

Reduced Differential Transform Method for Solving Nonlinear Biomathematics Models

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Abstract: In this paper, we study the approximate solutions for some of nonlinear Biomathematics models via the e-epidemic SI₁I₂R model characterizing the spread of viruses in a computer network and SIR childhood disease model. The reduced differential transforms method (RDTM) is one of the interesting methods for finding the approximate solutions for nonlinear problems. We apply the RDTM to discuss the analytic approximate solutions to the SI₁I₂R model for the spread of virus HCV-subtype and SIR childhood disease model. We discuss the numerical results at some special values of parameters in the approximate solutions. We use the computer software package such as Mathematical to find more iteration when calculating the approximate solutions. Graphical results and discussed quantitatively are presented to illustrate behavior of the obtained approximate solutions.

Keywords: Reduced differential transforms method, nonlinear biomathematics models, SI₁I₂R model, SIR model, analytic approximate solutions, qualitative analysis, stability and equilibrium.

1 Introduction

Many applications of science and engineering the nonlinear equations appear such as fluid dynamics, plasma physics, hydrodynamics, solid-state physics, optical fibers, acoustics and other disciplines [Adomian (1994)]. The analytic and approximate solutions many effective methods for obtaining to the NPDEs among of these methods are discussed in Ablowitz et al. [Ablowitz and Clarkson (1991); Singh, Dhar, Bhatti et al. (2016)]. In the present article, we use the reduced differential transform method (RDTM) which discussed in Keskin et al. [Keskin and Oturanc (2010); Keskin (2010)]; [Amer, Mahdy and Youssef (2018)], to construct an approximate numerical solution of some highly nonlinear differential equations in biomathematics. Reduced differential transform technique is iterative procedure a Taylor series solution of differential equations. This method reduces the size of work computational and easily applicable to many nonlinear physical problems. The results show that RDTM is a powerful mathematical tool for handling nonlinear ODEs.

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The solution approach of RDTM is observed simpler than other approximate methods. Also, is highly accurate, rapidly converge and easily implementable mathematical tool for the multidimensional biomathematics models, physical problems emerging in various domains of engineering and applied sciences. Effectively, the analytic approximate solutions are discussed for two nonlinear systems of biomathematics models such as SI1I2R model for the spread of virus HCV-subtype4a and SIR childhood disease mode. These systems can be seen in El-Shahed et al. [El-Shahed, Ahmed and Abdelstar (2016); Haq, Shahzad, Muhammad et al. (2017)]. In biomathematics models, they play a major role in various fields, such as Childhood diseases are the most serious infectious diseases. Measles, poliomyelitis, and rubella are famous among them.

1.1 SI1I2R model

Model SI1I2R for the spread of virus HCV-subtype4 can be written as follows [El-Shahed, Ahmed and Abdelstar (2016)]:

$$\begin{aligned}\frac{dS}{dt} &= -(k_1 I_1 + k_2 I_2)S - bS + A, \\ \frac{dI_1}{dt} &= k_1 S I_1 - b I_1 + \mu I_2 - \gamma I_1, \\ \frac{dI_2}{dt} &= k_2 S I_2 - b I_2 - \mu I_2 - \delta I_2, \\ \frac{dR}{dt} &= \gamma I_1 + \delta I_2 - b R,\end{aligned}\tag{1}$$

where R denotes densities of individuals recovered. Rate of birth is equal a rate positive constant (c), (b), γ , δ rate the susceptible individuals a removed after taking the medicine from I1, I2, respectively.

1.2 SIR model

The mathematical model plays an important comprehend the process of transmission disease and provides different techniques to control propagation. Many mathematicians investigated childhood disease; for instance, Henderson et al. [Henderson (1984); Singh, Dhar, Bhatti et al. (2016)] studied the diseases vaccination of childhood. Makinde [Makinde (2007)] presented the Susceptible-Infected-Recovered.

$$\begin{aligned}\frac{dS}{dt} &= (1-p)\pi + \beta SI - \pi S \\ \frac{dI}{dt} &= \beta SI - (\gamma + \pi)I, \\ \frac{dR}{dt} &= \rho\pi + \gamma I - \pi R.\end{aligned}\tag{2}$$

This model shows vaccination is 100 percent efficient and rate the natural death μ is unequal. So, size the total population N is not constant. Rate birth is π while the rate of mortality of

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the childhood disease is very low. The parameter, P is vaccinated population at birth, where $0 < \rho < 1$, rest of population is susceptible. The rate of susceptible individual suffers from through contact with infected individuals is β . Rate the infected individuals recover is γ . More many applications of models fractional [El-Shahed, Ahmed and Abdelstar (2016); Haq, Shahzad, Muhammad et al. (2017)]. Researchers and mathematicians used fractional models problems [El-Shahed, Ahmed and Abdelstar (2016); Henderson (1984)].

This paper are organized as follows. Preliminaries and notations of RDTM are given in Section 2. In Section 3, we apply the RDTM to solve two models of nonlinear biomathematics models (SIIIR model for the spread of virus HCV-subtype4a and SIR childhood disease mode). In Section 4, we have shown the qualitative analysis for the model SIR. Conclusions are given in Section 5.

2 Preliminaries and notations

The basic idea, basic definitions and property properties of the RDTM are discussed in many new articles such as Mohamed et al. [Mohamed, Sayed and Al-Qarshi (2016); Keskin and Oturanc (2009); Keskin (2010)]. We summarized the RDTM in the following Tab. 1.

Table 1: The fundamental operations of RDTM

Functional Form	Transformed Form
$z(x, t)$	$\frac{1}{k!} \left[\frac{\partial^k}{\partial t^k} z(x, y, t) \right]_{t=0},$
$w(x, t) = z(x, t) \pm v(x, t)$	$W_k(x) = Z_k(x) \pm V_k(x),$
$w(x, t) = \alpha z(x, t)$	$W_k(x) = \alpha Z_k(x, t) (\alpha \text{ is a constant}),$
$w(x, t) = x^m t^n$	$W_k(x) = x^m \delta(k - n), \delta(k - m) = \begin{cases} 1 & k = n \\ 0 & k \neq n \end{cases}$
$w(x, t) = x^m t^n z(x, t)$	$W_k(x) = x^m Z(k - n)$
$w(x, t) = z(x, t)v(x, t)$	$W_k(x) = \sum_{r=0}^k Z_r(x) V_{k-r}(x) = \sum_{r=0}^k V_r(x) Z_{k-r}(x)$
$w(x, t) = \frac{\partial^r}{\partial t^r} z(x, t)$	$W_k(x) = (k + 1) \dots (k + r) Z_{k+r}(x) = \frac{(k + r)!}{k!} Z_{k+r}(x)$
$w(x, t) = \frac{\partial}{\partial x} z(x, t)$	$W_k(x) = \frac{\partial}{\partial x} Z_k(x)$
$w(x, t) = \frac{\partial^2}{\partial x^2} z(x, t)$	$W_k(x) = \frac{\partial^2}{\partial x^2} Z_k(x).$

3 Numerical results

In this section, we used RDTM to construct analytic approximate solutions two systems of nonlinear biomathematics models (SI1I2R) model for the spread of virus HCV-subtype4a and SIR childhood disease mode. The results have been provided by software packages such as Mathematica 9.

3.1 Example 1

Let us consider SI1I2R model for the spread of virus HCV-subtype4a on homogenous networks is given by El-Shahed et al. [El-Shahed, Ahmed and Abdelstar (2016)]:

$$\begin{aligned}\frac{ds}{dt} &= -(k_1 I_1 + k_2 I_2)S - bS + A \\ \frac{dI_1}{dt} &= k_1 S I_1 - b I_1 + \mu I_2 - \gamma I_1 \\ \frac{dI_2}{dt} &= k_2 S I_2 - b I_2 - \mu I_2 - \delta I_2, \\ \frac{dR}{dt} &= \gamma I_1 + \delta I_2 - b R,\end{aligned}\tag{3}$$

where $b = 0.02$, $c = 0.04$, $N = 1000000$, $\mu = 0.02$, $\gamma = 0.001$, $\delta = 0.001$
 $k_1 = 0.42 \times 10^{-6}$, $k_2 = 0.164 \times 10^{-5}$.

Subject to the initial conditions:

$$S(0) = \frac{A}{b}, I_1(0) = 10, I_2(0) = 20, R(0) = 10\tag{4}$$

From RDTM, we have following iteration relations:

$$\begin{aligned}(k+1)S_{k+1}(t) &= -k_1 \sum_{r=0}^k I_{1r}(t) S_{(k-r)}(t) - k_2 \sum_{r=0}^k I_{2r}(t) S_{(k-r)}(t) - bS_k + A\delta(k) \\ (k+1)I_{1k+1}(t) &= k_1 \sum_{r=0}^k S_r(t) I_{1(k-r)}(t) - bI_{1k}(t) + \mu I_{2k}(t) - \gamma I_{1k}(t) \\ (k+1)I_{2k+1}(t) &= k_2 \sum_{r=0}^k S_r(t) I_{2(k-r)}(t) - bI_{2k}(t) - \mu I_{2k}(t) - \delta I_{2k}(t) \\ (k+1)R_{k+1}(t) &= \gamma I_{1k}(t) + \delta I_{2k}(t) - bR_k(t)\end{aligned}\tag{5}$$

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$$\begin{aligned}
 S_{k+1}(t) &= \frac{1}{(k+1)} \left[-k_1 \sum_{r=0}^k I_{1r}(t) S_{(k-r)}(t) - k_2 \sum_{r=0}^k I_{2r}(t) S_{(k-r)}(t) - bS_k + A\delta(k) \right] \\
 I_{1k+1}(t) &= \frac{1}{(k+1)} \left[k_1 \sum_{r=0}^k S_r(t) I_{1(k-r)}(t) - bI_{1k}(t) + \mu I_{2k}(t) - \gamma I_{1k}(t) \right] \\
 I_{2k+1}(t) &= \frac{1}{(k+1)} \left[k_2 \sum_{r=0}^k S_r(t) I_{2(k-r)}(t) - bI_{2k}(t) - \mu I_{2k}(t) - \delta I_{2k}(t) \right] \\
 R_{k+1}(t) &= \frac{1}{(k+1)} [\gamma I_{1k}(t) + \delta I_{2k}(t) - bR_k(t)]
 \end{aligned} \tag{6}$$

Eqs. (4) and (6) lead to get the results as the following table:

$$S_1 = 1.99999 \times 10^6, \quad I_{11} = 10.9025, \quad I_{21} = 27.6404, \quad R_1 = 9.98342$$

$$S_2 = 1.99998 \times 10^6, \quad I_{12} = 11.8993, \quad I_{22} = 38.0585, \quad R_2 = 9.96782$$

and so on.

By using the software Mathematica, we obtained the component of $S(t), I_1(t), I_2(t)$ and $R(t)$ to the tenth iteration and we write two only for convenience.

Finally, the differential inverse transforms are given by:

$$S(t) = \sum_{n=0}^N S_n t^n, \quad I_1(t) = \sum_{n=0}^N I_{1n} t^n, \quad I_2(t) = \sum_{n=0}^N I_{2n} t^n, \quad R(t) = \sum_{n=0}^N R_n t^n,$$

Consequently, the approximate series solutions take the form

$$S(t) = 2 \times 10^6 - 74t - 109.11t^2 + \dots$$

$$I_1(t) = 10 + 8.59t + 4.165t^2 + \dots$$

$$I_2(t) = 20 + 64.78t + 104.91t^2 + \dots$$

$$R(t) = 10 - 0.17t + 0.0384t^2 + \dots$$

(7)

Table 2: Numerical solution of the proposed model using RDTM

t	$S(t)$	$I_1(t)$	$I_2(t)$	$R(t)$
0.0	2 e+6	10	20	10.
0.1	1.9999 e+6	10.9025	27.6404	9.98342
0.2	1.99998 e+6	11.8993	38.0585	9.96782
0.3	1.99996 e+6	13.0015	51.934	9.95343
0.4	1.99995 e+6	14.22	69.9465	9.94045
0.5	1.99992 e+6	15.5658	92.7755	9.92911
0.6	1.99989 e+6	17.0501	121.101	9.91962
0.7	1.99986 e+6	18.6838	155.601	9.91219
0.8	1.99981 e+6	20.4779	196.958	9.90705
0.9	1.99976 e+6	22.4435	245.849	9.90441
1.0	1.9997 e+6	24.5915	302.954	9.90449

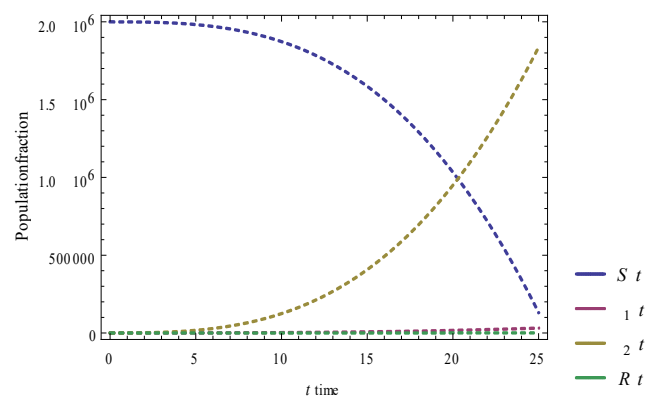


Figure 1: Numerical simulations for the (S I₁ I₂ R) model at various for the social and infection

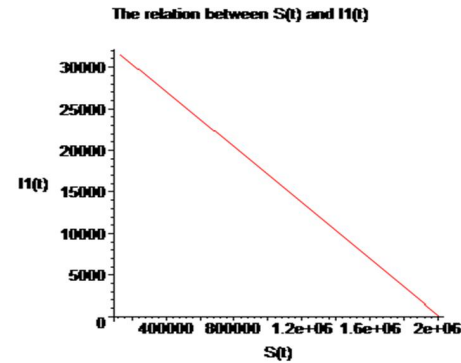


Figure 2: The relation between $S(t)$ and $I_1(t)$

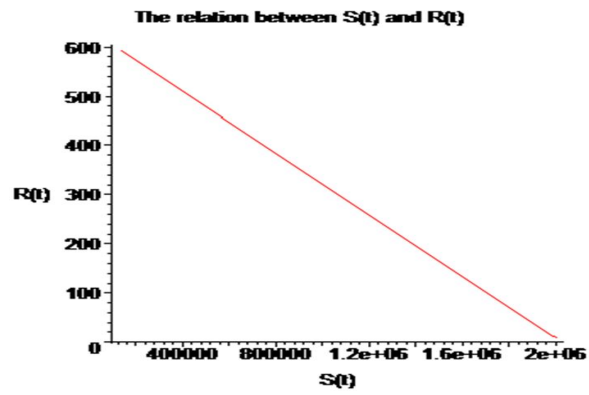


Figure 3: The relation between $S(t)$ and $R(t)$

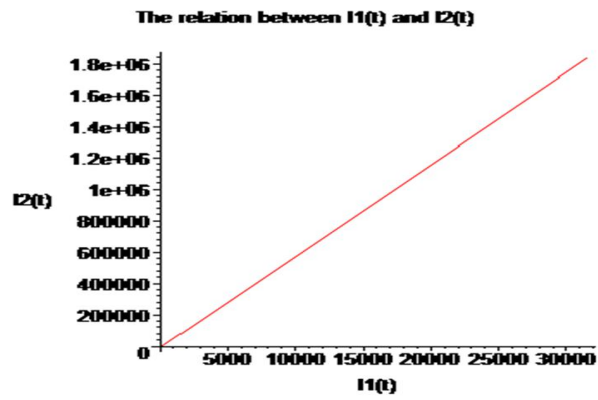


Figure 4: The relation between $I_1(t)$ and $I_2(t)$

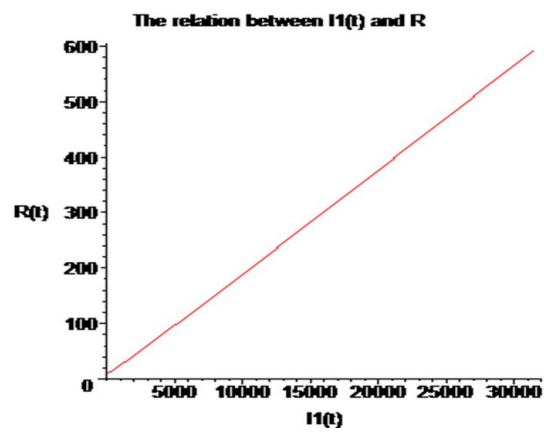


Figure 5: The relation between $I_1(t)$ and $R(t)$

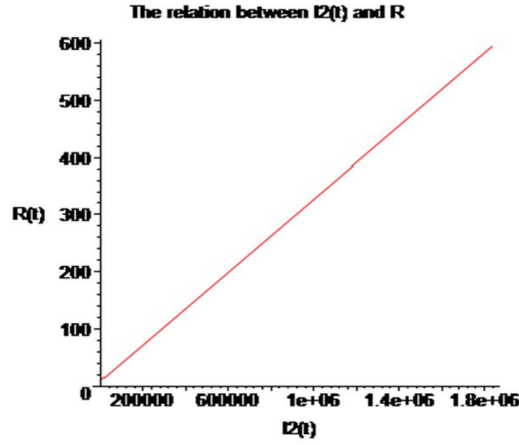


Figure 6: The relation between $I_2(t)$ and $R(t)$

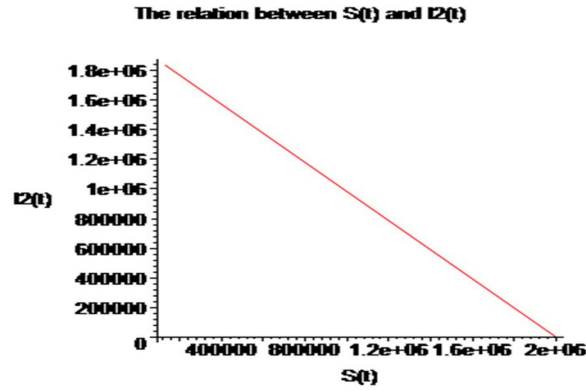


Figure 7: The relation between $S(t)$ and $I_2(t)$

This approach of efficiency is greatly enhanced by calculation further terms of $S(t), I_1(t), I_2(t)$ and $R(t)$ by using RDTM. Figs. (1)-(7) show the approximate solution of SIIIR model. From Figs. 2 to 7, showing the relation between $S(t)$ and $I_1(t)$; $I_1(t)$ and $I_2(t)$; $I_1(t)$ and $R(t)$; $I_2(t)$ and $R(t)$; $I_2(t)$ and $S(t)$. From the above Fig. 2, we $S(t)$ is decreasing with increasing the $I_1(t)$. Also, from Fig. 3, we get $S(t)$ is decreasing with increasing the $R(t)$. From Fig. 4, we $I_1(t)$ is increasing the $I_2(t)$. Fig. 5, leads to get $I_1(t)$ is increasing the $R(t)$. In Fig. 6, $I_2(t)$ is increasing $R(t)$. In Fig. 7, $S(t)$ is increasing the $I_2(t)$.

3.2 Example 2

Let us consider SIR model [Makinde (2007)]:

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$$\begin{aligned}\frac{dS}{dt} &= (1-p)\pi - \beta SI - \pi S \\ \frac{dI}{dt} &= \beta SI - (\gamma + \pi)I, \\ \frac{dR}{dt} &= \rho\pi + \gamma I - \pi R.\end{aligned}\tag{8}$$

where $p = 0.9$, $\mu = 0.4$, $\gamma = 0.03$, $\beta = 0.8$,

with initial conditions:

$$S(0) = 0.8, I(0) = 0.2, R(0) = 0\tag{9}$$

First by applying RDTM on both sides of Eq. (8), thus we get :

$$\begin{aligned}(k+1)S_{k+1}(t) &= (1-p)\pi\delta(k) - \beta \sum_{r=0}^k S_r(t) I_{(k-r)}(t) - \pi S_k(t) \\ (k+1)I_{k+1}(t) &= \beta \sum_{r=0}^k S_r(t) I_{(k-r)}(t) - (\gamma + \pi)I_k(t) \\ (k+1)R_{k+1}(t) &= p\pi\delta(k) + \gamma I_k(t) - \pi R_k(t)\end{aligned}\tag{10}$$

$$\begin{aligned}S_{k+1}(t) &= \frac{1}{(k+1)} \left[(1-p)\pi\delta(k) - \beta \sum_{r=0}^k S_r(t) I_{(k-r)}(t) - \pi S_k(t) \right] \\ I_{k+1}(t) &= \frac{1}{(k+1)} \left[\beta \sum_{r=0}^k S_r(t) I_{(k-r)}(t) - (\gamma + \pi)I_k(t) \right] \\ R_{k+1}(t) &= \frac{1}{(k+1)} \left[p\pi\delta(k) + \gamma I_k(t) - \pi R_k(t) \right]\end{aligned}\tag{11}$$

By substituting Eq. (9) in Eq. (11) we have :

$$S_1 = -0.408, I_1 = 0.042, R_1 = 0.366, S_2 = 0.1008, I_2 = -0.02823, R_2 = -0.073$$

and so on.

The components can obtain by Mathematica software. Taking transformation inverse to get following results.

$$S(t) = \sum_{n=0}^N S_n t^n, \quad I(t) = \sum_{n=0}^N I_n t^n, \quad R(t) = \sum_{n=0}^N R_n t^n,$$

Consequently,

$$\begin{aligned}S(t) &= 0.8 - 0.408t + 0.1008t^2 + \dots \\ I(t) &= 0.2 + 0.042t - 0.02823t^2 + \dots \\ R(t) &= 0.366t + 0.073t^2 + \dots\end{aligned}\tag{12}$$

Table 3: Coverage the various parameter values of effect of vaccination ($p_c = 0.4625$)

Case	S_0	I_0	R_0	β	ν	Π	P	R_v	Comments
1	0.8	0.2	0	0.8	0.03	0.4	0.9	0.18604	
2	0.8	0.2	0	0.8	0.03	0.4	0.3	1.30232	

Table 4: Numerical solution of the proposed model using RDTM

(a): Case 1				(b) case 2			
t	$S(t)$	$I(t)$	$R(t)$	t	$S(t)$	$I(t)$	$R(t)$
0.0	0.800	0.2000	0.0000	0.0	0.8000	0.2000	0.0000
0.1	0.760	0.2039	0.0359	0.1	0.7835	0.2041	0.0124
0.2	0.722	0.2073	0.0704	0.2	0.7677	0.2080	0.0242
0.3	0.686	0.2100	0.1035	0.3	0.7526	0.2118	0.0357
0.4	0.652	0.2123	0.1354	0.4	0.7380	0.2153	0.0467
0.5	0.620	0.2140	0.1660	0.5	0.7241	0.2187	0.0572
0.6	0.589	0.2151	0.1954	0.6	0.7107	0.2218	0.0674
0.7	0.561	0.2158	0.2237	0.7	0.6980	0.2248	0.0771
0.8	0.533	0.2160	0.2508	0.8	0.6858	0.2276	0.0867
0.9	0.507	0.2160	0.2769	0.9	0.6741	0.2302	0.0957
1.0	0.483	0.2150	0.3020	1.0	0.6630	0.2327	0.1043

4 Analysis qualitative of SIR

Observed, R is not appear in first and second Eq. (8), we analyze model qualitatively by studying subsystem in closed set $\Gamma = \{(S, I) \in R_+ | 0 \leq S + I \leq 1\}$. The subsystem described analysis qualitatively of the long-term behavior falls into two categories: die out or endemic. The solution asymptotically approaches a disease free equilibrium (DFE) at the disease dies out naturally E_0 of the form $E_0 = (1 - p, 0)$. The stability of this equilibrium is reproduction number $R_v = \frac{\beta(1-p)}{\gamma + \pi}$.

The DF is locally stable if $R_v < 1$. Global asymptotic stability for DFE is also achieved using a Bendixson-Dulac argument for $R_v < 1$ i.e., there are no periodic solutions [Brauer and Castillo-Chavez (2001); Makinde (2007)]. For many details of eigenvalues in Makinde [Makinde (2007)].

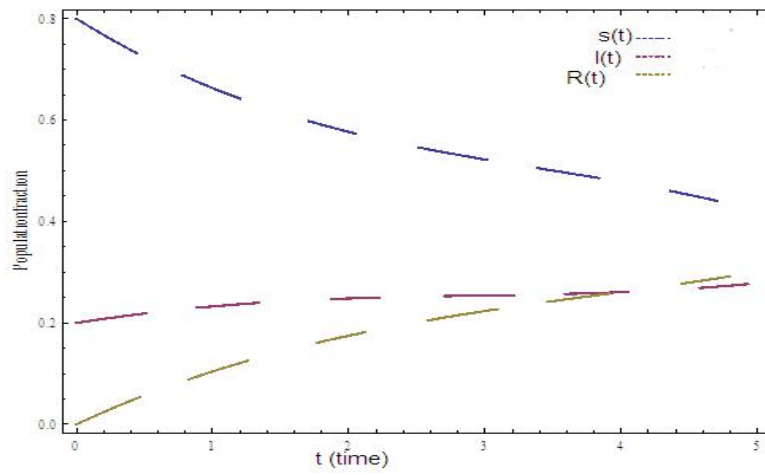


Figure 8: Population fraction versus time for Case1 at $p = 0.9$

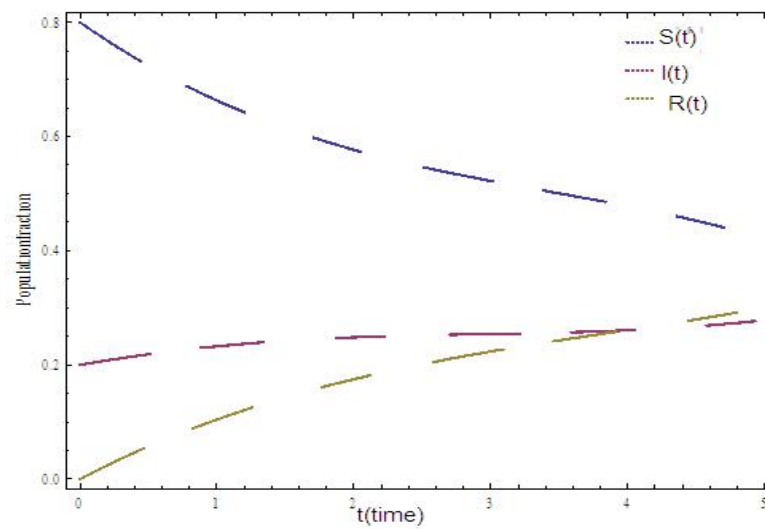


Figure 9: Population fraction versus time for Case2 at $p = 0.3$

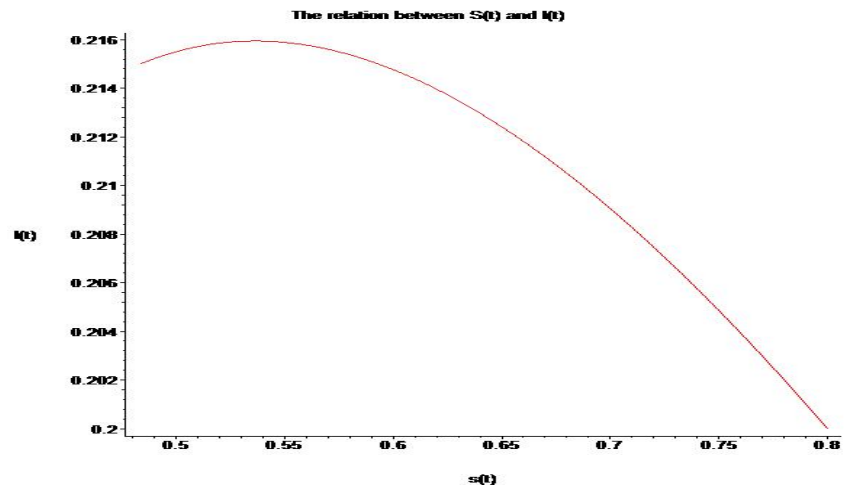


Figure 10: The relation between $S(t)$ and $I(t)$

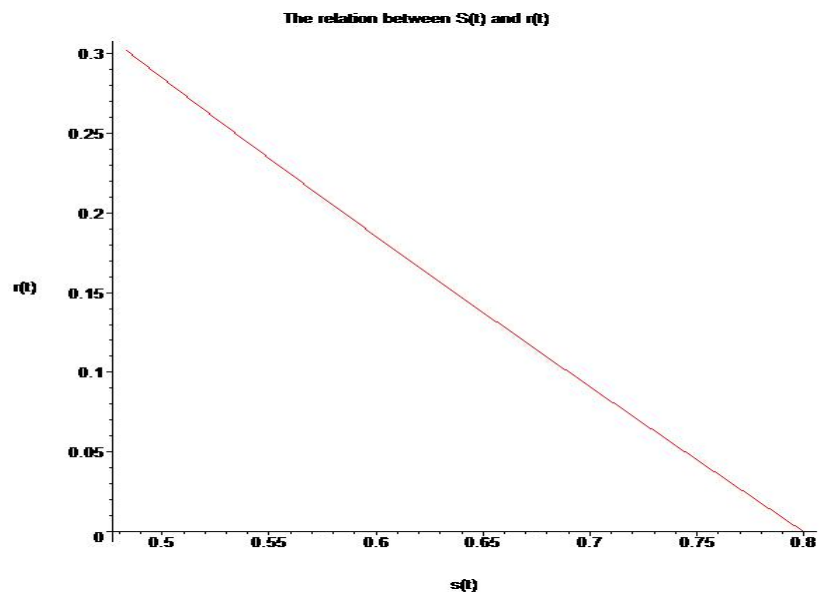


Figure 11: The relation between $S(t)$ and $R(t)$

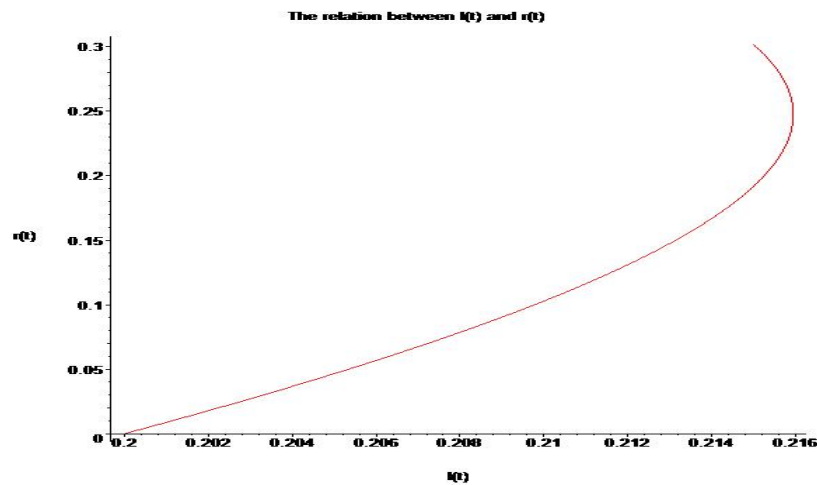


Figure 12: The relation between $I(t)$ and $R(t)$

This approach of efficiency is greatly enhanced by calculation further terms of $S(t)$, $I(t)$ and $R(t)$ at $p = 0.3$ by using RDTM. From Figs. (9)-(12) show the approximate solution of SIR model. From Fig. 10, the approximate solution $S(t)$ is decreasing with increasing $I(t)$. In Fig. 11, the approximate solution $S(t)$ is decreasing with increasing $R(t)$. In Fig. 12, the approximate solution $I(t)$ is increasing with increasing $R(t)$.

5 Discussion

In this work, we present new applications of the reduced differential transform method (RDTM) by handling two nonlinear biomathematics models (SIIIR model for the spread of virus HCV-subtype4a and SIR childhood disease mode). RDTM, which does not require linearization, perturbation or discretization, form the solution of this method is convergent power series with elegantly computed components. So, the solution procedure is simpler than other traditional methods.

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