Int. J. Adv. Appl. Math. and Mech. 7(1) (2019) 9 – 19 (ISSN: 2347-2529)

Journal homepage: www.ijaamm.com

IJAAMM

International Journal of Advances in Applied Mathematics and Mechanics

Partitioning differential transformation method to a SIR epidemic model under vaccination strategy

Research Article

Atika RADID[a, *], **Karim RHOFIR**[b]

[a] *University Hassan II Casablanca, FSAC-MACS, BP. 5366 Maarif, Casablanca, MOROCCO*

[b] *University Sultan Moulay Slimane, LISERT-ENSA, Bd. Beni Amir, BP. 77, Khouribga, MOROCCO*

Received 03 June 2019; accepted (in revised version) 10 August 2019

Abstract: In this paper, we introduce a new solution of the SIR model under vaccination strategies by using the partitioning differential transformation method. The corresponding mathematical model is described by nonlinear first order ordinary differential equations. First, we recall some properties of the differential transformation method and show the limitation of this method as it is the case for adomian decomposition method and the homotopy perturbation method. To overcome these limitations, we introduce the partitioning differential transformation method. In order to measure its efficiency, we compare the results obtained by the differential transformation method to the homotopy perturbation and adomian decompostion methods. Several numerical tests are performed and compared between these different methods for different cases of the SIR model under vaccination strategies.

MSC: 35C10 • 41A58 • 74S30

Keywords: SIR epidemic models • Differential transformation approach • Adomian decomposition method • Homotopy perturbation method

1. Introduction

Mathematical models are an essential tool for understanding, analyzing and describing results from natural phenomena modeling. One of the important topics studied in the field of mathematical modeling is epidemiology. Because it can provide very useful results and help public health agencies better manage epidemics.

Kermack [14], a pioneer in epidemiological modeling, proposed a first SIR model describing the spread of an infectious disease following a division of population into three distinct categories: susceptible S, infected I, and recovered R. This propagation is governed by a system of differential equations which is fed with parameters representing the intrinsic characteristics of the population/epidemic, such as the rate of infection. More recent studies have developed mathematical models that take into account specific aspects of distinct epidemics, such as seasonal influences, cross-immunity, and disease containment measures [24], [22]. For several years, the most common infectious diseases have been childhood diseases in children under five years of age (such as measles, mumps, influenza, smallpox, rubella, polio, etc...). Since vaccination is considered to be the most effective strategy against childhood diseases, the development of a framework that would predict the optimal vaccine coverage level needed to prevent the spread of these diseases is crucial. Several mathematical models allow the vaccination study in a certain population. Vaccination strategies are considered a measure that presents one of the best outcomes in preventing infectious diseases [25]. In

* Corresponding author.

E-mail address(es): atikaradid@gmail.com (Atika RADID), krhofir@gmail.com (Karim RHOFIR).

the case of constant vaccination strategies, there is some recent work on the subject discussed here that we can use as comparisons in our numerical tests [3] [17].

Mathematical models derived from the modeling of some epidemiological models using differential equations require efficient methods of solving problems. These methods must take into account the sensitivity of these equations with respect to the parameters to represent and describe the diseases mathematically. There are a variety of methods, exact, approximate, and purely numerical are available for such a system. But most of theme are computationally intensive, trial-and-error or need complicated symbolic computations [1]-[2]. In [11], the classic method as Euler method, Taylor method and Runge-Kutta methods are used as an introduction to numerical method for solving systems of differential equations.

In this paper, we apply the partitioning differential transformation method (PDTM) to systems of differential equations resulting from the modeling of the epidemic. The differential transformation method (DTM) is an alternative procedure for obtaining an analytic Taylor series solution of differential equations. The main advantage of this method is that it can be applied directly to nonlinear differential equations without requiring linearization and discretization, and therefore, it is not affected by errors associated with discretization. The concept of DTM was first introduced by [21] and by [26], who solved linear and nonlinear problems in electrical circuits. The DTM method can be used to evaluate the approximating solution by the finite Taylor series and by an iteration procedure described by the transformed equations obtained from the original equation using the operations of differential transformation. The homotopy analysis method (HAM), homotopy perturbation method (HPM), adomian decomposition method (ADM), variational iterative method (VIM), etc., are some common and classical analytical methods have been presented in the literature for solving nonlinear problems ([1], [17], [10]).

As the DTM is based on the Taylor series, then, it is difficult to obtain accurate results in the case of a large domain. To overcome this difficulty, the partitioning differential transformation method has been introduced and has provided reliable approximate solutions for many problems. The method is proposed to accelerate the convergence of the truncated approximation in a large domain as well as to improve the accuracy of the standard DTM.

In this work, we present a model containing two vaccination strategies: a vaccination at birth for a number of the population that represents a constant vaccination and vaccination pulses in which a certain part of the population is vaccinated periodically. In the case of constant vaccination, we give a comparison of the PDTM with ADM method, HPM method and the DTM method, and show the convergence of the method when the others have difficulty approaching the solution or fail when the interval is large.

The present paper has been organized as following: In Section 2, the governing equations for the SIR model is presented. In section 3, basic definitions of the differential transformation method are introduced and applied to SIR model. The partitioning differential transformation are presented. In Section 3. Numerical examples have been presented and compared to ADM, HPM and HAM in order to illustrate the effectiveness of the proposed method.

2. The governing equations for the SIR model

The SIR model is a standard compartmental model that has been used to describe many epidemiological diseases [13][15][20]. The way several childhood diseases spread through a population fits into this framework. The model has a susceptible group designated by S, an infected group I, and a removed group R, denoting vaccinated as well as recovered people with permanent immunity.

As in [17], this model assumes that the efficacy of the vaccine is 100% and the natural death rates μ in the classes remain unequal to births, so that the population size N is realistically not constant. Citizens are born into the population at a constant birth rate ρ with extremely very low childhood disease mortality rate.

In this section, we presented and analyzed a model that contains two vaccination strategies: a constant vaccination, wherein a certain parcel of the population that is born is immediately vaccinated; and vaccination in pulses, wherein a certain parcel of the population is vaccinated periodically. It is proposed the utilization of a function that illustrates the vaccination in pulses behavior.

In order to use such model, it is necessary to describe some parameters that represent characteristics inherent of each disease. Thus, ρ, β, μ and γ represents birth rate, average contact rate and natural death rate respectively with an infected individual recovers at a rate γ.

Considering $S(t)$ the class of susceptible individuals, $I(t)$ the class of infected individuals and $R(t)$ the class of recovered individuals, the equations that describe the SIR model in this specific vaccination situation are [22]:

$$\begin{cases} \frac{dS}{dt} = (1-V)\rho N - \beta\frac{SI}{N} - \mu S, \\ \frac{dI}{dt} = \beta\frac{SI}{N} - (\gamma+\mu)I \\ \frac{dR}{dt} = V\rho N + \gamma I - \mu R. \end{cases} \tag{1}$$

In these cases, groups considered at risk are repeatedly vaccinated until the level of transmission and infection is reduced or stopped. So, defining ω as the period of the pulses and ϕ as their phase, the pulse modeling of this kind of

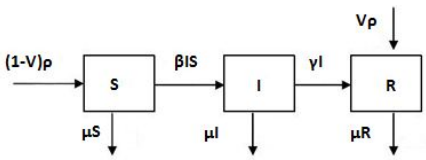

Fig. 1. Flow chart diagram for the SIR model

vaccination is proposed by the insertion of a function V given by:

$$V = \begin{cases} 0 & \text{if } \cos(\omega t + \phi) \le 0 \\ \alpha \cos(\omega t + \phi) & \text{if } \cos(\omega t + \phi) > 0 \end{cases} \tag{2}$$

We also have the relationship $N = S + I + R$ and assume α, ρ, β, γ and μ are all positive constant parameters.

Adding the equations in (1), we obtain

$$\frac{dN}{dt} = (\rho - \mu) N, \tag{3}$$

so that we are now dealing with a varying total population [19]. A summary of the process is drawn in a flow chart in Fig. 1. The groups can be scaled by population N using the new variables, $s = S/N$, $i = I/N$, and $r = R/N$. The population is now normalised, meaning $s + i + r = 1$, and we have the new system,

$$\begin{cases} \frac{ds}{dt} = (1 - V)\rho - \beta si - \mu s \\ \frac{di}{dt} = \beta si - (\gamma + \mu) i \\ \frac{dr}{dt} = V\rho + \gamma i - \mu r \end{cases} \tag{4}$$

When the vaccination is constant, more details on qualitative and quantitative analysis can be found in [17] and [3].

3. The differential transformation Approach

The definitions of the basic one dimensional differential transformation approach are introduced as follows [26], [2], [12].

3.1. Definition

With reference to the articles, we introduce in this section the basic definition of the differential transformation:

Assume that $u(t)$ is analytic in the time domain $[0, T]$, then it will be differentiated continuously with respect to time t,

$$\frac{d^k u(t)}{dt^k} = \phi(t, k), \text{ for all } t \in [0, T], \tag{5}$$

where k belongs to the set of non-negative integers, denoted as the K-domain.

For $t = t_i$, $\phi(t, k) = \phi(t_i, k)$, therefore, Eq. (5) can be rewritten as

$$U(k) = \phi(t, k) = \left[\frac{d^k u(t)}{dt^k} \right]_{t=t_i}, \tag{6}$$

where $U(k)$ is called the spectrum or the transformer of $u(t)$ at $t = t_i$ in K-domain.

If $u(t)$ can be expressed by Taylor's series, then $u(t)$ can be represented as

$$u(t) = \sum_{k=0}^{\infty} \frac{(t - t_i)^k}{k!} U(k). \tag{7}$$

Eq. (7) is known as the inverse transformation of $U(k)$. Using the symbol "D" denoting the differential transformation process and combining the previous equations, it is obtained that

$$u(t) = \sum_{k=0}^{\infty} \frac{(t - t_i)^k}{k!} U(k) \equiv D^{-1} U(k).$$

Using the differential transformation, a differential equation in the domain of interest can be transformed to an algebraic equation in the K-domain and the $u(t)$ can be obtained by a finite-term of Taylor's series plus a remainder. Thus

$$u(t) = \sum_{k=0}^{n} \frac{(t-t_i)^k}{k!} U(k) + Res_{n+1}.$$

Properties of differential transformation method: If $u(t)$ and $v(t)$ are two uncorrelated functions with time t where $U(k)$ and $V(k)$ are the transformed functions corresponding to $u(t)$ and $v(t)$, then we can easily proof the fundamental mathematics operations performed by differential transformation and are listed as follows :

Origin Function	Transformed Function
$u(t) = \alpha v(t) \pm \beta w(t)$	$U(k) = \alpha V(k) \pm \beta W(k)$
$u(t) = \frac{d^m v(t)}{dt^m}$	$U(k) = \frac{(k+m)!V(k+m)}{k!}$
$u(t) = v(t)w(t)$	$U(k) = \sum_{l=0}^{k} V(l)W(k-l)$
$u(t) = t^m$	$U(k) = \delta_{(k-m)} = \begin{cases} 1, & \text{if } k = m, \\ 0, & \text{if } k \neq m. \end{cases}$
$u(t) = \exp(t)$	$U(k) = \frac{1}{k!}$
$u(t) = \sin(\omega t + \varphi)$	$U(k) = \frac{\omega^k}{k!} \sin(\frac{k\pi}{2} + \varphi)$
$u(t) = \cos(\omega t + \varphi)$	$U(k) = \frac{\omega^k}{k!} \cos(\frac{k\pi}{2} + \varphi)$

In order to construct an approximate solution of the system described by Eqs.(4), the differential transformation method is employed. The advantage of this method is that it provides a direct scheme for solving the problem, i.e., without the need for linearization, perturbation or any transformation. The new system is as follows:

$$\begin{cases} S(k+1) = \frac{1}{k+1}\left[\rho\delta_{(k-0)} - \rho\overline{V}(k) - \beta\sum_{l=0}^{k} S(l)I(k-l) - \mu S(k)\right], \\ I(k+1) = \frac{1}{k+1}\left[\beta\sum_{l=0}^{k} S(l)I(k-l) - (\gamma+\mu)I(k)\right], \\ R(k+1) = \frac{1}{k+1}\left[\rho\overline{V}(k) + \gamma I(k) - \mu R(k)\right]. \end{cases} \tag{8}$$

with

$$\overline{V}(k) = \begin{cases} 0 & \text{if} \cos(\frac{k\pi}{2} + \varphi) \leq 0 \\ \alpha\frac{\omega^k}{k!}\cos(\frac{k\pi}{2} + \varphi) & \text{if } \cos(\frac{k\pi}{2} + \varphi) > 0 \end{cases}$$

and where $S(0) = S_0, I(0) = I_0$ and $R(0) = R_0$ are given by s_0, i_0 and r_0 respectively.

Then, for $k = 0$, we have

$$\begin{cases} S_1 &= \left(1 - \overline{V}(0)\right)\rho - \beta S_0 I_0 - \mu S_0 \\ I_1 &= \beta S_0 I_0 - (\gamma+\mu) I_0 \\ R_1 &= \overline{V}(0)\rho + \gamma I_0 - \mu R_0 \end{cases} \tag{9}$$

and for $k = 1$, we have

$$\begin{cases} S_2 &= (\overline{V}(0)\rho - \beta S_0 I_1 - \beta S_1 I_0 - \mu S_1)/2 \\ I_2 &= \left(\beta S_0 I_1 + \beta S_1 I_0 - (\gamma+\mu) I_1\right)/2 \\ R_2 &= \left(\overline{V}(0)\rho + \gamma I_1 - \mu R_1\right)/2 \end{cases} \tag{10}$$

We can repeat this soon as for all k.

The solution approximation of the system is then given by : for all $t \in [0, T]$,

$$\begin{cases} s(t) = \sum_{k=0}^{n} S_k t^k \\ i(t) = \sum_{k=0}^{n} I_k t^k \\ r(t) = \sum_{k=0}^{n} R_k t^k \end{cases}$$

3.2. The partitioning differential transformation method

In the previous section, we apply the DTM method to approximate the solution of the system described by Eqs.(4). Although this method has some disadvantages: the solutions converge in a very small region and a slow convergence rate (see [18]). To overcome this, we present a partitioning differential transformation method (PDTM) as follow :

Let $[0, T]$ be the time interval of interest. We want to find the solutions of the initial value problem over the interval. In the classical DTM, the approximate solution can be obtained by the finite series

$$y(t) = \sum_{k=0}^{\infty} U(k)\, t^k \text{ for } t \in [0, T] \tag{11}$$

In the partitioning DTM, the time interval $[0, T]$ is subdivised into M sub-interval $[t_{m-1}, t_m]$, $m = 1, 2, ..., M$. First, the classical DTM method is applied to nonlinear equations over the interval $[0, t_1]$ and hence we obtain

$$y_1(t) = \sum_{k=0}^{\infty} Y_1(k)\, t^k \text{ for } t \in [0, t_1] \tag{12}$$

The value at $t = t_1$ is used as initial condition for the next time step. The initial condition for the next time step is written as

$$y_m(t_{m-1}) = y_{m-1}(t_{m-1}) \tag{13}$$

In general, the value at the last time in the interval is used as initial conditions for the next time step and the solution is approximated as

$$y_m(t) = \sum_{k=0}^{n} Y_m(k)(t - t_{m-1})^k \text{ for } t \in [t_{m-1}, t_m] \tag{14}$$

According to the partitioning DTM method, the approximation of the SIR model Eqs. (4) solution is given by :

$$X(t) = \begin{cases} \sum\limits_{k=0}^{n} X_1(k)\, t^k & t \in [0, t_1] \\ \sum\limits_{k=0}^{n} X_2(k)(t - t_1)^k & t \in [t_1, t_2] \\ \vdots & \vdots \\ \sum\limits_{k=0}^{n} X_M(k)(t - t_{M-1})^k & t \in [t_{M-1}, t_M] \end{cases} \tag{15}$$

where X denote S, I or R and S_j, I_j and R_j for $j = 1, ..., M$, satisfy the following recurrence relations :

$$\begin{cases} S_j(k+1) = \frac{1}{k+1}\left[\rho\delta_{(k-0)} - \rho\overline{V} - \beta \sum\limits_{l=0}^{k} S_j(l) I_j(k-l) - \mu S_j(k)\right], \\ I_j(k+1) = \frac{1}{k+1}\left[\beta \sum\limits_{l=0}^{k} S_j(l) I_j(k-l) - (\gamma + \mu) I_j(k)\right], \\ R_j(k+1) = \frac{1}{k+1}\left[\overline{V}\rho + \gamma I_j(k) - \mu R_j(k)\right]. \end{cases} \tag{16}$$

With the initial conditions $S_j(0) = S_{j-1}(0), I_j(0) = I_{j-1}(0)$ and $R_j(0) = R_{j-1}(0)$.

Finally, we start with initial conditions $S(0) = S_0, I(0) = I_0$ and $R(0) = R_0$, and use the recurrence relation given in the above system, we can obtained the partitioning differential transformation solution given in (15) by X. Therefore, to obtain the approximated values of the $s(t)$, $i(t)$ and $r(t)$ at any grid point, we define

$$\chi_{[t_i, t_{i+1}]}(t) = \begin{cases} 1 & \text{if } t \in [t_i, t_{i+1}] \\ 0 & \text{otherwise} \end{cases}$$
$$\forall i \in \{0, ..., M-1\} \text{ and } [0, T] = \bigcup_{i=0}^{M-1} [t_i, t_{i+1}]$$

and for all $t \in [0, T]$, we have

$$\begin{cases} s(t) = \sum_{j=0}^{M-1} s_j(t)\chi_{[t_j, t_{j+1}]}(t) \\ i(t) = \sum_{j=0}^{M-1} i_j(t)\chi_{[t_j, t_{j+1}]}(t) \\ r(t) = \sum_{j=0}^{M-1} r_j(t)\chi_{[t_j, t_{j+1}]}(t) \end{cases}$$

Table 1. Source [17] with time interval [0,10].

Case	s_0	i_0	r_0	β	γ	ρ	V	R_ν	E_u
1	1	0	0	0.8	0.03	0.4	0.9	0.18604	E_0 stable
2	0.8	0.2	0	0.8	0.03	0.4	0.9	0.18604	E_0 stable
3	0.8	0.2	0	0.8	0.03	0.4	0.3	1.30232	E_u stable
4	0.8	0.2	0	0.8	0.03	0.4	0.0	1.86046	E_u stable

4. Numerical results, comparisons and discussion

In this section, in order to monitor the effect of vaccination on the dynamics of a childhood disease described by the SIR model Eqs.(4) using differential transformation approach, we use the numerical results presented in [17], [3] for the ADM and HPM methods in the case of a constant vaccination. More specifically, we consider only the most significant case for our comparison and discuss why the partitioning differential transformation method gives good results when the others fails.

Now, we consider the effect of vaccination on the dynamics of a childhood disease described by the SIR model using ADM [17] and HPM [3]. All calculations were performed on a PC equipped with Intel Atom, Quad Core at 1.44 GHz and 2G of RAM using Matlab 2012. For illustration purposes the parameter values in Table 1 are used.

4.1. Numerical comparison case study (case 2)

Since $R_\nu < 1$, E_0 is stable, E_u is unstable and have disease eradication. The numerical results for DTM, ADM [17] and HPM [3] are given by the following approximate solutions

for DTM :

$$\begin{aligned}
s(t) = {} & 0.8 - 0.408t + 0.0884544t^2 - 14.512832\times10^{-3}t^3 + 0.2261847\times10^{-2}t^4 \\
& -3.92\times10^{-4}t^5 + 7.64\times10^{-5}t^6 - 1.57\times10^{-5}t^7 + 3.25\times10^{-6}t^8 \\
& -6.65\times10^{-7}t^9 + 1.35\times10^{-7}t^{10}.\\
i(t) = {} & 0.2 + 0.42\times10^{-1}t - 0.158844\times10^{-1}t^2 + 0.4995676\times10^{-2}t^3 \\
& -0.1347599\times10^{-2}t^4 + 0.326651\times10^{-3}t^5 - 7.37\times10^{-5}t^6 \\
& +1.59\times10^{-5}t^7 - 3.31\times10^{-6}t^8 + 6,79\times10^{-7}t^9 - 1.38\times10^{-7}t^{10}.\\
r(t) = {} & 0 + 0.366t - 0.7257\times10^{-1}t^2 + 0.9517156\times10^{-2}t^3 - 0.914248\times10^{-3}t^4 \\
& +6.51\times10^{-5}t^5 - 2.70\times10^{-6}t^6 - 1.61\times10^{-7}t^7 + 6.76\times10^{-8}t^8 \\
& -1.41\times10^{-8}t^9 + 2.60\times10^{-9}t^{10}.
\end{aligned}$$

For ADM:

$$\begin{aligned}
s(t) = {} & 0.8 - 0.408t + 0.1008t^2 - 8.224\times10^{-3}t^3 - 0.1811776\times10^{-2}t^4 \\
& +0.2838500158\times10^{-3}t^5 - 0.4866281149\times10^{-4}t^6 - 0.1973168518\times10^{-5}t^7 \\
& +0.1567280763\times10^{-7}t^8 + 0.4557699387\times10^{-9}t^9 - 0.1747626667\times10^{-11}t^{10}.\\
i(t) = {} & 0.2 + 0.42\times10^{-1}t - 0.2823\times10^{-1}t^2 - 0.11697\times10^{-2}t^3 + 0.2759918751\times10^{-2}t^4 \\
& -0.3762609484\times10^{-3}t^5 + 0.4741940899\times10^{-4}t^6 + 0.199013997\times10^{-5}t^7 \\
& -0.1540349563\times10^{-7}t^8 - 0.4575903832\times10^{-9}t^9 + 0.1747626667\times10^{-11}t^{10}.\\
r(t) = {} & 0 + 0.366t - 0.7257\times10^{-1}t^2 + 0.93937\times10^{-2}t^3 - 0.94814275\times10^{-3}t^4 \\
& +0.9241093251\times10^{-4}t^5 + 0.4445486401\times10^{-5}t^6 - 0.1697145904\times10^{-7}t^7 \\
& -0.269312\times10^{-9}t^8 + 0.182044444\times10^{-11}t^9.
\end{aligned}$$

For HPM:

$$\begin{aligned}
s(t) = {} & 0.8 - 0.408t + 0.1008t^2 - 8.224\times10^{-3}t^3 - 0.1812\times10^{-2}t^4 + 0.2839\times10^{-3}t^5 \\
& -0.487\times10^{-4}t^6 - 0.197\times10^{-5}t^7 + 0.1567\times10^{-7}t^8 + 0.456\times10^{-9}t^9 \\
& -0.175\times10^{-11}t^{10}.\\
i(t) = {} & 0.2 + 0.042t - 0.02823t^2 - 0.117\times10^{-2}t^3 + 0.276\times10^{-2}t^4 - 0.376\times10^{-3}t^5 \\
& +0.474\times10^{-4}t^6 + 0.199\times10^{-5}t^7 - 0.154\times10^{-7}t^8 - 0.457\times10^{-9}t^9 \\
& +0.175\times10^{-11}t^{10}.\\
r(t) = {} & 0 + 0.366t - 0.07257t^2 + 0.9394\times10^{-2}t^3 - 0.948\times10^{-3}t^4 + 0.924\times10^{-4}t^5 \\
& +0.445\times10^{-5}t^6 - 0.1697\times10^{-7}t^7 - 0.269\times10^{-9}t^8 + 0.182\times10^{-11}t^9.
\end{aligned}$$

Remark 4.1.
All of these method are local convergent, and when the time interval is large these methods do not give the good

results. Using the previous approximation solutions for DTM, ADM and HPM in the time interval [0,10], we remark that is difficult to obtain accurate results in the case of a large domain and fails when there are implemented in Matlab.

To overcome this difficulty, we introduce the partitioning differential transformation method and provide reliable approximate solutions for many cases. The method is proposed to accelerate the convergence of the truncated approximation in a large domain as well as to improve the accuracy of the standard DTM. We investigate the approximation solution in the interval $[0,10]$ that is divided into 5 subintervals : $[0,10] = [0,2]\bigcup[2,4]\bigcup[4,6]\bigcup[6,8]\bigcup[8,10]$, and the graphical approximations are illustrated in the Figs. 2 - 5.

4.2. Case 1:

Since $R_v < 1$, E_0 is stable, E_u is unstable and have disease eradication. The approximation solution can be derived from Table 2 and Table 3:

Table 2. A sequence of S_j, $j = 1,\cdot\cdot,4$ and $k = 1,2,\cdots$ for case 1.

k	S_0	S_1	S_2	S_3	S_4	$\cdots$
1	-0,36	-0,161757052	-0,072681511	-0,032657631	-0,014673895	$\cdots$
2	0,072	0,03235141	0,014536302	0,006531526	0,002934779	$\cdots$
3	-0,0096	-0,004313521	-0,001938174	-0,00087087	-0,000391304	$\cdots$
4	0,00096	0,000431352	0,000193817	8,71E-05	3,91E-05	$\cdots$
5	-7,68E-05	-3,45E-05	-1,55E-05	-6,97E-06	-3,13E-06	$\cdots$
6	5,12E-06	2,30E-06	1,03E-06	4,64E-07	2,09E-07	$\cdots$
7	-2,93E-07	-1,31E-07	-5,91E-08	-2,65E-08	-1,19E-08	$\cdots$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$

$\forall\, t \in [0,10]$, $\forall\, j = 0,1,2,3,4$, we have $i(t) = 0$.

Table 3. A sequence of R_j, $j = 1,\cdot\cdot,4$ and $k = 1,2,...$ for case 1.

k	R_0	R_1	R_2	R_3	R_4	$\cdots$
1	0,36	0,161757052	0,072681511	0,032657631	0,014673895	$\cdots$
2	-0,072	-0,03235141	-0,014536302	-0,006531526	-0,002934779	$\cdots$
3	0,0096	0,004313521	0,001938174	0,00087087	0,000391304	$\cdots$
4	-0,00096	-0,000431352	-0,000193817	-8,71E-05	-3,91E-05	$\cdots$
5	7,68E-05	3,45E-05	1,55E-05	6,97E-06	3,13E-06	$\cdots$
6	-5,12E-06	-2,30E-06	-1,03E-06	-4,64E-07	-2,09E-07	$\cdots$
7	2,93E-07	1,31E-07	5,91E-08	2,65E-08	1,19E-08	
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$

and the corresponding Fig. 2 shows the impact of high vaccination coverage on the disease free initial population groups :

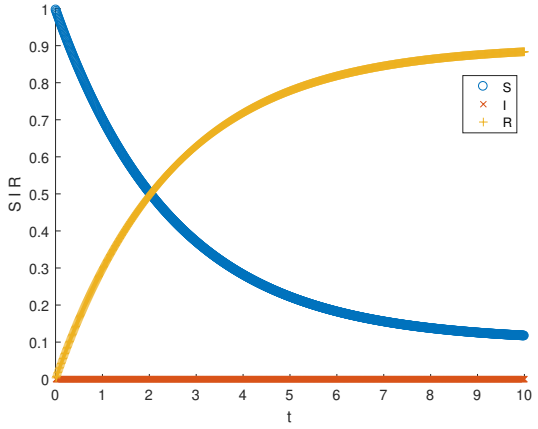

Fig. 2. Population fraction versus time for Case 1

4.3. Case 2:

Since $R_v < 1$, E_0 is stable, E_u is unstable and have disease eradication.
The approximation solution can be derived from Tables 4-6 :

Table 4. A sequence of S_j, $j = 1,...,4$ and $k = 1,2,...$ for case 2.

k	S_0	S_1	S_2	S_3	S_4	$\cdots$
1	-0,408	-0,108281343	-0,011145863	0,002607376	0,003873484	$\cdots$
2	0,0884544	0,019184391	0,001953864	-0,000486269	-0,000748381	$\cdots$
3	-0,014512832	-0,001840277	-0,000188062	5,54E-05	9,26E-05	$\cdots$
4	0,002261847	4,52E-05	6,70E-06	-3,93E-06	-8,01E-06	$\cdots$
5	-3,92E-04	1,75E-05	9,76E-07	1,04E-07	4,71E-07	$\cdots$
6	7,64E-05	-3,81E-06	-2,11E-07	1,51E-08	-1,24E-08	$\cdots$
7	-1,57E-05	4,86E-07	2,23E-08	-2,74E-09	-1,06E-09	$\cdots$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$

Table 5. A sequence of I_j, $j = 1,\cdot,4$ and $k = 1,2,\cdots$ for case 2.

k	I_0	I_1	I_2	I_3	I_4	$\cdots$
1	0,042	-0,057070706	-0,061751202	-0,033756802	-0,016984902	$\cdots$
2	-0,0158844	0,014742079	0,013551817	0,007222506	0,003625438	$\cdots$
3	0,004995676	-0,002830674	-0,00201488	-1,03E-03	-5,13E-04	$\cdots$
4	-0,001347599	4,43E-04	2,29E-04	1,09E-04	5,38E-05	$\cdots$
5	3,27E-04	-5,92E-05	-2,12E-05	-9,13E-06	-4,46E-06	$\cdots$
6	-7,37E-05	6,88E-06	1,66E-06	6,33E-07	3,01E-07	$\cdots$
7	1,59E-05	-6,91E-07	-1,13E-07	-3,70E-08	-1,67E-08	$\cdots$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$

Table 6. A sequence of R_j, $j = 1, \cdot\cdot, 4$ and $k = 1, 2, \cdots$ for case 2.

k	R_0	R_1	R_2	R_3	R_4	$\cdots$
1	0,366	0,165352049	0,072897064	0,031149426	0,013111418	$\cdots$
2	-0,07257	-0,03392647	-0,015505681	-0,006736237	-0,002877057	$\cdots$
3	0,009517156	0,00467095	0,002202942	9,70E-04	4,20E-04	$\cdots$
4	-0,000914248	-4,88E-04	-2,35E-04	-1,05E-04	-4,58E-05	$\cdots$
5	6,51E-05	4,17E-05	2,02E-05	9,03E-06	3,99E-06	$\cdots$
6	-2,70E-06	-3,08E-06	-1,45E-06	-6,48E-07	-2,88E-07	$\cdots$
7	-1,61E-07	2,05E-07	9,02E-08	3,97E-08	1,78E-08	$\cdots$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$

And the corresponding Fig. 3 illustrates the impact of high vaccination coverage on the initial population groups with low level of infective group :

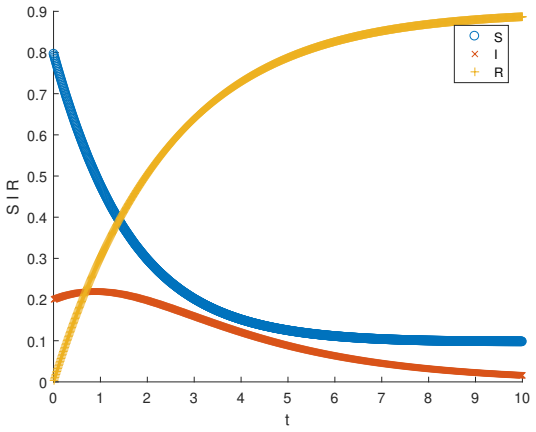

Fig. 3. Population fraction versus time for Case 2

4.4. Case 3:

Since $R_v > 1$, , E_0 is stable, E_u is stable and we don't have disease eradication. Case 3 is represented in Fig. 4 and illustrates the effect of low vaccination coverage on the initial population groups with low levels of infective group :

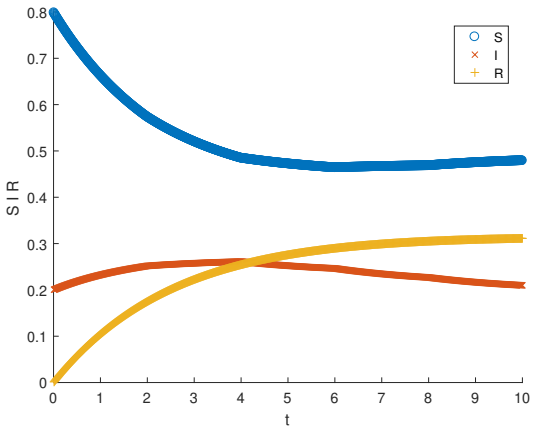

Fig. 4. Population fraction versus time for Case 3

4.5. Case 4:

Since $R_v > 1$, E_0 is stable, E_u is stable and we don't have disease eradication. Case 4 is shown in Fig. 5 and illustrates the impact of initial low levels of infective group on the vaccination free population :

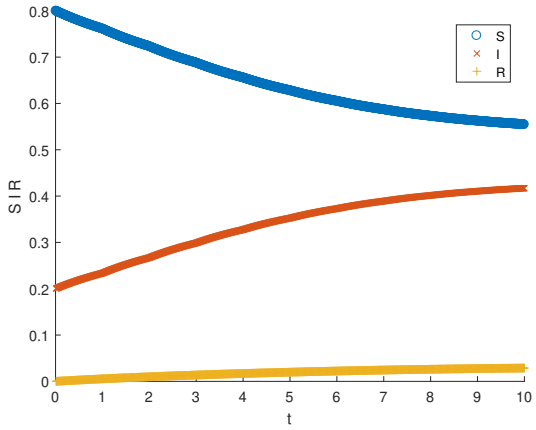

Fig. 5. Population fraction versus time for Case 4

5. Conclusion

In this paper, a three-compartmental deterministic mathematical model for the transmission dynamics of a childhood disease under vaccination strategies, was qualitatively and quantitatively studied. The analytical approximations to the solutions are reliable, and confirm the power and ability of the partitioning DTM methods as an easy device for computing the solution of a non-linear system of differential equations. The merit of this method is that it is more efficient than the basic differential transformation, adomian decomposition or homotopy methods when system of differential equations are solved in large interval. The advantage of using these method is clearly demonstrated by the different numerical cases. The obtained results show that the convergence to the accurate approximation is assured by the partitioning differential transformation method for the SIR epidemic problems.

Acknowledgements

The authors thanks the referees very much for their constructive suggestions, helpful comments and fast response, which led to significant improvement of the original manuscript of this paper.

References

[1] I.H. Abdel-Halim Hassan, Differential transformation technique for solving higher-order initial value problems. Appl. Math. Comput. 154 (2004), 299-311.
[2] I.H. Abdel-Halim Hassan, Application to differential transformation method for solving systems of differential equations. Applied Mathematical Modelling 32(12) (2008), 2552-2559.
[3] Ahmet Yıldırım, Yves Cherruault, Analytical approximate solution of a SIR epidemic model with constant vaccination strategy by homotopy perturbation method. Kybernetes, 38(9) (2009), 1566-1575.
[4] A. J. Arenas, G. Gonzales-Parra, and B. M. Chen-Charpentier, Dynamical analysis of the transmission of seasonal disease using the differential transformation method. Mathematical and Computer Modelling 50 (2009), 765-776.
[5] J. Biazzar, E. Babolian, R. Islam, Solution of the system of ordinary differential equations by Adomian decomposition method. Appl. Math. Comput. 147 (2004), 713-719.
[6] R.L. Burrden, J.D. Faires, Numerical Analysis, PWS-KENT Publishing Company, Boston, 1993.
[7] S. Busenberg, P. van den Driessche, Analysis of a disease transmission model in a population with varying size. J. Math. Biol. 28 (1990), 257-270.
[8] C.L. Chen, S.H. Lin, C.K. Chen, Application of Taylor transformation to nonlinear predictive control problem. Appl. Math. Model. 20 (1996), 699-710.

[9] C.K. Chen, S.H. Ho, Application of differential transformation to eigenvalue problems. Appl. Math. Comput. 79 (1996), 173-188.
[10] Ghotbi, Abdoul R.; Barari, Amin; Omidvar, M.; Domairry, G. Application of Homotopy Perturbation and Variational Iteration Methods to SIR Epidemic Model. Journal of Mechanics in Medicine and Biology, 11(1) (2011), 149-161.
[11] T. Guyer, K. Onur, B. Goksal, M. Seref, A new method for computing the solutions of differential equation systems using generalized inverse via Maple, Appl. Math. Comput. 121 (2001), 291-299.
[12] Mohammad Hatami, Davood Domairry Ganji, Mohsen Sheikholeslami, Differential Transformation Method for Mechanical Engineering Problems. Academic Press, 2017.
[13] H.W. Hethcote, The mathematics of infectious diseases. Siam Rev. 42(4) (2000), 599-653.
[14] William Ogilvy Kermack, A. G. McKendrick, and Gilbert Thomas Walker, A contribution to the mathematical theory of epidemics, 115 Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character.
[15] Z. Lu, X. Chi, L. Chen, The effect of constant and pulse vaccination of SIR epidemic model with horizontal and vertical transmission. *Math. Comput. Model.* **36** (2002), 1039-1057.
[16] M. Malik, H.H. Dang, Vibration analysis of continuous system by differential transformation. *Appl. Math. Comput.* **96** (1998), 17-26.
[17] O.D.Makinde, Adomian decomposition approach to a SIR epidemic model with constant vaccination strategy. Appl. Math. & Computation 184(2) (2007), 842-848.
[18] Z. M. Odibat, C. Bertelle, M.A. Aziz-Alaoui, and G. H.E. Duchamp. A multi-step differential transform method and application to non-chaotic or chaotic systems. Computers and Mathematics with Applications 59(4) (2010), 1462-1472.
[19] D. B. Prates et all, Vaccination Strategies: a comparative study in an epidemic scenario. Journal of Physics: Conference Series 738(1) (2016), 012083.
[20] C. Piccolo III, L. Billings, The effect of vaccinations in an immigrant model. Math. Comput. Model. 42 (2005), 291-299.
[21] Georgii Evg. Pukhov, Differential transforms and circuit theory. Circuit theory and applications 10 (1982), 265-276.
[22] M. Sabeti, A. R. Castilho, Model Discrete Epidemiological SIR with ethereal structure and application of vaccination with pulses and constant. In portuguese language , Tese de Doutorado, UFPE, 2011.
[23] H.L. Smith, Subharmonic bifurcation in SIR epidemic model. J. Math. Biol. 17 (1983), 163-177.
[24] Stone, L., Shulgin, B. and Agur, Z., Theoretical examination of the pulse vaccination policy in the SIR epidemic model. Mathematical and computer modelling 31(4) (2000), 207-215.
[25] Zhi-Long He and Lin-Fei Nie, The Effect of Pulse Vaccination and Treatment on SIR Epidemic Model with Media Impact. Discrete Dynamics in Nature and Society, vol. 2015, Article ID 532494, 12 pages, 2015.
[26] J.K. Zhou, Differential transformation and its application for electrical circuits. Huarjung University Press, Wuuhahn, China, 1986 (in Chinese).