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Numerical Solution of Stochastic SEIQR epidemic model with Differential Transformation Method

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Abstract: In this we solve the Policy Decision-Making for quarantine Policy. The quarantine variable in the SEIQR model enables the policy-makers to examine the relative impact of isolation measures on controlling disease transmission. Real-World Disease Modeling can be used to model different infectious diseases like COVID-19, SARS, MERS and influenza, where quarantine is an important factor. The Reproduction Number and Disease Dynamics, derivation of equilibrium points under which a disease dies out or continues to multiple. The research compares (DTM) with the (RK4) method to determine its accuracy and efficiency. The aim of this research is to examine the application of the differential transformation to determine the approximate solutions to the SEIQR epidemiology model. In solving differential and integral equations, numerical and semi-analytical techniques are employed respectively through this method. Through the application of the DTM (Differential Transformation Method), a SEIQR model was solved and two cases were discussed, one of which is endemic and another is disease-free case. In addition, we solve the solutions using Runge-Kutta method of order four. At last, we compare both the solutions obtained by using Differential Transformation Method (DTM) and the (RK4) method. The solution, so obtained is more precise to use than DTM.

Keywords: Differential Transformation Method, SEIQR epidemiology model, RK4 Method, Transformed function, Numerical Solutions.

1. Introduction

The study of Mathematics is the Science of order, relation and structure which is used across a variety of disciplines. It is possible to solve many problems mathematically. Solving and analyzing differential equations involves analytical and numerical methods. We use analytical Taylor series method; the differential transform method (DTM) solves integral equations as well as differential equations. As a result of all these activities, we should be able to gain information about how the disease is spreading throughout the population, how we can control the spread, and how to eradicate the disease completely [1]. It is most often infectious diseases that are modeled, i.e. disease that can be transmitted from one person to another. In many diseases affect children, including measles, rubella, chicken pox and mumps, along with gonorrhea, syphilis and HIV/AIDS, as well as sexually transmitted diseases.

Runge-Kutta methods are a class of methods that extrapolate the solution to the next time step by carefully using the information on the "slope" at many points. The fourth order Runge Kutta (RK4) method is explicit and one of the most used approaches for solving IVPs. There is a need for a method that precisely use the nonlinear terms easily without any restrictions and with less number of computations. Indeed, the so called Differential Transform Method (DTM) which gives a series solutions can overcome some of the above difficulties. The DTM is very effective numerical and analytical method for solving different types of differential equations as well as integral equations. This method converts the differential equations into recurrence relations and then by Taylor series expansion will give a different approach to obtain the convergent series solutions.

The differential transformation method is very much familiar technique to solve all the kinds of differential equations. The method was originally developed by Zhou [2] for solving both linear and non-linear initial value problems in electrical circuits. Later, several researches have been conducted in applying differential transform method to different types of equations. These researches confirm the fact that this method is reliable, efficient as well as having a wider applicability.

According to Hasan [3] the differential equation system was completed by using DTM and compared with RK method in 2008. In his opinion, DTM is one of the most accurate and easiest to explore the technologies. Despite its advantages, the only disadvantage of the DTM is that it produces an approximate solution in the truncated series form and also the convergence interval is pretty limited. In a tiny area, DTM produces a series of solution which is not reflect the real time behavior of the given problem, but does provide a good estimate to the correct solution.

A number of differential algebraic equations have been solved by using this method, as well as Schrödinger equations [4], fractional differential equations [5,10] an equation of the type Lane-Emden and equations describing the unsteady movements of rotating spheres in inclined tubes. There are many advantages in this method, including the fact that it can be used directly with all ODEs without the requirement of perturbation, discretization or linearization. In [9] an artificial infectious disease optimization algorithm based on the SEIQR epidemic model is constructed. This method have an advantage in the way it is able to reduce the amount of computations needed to compute the series of solution while even maintaining accuracy and providing the series solution’s fast convergence as well. The Runge-Kutta method has been used by many authors to solve nonlinear ODEs [6, 7, 8].

In this paper, we apply the application of the Differential Transform Method to the proposed model and verify that Maple 18 and Matlab’s classical (RK4) method is valid for solving the model. Throughout this paper, the following topics are discussed. The approach of differential transformation method is covered in Section 2. To construct the SEIQR model in a dynamical system is discussed in Section 3. The equilibrium point of the model is analyzed in Section 4. In Section 5, an application of the differential transformation method and graphical representation for SEIQR model is seen. In Section 6, the comparison of the values of Runge-Kutta method of fourth order and DTM are shown in the table.

2. Methodology

The purpose of this Section is to provide insight into the methodology we used to solve our problem.

2.1. Method of Differential Transformation

If a function $h(x)$ has k^{th} derivatives, then it can be written in Taylor series expansion about a point at $x = x_0$ as

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

Table 1: A description of the fundamental operations of Differential Transformation Methods (DTMs)

S.No	Original Function	Transformed Function
1	$h(x) = m(x) \pm n(x)$	$H(k) = M(k) \pm N(k)$
2	$h(x) = cm(x)$	$H(k) = cM(k)$, where c is constant.
3	$h(x) = \frac{dm(x)}{dx}$	$H(k) = (k+1)M(k+1)$
4	$h(x) = \frac{d^2m(x)}{dx^2}$	$H(k) = (k+1)(k+2)M(k+2)$
5	$h(x) = \frac{d^rm(x)}{dx^r}$	$H(k) = (k+1)(k+2) + \ldots + (k+l)M(k+l)$
6	$h(x) = 1$	$H(k) = \delta(k)$
7	$h(x) = x$	$H(k) = \delta(k-1)$, where δ is Kronecker delta.
8	$h(x) = e^{\lambda x}$	$H(k) = \frac{\lambda^k}{k!}$
9	$H(x) = m(x)n(x)$	$H(k) = \sum_{l=0}^{k} M(l)N(k-l)$
10	$h(x) = (1+x)^r$	$H(k) = \frac{r(r-1)(r-2)\ldots(r-k+1)}{k!}$

If $h(x)$ is differentially transformed, it has the following definition

$$H(x) = \frac{1}{k!}\left[\frac{d^k h(x)}{dx^k}\right]_{x=x_0}.$$

The inverse of differential transformation method of $H(x)$ is

$$h(x) = \sum_{k=0}^{\infty} x^k H(k) .$$

Table-1 will provide a comprehensive overview of the strong fundamental mathematical operations that are accomplished with differential transforms.

3. Stochastic SEIQR model

To understand the dynamics of epidemics in mathematical terms, several models incorporating quarantine have been developed. According to this model, the whole population can be classified into five groups: susceptible, exposed, infectious, quarantined, and recovered.

Table 2: Model Variables and Description [11]

Variable	Description
S(t)	Susceptible population
E(t)	Exposed population
I(t)	Infected population
Q(t)	Quarantined population
R(t)	Recovered population

In this study, we examine the SEIQR model as described below,

$$\frac{ds}{dt} = b - \mu S - \frac{\beta SI}{N}$$

$$\frac{dE}{dt} = \frac{\beta SI}{N} - (\gamma + \mu)E$$

$$\frac{dI}{dt} = \gamma E - (\xi + \eta + \alpha_1 + \mu)I \qquad (3.1)$$

$$\frac{dQ}{dt} = \eta I - (\delta + \alpha_2 + \mu)Q$$

$$\frac{dR}{dt} = \xi I + \delta Q - \mu R.$$

In total, the size of the population $\mathrm{N(t) = S(t) + E(t) + I(t) + R(t)}$. Obviously the region $\mathrm{D} = \{(\mathrm{S, E, I, Q, R})/S \geq 0, \mathrm{E} \geq 0, \mathrm{I} \geq 0, \mathrm{Q} \geq 0, \mathrm{R} \geq 0, \mathrm{S + E + I + Q + R} \leq \mathrm{b}/\mu\}$

is a collection of model (3.1) that is positively invariant. The reproduction number of the model is

$$\mathbf{R_0} = \frac{\beta b \gamma}{\mu(\gamma+\mu)(\xi+\mu+\alpha_1+\eta)}.$$

Table 3: Model Parameter and Units

Parameter	Description	Units
b	Birth rate	Individual/day
β	Transmission co-efficient	(Individual× day)−1
μ	Natural death rate	1/day
γ	Infective individuals of exposed people	1/day
η	Infective individuals of quarantined recovery rate	1/day
ε	Recovered rate of infective people	1/day
α_1	Disease induced death rate of infected people	1/day
α_2	Disease induced death rate of quarantined people	1/day
δ	Recovered people quarantined people rate	1/day

4. Equilibrium Analysis

The following section discusses the endemic equilibrium as well as the disease-free equilibrium that will prevail in the future. There are two ways to analyze the qualitative system:

1. Disease-free equilibrium
2. Endemic equilibrium.

4.1 Disease Free Equilibrium

In the event of disease death naturally, an equilibrium resulting from the above system takes the form of a disease-free population or a disease-free equilibrium,

$S = b/\mu, E = 0, I = 0, Q = 0, R = 0,$

Hence $(S, E, I, Q, R) = \left(\frac{B}{\mu}, 0, 0, 0, 0\right)$.

The disease-free equilibrium is locally stable when $R_0 < 1$, but it is unstable when $R_0 > 1$.

4.2 Endemic Equilibrium

In the case of $R_0 > 1$, the endemic equilibrium is always stable. It will take the form of an endemic equilibrium if there is a disease-free equilibrium by the population and diseases remain unstable. We set the RHS of equation (3.1) equal to zero. The disease endemic equilibrium (S^*, E^*, I^*, Q^*, R^*) with the positive components, where

$S^* = \frac{1}{R_0}$, $E^* = \frac{b}{\mu} - \frac{(\epsilon+\eta+\mu+\alpha_1)\mu}{\beta\gamma}$, $I^* = \frac{b\gamma}{(\gamma+\mu)(\epsilon+\eta++\alpha_1)} - \frac{\mu}{\beta}$,

$$Q^* = \frac{\eta I^*}{(\delta+\alpha_2+\mu)} \quad \& \quad R^* = H + \frac{\delta\eta}{\mu(\delta+\alpha_2+\mu)} - \frac{\epsilon}{\beta}$$

where $H = \frac{b\gamma}{(\gamma+\mu)(\epsilon+\eta++\alpha_1)}(\epsilon - \frac{\delta\eta}{\mu(\delta+\alpha_2+\mu)})$.

5. An application of the DTM

Based on the transformed function of the given function in table 1, equation (1) has the following recurrence relation:

$$S(1+k) = \frac{1}{k+1}\left[b - \frac{\beta}{N}\sum_{r=0}^{k} I(k-r) - \mu\, S(k)\right]$$
$$E(1+k) = \frac{1}{k+1}\left[\frac{\beta}{N}\sum_{r=0}^{k} I(k-r) - \gamma E(k) - \mu\, S(k)\right]$$
$$I(1+k) = \frac{1}{k+1}[\gamma E(k) - \epsilon I(k) - \eta I(k) - \alpha_1 I(k) - \mu I(k)] \quad (5.1)$$
$$Q(1+k) = \frac{1}{k+1}[\eta I(k) - \delta Q(k) - \alpha_2 Q(k) - \mu Q(k)]$$
$$R(1+k) = \frac{1}{k+1}[\xi I(k) - \delta Q(k) - \mu R(k)]$$

with the initial points $S(0) = 500$, $E(0) = 100$, $I(0) = 100$, $Q(0) = 200$, $R(0) = 100$ and the parameters $N = 1000$, $b = 5$, $\gamma = 0.75$, $\alpha_1 = 0.01$, $\alpha_2 = 0.01$, $\eta = 0.5$, $\mu = 0.5$, $\beta = 1.5$, $\epsilon = 0.5$, $\delta = 0.75$.

Based on the equation, we can derive the DTM series solution of the SEIQR model as follows:

$$S(t) = \sum_{l=0}^{k} S(k)t^k$$

$$E(t) = \sum_{l=0}^{k} E(k)t^k$$

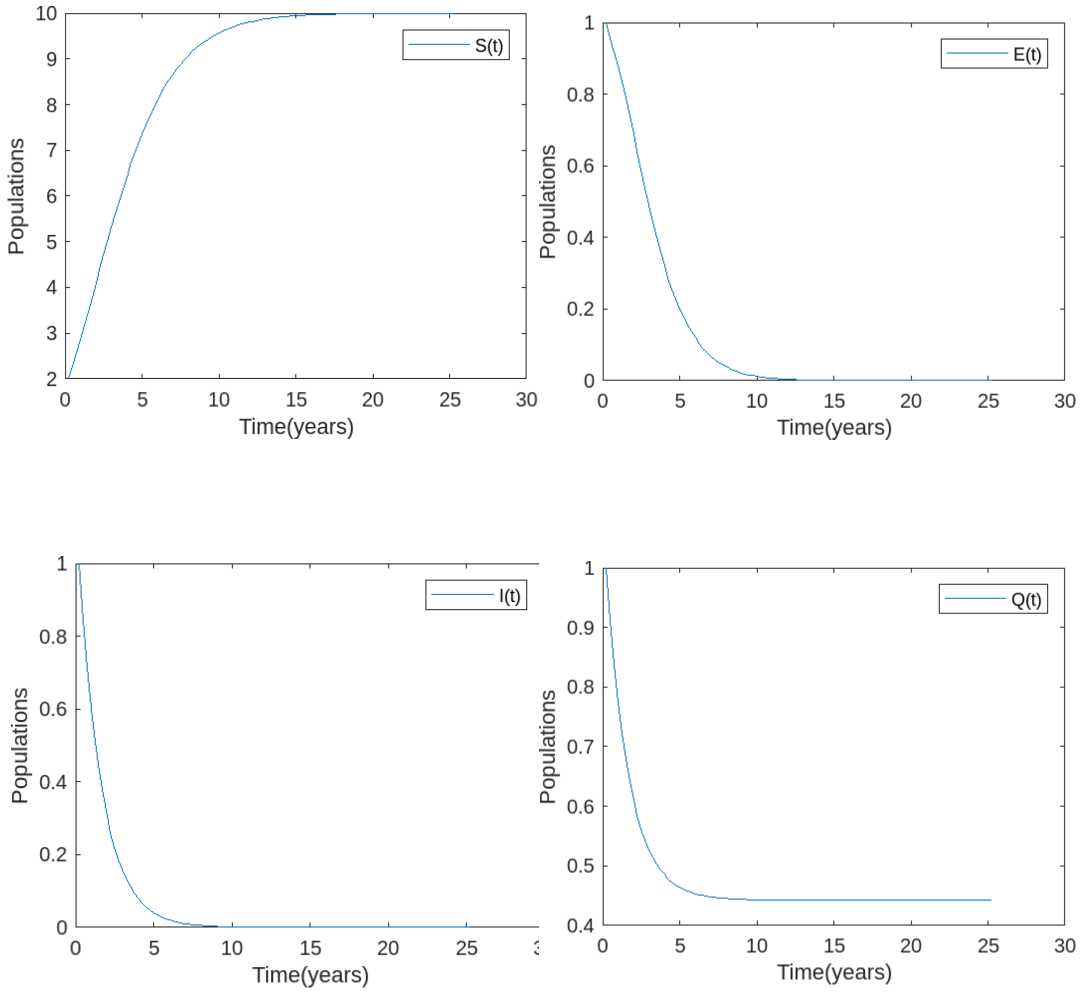
$$I(t) = \sum_{l=0}^{k} I(k)t^k$$

$$Q(t) = \sum_{l=0}^{k} S(k)t^k$$

$$R(t) = \sum_{l=0}^{k} R(k)t^k.$$

By applying the condition in (5.1), we get

$$\begin{array}{llll}
S(1) = -245, & S(2) = 129, & S(3) = -60.52083, & S(4) = 17.6802, \\
E(1) = -50 & E(2) = -34, & E(3) = 27.66875, & E(4) = -32.6418, \\
I(1) = -125 & I(2) = 75.625, & I(3) = -46.5646, & I(4) = 22.7660, \\
Q(1) = -250 & Q(2) = 126.25, & Q(3) = -40.4208, & Q(4) = 2.3646, \\
R(1) = 150 & R(2) = -162.5, & R(3) = 71.25, & R(4) = -22.3057.
\end{array}$$



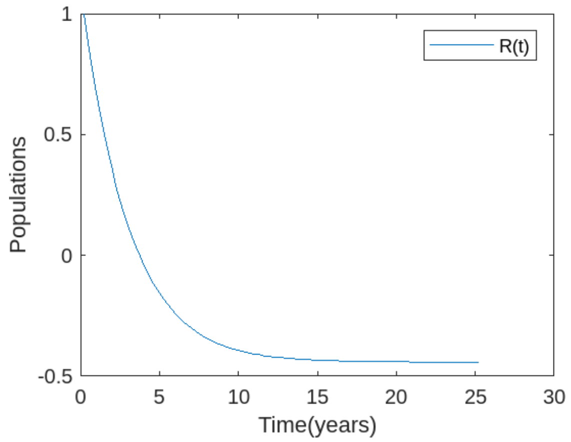


Figure 1: A relationship between S(t), E(t), I(t), Q(t) and R(t) population and time in years.

Hence the closed form of a solution, with k = 4, is as follows:

$S(t) = \sum_{l=0}^{k} S(k)t^k = 500 - 245t + 129t^2 - 60.52083t^3 + 17.6802t^4 + \ldots$

$E(t) = \sum_{l=0}^{k} E(k)t^k = 100 - 50t - 34t^2 + 27.66875t^3 - 32.6418t^4 + \ldots$

$I(t) = \sum_{l=0}^{k} I(k)t^k = 100 - 125t + 75.625t^2 - 46.5646t^3 + 22.76660t^4 + \ldots$

$Q(t) = \sum_{l=0}^{k} S(k)t^k = 200 - 250t + 126.25t^2 - 40.4208t^3 + 2.3646t^4 + \ldots$

$R(t) = \sum_{l=0}^{k} R(k)t^k = 100 + 150t - 162.5t^2 + 71.25t^3 - 22.3057t^4 + \ldots$

6. The Comparison between RK4 method and DTM

Now take the solution of the SEIQR model and compute it by the DTM and RK4 method. The values are discussed in the Table 4.

Table 4: Comparison between RK4 and DTM

t_i		0	0.25	0.5	0.75	1
Susceptible	RK4	500	444.3097	395.7261	353.2100	315.8906
	DTM	500	445.9359	403.2899	368.8744	341.1594
Exposed	RK4	100	86.8303	75.0636	64.6330	55.4509
	DTM	100	85.6798	67.9184	44.7196	11.0269
Infected	RK4	100	87.9395	76.9315	66.9970	58.1147
	DTM	100	72.8379	52.0085	36.3481	26.8270
Quarantined	RK4	200	191.1697	183.4350	176.6936	170.8434
	DTM	200	144.7683	101.6576	67.2112	38.1938

Recovered	RK4	100	82.9566	66.7665	51.4759	37.1038
	DTM	100	128.3698	141.8871	144.0946	136.4443

It is evident from Table 4 that Susceptible and Recovered populations are increasing in our cases. It is noticeable that Exposed, Infected and Quarantined populations are decreasing.

7. Conclusion

The SEIQR model with starting conditions has successfully been solved approximately in this study using the differential transformation method (DTM). We have applied the presented methods directly, without linearizing, discretizing, or perturbing. In this method, results show excellent agreement, indicating reliability and effectiveness. This tool can be used in a wide range of fields of study to solve linear problems and non-linear too. We used the Differential Transformation Method (DTM) in this work to analyze the Stochastic SEIQR Model that explains infectious disease transmission with quarantine strategies. The method offered is an efficient approximate solution method that does not need linearization, discretization, or perturbation. Comparison between the (DTM) and (RK4) methods confirms the precision and efficacy of the DTM approach to nonlinear epidemiological models. This paper suggesting that quarantine playing a vital role in the control of the spread of infection, and the model can predict disease development under varying parameter conditions. Moreover, the equilibrium analysis shows that the disease-free equilibrium is stable if $R_0 < 1$ and an endemic equilibrium exists and indicating the threshold value for disease control if $R_0 > 1$. SEIQR model and DTM framework can be generalized to other contagious diseases, such as COVID-19, SARS, and influenza, in support of public health decision-making and policy design. Research should be done on fractional-order models, stochastic phenomena, and vaccine strategies inorder to extend this approach towards applications in real epidemiology.

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