model and its plane figure [1].

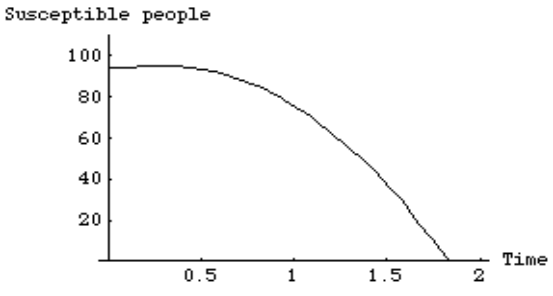

Figure. 6 Approximate solution for susceptibles in the location [2]

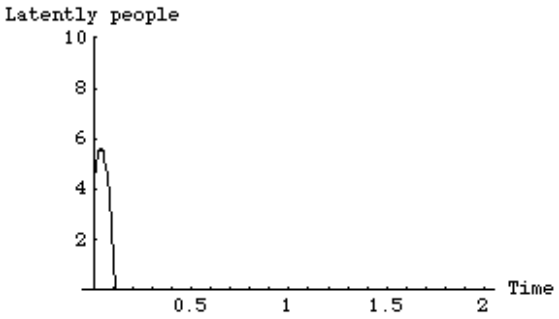

Figure. 7 Approximate solution for the exposed population [2]

The numerical simulations show that, the approximate solutions are continuous functions of the non-integer order derivative. It is worth nothing that the standard mathematical models of integer-order derivatives, including nonlinear models, do not work poperly in many cases. It is therefore advisable to use the fractional model for describing this problem.

4. Conclusion

The tuberculosis model was investigated for the case of integer and non-integer order derivatives. Both systems of nonlinear equations were considered and iteratively analytically solved using homotopy decomposition methods. The approximate solutions of the non-integer case are increasing continuous functions of the fractional order derivative. The numerical solutions in both cases displayed critical biological behavior.

5. References

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