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Stochastic SEIR Model for Measles with Differential Transformation Method (DTM)

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ABSTRACT

The epidemic models are important to study and control epidemiological diseases. The SEIR model of measles disease in children has been solved and evaluated using the differential transformation method (DTM). This is a numerical and semi-analytic technique that is used to solve differential and integral equations. We solved a measles model with the help of differential transformation method and discussed two cases one is endemic and other is a disease-free state. In both cases, if threshold number $R_0 < 1$ then we get a locally stable situation while at $R_0 > 1$ we get a locally unstable situation. Also, compared it with [6] to prove better convergence of differential transformation method. This approach offers solutions for converging a series of conveniently computable components. DTM is an efficient tool to solve linear and non-linear differential equations. We compare results with Runge-Kutta fourth order. DTM is much convenient and gives better results.

Keywords

Deterministic and stochastic modeling, numerical method, differential transformation method, solution of the measles SEIR model

1. INTRODUCTION

Most mathematical modeling in human geography is stochastic. These models offer a framework that is recognized as an essential issue of spatial uncertainty in mathematical modeling. In the field of epidemiology, mathematical modeling is used to understand the previous outbreaks of diseases.

We will use the differential transformation method(DTM) in this paper. Zhou (1986) [15] proposed the concept of DTM and in the last two decades, DTM has been used extensively to solve various initial value problems of linear and non-linear in the electric circuit analysis efficiently and easily. The major benefits of these methods are that they can be extended directly to the differential equations without requiring linearization, discretization or perturbation.

Farshid Mirzaee et al. [11] used a DTM to solve ODE's linear and nonlinear systems. Sucheta Moharir and Narhari Patil [12] gives the application of DTM for both differential and integral equations. Alexander D. Becker et al. [3] explained London's long-term measles dynamics: the impact of wars, pandemics and vaccination in 1918. Strong agreement was also found between the data and the sophisticated model, which indicates both time dynamics such as the epidemic form and size, as well as bifurcations, could be predicted accurately.

So, we will discuss the epidemiological disease model which is divided into four categories SEIR (Susceptible, Exposed, Infected, Recovered). Measles, ebola virus, influenza and Covid-19 are common examples of SEIR and discussed extensively in [1], [2], [5], [7], [8], [9]. A.A. Momoh et al. [13] uses a mathematical model to discuss epidemiological control of measles. The impact of the exposed individuals on the dynamics of measles transmission in latent times are investigated by an SEIR epidemic model.

M. H. A. Biswas et al. [10] discussed the SEIR model for infectious disease prevention with constraints and they proposed the introduction of constraints involving state variables in a compartmental SEIR model for an optimal control problem.

M. Farman et al. [4] using the Laplace-Adomian decomposition process, evaluate and explore the numerical solution of the epidemic SEIR model of measles with non-integer time-fractional derivatives.

Numerical Simulations for measles disease and its existence, uniqueness and stability of solution discussed by Samuel O. Sowole et al. [14]. And model recognized that exposed individuals play a significant role in the control of disease during a latent phase.

Below we discuss the differential transformation method with the application. We use the differential transformation method on the measles SEIR model and discuss two cases. One is endemic and the second is disease free. Then at the last, we compared the results of the measles SEIR model with Runge-Kutta fourth-order to show the convergence of the differential transformation method.

2. METHODOLOGY

Here we will discuss the methodology which we used in our problem.

2.1 Differential Transformation Method

If k^{th} derivative of function $u(x)$ exist at $x = x_0$then differential transformation of $u(x)$ is defined as:

$$U(K) = \frac{1}{k!}\left[\frac{d^k u(x)}{dx^k}\right]_{x=x_0} \tag{1}$$

Here the $U(K)$ is a transformed function. The inverse of differential transformation of $U(K)$ is

$$u(x) = \sum_{k=o}^{\infty} (x - x_0)^k U(k) \tag{2}$$

by putting equation (1) in equation (2), we have

$$u(x) = \sum_{k=0}^{\infty} (x - x_0)^k \frac{1}{k!} \left[\frac{d^u(x)}{dx^k} \right]_{x=x_0}$$

The following section summarizes some of the fundamental outcomes of the $1 - D$ transformation method.

Table 1. : Basic Fundamental results

case	**Transformed function**
z(t)=a(t) $\pm$ b(t)	Z(k)=A(k) $\pm$ B(k)
z(t)=β a(t)	Z(k)= β A(k)
z(t)=∂ a(t)/ ∂ t	Z(k)=(k+1)A(k+1)
z(t)=∂^s a(t)/ ∂t^s	Z(k)=(k+1)(k+2) ...(m+s)A(k+s)
z(t)=u(t)v(t)	Z(k)= $\sum_{p=0}^{k}$ U(k-l)V(l)
z(t)=exp(μ t)	Z(k)=μ^k / k! then 1, if k = m 0, if k $\pm$ m
z(t)=sin($\omega t + \alpha$)	Z(k)=$\frac{\omega^k}{k!} sin\left(\frac{\pi}{2}k + \alpha\right)$
z(t)= $cos(\omega t + \alpha)$	Z(k)=$\frac{\omega^k}{k!} cos\left(\frac{\pi}{2}k + \alpha\right)$
D[c]	$\delta(k)$
z(t)=$\int_{u_0}^{u} a(t)dt$	Z(m)=$\frac{A(m-1)}{m}$ where m $\geq$ 1, A(0)=0

3. MEASLES SEIR MODEL

This model categorizes the entire population into four groups, with one vulnerable, the second exposed, the third infectious and the fourth recovered. Individuals who have not been exposed to the disease are susceptible, whereas those who lead compartment of exposed who contract sickness but are unable to transmit it for a specified period of time (i.e. period of incubation) when they move to the exposed category moving onto an infected category. The infectious person can pass disease and in the last recovered category are the individuals who get a permanent immunity and recovery and can no longer transmit infection in the cured group. The flow chart for the SEIR measles model is as follows:

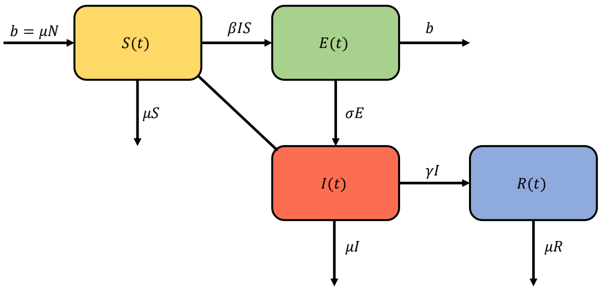

Fig. 1: Compartmental figure for SEIR model

The mathematical representation of the preceding model

$$\frac{dS}{dt} = b - \beta Si - \mu S \quad t > 0 \tag{3}$$

$$\frac{dE}{dt} = -\mu E + \beta SI - \sigma E \quad t > 0 \tag{4}$$

$$\frac{dI}{dt} = -\mu I + \sigma E - \gamma I \quad t > 0 \tag{5}$$

$$\frac{dR}{dt} = \gamma I - \mu R \quad t > 0 \tag{6}$$

where

$$S(0) = S^0 \ , \quad E(0) = E^0 \ , \quad I(0) = I^0 \ , \quad R(0) = R^0 \tag{7}$$

Consider for size N total population is constant.
Therefore, N is the sum of S, E, I and R.
Where $S(t)$ is representing the vulnerable and those persons that catch the illness, $E(t)$ represents those persons exposed to the illness, but not infected by it, $I(t)$ shows infected individuals, while $R(t)$ represents permanent immunity or resistance population.
μ, σ, β and γ are concerned with population reproduction and mortality, the rate at which persons who have been exposed to disease become infected, infection rate and recovery rate respectively. Qualitatively system is analyzed in two ways.

—Disease-free equilibrium

—Endemic equilibrium

4. EQUILIBRIUM ANALYSIS

In this section endemic equilibrium and disease-free equilibrium are discussed.

4.1 Disease Free Equilibrium

When the disease naturally dies, asymptotically solution of the above system leads to a disease-free population or equilibrium takes the form

$$S = N \ , \ E = 0 \ , \ I = 0 \ , \ R = 0$$

$$i.e \ \ (S, E, I, R) = (N, 0, 0, 0) \tag{8}$$

If $R_0 < 1$ disease free equilibrium is locally stable and unstable if $R_0 > 1$

4.2 Endemic Equilibrium

When $R_0 > 1$ then endemic equilibrium is stable.
If disease-free equilibrium persists in the population and disease remains unstable then endemic equilibrium takes the form

$$(S, E, I) = \left[\frac{(\mu + \sigma)(\mu + \gamma)}{\beta\sigma} \ , \ \frac{\mu N}{\mu + \sigma} - \frac{\mu(\mu + \gamma)}{\sigma\beta} \ , \right.$$
$$\left. \frac{\mu\sigma N}{(\mu + \sigma)(\mu + \gamma)} - \frac{\mu}{\beta} \right]$$

4.3 Application of differential transformation method

Now we have a recurrence relation of the system (3 , 4 , 5 , 6) w.r.t time t and by applying the differential transformation method, we get

$$\begin{aligned} S(k+1) =& \frac{1}{k+1}\left[b - \beta\sum_{l=0}^{k} S(l)I(k-l) - \mu S(k)\right] \\ E(k+1) =& \frac{1}{k+1}\left[\beta\sum_{l=0}^{k} S(l)I(k-l) - E(k)(\mu+\sigma)\right] \\ I(k+1) =& \frac{1}{k+1}\left[\sigma E(k) - I(k)(\mu+\gamma)\right] \\ R(k+1) =& \frac{1}{k+1}\left[\gamma I(k) - \mu R(k)\right] \end{aligned}$$

We are now starting to iterate the above system for the various parameter values and we are looking at the effects of high or low vaccination on childhood diseases with these parameters, hence we discussed stability.

Table 2. : Initial Conditions [6]

Parameters	Values
b	0
β	0.5
σ	0.75
μ	0.25
γ	0.75
N	2
S(0)	1
E(0)	0
I(0)	1
R(0)	0

$$R_0 = \frac{\beta\sigma S}{(\mu+\sigma)(\mu+\gamma)} = 0.375 \; < \; 1$$

Thus, the solution converges to disease-free equilibrium
Tabular form will be

$$S(t) = 1 + (-0.75)t + (0.53125)t^2 + (-0.3723958)t^3 + (0.2508138)t^4 + ...$$

$$E(t) = (0.5)t + (-0.6875)t^2 + (0.5572917)t^3 + (-0.366862)t^4 + ...$$

$$I(t) = 1 + (-1)t + (0.6875)t^2 + (-0.4010417)t^3 + (0.2047526)t^4 + ...$$

$$R(t) = (0.75)t + (-0.46875)t^2 + (0.2109375)t^3 + (-0.08837891)t^4 + ...$$

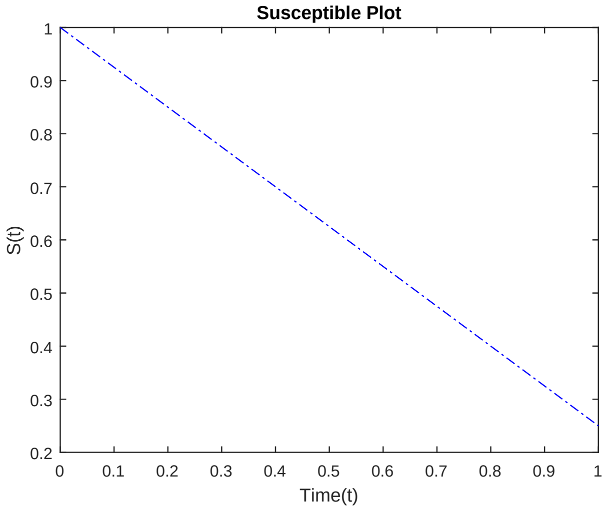

Fig. 2: Relation between susceptible and time in years

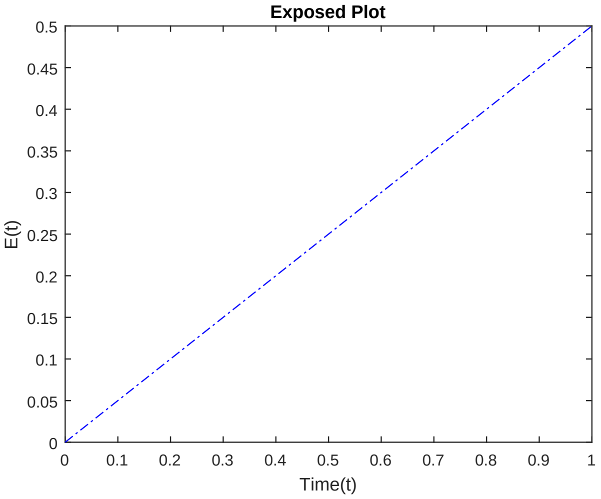

Fig. 3: Relation between exposed and time in years

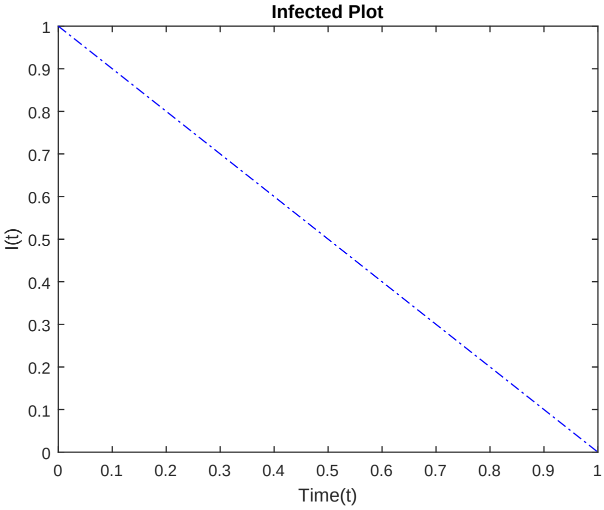

Fig. 4: Relation between infected and time in years

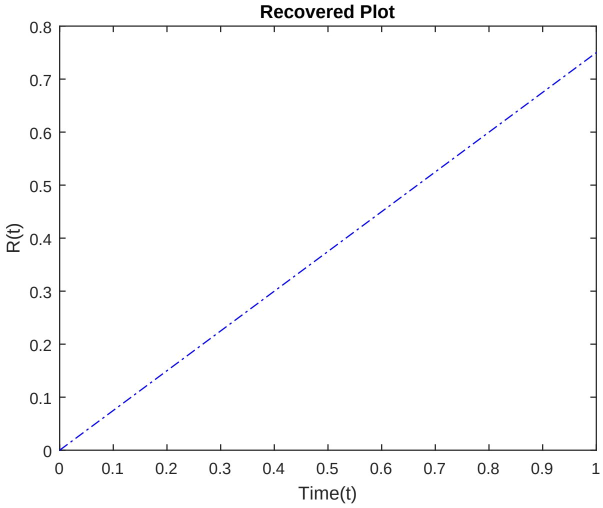

Fig. 5: Relation between recovered and time in years

5. COMPARISON BETWEEN RUNGE-KUTTA 4^{TH} ORDER AND DIFFERENTIAL TRANSFORMATION METHOD

We take the example from [6] and compute the differential transformation method. Results are discussed below

Table 3. : Comparison between RK4 and DTM

t_i		0	0.25	0.5	0.75	1
Susceptible	RK [6]	1	0.88986	0.79351	0.71554	0.64883
	DTM	1	0.84086	0.72694	0.65858	0.65967
Exposed	RK [6]	0	0.03089	0.05201	0.0636	0.06964
	DTM	0	0.08931	0.12486	0.10731	0.00293
Infected	RK [6]	1	0.86659	0.75167	0.65096	0.56374
	DTM	1	0.7875	0.63454	0.53231	0.49121
Recovered	RK [6]	0	0.10205	0.19183	0.25993	0.31443
	DTM	0	0.16115	0.27866	0.35985	0.40381

The table (3) shows that there are more exposed and recovered in our case. Whereas the number of susceptible and infectious are decreasing in our case.

6. RESULTS AND DISCUSSION

In the SEIR measles model, the differential transformation approach is used to solve and analyze vaccines. As we know recovery rate γ will increase if we develop a strong immunity. For this reason, proper steps should be taken to reduce contact between infectious and susceptible children. However, the study of disease models using the differential transformation approach shows that the method offers a quickly converging sequence solution with fewer iterations and prevents massive computational work. This approach is fairly simple to implement and provides higher accuracy for a limited number of terms than the previous method.

The differential transformation method is proposed to solve a mixing problem. The small number of computations as compared to the computational size required in traditional numerical methods and the rapid convergence shows that the method is reliable and significantly improves the solution of differential equations over the existing methods. This method is about to be used as an alternative approach to the current techniques used for a wide range of physical problems. It is observed that the differential transformation method is an effective and reliable tool for solving the system of ordinary differential equations. This method provides a rapidly convergent series of solutions. By taking more terms in the result, the accuracy of obtained results can be improved. In most cases, the series solutions obtained by differential transformation method maybe written in exact closed form. As the present approach eliminates the analytical complexities of the other conventional approaches and all the calculations can be rendered with easy manipulations. Many cases have been checked by using the differential transformation approach and the findings have shown outstanding success.

We compared the results by the Runge-Kutta fourth-order [6] and differential transformation method. While differential transformation method gives better converging results with fewer calculations.

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