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Solution of HIV and Malaria Coinfection Model Using Msgdtm

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Abstract

In this paper, we investigate an epidemic model of HIV and Malaria co-infection using fractional order Calculus (FOC). The multistep generalized differential transform method (MSGDTM) is employed to obtain an accurate approximate solution to the epidemic model of HIV and Malaria co-infection disease in fractional order. A unique positive solution for HIV and Malaria co-infection is presented in fractional order form. For the integer case derivatives, the approximate solution of MSGDTM and the Runge–Kutta–order four scheme are compared. Numerical results are produced for the justification for this method.

Keywords: Fractional differential equations, Caputo fractional derivative, multi-step generalized differential transform, co-infection.

1. Introduction

Malaria and human immunodeficiency virus (HIV) are the most deadly and important global health problems of our time. Malaria accounts for more than a million deaths each year, of which about 90% occur in tropical Africa, where malaria is the leading cause of mortality in children below five years [WHO, 2004]. Sub-Saharan Africa is also home to more than 29 million people living with HIV/AIDS. Both Malaria and HIV are considered as diseases of poverty, since they hinder sustainable development and contribute to poverty by taking a great toll on the young productive generation who would otherwise enter the workforce and contribute to the nation's economy. The global distribution of Malaria and HIV is the same, with the majority of those affected living in sub-Saharan Africa, the Indian subcontinent, and Southeast Asia. Owing to the overlap of their geographic distribution and resultant rates of co-infection, interactions between the two diseases pose major public health problems. For instance, in 2007, together they accounted for over 3 million deaths and millions more are adversely affected each year [Hochman and Kim, 2009].

HIV is a lenti-virus that brings about Acquired Immuno deficiency Syndrome (AIDS).This is a state in humans in which gradual failure of the immune system provides life-threatening opportunistic infections such as Malaria, TB and more to thrive [Gendelman et al. 2005]. HIV has become one of the life threatening diseases all over the globe, especially in developing countries where incomes are low. HIV disease was first noticed in 1981 based on a Weekly Morbidity and Mortality Report by Centers for Disease Control and Prevention, USA.

Malaria is caused by the protozoan parasite *Plasmodium* and is transmitted by *Anopheles* mosquitoes through biting of humans. If left unattended to it infects the liver and carries through the bloodstream creating problems for all the organs which will eventually lead to death. It is endemic in most tropical and subtropical regions of the world. Worldwide, 1.2 billion people are at risk for malaria infection, resulting in 500 million infections and more than 1 million deaths each year. It is well- known that the majority of these deaths occur in young children in sub-Saharan Africa, as well as pregnant women who are heavily affected with resultant effects on maternal health and birth outcomes.

A recent study from sub-Saharan Africa has pinpointed malaria as a risk factor of concurrent HIV infection at the population level [Cuadros et al. 2011]. Malaria negatively affects the viral load by increasing HIV replication in *vitro* and in *vivo*. However, this situation may be eradicated with good malaria treatment [Driessche and Watmough, 2002]. Studies indicate that malaria-HIV co-infection triggers malaria disease progression, increases the risk of severe malaria in adults, increases risk of congenital infection and this dual infection fuels the spread of both diseases especially in sub-Saharan Africa [Sanyaolu et al. 2013]

Mathematical modeling has been an important tool in understanding the dynamics of disease transmission and also in decision-making processes in regard to intervention mechanisms for disease control. Nikolaos et al. [1997] proposed a detailed analysis of a dynamical model to describe pathogenesis of HIV infection. A deterministic model for the co-infection of tuberculosis and malaria was presented by Mtisi et al. [2009]. Nielan et al. [2010] proposed a mathematical model for cholera to incorporate vital components such as hyper-infectious, short-lived bacterial states, taking into account separate classes, mild human infections and waning disease immunity using distributes delay. A co-infection model for TB-HIV/AIDS was proposed by Sharomi et al. [2008] to determine the basic reproduction number with the aim of maximizing the control of the diseases. Recently, Abu-Raddad et al. [2006] proposed a mathematical model to examine the transmission dynamics of HIV and malaria co-infection. In his model, he investigated the magnitude of the epidemic synergy that exists between HIV-1 and malaria.

Mathematical modeling associated with multifaceted biological dynamics is a great concern to many researchers. The simple fractional integer order is capable of dealing with such biological processes and dynamics. However, when the biological process is complex the integer order falls short owing to properties such as nonlinearity, mathematical relation associated with the parameters and multiscale behaviour [Leszczynski, 2011]. To study such complex biological systems, fractional derivatives offer the tools to deal with dynamics of such systems. The nonexistence differential operator of integer is the key fundamental property of fractional derivatives models. These properties are able to provide information about the current as well as the past state.

The use of fractional derivatives and fractional integrals to model biomaterials and examine the relation between the material and stress- strain was first undertaken by Magin et al. [2006]. Ding and Ye applied a fractional-order differential equation to model of HIV infection of CD4+ T-cells in humans. Diethelm Ding and Ye [2009] applied fractional calculus to model dengue fever disease outbreak. Doungmo et al. [2014] employed a fractional SEIR epidemic model for spatial and temporal spread of measles in metapopulations in some cities in South Africa. Carla Gendelman et al. [2005] explored computer virus dynamics based on fraction order differential equation. Currently, fractional calculus has been intensively been utilised in modelling process [Alawneh et al. 2011, Alawneh 2013 and Leszczynski 2011].

Recently, Mukandavire et al. [2009] developed a deterministic model for the analysis of co-infection of HIV and malaria in a certain community.

To the best of our knowledge, there is no fractional order coinfection model for HIV and malaria coinfection model for obtaining analytical approximate solution. By reason of this, we propose multistep generalized differential transform method (MSGDTM) which gives accurate solutions over a longer time frame as compared to the standard generalized differential transform method (GDTM) to obtain approximate solution of HIV and malaria coinfection model.

This paper is arranged as follows, In Section 2, we present the HIV and malaria coinfection model. In Section 3, we present some vital definitions and notations related to fractional calculus. The non-negativity solution of the model is presented in Section 4. The proposed method is described in Section 5. In Section 6, the method is applied to problem (2) and numerical simulations graphically shown. Finally, the conclusions are presented in Section 7.

2. The HIV and Malaria Coinfection Model

The model sub - divides the total human population, denoted by $N_h(t)$, into sub-populations of susceptible humans ($S_h(t)$) individuals infected with malaria only $I_{ma}(t)$, individuals infected with only HIV $I_h(t)$, individuals dually infected with malaria and HIV $I_{mh}(t)$. Therefore, the total human population $N_h(t)=S_h(t)+I_{ma}(t)+I_h(t)+I_{mh}(t)$. The total mosquito population (vector), denoted by $N_v(t)$, is also sub-divided into susceptible vector $S_v(t)$ and infected mosquito denoted by $I_v(t)$. Thus, $N_v(t)= S_v(t)+ I_v(t)$. The population of size $N_v(t)$, at time t, has inflow, $\mu_h N_h$, of susceptible, $S_h(t)$, where π is the recruitment rate. The natural mortality rate is for all human populations class is denoted by μ_h.

Susceptible humans, $S_h(t)$, are infected with malaria through biting of mosquito, at a rate $\beta_m \theta I_v S_h$ and move to the malaria infectious class $I_{ma}(t)$. They can get infected with HIV at a contact rate $\beta_h (I_h + \eta_{mh} I_{mh})$ and then move to HIV infectious class $I_h(t)$. Infected individuals with malaria only, either recover with partial immunity and move to susceptible class at a rate ν_1 or acquire HIV infection following effective contact with infected humans at a rate $\delta\beta_h (I_h + \eta_{mh} I_{mh})$ where the parameter $0 < \delta \le 1$ examines the expected decrease in sexual activity (contact) by individuals with malaria infection (because of ill health) and move to the HIV malaria dually-infectious class $I_{mh}(t)$. They pass away due to the disease at a rate α_{ma}. Infected individuals with HIV only, either acquire infection with malaria following effective contact with infected mosquitoes at a rate $\omega\beta_m \theta I_v$, where $\omega > 1$ accounts for the assumed increase in susceptibility to malaria infection as a result of HIV infection and move to the HIV malaria dually-infectious class I_{mh} or die from HIV at rate α_h. Dually-infected individuals either recover with partial immunity and move into HIV only infectious class at a rate ν_2 or die from the malaria at a rate $r\alpha_{ma}$, where $r \ge 1$ accounts for the increased mortality of the $I_{mh}(t)$ individuals in comparison with individuals with malaria infection but not infected with HIV or from HIV at

a rate $q\alpha_H$, where $q \geq 1$ accounts for the increased mortality of the $I_{mh}(t)$ individuals in comparison with individuals with HIV infection but not infected with malaria.

Susceptible mosquitoes are recruited into the population at a constant rate $\pi_v N_v$. They either die at a rate μ_v or acquire malaria infection (following effective contacts with infected humans) at a rate $\beta_h \theta (I_m + \eta_v I_{mh})$. Each infected mosquito becomes infectious and moves to the infectious class (I_v) after a time *t*. Here β_h refers to the effective contact rate for HIV infection, the modification parameter accounts for the relative infectiousness of individuals dually-infected with HIV and malaria $I_{mh}(t)$ in comparison to those with HIV only infection $I_h(t)$. For malaria, θ is the per capita biting rate of mosquitoes, β_m (resp. β_v) is the transmission probability per bite for human (resp. mosquito) infection. Whereas, $\eta_v \geq 1$ is a modification parameter accounting for the increased likelihood of infection of vectors from humans with dual HIV-malaria infection in relation to acquiring infection from humans with malaria only. The use of this force of infection is due to the fact that female mosquitoes only take a fixed number of blood meals per unit of time, irrespective of the absolute numbers of mosquitoes and human.

We present a modified version proposed by Mukandavire et al. [2009].

$$\begin{cases} \frac{dS_h}{dt} = \pi_h + v_1 i_{ma} - \beta_{ma}\theta I_v S_h - \beta_h I_h S_h - \beta_h \eta_{mh} I_{mh} S_h - \mu_h S_h, \\ \frac{dI_{ma}}{dt} = \beta_{ma}\theta I_v S_h - \delta\beta_h I_h I_{ma} - \delta\beta_h \eta_{mh} I_h I_{ma} - (\mu_h + \alpha_{ma} + v_1) I_{ma}, \\ \frac{dI_h}{dt} = \beta_h I_h S_h + \beta_h \eta_{mh} I_{mh} S_h + v_2 I_{mh} - \omega\beta_{ma}\theta I_v I_h - (\mu_h + \alpha_h) I_h, \\ \frac{dI_{mh}}{dt} = \delta\beta_h I_h I_{ma} + \delta\beta_h \eta_{mh} I_{mh} I_{ma} + \omega\beta_{ma}\theta I_v I_h - (\mu_h + r\alpha_{ma} + q\alpha_h + v_2) I_{mh}, \\ \frac{dS_v}{dt} = \pi_v - \beta_v \theta I_{ma} S_v - \beta_v \theta \eta_v I_{mh} S_v - \mu_v S_v, \\ \frac{dI_v}{dt} = \beta_v \theta I_{ma} S_v + \beta_v \theta \eta_v I_{mh} S_v - \mu_v I_v \end{cases} \tag{1}$$

with the initial conditions;

$S_h(0) = e_1,\ I_{ma}(0) = e_2,\ I_h(0) = e_3,\ I_{mh}(0) = e_4,$

$S_v(0) = e_5$ and $I_v(0) = e_6$.

The slightly modified model given by system (1) is thus written in fractional order differential equations version as:

$$\begin{aligned} D_t^\alpha S_h(t) &= \pi_h + v_1 i_{ma} - \beta_{ma}\theta I_v S_h - \beta_h I_h S_h - \beta_h \eta_{mh} I_{mh} S_h - \mu_h S_h, \\ D_t^\alpha I_{ma}(t) &= \beta_{ma}\theta I_v S_h - \delta\beta_h I_h I_{ma} - \delta\beta_h \eta_{mh} I_h I_{ma} - (\mu_h + \alpha_{ma} + v_1) I_{ma}, \\ D_t^\alpha I_h(t) &= \beta_h I_h S_h + \beta_h \eta_{mh} I_{mh} S_h + v_2 I_{mh} - \omega\beta_{ma}\theta I_v I_h - (\mu_h + \alpha_h) I_h, \\ D_t^\alpha I_{mh}(t) &= \delta\beta_h I_h I_{ma} + \delta\beta_h \eta_{mh} I_{mh} I_{ma} + \omega\beta_{ma}\theta I_v I_h - (\mu_h + r\alpha_{ma} + q\alpha_h + v_2) I_{mh}, \\ D_t^\alpha S_v(t) &= \pi_v - \beta_v \theta I_{ma} S_v - \beta_v \theta \eta_v I_{mh} S_v - \mu_V S_v, \\ D_t^\alpha I_v(t) &= \beta_v \theta I_{ma} S_v + \beta_v \theta \eta_v I_{mh} S_v - \mu_v I_v \end{aligned} \tag{2}$$

where D_t^α characterizes the fractional derivative in Caputo derivative version and the order of the fractional derivative is represented by the parameter α and $0 < \alpha < 1$, with the related initial conditions (2).

The variation of the parameter that represents the order of fractional derivative leads to different results for different values. Clearly, the integer-order differential can be viewed as fractional derivatives when $\alpha = 1$. Mostly, for higher order, the dynamics of integer-order and fraction order is the same.

3. Basic Definitions and Notations

This part covers some basic definitions and notations of fractional calculus that will assist in the subsequent sections.

Definition 1: A function $p(x)$ having the positive values of x is identified in the space B_α $(\alpha \in \mathrm{R})$ if it is expressed in the form $p(x) = x^q p_1(x)$ and for some $\mathrm{q} > \alpha$, where $p_1(x)$ is continuous in $[0, \infty)$, and it is identified to be in the space B_α^n if $p^{(n)} \in B_{n,} n \in N$.

Definition 2: The Riemann Liouville integral operator of a given order $\alpha > 0$ with $a \geq 0$ is expressed as

$$\left(J_a^{\alpha} p\right)(x) = \frac{1}{\Gamma(\alpha)} \int_a^x (x-t)^{n-1} p(t)dt, \quad x > \alpha, \tag{3}$$
$$\left(J_a^{0} p\right)(x) = p(x),$$

For the properties of the operator, we require only the following. For $p \in B_n, \alpha > 0, \beta > 0, c \in R$ and γ >-1, one obtains

$$\left(J_a^{\alpha} J_a^{\beta} p\right)(x) = \left(J_a^{\beta} J_a^{\alpha} p\right)(x) = \left(J_a^{\alpha+\beta} p\right)(x), \tag{4}$$
$$J_a^{\alpha} x^{\gamma} = \frac{x^{\gamma+\alpha}}{\Gamma(a)} \beta_{(x-a)/x}(\alpha, \gamma+1),$$

where $\beta_{\tau}(\alpha, \gamma+1)$ characterizes the incomplete beta function stated as

$$B_{\tau}(\alpha, \gamma+1) = \int_0^{\tau} t^{\alpha_1} (1-t)^{\gamma} dt,$$
$$J_a^{\alpha} e^{cx} = e^{cx} (x-a)^{\alpha} \sum_{k=0}^{\infty} \frac{\left[c(c-a)\right]^k}{\Gamma(\alpha+k+1)}. \tag{5}$$

The Riemann Liouville derivative possesses some set-backs when applied to real life situations with fractional differential equations. Thus, at this point we exploit a modified version of fractional differential operator D_a^{α} which has been employed in Caputo work on the theory of viscoelasticity.

Definition 3: The Caputo fractional derivative of $p(x)$ order $\alpha > 0$ with $a \geq 0$ is expressed as

$$\left(D_a^{\alpha} p\right)(x) = \left(J_a^{m-\alpha} p^{(m)}\right)(x) = \frac{1}{\Gamma(m-\alpha)} \int_a^x \frac{p^{(m)}(t)}{(x-t)^{(\alpha+1-m)}} dt, \tag{6}$$

for $m-1 < \alpha \leq m,\ m \in N,\ x \geq a,\ f(x) \in \mathrm{B}_{-1}^m$. Many researchers examined the Caputos fractional order derivatives for $m-1 < \alpha \leq m,\ p(x) \in \mathrm{B}_{\alpha}^m$, and $\alpha \geq -1$, one obtains

$$\left(J_a^{\alpha} D_a^{\alpha} p\right)(x) = J^{(m)} D^{(m)} p(x) = p(x) - \sum_{k=0}^{m-1} p^k(a) \frac{(x-a)^k}{k!}, \tag{7}$$

4. Non- negativity Solution

Assume $R_+^6 = \left\{ X \in R^6 : \ \mathrm{X} \geq 0 \right)$ and $\mathrm{X(t)} = \left(S_h(t), I_{ma}(t), I_h(t), I_{mh}(t), S_v(t), I_v(t)\right)^{\mathrm{T}}$. In order to prove the theorem, first, we state the following lemma.

Lemma 1: Suppose $p(x) \in B[a,b]$ and $D^{\alpha} p(x) \in B[a,b]$ for $\alpha \in (0,1]$. Then one gets

$$p(x) = p(a) + \frac{1}{\Gamma(\alpha)} D^{\alpha} p(\eta)(x-a)^{\eta}, \tag{8}$$

with $0 \leq \eta \leq x,$ for all $x \in [a,b]$. This is also known as generalized mean value theorem.

Remarks 5: Assume $p(x) \in B[a,b]$ and $D^{\alpha} p(x) x \in [a,b]$ for $0 \leq \eta \leq x$. It is obvious from **Lemma 1** that if $D^{\alpha} p(x) \geq 0\ \forall x \in (0,b)$, then the p behaves as nonincreasing function.

Theorem 6: Therefore, given the initial value problems (3), a unique solution exists and remains in R_+^6.

Proof: The existence and uniqueness of the solution of (3) in $(0,\infty)$ can be derived from Magin [2006]. We just require to establish that the domain R_+^6 is positive invariant. Since

$$\begin{aligned}
&D_t^{\alpha} S_h(t)\big|_{S_h=0} = \pi_h + \nu_1 i_{ma} \geq 0,\\
&D_t^{\alpha} I_{ma}(t)\big|_{I_{ma}=0} = \beta_{ma} \theta I_v S_h \geq 0,\\
&D_t^{\alpha} I_h(t)\big|_{I_h=0} = \beta_h \eta_{mh} I_{mh} S_h + \nu_2 I_{mh} \geq 0,\\
&D_t^{\alpha} I_{mh}(t)\big|_{I_{mh}=0} = \delta\beta_h I_h I_{ma} + \omega\beta_{ma} \theta I_v I_h \geq 0,\\
&D_t^{\alpha} S_v(t)\big|_{S_v=0} = \pi_v \geq 0,\\
&D_t^{\alpha} I_v(t)\big|_{I_v=0} = \beta_v \theta I_{ma} S_v + \beta_v \theta \eta_v I_{mh} S_v \geq 0,
\end{aligned} \tag{9}$$

On every hyperplane bounding the nonnegative orthant, the vector field move towards to R_+^6.

5. Multi-step Generalized Differential Transform Method

The nonlinear fractional equations can be best dealt with by employing the approach in Alawneh et al. [2011]. MSGDTM is obtained from GDTM [Leszczynski, 2011, Magin et al. 2006] which provides small step sequentially leading to an accurate approximation solution of a given model. Multistep generalized differential transform method (MSGDTM) provides long time solution and generalized differential transform method (GDTM) also associated with short term solution. The unique property of MSGDTM also conforms to classical Runge – Kutta numerical solution method, having a unity of order of derivative [Leszczynski, 2011]. The solution to such nonlinear fractional equation can also be obtained by using an efficient approach [Ding, 2009]. The MSGDTM is a modified form of the GDTM [Leszczynski, 2011, Magin et al. 2006], in which it is treated as an algorithm in a sequence of small steps, to obtain the accurate approximate solution to the desired models. By using GDTM, the obtained solution is valid for a short interval of time while the solution obtained from multistep generalized differential transform method (MSGDTM) is valid for a long time. To obtain the solution, using MSGDTM is more accurate and valid for long interval of time and agrees well with the classical Runge – Kutta numerical solution method, with the unity order derivative [Magin et al. 2006].

We use the multi-step generalized differential transform method to obtain the approximate solution of system (3), which leads to an accurate solution over a longer time frame as compared to the standard generalized differential transform method. By taking the differential transform of the system (2) with respect to time we have:

$$S_h(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right.}\times\Bigg(\pi_h+v_1 i_{ma}(k)-\beta_{ma}\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_h(k_2-k_1)I_v(k-k_2)$$

$$-\beta_h(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_h(k_2-k_1)I_h(k-k_2)-\beta_h\eta_{mh}(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_h(k_2-k_1)I_{mh}(k-k_2)-\mu_h S_h(k)\Bigg),$$

$$I_{ma}(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\beta_{ma}\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_h(k_2-k_1)I_v(k-k_2)-\delta\beta_h(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{ma}(k_2-k_1)I_h(k-k_2)$$

$$\delta\beta_h\eta_{mh}(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{ma}(k_2-k_1)I_h(k-k_2)-(\mu_h+\alpha_{ma}+v_1)I_{ma}(k)\Bigg),$$

$$I_h(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\delta\beta_h(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{ma}(k_2-k_1)I_h(k-k_2)-\delta\beta_h\eta_{mh}(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{ma}(k_2-k_1)I_{mh}(k-k_2)+v_2 I_{mh}(k)$$

$$-\omega\beta_{ma}\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_h(k_2-k_1)I_v(k-k_2)-(\mu_h+\alpha_h)I_h(k)\Bigg),$$

$$I_{mh}(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\delta\beta_h(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{ma}(k_2-k_1)I_h(k-k_2)-\delta\beta_h\eta_{mh}(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{ma}(k_2-k_1)I_{mh}(k-k_2)+v_2 I_{mh}(k)$$

$$+\omega\beta_{ma}\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_v(k_2-k_1)I_h(k-k_2)-(\mu_h+r\alpha_{ma}+q\alpha_h+v_2)I_{mh}(k)\Bigg),$$

$$S_v(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\pi_v-\beta_v\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_v(k_2-k_1)I_{ma}(k-k_2)-\beta_v\theta\eta_v(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mh}(k_2-k_1)S_V(k-k_2)-\mu_v S_v(k)\Big),$$

$$I_v(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\beta_v\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_v(k_2-k_1)I_{ma}(k-k_2)+\beta_v\theta\eta_v(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mh}(k_2-k_1)S_V(k-k_2)-\mu_v I_v(k)\Big),\tag{10}$$

where $S_{(h)}(k)$, $I_{(ma)}(k)$, $I_{(h)}(k)$, $I_{(mh)}(k)$, $S_{(v)}(k)$, $\beta_h(k)$, $\beta_{ma}(k)$, $\beta_v(k)$, $\theta(k)$, $\delta(k)$ $\eta_{mh}(k)$, $\eta_v(k)$ and $I_{(v)}(k)$ stand for the differential transformation of $S_{(h)}(t)$, $I_{(ma)}(t)$, $I_{(h)}(t)$, $I_{(mh)}(t)$, $S_{(v)}(t)$, $\beta_h(t)$, $\beta_{ma}(t)$, $\beta_v(t)$, $\theta(t)$, $\delta(t)$ $\eta_{mh}(t)$, $\eta_v(t)$ and $I_{(v)}(t)$. The initial conditions in terms of differential transform from are represented as $S_h(0)=e_1$, $I_{ma}(0)=e_2$, $I_h(0)=e_3$, $I_{mh}(0)=e_4$, $S_v(0)=e_5$ and $I_v(0)=e_6$. From differential inverse transform vision, the differential transform series solution for the system (2) can be obtained as

$$
\begin{aligned}
S_{(h)}(t) &= \sum_{k=0}^{K} S_{(h)}(k)\, t^{\alpha k}, \\
I_{(ma)}(t) &= \sum_{k=0}^{K} I_{(ma)}(k)\, t^{\alpha k}, \\
I_{(h)}(t) &= \sum_{k=0}^{K} I_{(h)}(k)\, t^{\alpha k}, \\
I_{(mh)}(t) &= \sum_{k=0}^{K} I_{(mh)}(k)\, t^{\alpha k}, \\
S_{(v)}(t) &= \sum_{k=0}^{K} S_{(v)}(k)\, t^{\alpha k}, \\
I_{(v)}(t) &= \sum_{k=0}^{K} I_{(v)}(k)\, t^{\alpha k}.
\end{aligned}
\tag{11}
$$

The series solution for the system (2), based on the MSGDTM is suggested as

$$
S_{(h)}(t) = \begin{cases}
\sum_{k=0}^{K} S_{(h1)}(k)\, t^{\alpha k} & t \in [0, t_1] \\
\sum_{k=0}^{K} S_{(h2)}(k)\, (t - t)^{\alpha k}, & t \in [t_1, t_2] \\
. & \\
. & \\
. & \\
\sum_{k=0}^{K} S_{(hM)}(k)\, (t_M - t_{M-1})^{\alpha k} & t \in [t_{M-1}, t_M],
\end{cases}
$$

$$
I_{(ma)}(t) = \begin{cases}
\sum_{k=0}^{K} I_{(ma1)}(k)\, t^{\alpha k} & t \in [0, t_1] \\
\sum_{k=0}^{K} I_{(ma2)}(k)\, (t - t)^{\alpha k}, & t \in [t_1, t_2] \\
. & \\
. & \\
. & \\
\sum_{k=0}^{K} I_{(maM)}(k)\, (t_M - t_{M-1})^{\alpha k} & t \in [t_{M-1}, t_M],
\end{cases}
$$

$$
I_{(h)}(t) = \begin{cases}
\sum_{k=0}^{K} I_{(h1)}(k)\, t^{\alpha k} & t \in [0, t_1] \\
\sum_{k=0}^{K} I_{(h2)}(k)\, (t - t)^{\alpha k}, & t \in [t_1, t_2] \\
. & \\
. & \\
. & \\
\sum_{k=0}^{K} I_{(hM)}(k)\, (t_M - t_{M-1})^{\alpha k} & t \in [t_{M-1}, t_M],
\end{cases}
$$

$$I_{(mh)}(t)=\begin{cases}\sum_{k=0}^{K} I_{(mh1)}(k)\ t^{\alpha k} & t\in[0,t_1]\\ \sum_{k=0}^{K} I_{(mh2)}(k)\ (t-\ t)^{\alpha k}, & t\in[t_1,t_2]\\ . & \\ . & \\ . & \\ \sum_{k=0}^{K} I_{(mhM)}(k)\ (t_M-\ t_{M-1})^{\alpha k} & t\in[t_{M-1},t_M],\end{cases}$$

$$S_{(v)}(t)=\begin{cases}\sum_{k=0}^{K} S_{(v1)}(k)\ t^{\alpha k} & t\in[0,t_1]\\ \sum_{k=0}^{K} S_{(v2)}(k)\ (t-\ t)^{\alpha k}, & t\in[t_1,t_2]\\ . & \\ . & \\ . & \\ \sum_{k=0}^{K} S_{(vM)}(k)\ (t_M-\ t_{M-1})^{\alpha k} & t\in[t_{M-1},t_M],\end{cases}$$

$$I_{(v)}(t)=\begin{cases}\sum_{k=0}^{K} I_{(v1)}(k)\ t^{\alpha k} & t\in[0,t_1]\\ \sum_{k=0}^{K} I_{(v2)}(k)\ (t-\ t)^{\alpha k}, & t\in[t_1,t_2]\\ . & \\ . & \\ . & \\ \sum_{k=0}^{K} I_{(vM)}(k)\ (t_M-\ t_{M-1})^{\alpha k} & t\in[t_{M-1},t_M],\end{cases} \tag{12}$$

where $S_{(hi)}(k),\ I_{(mai)}(k),\ I_{(hi)}(k),\ I_{(mhi)}(k),\ S_{(vi)}(k)$ and $I_{(vi)}(k)$ for $i=1,2,3,...,M$ satisfy the following recurrence relations:

$$S_{hi}(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right.}\times\Bigg(\pi_h+\nu_1 i_{mai}(k)-\beta_{ma}\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_{hi}(k_2-k_1)I_{vi}(k-k_2)$$
$$-\beta_h(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_{hi}(k_2-k_1)I_{hi}(k-k_2)-\beta_h\eta_{mh}(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_{hi}(k_2-k_1)I_{mhi}(k-k_2)-\mu_h S_{hi}(k)\Bigg),$$

$$I_{mai}(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right.}\times\Bigg(\beta_{ma}\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_{hi}(k_2-k_1)I_{vi}(k-k_2)-\delta\beta_h(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mai}(k_2-k_1)I_{hi}(k-k_2)$$
$$\delta\beta_h\eta_{mh}(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mai}(k_2-k_1)I_{hi}(k-k_2)-(\mu_h+\alpha_{ma}+\nu_1)I_{mai}(k)\Bigg),$$

$$I_h(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\delta\beta_h(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mai}(k_2-k_1)I_{hi}(k-k_2)-\delta\beta_h\eta_{mh}(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mai}(k_2-k_1)I_{mhi}(k-k_2)+v_2I_{mhi}(k)$$
$$-\omega\beta_{ma}\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{hi}(k_2-k_1)I_{vi}(k-k_2)-(\mu_h+\alpha_h)I_{hi}(k)\Bigg),$$

$$I_{mhi}(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\delta\beta_h(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mai}(k_2-k_1)I_{hi}(k-k_2)-\delta\beta_h\eta_{mh}(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mai}(k_2-k_1)I_{mhi}(k-k_2)+v_2I_{mhi}(k)$$
$$+\omega\beta_{ma}\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{vi}(k_2-k_1)I_{hi}(k-k_2)-(\mu_h+r\alpha_{ma}+q\alpha_h+v_2)I_{mhi}(k)\Bigg),$$

$$S_{vi}(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\pi_v-\beta_v\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_{vi}(k_2-k_1)I_{mai}(k-k_2)-\beta_v\theta\eta_v(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mhi}(k_2-k_1)S_{vi}(k-k_2)-\mu_v S_{vi}(k)\Big),$$

$$I_{vi}(k+1)=\frac{\Gamma(\alpha k+1)}{\Gamma\left(\alpha(k+1+1)\right)}\times\Bigg(\beta_v\theta(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}S_{vi}(k_2-k_1)I_{mai}(k-k_2)+\beta_v\theta\eta_v(k_1)\sum_{k_2=0}^{k}\sum_{k_1=0}^{k_2}I_{mhi}(k_2-k_1)S_{vi}(k-k_2)-\mu_v I_V(k)\Big), \tag{13}$$

such that $S_{h(i)}(t_{i-1})=S_{h(i-1)}(t_{i-1}),\ I_{ma(i)}(t_{i-1})=I_{ma(i-1)}(t_{i-1}),\ I_{h(i)}(t_{i-1})=I_{h(i-1)}(t_{i-1})$,

$I_{mh(i)}(t_{i-1})=I_{mh(i-1)}(t_{i-1}),\ S_{v(i)}(t_{i-1})=S_{v(i-1)}(t_{i-1})$ and $I_{v(i)}(t_{i-1})=I_{v(i-1)}(t_{i-1})$. Initially, beginning from

$S_{h(0)}=e_1,\ I_{ma(0)}=e_1,\ I_{h(0)}=e_1,\ I_{mh(0)}=e_1,\ S_{v(0)}=e_1$ and $I_{v(0)}=e_1$, by employing (12)

6. Numerical Methods and Simulation

We solve analytically the system (2) with transform initial condition by applying the multi-step generalized differential transform method (MSGDTM) and employ Runge – Kutta order four method for integer order derivative for numerical results. We investigate the system (2) numerically in the interval [0, 30] for the approximate solution of nonlinear fractional differential equation. For K=10 and M= 3000, the final output (results) are determined. By employing Mathematica the results were obtained. The initial condition $e_1=60,\ e_2=20,\ e_3=10,\ e_4=30\ e_5=30$ and $e_5=10$ are employed in the computation of the numerical results. The values for the parameters assumed are indicated in Table 1. In Figures 1,2,3,4,5 and 6, the approximate solution is obtained by MSGDTM and the classical Runge – Kutta method order four scheme for $\alpha=1$. The approximate solution of MSGDTM matches with the results obtained using the 4^{th} order Runge – Kutta iteration scheme. Figure 7,8,9,10,11 and 12 represent the approximate solution obtained by MSGDTM and classical Runge – Kutta order four scheme considering different values of α. We conclude from the two algorithms graphical results that the MSGDTM and classical Runge – Kutta behave similarly.

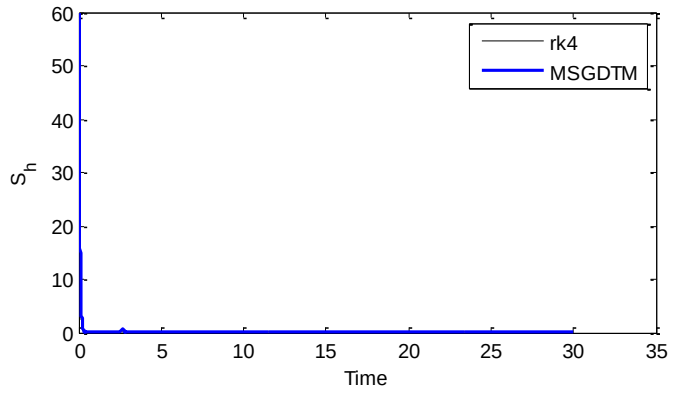

Figure 1. The plot shows susceptible humans with comparison of rk4 and MSGDTM

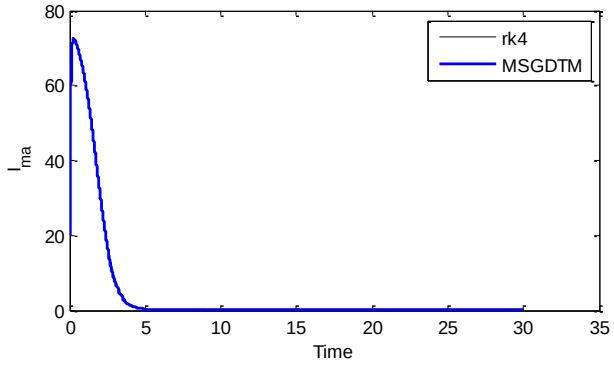

Figure 2. The plot shows individuals infected with malaria only with comparison of rk4 and MSGDTM

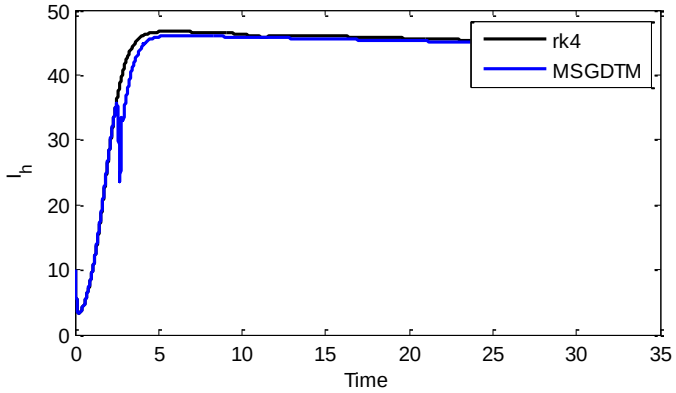

Figure 3. The plot depicts individuals infected with only HIV with comparison of rk4 and MSGDTM

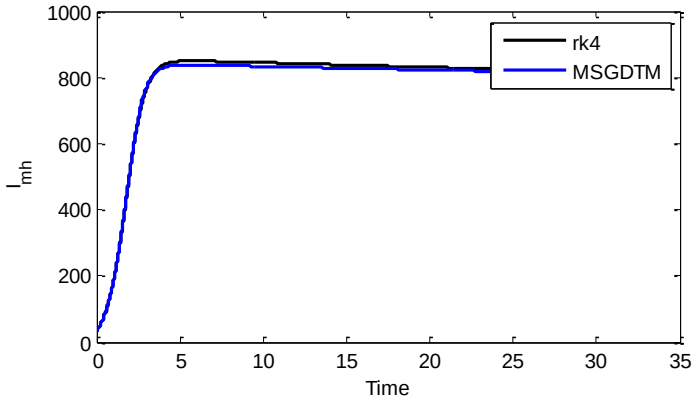

Figure 4. The plot shows individuals infected dually with malaria and HIV with comparison of rk4 and MSGDTM

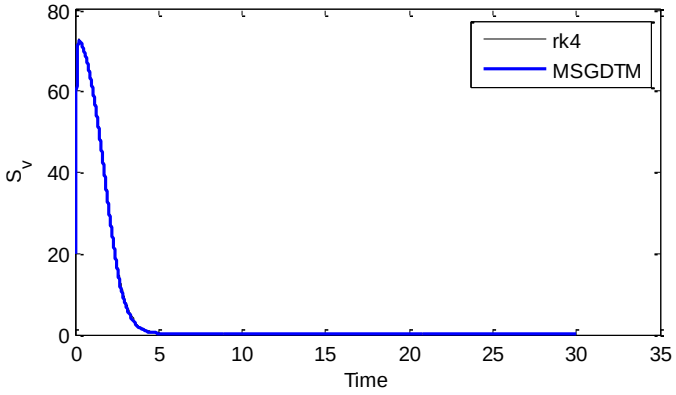

Figure 5. The plot depicts susceptible vector with comparison of rk4 and MSGDTM

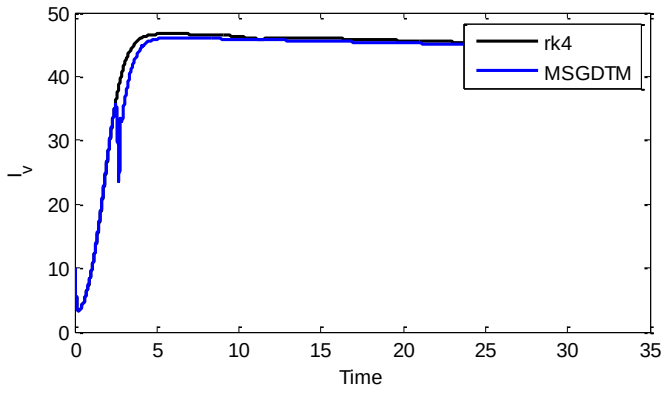

Figure 6. The plot shows an infected mosquito with comparison of rk4 and MSGDTM

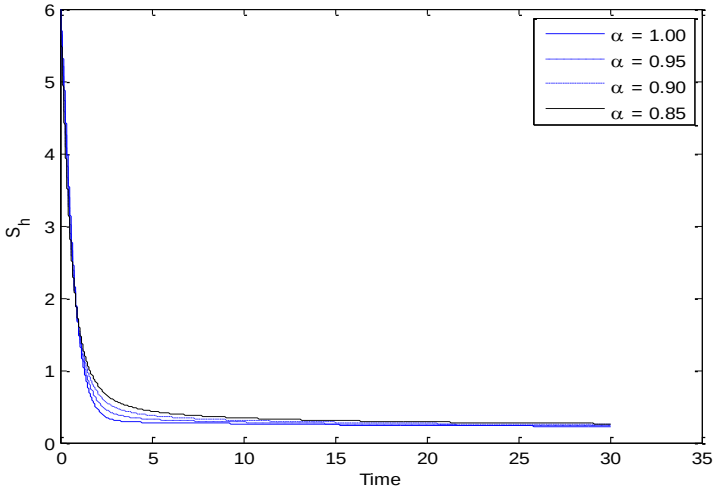

Figure 7. The plot shows susceptible humans with different values of $\alpha = (1.00, 0.95, 0.90, 0.85)$

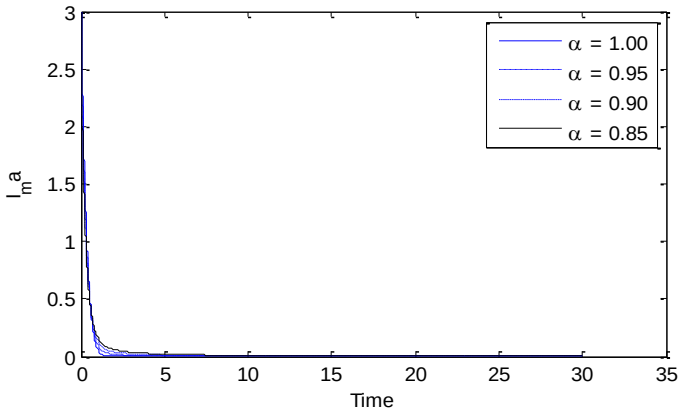

Figure 8. The plot shows individuals infected with different values of $\alpha = (1.00, 0.95, 0.90, 0.85)$

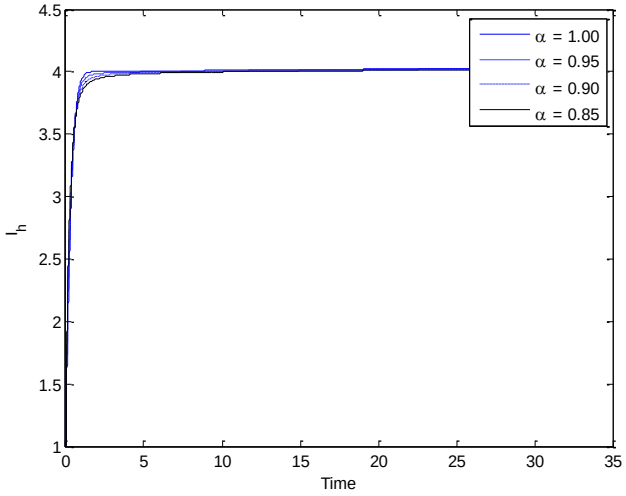

Figure 9. The plot depicts individuals infected with different values of $\alpha = (1.00, 0.95, 0.90, 0.85)$

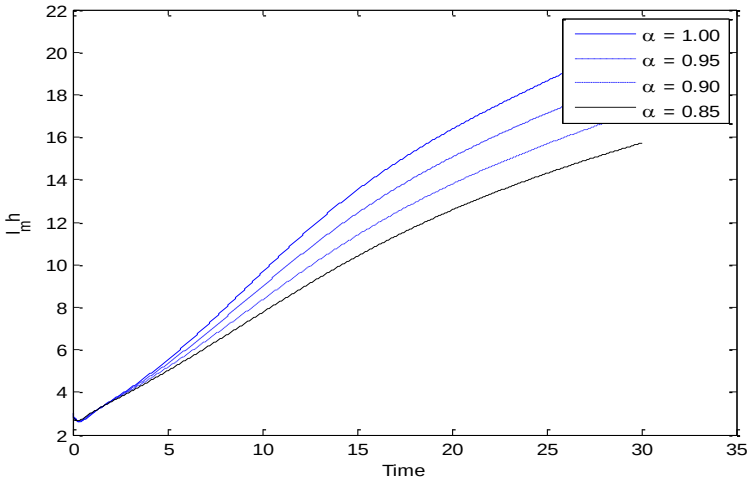

Figure 10. The plot shows individuals infected dually with different values of $\alpha = (1.00, 0.95, 0.90, 0.85)$.

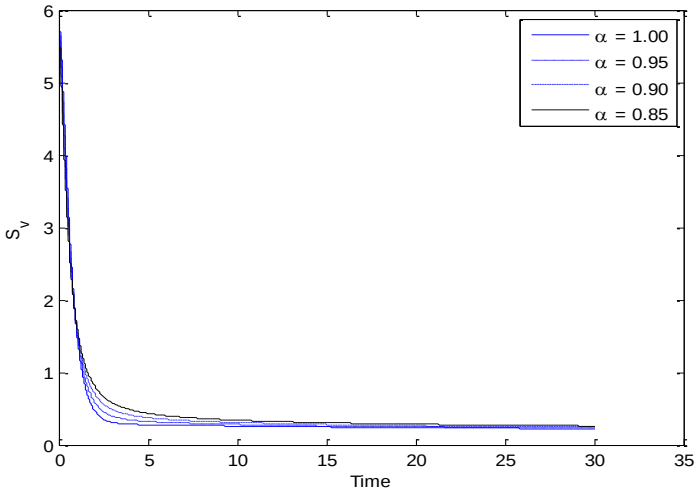

Figure 11. The plot depicts susceptible vector with different values of $\alpha = (1.00, 0.95, 0.90, 0.85)$

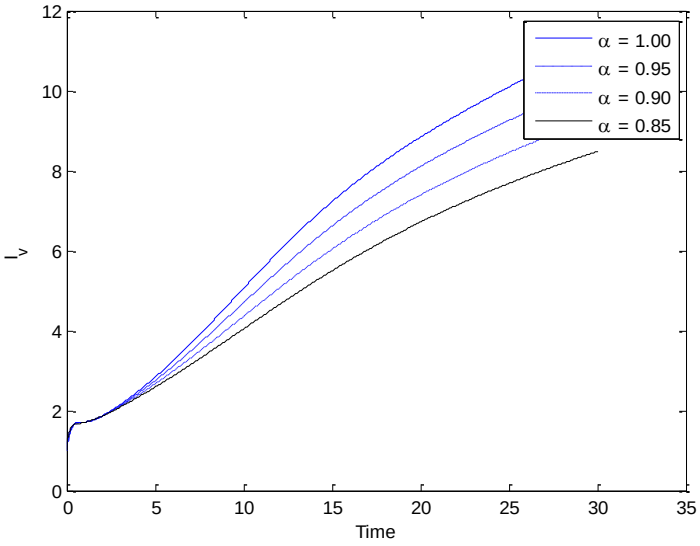

Figure 12. The plot shows an infected mosquito with different values of $\alpha = (1.00, 0.95, 0.90, 0.85)$.

Table 1. Parameters used in the numerical simulations of model (4)

Parameter	Value/Range	Sources
π_h	0.55	Chiyaka et al., 2007
π_v	0.001	Chiyaka et al., 2007
α_{ma}	0.00041	Chitnis et al., 2008
α_h	0.0049139	Chitnis et al., 2008
θ	0.57	Chiyaka et al., 2008
v_1	0.02	Abu-Raddad et al., 2006
v_2	1.002	Abu-Raddad et al., 2006
β_h	0.015	Chiyaka et al., 2007
β_v	0.8	Chiyaka et al., 2007
β_m	0.8	Chiyaka et al., 2007
η_{mh}	1.500	Chiyaka et al., 2007
η_v	1.500	Chitnis et al., 2008
ω	1.00	Chitnis et al., 2008
q	1.00	Chiyaka et al., 2008
δ	1.00	Abu-Raddad et al., 2006
r	1.00	Chiyaka et al., 2008

7. Conclusion

In this paper, a new numerical method to deal with a time- fractional HIV and malaria coinfection is proposed and non-negativity solution of the proposed model determined. The method is a modification of standard GDTM. Comparison of the results obtained using the MGDTM with that of the one obtained by Runge – Kutta fourth order shows that MGDTM matches excellently with the RK4 method. The numerical solutions obtained using MGDTM with different α values were also very good. The MGDTM results are also valid for a larger t.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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