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A new analytic numeric method solution for fractional modified epidemiological model for computer viruses

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Abstract

Computer viruses are an extremely important aspect of computer security, and understanding their spread and extent is an important component of any defensive strategy. Epidemiological models have been proposed to deal with this issue, and we present one such here. We consider the modified epidemiological model for computer viruses (SAIR) proposed by J. R. C. Piqueira and V. O. Araujo. This model includes an antidotal population compartment (A) representing nodes of the network equipped with fully effective anti-virus programs. The multi-step generalized differential transform method (MSGDTM) is employed to compute an approximation to the solution of the model of fractional order. The fractional derivatives are described in the Caputo sense. Figurative comparisons between the MSGDTM and the classical fourth-order Runge-Kutta method (RK4) reveal that this method is very effective. Mathematica 9 is used to carry out the computations. Graphical results are presented and discussed quantitatively to illustrate the solution.

Keywords: Fractional differential equations, Caputo fractional derivative, multi-step generalized differential transform, Epidemiological model, computer viruses

MSC 2010 No.: 74H15

1. Introduction

Computer virus is a kind of computer program that can replicate itself and spread from one computer to others. Viruses mainly attack the file system and worms use system vulnerability to search and attack computers. As hardware and software technology develop and computer networks become an essential tool for daily life, the computer virus starts to be a major threat. Consequently, the trial on better understanding of the computer virus propagation dynamics is an important matter for improving the safety and reliability in computer systems and networks. Similar to the biological virus, there are two ways to study this problem: microscopic and macroscopic models. Following a macroscopic approach, since [Kephart and White (1993), Kephart et al. (1993)] took the first step towards modeling the spread behavior of computer virus, much work has been done in the area of developing a mathematical model for the computer virus propagation [Billings et al. (2002), Han and Tan (2010), Piqueira and Araujo (2009), Ren et al. (2012), Wierman and Marchette (2004)].

Epidemic models for computer virus spread have been investigated since at least 1988. Murray (1988) appears to be the first to suggest the relationship between epidemiology and computer viruses. Although he did not propose any specific models, he pointed out analogies to some public health epidemiological defense strategies. Gleissner (1989) examined a model of computer virus spread on a multi-user system, but no allowance was made for the detection and removal of viruses or alerting other users of the presence of viruses. More recently, a group at IBM Watson Research Center [Kephart et al. (1997), Kephart and White (1991), Kephart et al. (1993), Kephart and White (1993)] has investigated susceptible infected- susceptible (SIS) models for computer virus spread.

Kephart and White (1991), formulated a directed random graph model and studied its behavior via deterministic approximation, stochastic approximation, and simulation. In [Kephart et al. (1993), Kephart and White (1993)], a combination of theory and observation led to a conclusion that computer viruses were much less prevalent than many have claimed, estimating that the number of infected machines is perhaps 3 or 4 per thousand PC's. They also claim that computer viruses are gradually becoming more prevalent, not because of any single viral strain, but because the number of viruses is growing with time. The classical SIR (Susceptible-Infected- Recovered) computer virus propagation model was proposed Piqueira and Araujo (2009), Wierman and Marchette (2004) which is formulated as the following system of differential equations:

$$\begin{aligned}\frac{dS}{dt} &= b - \lambda S(t)I(t) - dS(t), \\ \frac{dI}{dt} &= \lambda S(t)I(t) - \varepsilon I(t) - dI(t), \\ \frac{dR}{dt} &= \varepsilon I(t) - dR(t).\end{aligned}\tag{1.1}$$

Here, it is assumed that all the computers connected to the network in question are classified into three categories: susceptible, infected, and recovered computers. Let $S(t)$, $I(t)$ and $R(t)$ denote

their corresponding numbers at time t , respectively. This model involves four positive parameters: b denotes the rate at which external computers are connected to the network, ε denotes the recovery rate of infected computers due to the anti-virus ability of the network, d denotes the rate at which one computer is removed from the network, λ denotes the rate at which, when having a connection to one infected computer, one susceptible computer can become infected. Recently, Jianguo Ren et. all in (Ren et al. 2012) introduced a new recovery function

$$T(I) = \begin{cases} \varepsilon I, & 0 \leq I \leq I_0 \\ m, & I > I_0 \end{cases}, \quad (1.2)$$

where ε is the recovery rate when the anti-virus ability is not fully utilized, $m = \varepsilon I_0$ to characterize the saturation phenomenon of the limited anti-virus ability of a network, and they carefully investigated the dynamics of the following computer virus propagation model

$$\begin{aligned} \frac{dS}{dt} &= rS \left(1 - \frac{S}{k} \right) - \lambda SI - dS, \\ \frac{dI}{dt} &= \lambda SI - T(I) - dI, \\ \frac{dR}{dt} &= T(I) - dR. \end{aligned} \quad (1.3)$$

Nowadays several researchers work on the fractional order differential equations because of best presentation of many phenomena. 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. In recent years, fractional calculus has played a very important role in various fields such as mechanics, electricity, chemistry, biology, economics, notably control theory, and signal and image processing; see for example [Ertürk, et al. (2011), Lin (2007), Miller and Ross (1993)].

In this paper, we intend to obtain the approximate solution of the fractional-order Model for computer viruses via the multi-step generalized differential transform method (MSGDTM). This method is only a simple modification of the generalized differential transform method (GDTM), in which it is treated as an algorithm in a sequence of small intervals (i.e., time step) for finding accurate approximate solutions to the corresponding systems. The approximate solutions obtained by using GDTM are valid only for a short time. The ones obtained by using the MSGDTM are more valid and accurate during a long time, and are in good agreement with the classical Runge-Kutta method of numerical solution when the order of the derivative is one.

2. Model description

Here, we consider the model taking by J. R. C. Piqueira and V. O. Araujo. (Piqueira and Araujo, 2009). In this model, they considered that the total population T , is divided into four groups: S , of

non-infected computers subjected to possible infection; A , of noninfected computers equipped with anti-virus; I , of infected computers; and R , of removed ones due to infection or not. The influx and mortality parameters of the model are defined as:

N : influx rate, representing the incorporation of new computers to the network;

μ : proportion coefficient for the mortality rate, not due to the virus.

The susceptible population S is infected with a rate that is related to the probability of susceptible computers to establish effective communications with infected ones. Therefore, this rate is proportional to the product SI , with proportion factor represented by β . Conversion of susceptible into antidotal is proportional to the product SA and is controlled by α_{SA} , that is an operational parameter defined by the anti-virus distribution strategy of the network administration.

Infected computers can be fixed by using anti-virus programs being converted into antidotal ones with a rate proportional to AI , with a proportion factor given by α_{IA} , or become useless and removed with a rate controlled by δ . Removed computers can be restored and converted into susceptible ones with a proportion factor σ . This model represents the dynamics of the propagation of the infection of a known virus and, consequently, the conversion of antidotal into infected is not considered. Therefore, by using this model, a vaccination strategy can be defined, providing an economical use of the anti-virus programs.

Considering these facts, the model can be described by:

$$\begin{aligned}\frac{dS}{dt} &= N - \alpha_{SA}SA - \beta SI - \mu S + \sigma R, \\ \frac{dI}{dt} &= \beta SI - \alpha_{IA}AI - \delta I - \mu I, \\ \frac{dR}{dt} &= \delta I - \sigma R - \mu R, \\ \frac{dA}{dt} &= \alpha_{SA}SA + \alpha_{IA}AI - \mu A.\end{aligned}\tag{2.1}$$

Here, the influx rate is considered to be $N = 0$, representing that there is no incorporation of new computers in the network during the propagation of the considered virus, because its action is faster than the network expansion. The same reason justifies the choice of $\mu = 0$, considering that the machines obsolescence time is larger than the time of the virus action.

Consequently, the Equation system (2.1) is simplified to:

$$\begin{aligned}
\frac{dS}{dt} &= -\alpha_{SA}SA - \beta SI + \sigma R, \\
\frac{dI}{dt} &= \beta SI - \alpha_{IA}AI - \delta I, \\
\frac{dR}{dt} &= \delta I - \sigma R, \\
\frac{dA}{dt} &= \alpha_{SA}SA + \alpha_{IA}AI.
\end{aligned} \tag{2.2}$$

Here, the total population of the network $T = S + I + R + A$ remains constant.

3. Fractional calculus

There are several approaches to define fractional calculus, e.g. Riemann-Liouville, Grünwald-Letnikov, Caputo, and Generalized Functions approach. Riemann-Liouville fractional derivative is mostly used by mathematicians but this approach is not suitable for real world physical problems since it requires the definition of fractional order initial conditions, which have no physically meaningful explanation yet. Caputo introduces an alternative definition, which has the advantage of defining integer order initial conditions for fractional order differential equations.

Definition 3.1.

A function $f(x)$ ($x >$) is said to be in the space C_α ($\alpha \in \mathbb{R}$) if it can be written as $f(x) = x^p f_1(x)$ for some $p > \alpha$ where $f_1(x)$ is continuous in $[0, \infty)$, and it is said to be in the space C_α^m if $f^{(m)} \in C_\alpha$, $m \in \mathbb{R}$.

Definition 3.2.

The Riemann–Liouville integral operator of order α with $a \geq 0$ is defined as

$$(J_a^\alpha f)(x) = \frac{1}{\Gamma(\alpha)} \int_a^x (x-t)^{\alpha-1} f(t) dt, \quad x > a, \tag{3.1}$$

$$(J_a^0 f)(x) = f(x). \tag{3.2}$$

Properties of the operator can be found in (Caputo, 1967), (Miller and Ross, 1993), (Podlubny, 1999). Here, we only need the following: For $f \in C_\alpha$, $\alpha, \beta > 0$, $a \geq 0$, $c \in \mathbb{R}$, $\gamma > -1$, we have

$$(J_a^\alpha J_a^\beta f)(x) = (J_a^\beta J_a^\alpha f)(x) = (J_a^{\alpha+\beta} f)(x), \tag{3.3}$$

$$J_a^\alpha x^\gamma = \frac{x^{\gamma+\alpha}}{\Gamma(\alpha)} B_{\frac{x-a}{x}}(\alpha, \gamma+1), \quad (3.4)$$

where $B_\tau(\alpha, \gamma+1)$ is the incomplete beta function which is defined as

$$B_\tau(\alpha, \gamma+1) = \int_0^\tau t^{\alpha-1} (1-t)^\gamma dt, \quad (3.5)$$

$$J_a^\alpha e^{cx} = e^{ac} (x-a)^\alpha \sum_{k=0}^{\infty} \frac{[c(x-a)]^k}{\Gamma(\alpha+k+1)}. \quad (3.6)$$

The Riemann–Liouville derivative has certain disadvantages when trying to model real-world phenomena with fractional differential equations. Therefore, we shall introduce a modified fractional differential operator D_a^α proposed by Caputo in his work on the theory of viscoelasticity.

Definition 3.3.

The Caputo fractional derivative of $f(x)$ of order $\alpha > 0$ with $a \geq 0$ is defined as

$$(D_a^\alpha f)(x) = (J_a^{m-\alpha} f^{(m)})(x) = \frac{1}{\Gamma(m-\alpha)} \int_a^x \frac{f^{(m)}(t)}{(x-t)^{\alpha+1-m}} dt, \quad (3.7)$$

for $m-1 < \alpha \leq m$, $m \in \mathbb{R}$, $x \geq a$, $f \in C_{-1}^m$.

The Caputo fractional derivative was investigated by many authors, for $m-1 < \alpha \leq m$, $f(x) \in C_{-1}^m$ and $\alpha \geq -1$, we have

$$(J_a^\alpha D_a^\alpha f)(x) = J_a^m D_a^m f(x) = f(x) - \sum_{k=0}^{m-1} f^{(k)}(a) \frac{(x-a)^k}{k!}. \quad (3.8)$$

For mathematical properties of fractional derivatives and integrals one can consult the mentioned references.

4. Multi-step generalized differential transform method (MSGDTM)

To describe the multi-step generalized differential transform method (MSGDTM) [Abuteen et al. (2014), Arshad et al. (2015), Ertürk et al. (2008), Freihat and Momani (2012), Freihat and Momani (2012), Momani and Odibat (2008), Odibat et al. (2008), Odibat and Momani (2008)].

We consider the following initial value problem for systems of fractional differential equations

$$\begin{aligned}
D_*^{\alpha_1} y_1(t) &= f_1(t, y_1, y_2, \dots, y_n), \\
D_*^{\alpha_2} y_2(t) &= f_2(t, y_1, y_2, \dots, y_n), \\
&\vdots \\
D_*^{\alpha_n} y_n(t) &= f_n(t, y_1, y_2, \dots, y_n),
\end{aligned} \tag{4.1}$$

subject to the initial conditions

$$y_i(t_0) = c_i, \quad i = 1, 2, \dots, n, \tag{4.2}$$

where $D_*^{\alpha_i}$ is the Caputo fractional derivative of order α_i , where $0 < \alpha_i \leq 1$, for $i = 1, 2, \dots, n$.

Let $[t_0, T]$ be an interval over which we wish to determine the solution of the initial value problem (4.1)-(4.2). In actual applications of GDTM, the K^{th} -order approximate solution of the initial value problem (4.1)-(4.2) can be expressed by the finite series

$$y_i(t) = \sum_{k=0}^K Y_i(k)(t-t_0)^{k\alpha_i}, \quad t \in [t_0, T], \tag{4.3}$$

where $Y_i(k)$ satisfies the recurrence relation

$$\frac{\Gamma((k+1)\alpha_i + 1)}{\Gamma(k\alpha_i + 1)} Y_i(k+1) = F_i(k, Y_1, Y_2, \dots, Y_n), \tag{4.4}$$

$Y_i(0) = c_i$ and $F_i(k, Y_1, Y_2, \dots, Y_n)$ are the differential transforms of functions $f_i(t, y_1, y_2, \dots, y_n)$ for $i = 1, 2, \dots, n$. The basics steps of the GDTM can be found in (Chongxin and Junjie, 2010), (Momani and Odibat, 2008), (Odibat et al. 2008).

Assume that the interval $[t_0, T]$ is divided into M subintervals $[t_{m-1}, t_m]$, $m = 1, 2, \dots, M$ of equal step size $h = (T - t_0) / M$ by using the nodes $t_m = t_0 + mh$. The main ideas of the MSGDTM are as follows:

Firstly, we apply the GDTM to the initial value problem (4.1)-(4.2) over the interval $[t_0, t_1]$, we will obtain the approximate solution $y_{i,1}(t)$, $t \in [t_0, t_1]$, using the initial condition $y_i(t_0) = c_i$, for $i = 1, 2, \dots, n$. For $m \geq 2$ and at each subinterval $[t_{m-1}, t_m]$, we will use the initial condition $y_{i,m}(t_{m-1}) = y_{i,m-1}(t_{m-1})$ and apply the GDTM to the initial value problem (4.1)-(4.2) over the interval $[t_{m-1}, t_m]$. The process is repeated and generates a sequence of approximate solutions $y_{i,m}(t)$, $m = 1, 2, \dots, M$, for $i = 1, 2, \dots, n$. Finally, the MSGDTM assumes the following solution

$$y_i(t) = \begin{cases} y_{i,1}(t), & t \in [t_0, t_1], \\ y_{i,2}(t), & t \in [t_1, t_2], \\ \vdots \\ y_{i,M}(t), & t \in [t_{M-1}, t_M]. \end{cases} \quad (4.5)$$

The new algorithm, MSGDTM, is simple for computational performance for all values of h . As we will see in the next section, the main advantage of the new algorithm is that the obtained solution converges for wide time regions.

5. Solving the fractional-order modified epidemiological model for computer viruses using the MSGDTM

In order to demonstrate the performance and efficiency of the multi-step generalized differential transform method for solving linear and nonlinear fractional-order equations, we have applied the method to the fractional-order modified epidemiological model for computer viruses.

Consider a fractional-order SAIR model of epidemics system (Piqueira and Araujo, 2009). In this system, the integer-order derivatives are replaced by the fractional-order derivatives, as follows:

$$D^{q_1} S(t) = -\alpha_{SA} SA - \beta SI + \sigma R, \quad (5.1)$$

$$D^{q_2} I(t) = \beta SI - \alpha_{IA} AI - \delta I, \quad (5.2)$$

$$D^{q_3} R(t) = \delta I - \sigma R, \quad (5.3)$$

$$D^{q_4} A(t) = -\alpha_{SA} SA + \alpha_{IA} AI, \quad (5.4)$$

where (S, I, R, A) are the state variables, $\alpha_{SA}, \beta, \sigma, \delta$ and α_{IA} are constants, $q_i, i=1,2,3,4$, are parameters describing the order of the fractional time-derivatives in the Caputo sense.

Applying the MSGDTM Algorithm to Equations (5.1)-(5.4) gives

$$S(k+1) = \frac{\Gamma(q_1 k + 1)}{\Gamma(q_1(k+1) + 1)} \begin{pmatrix} -\alpha_{SA} \left(\sum_{l=0}^k S(l) A(k-l) \right) \\ -\beta \left(\sum_{l=0}^k S(l) I(k-l) \right) + \sigma R(k) \end{pmatrix},$$

$$I(k+1) = \frac{\Gamma(q_2 k + 1)}{\Gamma(q_2(k+1) + 1)} \begin{pmatrix} \beta \left(\sum_{l=0}^k S(l) I(k-l) \right) \\ -\alpha_{IA} \left(\sum_{l=0}^k A(l) I(k-l) \right) - \delta I(k) \end{pmatrix},$$

$$R(k+1) = \frac{\Gamma(q_3 k + 1)}{\Gamma(q_3(k+1) + 1)} (\delta I(\kappa) - \sigma R(k)), \quad (5.5)$$

$$A(k+1) = \frac{\Gamma(q_4 k + 1)}{\Gamma(q_4(k+1) + 1)} \left(-\alpha_{SA} \left(\sum_{l=0}^k S(l)A(k-l) \right) - \alpha_{IA} \left(\sum_{l=0}^k A(l)I(k-l) \right) \right),$$

where $S(k), I(k), R(k)$ and $A(k)$ are the differential transforms of $S(t), I(t), R(t)$ and $A(t)$ respectively. The differential transform of the initial conditions are given by

$$S(0) = c_1, I(0) = c_2, R(0) = c_3 \text{ and } A(0) = c_4.$$

In view of the differential inverse transform, the differential transform series solution for the system (5.1)-(5.4) can be obtained as

$$\left\{ \begin{array}{l} s(t) = \sum_{n=0}^N S(n)t^{q_1 n}, \\ i(t) = \sum_{n=0}^N I(n)t^{q_2 n}, \\ r(t) = \sum_{n=0}^N R(n)t^{q_3 n}, \\ a(t) = \sum_{n=0}^N A(n)t^{q_4 n}. \end{array} \right. \quad (5.6)$$

According to the multi-step generalized differential transform method, the series solution for the system (5.1)-(5.4) is

$$s(t) = \left\{ \begin{array}{ll} \sum_{n=0}^K S_1(n)t^{q_1 n}, & t \in [0, t_1], \\ \sum_{n=0}^K S_2(n)(t-t_1)^{q_1 n}, & t \in [t_1, t_2], \\ \vdots & \\ \sum_{n=0}^K S_M(n)(t-t_{M-1})^{q_1 n}, & t \in [t_{M-1}, t_M]. \end{array} \right. \quad (5.7)$$

$$i(t) = \begin{cases} \sum_{n=0}^K I_1(n)t^{q_2^n}, & t \in [0, t_1], \\ \sum_{n=0}^K I_2(n)(t-t_1)^{q_2^n}, & t \in [t_1, t_2], \\ \vdots \\ \sum_{n=0}^K I_M(n)(t-t_{M-1})^{q_2^n}, & t \in [t_{M-1}, t_M]. \end{cases} \quad (5.8)$$

$$r(t) = \begin{cases} \sum_{n=0}^K R_1(n)t^{q_3^n}, & t \in [0, t_1], \\ \sum_{n=0}^K R_2(n)(t-t_1)^{q_3^n}, & t \in [t_1, t_2], \\ \vdots \\ \sum_{n=0}^K R_M(n)(t-t_{M-1})^{q_3^n}, & t \in [t_{M-1}, t_M]. \end{cases} \quad (5.9)$$

$$a(t) = \begin{cases} \sum_{n=0}^K A_1(n)t^{q_4^n}, & t \in [0, t_1], \\ \sum_{n=0}^K A_2(n)(t-t_1)^{q_4^n}, & t \in [t_1, t_2], \\ \vdots \\ \sum_{n=0}^K A_M(n)(t-t_{M-1})^{q_4^n}, & t \in [t_{M-1}, t_M], \end{cases} \quad (5.10)$$

where $S_i(n)$, $I_i(n)$, $R_i(n)$ and $A_i(n)$ for $i = 1, 2, \dots, M$ satisfy the following recurrence relations

$$S_i(k+1) = \frac{\Gamma(q_1 k + 1)}{\Gamma(q_1(k+1) + 1)} \begin{pmatrix} -\alpha_{SA} \left(\sum_{l=0}^k S_i(l) A_i(k-l) \right) \\ -\beta \left(\sum_{l=0}^k S_i(l) I_i(k-l) \right) + \sigma R_i(k) \end{pmatrix},$$

$$I_i(k+1) = \frac{\Gamma(q_2 k + 1)}{\Gamma(q_2(k+1) + 1)} \begin{pmatrix} \beta \left(\sum_{l=0}^k S_i(l) I_i(k-l) \right) \\ -\alpha_{IA} \left(\sum_{l=0}^k A_i(l) I_i(k-l) \right) - \delta I_i(k) \end{pmatrix},$$

$$R_i(k+1) = \frac{\Gamma(q_3 k+1)}{\Gamma(q_3(k+1)+1)} (\delta I_i(k) - \sigma R_i(k)), \quad (5.9)$$

$$A_i(k+1) = \frac{\Gamma(q_4 k+1)}{\Gamma(q_4(k+1)+1)} \left(-\alpha_{SA} \left(\sum_{l=0}^k S_i(l) A_i(k-l) \right) - \alpha_{IA} \left(\sum_{l=0}^k A_i(l) I_i(k-l) \right) \right),$$

Such that

$$S_i(0) = s_i(t_{i-1}) = s_{i-1}(t_{i-1}), \quad I_i(0) = i_i(t_{i-1}) = i_{i-1}(t_{i-1}),$$

$$R_i(0) = r_i(t_{i-1}) = r_{i-1}(t_{i-1}) \quad \text{and} \quad A_i(0) = a_i(t_{i-1}) = a_{i-1}(t_{i-1}).$$

Finally, we start with $S_0(0) = c_1, I_0(0) = c_2, R_0(0) = c_3$ and $A_0(0) = c_4$ and using the recurrence relation given in (5.11), then we can obtain the multi-step solution given in (5.7)-(5.10).

6. Non-negative solutions

Let $R_+^4 = (S(t), I(t), R(t), A(t))^T$. For the proof of the theorem about non-negative solutions we shall need the following Lemma

Lemma 6.1. Lin (2007). (Generalized Mean Value Theorem)

Let $f(x) \in C[a, b]$ and $D^\alpha f(x) \in C[a, b]$ for $0 < \alpha \leq 1$. Then we have,

$$f(x) = f(a) + \frac{1}{\Gamma(\alpha)} D^\alpha f(\zeta)(x-a)^\alpha,$$

with $0 \leq \zeta < x$, for all $x \in (a, b]$.

Remark 6.2. Zeb et al. (2013)

Suppose $f(x) \in C[a, b]$ and $D^\alpha f(x) \in C[a, b]$ for $0 < \alpha \leq 1$. It is clear from the above Lemma that if $D^\alpha f(x) \geq 0$, for all $x \in (0, b)$, then the function f is non-decreasing, and if $D^\alpha f(x) \leq 0$, for all $x \in (0, b)$, then the function f is non-increasing.

Theorem 6.3.

There is a unique solution for the initial value problem given by (5.1)-(5.4), and the solution remains in R_+^4 .

Proof:

The existence and uniqueness of the solution of (5.1)-(5.4), in $(0, \infty)$ can be obtained from ((Lin, 2007), Theorem 3.1 and Remark 3.2). We need to show that the domain R_+^4 is positively invariant. Since $D^{q_1} S|_{S=0} = \sigma R \geq 0$, $D^{q_2} I|_{I=0} = 0$, $D^{q_3} R|_{R=0} = \delta I \geq 0$ and $D^{q_4} A|_{A=0} = 0$. On each hyper-plane bounding the nonnegative orthant, the vector field points into R_+^4 .

7. Numerical results

We shall demonstrate the accuracy of the MSGDTM against Mathematica's built-in fourth-order Runge–Kutta (RK4) procedure for the solutions of modified epidemiological model for computer viruses in the case of integer order derivatives. The MSGDTM is coded in the computer algebra package Mathematica. The Mathematica environment variable digits controlling the number of significant digits are set to 20 in all the calculations done in this paper. The time range studied in this work is $[0, 25]$ and the step size $\Delta t = 0.025$ and the value of K is 10. We take the initial condition for epidemiological model for computer viruses such as $S(0) = 3$, $I(0) = 95$, $R(0) = 1$ and $A(0) = 1$. The parameters are: $\alpha_{SA} = 0.025$, $\alpha_{IA} = 0.25$, $\beta = 0.1$, $\delta = 9$, $\sigma = 0.8$.

Figure 1 shows the phase portrait for the classical SIRA models using the fourth-order Runge–Kutta method (RK4). Figure 2 shows the phase portrait for the classical SIRA models using multi-step generalized differential transform method. From the graphical results in Figure 1 and Figure 2 it can be seen the results obtained using the multi-step generalized differential transform method match the results of the RK4 very well, which implies that the multi-step generalized differential transform method can predict the behavior of these variables accurately for the region under consideration. Figure 3, Figure 4 and Figure 5 show the phase portrait for the fractional SIRA models of epidemics system using the multi-step generalized differential transform method. From the numerical results in Figure 3, Figure 4 and Figure 5, it is clear that the approximate solutions depend continuously on the time-fractional derivative $q_i, i = 1, 2, 3, 4$.

The effective dimension Σ of Equations (5.1)–(5.4) is defined as the sum of orders $q_1 + q_2 + q_3 + q_4 = \Sigma$. Also in Figure 5 we can see that the numerical results exist in the fractional-order SIRA model of modified epidemiological system with order as low as 2.63. From the graphical results in Figure 6, it can be seen that the results obtained using the MSGDTM match the results of the RK4 very well, and it shows non-infected computers, infected computers and removed ones due to infection or not vanish, while the noninfected computers equipped with anti-virus, in the long term, is in a good operational state.

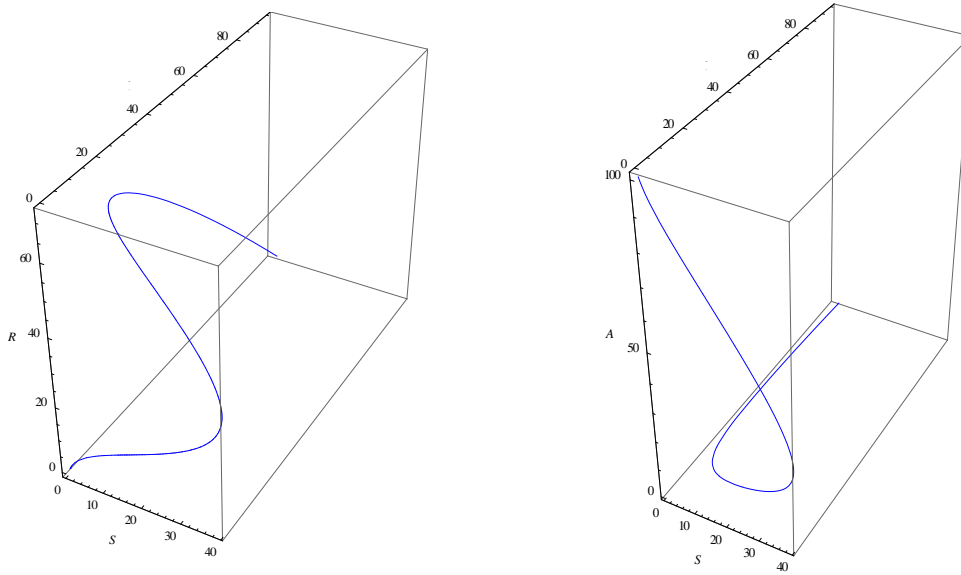


Figure 1. Phase plot in the (S, I, R) and (S, I, A) , with $q_1 = q_2 = q_3 = q_4 = 1$. (Using RK4)

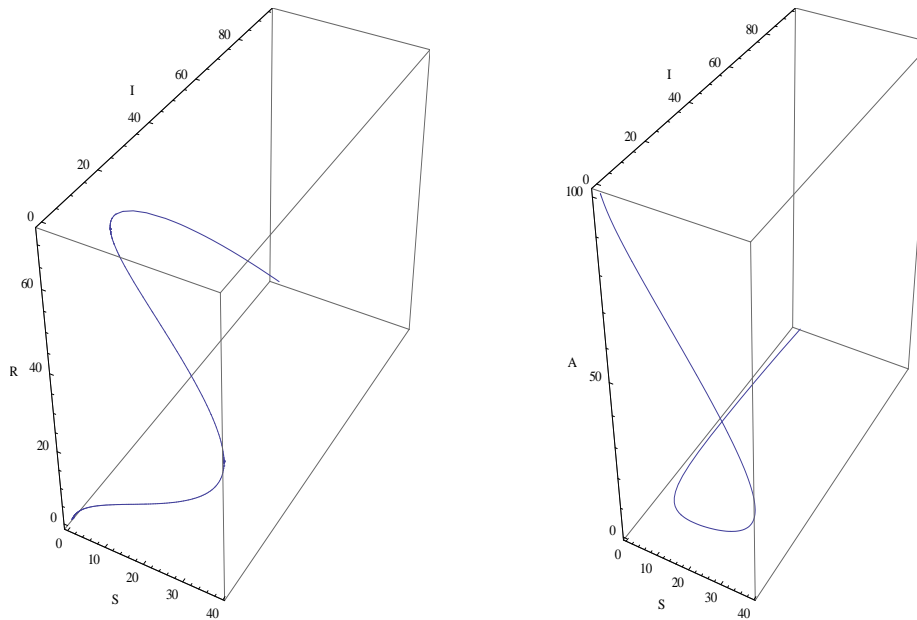


Figure 2. Phase plot in the (S, I, R) and (S, I, A) , with $q_1 = q_2 = q_3 = q_4 = 1$. (Using MSGDTM)

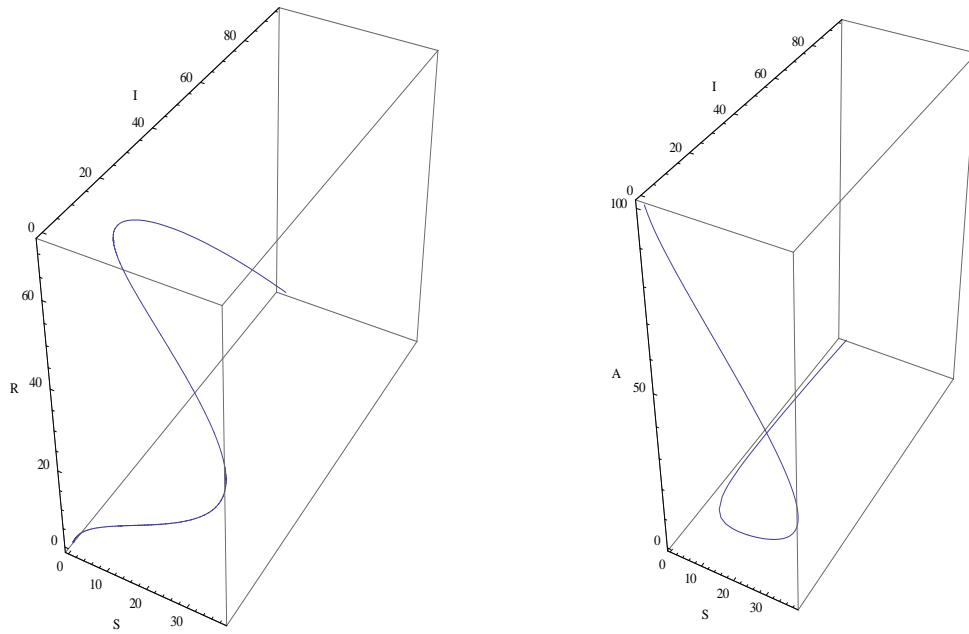


Figure 3. Phase plot in the (S, I, R) and (S, I, A) , with $q_1 = q_2 = q_3 = q_4 = 0.85$.

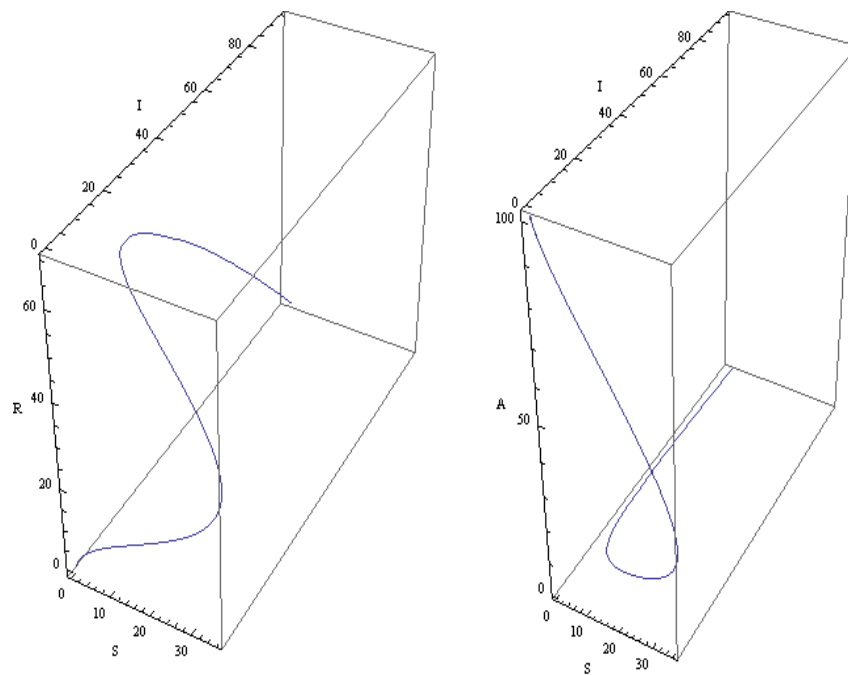


Figure 4. Phase plot in the (S, I, R) and (S, I, A) , with $q_1 = q_2 = q_3 = q_4 = 0.7$.

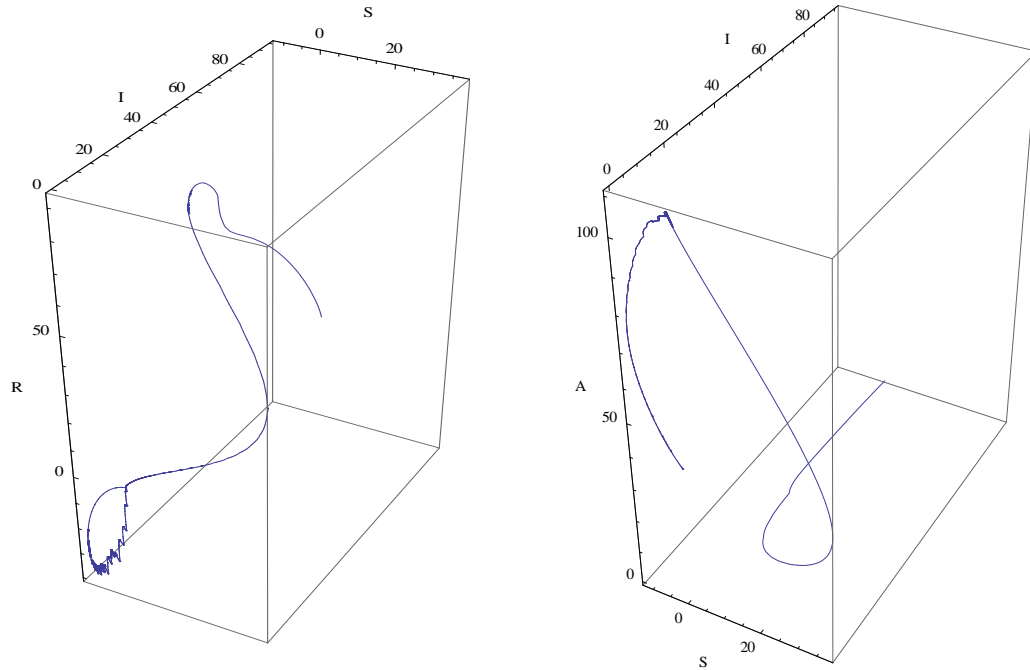


Figure 5. Phase plot in the (S, I, R) and (S, I, A) , with $q_1 = 0.67$, $q_2 = 0.7$, $q_3 = 0.6$ and $q_4 = 0.66$.

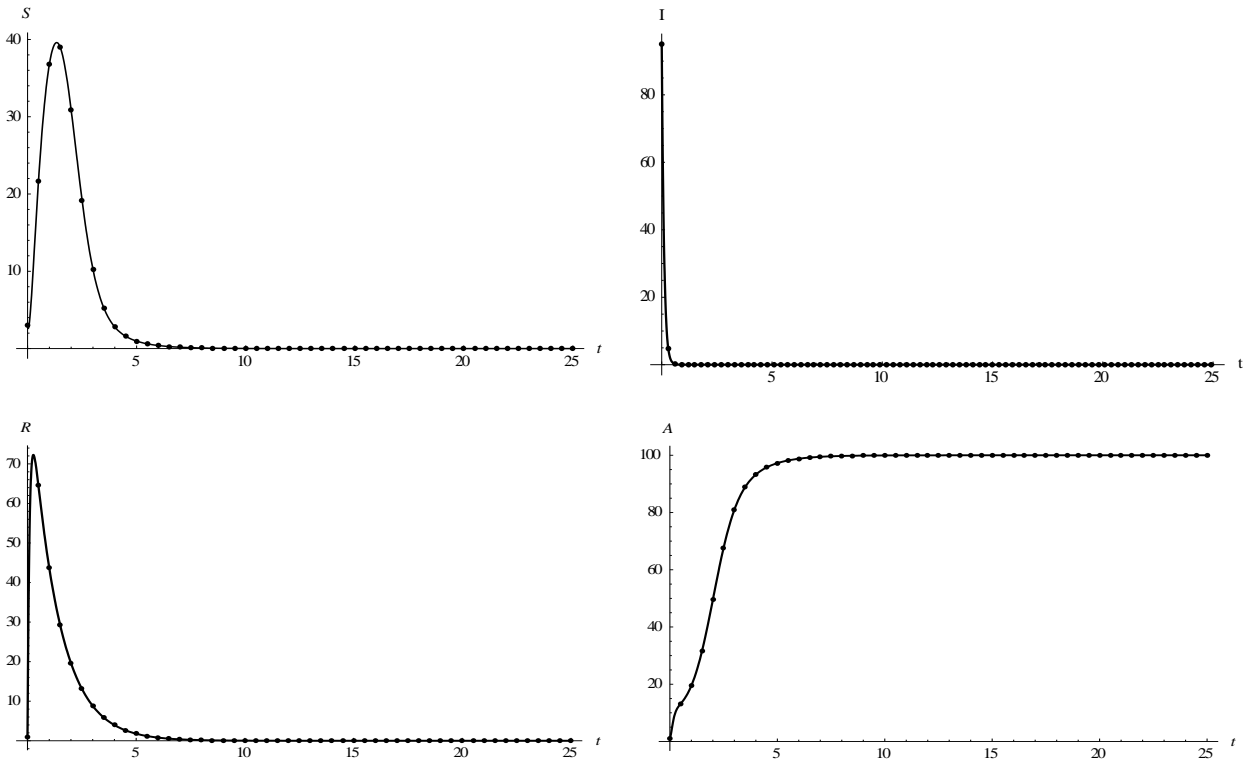


Figure 6. The displacement for modified epidemiological model for computer viruses when $\alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = 1$: solid line: RK4 method solution, dotted line: MSGDTM solution

8. Conclusions

The analytical approximations to the solutions of the epidemiological models are reliable and confirm the power and ability of the MSGDTM as an easy device for computing the solution of nonlinear problems, This method has the advantage of giving an analytical form of the solution within each time interval which is not possible using purely numerical techniques like the fourth-order Runge–Kutta method (RK4). We conclude that MSGDTM is a very reliable method in solving a broad array of dynamical problems in fractional calculus due to its consistency used in a longer time frame.

In this paper, a fractional order differential SIRA model is studied and its approximate solution is presented using a MSGDTM. The approximate solutions obtained by MSGDTM are highly accurate and valid for a long time. The reliability of the method and the reduction in the size of computational domain give this method a wider applicability. Finally, the recent appearance of nonlinear fractional differential equations as models in some fields such as models in science and engineering makes it is necessary to investigate the method of solutions for such equations. and we hope that this work is a step in this direction.

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