Time-Fractional Epidemiological Models with Applications

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Abstract: Epidemiological models are characterized by the fact that events happen at different time scales. Fractional derivatives are sensitive enough to capture the uncertainties induced of the models. In this paper we investigate the time-fractional derivatives of compartmental models and discuss some examples. The evolution equation is solved numerically via the Crank-Nicholson scheme. The stability and convergence of the numerical scheme are explored. [Oukouomi Noutchie, SC. **Time-Fractional Epidemiological Models with Applications**. *Life Sci J* 2013;10(3):622-630] (ISSN:1097-8135). http://www.lifesciencesite.com. 92

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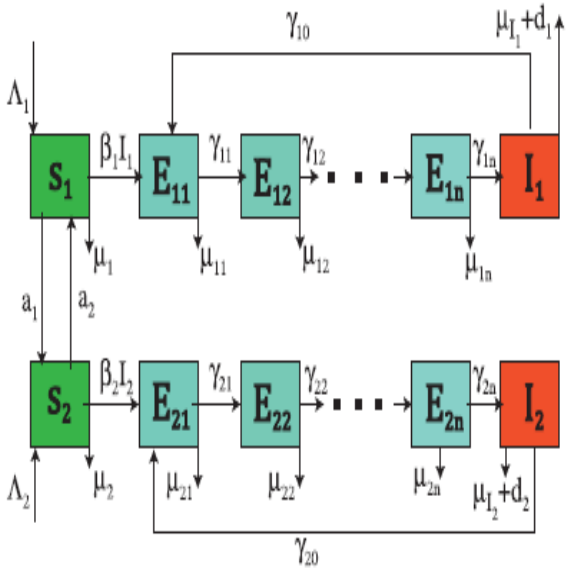
1. Introduction

Compartmental models have been used extensively in the past decades to model and understand the evolution of major diseases including HIV, Tuberculosis, Malaria, Influenza and tumors. The population is in general subdivided into several classes including the susceptible, the infected, the recovered, the latently infected individuals who cannot transmit the disease. In epidemiology, the dynamics in the compartments occur at different time scale and different speeds. Failing to take into consideration the impact of key aspects driving the problem may lead in general to solutions that do not reflect the reality. There are several papers dealing with epidemiology that overlook this aspect resulting in inexact models. In this paper we consider a model with two susceptible classes, two infected classes and several latently infected classes as described by the diagram below:



The equation describing this compartmental model is as follows:

$$
\begin{cases}
\dot{S}_1 = \Lambda_1 - (\mu_1 + a_1)S_1 - \beta_1 I_1 S_1 + a_2 S_2, \\
\dot{E}_{11} = \beta_1 I_1 S_1 - (\mu_{11} + \gamma_{11})E_{11} + \gamma_{10} I_1, \\
\dot{E}_{12} = \gamma_{11} E_{11} - (\mu_{12} + \gamma_{12})E_{12}, \\
\vdots \\
\dot{E}_{1n} = \gamma_{1,n-1} E_{1,n-1} - (\mu_{1n} + \gamma_{1n})E_{1n}, \\
\dot{I}_1 = \gamma_{1n} E_{1n} - (\mu_{I_1} + d_1 + \gamma_{10})I_1, \\
\dot{S}_2 = \Lambda_2 - (\mu_2 + a_2)S_2 - \beta_2 I_2 S_2 + a_1 S_1, \\
\dot{E}_{21} = \beta_2 I_2 S_2 - (\mu_{21} + \gamma_{21})E_{21} + \gamma_{20} I_2, \\
\dot{E}_{22} = \gamma_{21} E_{21} - (\mu_{22} + \gamma_{22})E_{22}, \\
\vdots \\
\dot{E}_{2n} = \gamma_{2,n-1} E_{2,n-1} - (\mu_{2n} + \gamma_{2n})E_{2n}, \\
\dot{I}_2 = \gamma_{2n} E_{2n} - (\mu_{I_2} + d_2 + \gamma_{20})I_2.
\end{cases}
$$

This model could describe 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 [1–4].

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. 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 [1–4].

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population-level outcome such as incidence or prevalence.

2. Application of the 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:

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

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

$$p^0: I_0(t) = I(0) \quad (11)$$

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

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

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

$$\vdots$$

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

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

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

Integrating the above, we obtain the following components:

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

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

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

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

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

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

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

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

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

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)

$$S(t) = 96 - 11.2162t + 62.1069t^2 - 29.5924t^3 - 149.2t^4 + 48.3455t^5 - 20.6378t^6 + 15.5857t^7 + \cdots$$
$$I_L(t) = 3 + 36.8527t - 62.9161t^2 - 797.302t^3 + 151.174t^4 - 48.8926t^5 + 20.7629t^6 - 15.6036t^7 + \cdots$$
$$I_A(t) = 1 - 0.706394t + 0.252053t^2 - 0.252832t^3 - 1.96203t^4 + 0.573666t^5 - 0.131459t^6 + 0.0190148t^7 + \cdots$$

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.

3. 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:

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

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For simplicity let us put:

$$a_0 = (\Lambda - \beta(N) S_0 I_0 - \mu S_0)$$
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$$p^1: E_1(t) = \int_0^t (\beta(N)(1-p) S_0 I_0(\tau) + r_2 I_0(\tau) - [\mu + k(1-r_1) E_0(\tau)]) d\tau, \ E_1(0) = 0.$$

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

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Integrating the above, we obtain the following components:

$$S_0(t) = S(0) \;\; ; \quad E_0(t) = E(0) \;\; ;$$
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For simplicity let us put:

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

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4. Numerical methods

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

$$p^1: S_1(t) = \int_0^t (\Lambda - \beta(N)S_0I_0(\tau) - \mu S_0(\tau))d\tau \;,\; S_1(0) = 0.$$

$$p^1{:}E_1(t)=\int_0^t(\beta(N)(1-p)S_0I_0(\tau)+r_2I_0(\tau)-[\mu+k(1-r_1)E_0(\tau)])d\tau,\ E_1(0)=0.$$

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

$$\vdots$$

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

$$p^n{:}E_n(t)=\int_0^t\left(\beta(N)(1-p)\sum_{j=0}^{n-1}I_jS_{n-j-1}(\tau)+r_2I_{n-1}(\tau)-[\mu+k(1-r_1)E_{n-1}(\tau)]\right)d\tau,\ E_n(0)=0$$

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

Integrating the above, we obtain the following components:

$$S_0(t)=S(0)\ ;\quad E_0(t)=E(0)\ ;$$
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$$S_1(t)=(\Lambda-\beta(N)S_0I_0-\mu S_0)t$$
$$E_1(t)=(\beta(N)(1-p)S_0I_0+r_2I_0-[\mu+k(1-r_1)E_0])t$$
$$I_1(t)=(\beta(N)pS_0I_0+k(1-r_1)E_0-(\mu+d+\zeta+r_2)I_0)t.$$

For simplicity let us put:

$$a_0=(\Lambda-\beta(N)S_0I_0-\mu S_0)$$
$$b_0=(\beta(N)(1-p)S_0I_0+r_2I_0-[\mu+k(1-r_1)E_0])$$
$$c_0=(\beta(N)pS_0I_0+k(1-r_1)E_0-(\mu+d+\zeta+r_2)I_0)$$

.

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)

$$S(t)=96-11.2162t+62.1069t^2-29.5924t^3-149.2t^4+48.3455t^5-20.6378t^6+15.5857t^7+\cdots$$
$$I_L(t)=3+36.8527t-62.9161t^2-797.302t^3+151.174t^4-48.8926t^5+20.7629t^6-15.6036t^7+\cdots$$

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

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)

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

$$p^1: S_1(t) = \int_0^t (\Lambda - \beta(N)S_0I_0(\tau) - \mu S_0(\tau))d\tau\ ,\ S_1(0) = 0.$$

$$p^1: E_1(t) = \int_0^t (\beta(N)(1-p)S_0I_0(\tau) + r_2I_0(\tau) - [\mu + k(1-r_1)E_0(\tau)])d\tau,\ E_1(0) = 0.$$

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

$$\vdots$$

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

$$p^n: E_n(t) = \int_0^t \left(\beta(N)(1-p)\sum_{j=0}^{n-1} I_jS_{n-j-1}(\tau) + r_2I_{n-1}(\tau) - [\mu + k(1 - r_1)E_{n-1}(\tau)]\right)d\tau,\ E_n(0) = 0$$

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

Integrating the above, we obtain the following components:

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

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

$$S_1(t) = (\Lambda - \beta(N)S_0I_0 - \mu S_0)t$$

$$E_1(t) = (\beta(N)(1-p)S_0I_0 + r_2I_0 - [\mu + k(1-r_1)E_0])t$$

$$I_1(t) = (\beta(N)pS_0I_0 + k(1-r_1)E_0 - (\mu + d + \zeta + r_2)I_0)t.$$

For simplicity let us put:

$$a_0 = (\Lambda - \beta(N)S_0I_0 - \mu S_0)$$

$$b_0 = (\beta(N)(1-p)S_0I_0 + r_2I_0 - [\mu + k(1-r_1)E_0])$$

$$c_0 = (\beta(N)pS_0I_0 + k(1-r_1)E_0 - (\mu + d + \zeta + r_2)I_0)$$

.

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

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

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

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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)

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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..

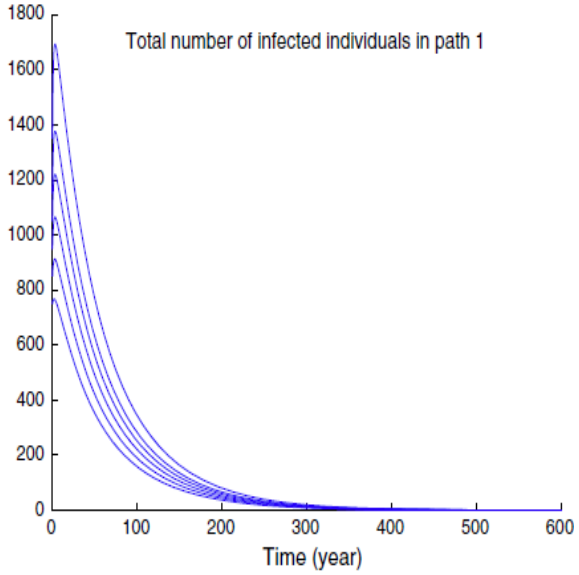

Fig. 1 Particles number of infected individual in path 1.

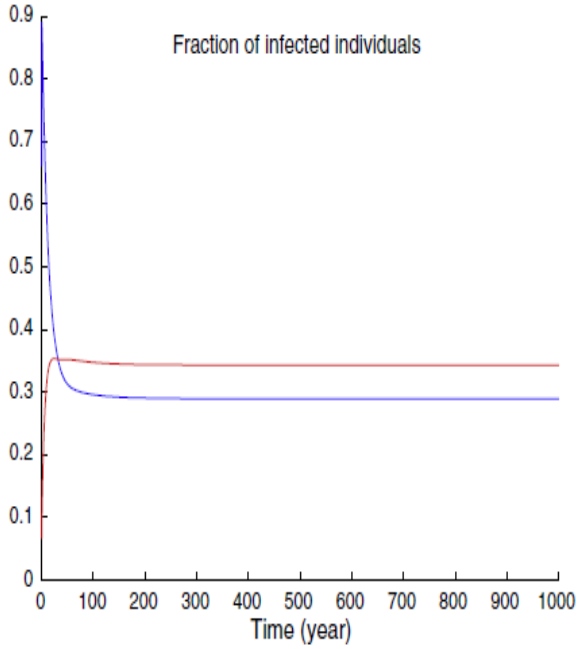

Fig. 2 Fraction number of infected individuals.

5. Conclusions

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..

6. References

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