Differential Transformation Method (DTM) for solving SIS and SI Epidemic Models

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LIST OF SYMBOLS

α	Recovery rate constant
β	Infectivity coefficient
γ	Removal rate constant
λ	Contact rate
μ	Death rate constant

LIST OF ABBREVIATIONS

DTM	Differential Transformation Method
SIR	Susceptible-Infective-Recovery
SIS	Susceptible-Infective-Susceptible
SI	Susceptible-Infective

Kaedah Penjelmaan Pembezaan (KPP) untuk menyelesaikan Model Wabak SIS dan SI

ABSTRAK

Persamaan pembezaan memainkan peranan yang penting dalam pemodelan masalah dunia nyata. Salah satu kepentingannya ialah memodelkan wabak SIS dan SIR. Banyak kajian telah dijalankan untuk menyelesaikan model wabak SIS dan SIR secara berangka. Walau bagaimanapun, tiada kajian yang menggunakan Kaedah Penjelmaan Pembezaan (KPP) dalam menyelesaikan model wabak SIS dan SI. Dalam kajian ini, KPP dicadangkan untuk menyelesaikan model wabak SIS dan SI bagi populasi tetap. Terlebih dahulu, latar belakang teori mengenai KPP telah dikaji dan diikuti dengan mendapatkan penyelesaian bagi model wabak SIS dan SI. Seterusnya, analisis penumpuan dilakukan melalui pembuktian dua teorem. Akhir sekali, penyelesaian berangka telah dijalankan dan membandingkannya dengan penyelesaian tepat. Hasil kajian mendapati penyelesaian berangka yang dihasilkan oleh KPP menghampiri penyelesaian tepat dan selari dengan teorem-teorem yang dicadangkan. Secara ringkasnya, KPP adalah satu teknik alternatif yang boleh digunakan untuk menyelesaikan banyak masalah praktikal yang melibatkan persamaan pembezaan.

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ABSTRACT

Differential equations play an important role in modeling real world problem. One of the importance of differential equations is seen in the SIS and SIR epidemic models. Many researches have been proposed to solve SIS and SIR models numerically. However, there is no study about the application of Differential Transformation Method (DTM) for solving SIS and SI epidemic models. In this study, DTM is proposed to solve the SIS and SI epidemic models for constant population. Firstly, the theoretical background of DTM is studied and followed by constructing the solutions of SIS and SI epidemic models. Furthermore, the convergence analysis of DTM is proven by proposing two theorems. Finally, numerical computations are made and compare with the exact solution. From the numerical result, the solution produced by DTM approaches the exact solution which agreed with the proposed theorems. In summary, DTM is an alternative technique to be considered in solving many practical problems involving differential equations.

CHAPTER 1

INTRODUCTION

The first chapter includes general ideas of the dissertation. This chapter comprises of eight sections which are organized as follow: The first section introduces the differential transformation method (DTM) and SIS and SIR epidemic models. The second section, rhetorically written background of study about DTM, SIS and SIR epidemic models. In the same line, problem statement is discussed in section three. Research questions and research objectives have been discussed in section four and five respectively. Significance of the study is being discussed in section six. This chapter is conclusion in the last section.

1.1 Introduction

There are many methods for solving differential equations. One of them is the Taylor series method. The Taylor series mehod, however, needs much work to find the derivatives of functions. Moreover, it is too complicated to find the higher order derivatives of functions. Due to this reason, this study uses a new form of the Taylor series method that makes the calculation of higher derivatives much easier, which is called the Differential Transformation Method (DTM). The idea of DTM is to determine the coefficients of the Taylor series of the function by solving the induced recursive equation from the given differential equation. The idea of DTM was introduced by Zhou (1986).

Many researchers have been useing DTM to solve initial and boundary value problems of ordinary differential equation, moreover, it was used to analyse the response of strongly non-linear damped system (Jang & Chen, 1997). DTM is often used to solve partial differential equation, system of differential equations, and some special differential equations (Bildik & Konuralp, 2006).

The value and significance of DTM gives a close result with the exact solution. Furthermore, DTM can be easily applied in linear and non-linear differential equations (Islam, Haq, & Ali, 2009; Borhanifar & Abazari, 2010).

The spread of diseases can be modeled using mathematical model, which forms an area of study in biology, called epidemiology. The first formulation of the physical real-life problem in epidemiology was introduced and described by using differential equations. The first mathematical model of epidemiology can be traced back to Bernoulli in 1763, who formulated and solved this problem. In fact, closed form solutions to mathematical models play a vital role in the proper understanding of qualitative features of natural science. In epidemiology, mathematical models describe some effects of the disease in some population, so one needs to be very careful while analyzing such models.

One of the tools which investigate the mechanisms for outbreaks and the spread of diseases is the mathematical modeling of infectious diseases. This tool includes two models. The first one was proposed by Daniel Bernoulli in 1763. The model showed that the universal inoculation against smallpox could increase the life expectancy. The second model called the modern mathematical epidemic modeling, which was an extension of the first mathematical epidemic model, proposed by Kermack and McKendrick (1927). Recently, the study of mathematical epidemiology has grown rapidly, with several types of models which are modeled and formulated in order to apply in the study of infectious diseases. In addition, this modeling considered effective in predicting the behavior of outbreaks in many recorded epidemics (Nelson & Williams, 2014; Fine & Lindqvist, 2014).

The main problem with models in epidemiology is that some of these models even the simplest one of natural phenomena with sets of first order ordinary differential equations are non-integrable. In order to avoid this problem, Nucci and Leach (2004) have studied these features and obtained an explicit solution for the SIS model by applying Lie theory of transformation groups. At the same time, they have obtained that the fatal disease with this model is also given a bad behavior.

Under this consideration, the community is divided into three disjoint classes: the first is a susceptible class (individuals who can incur the disease but are not yet infective). The second class called the infective class that is transmitting the disease to others. Finally, the third class called removed class consists of those classes that are removed from the susceptible-infective.

1.2 Research Background

The DTM was first proposed by Zhou (1986), who solved linear and nonlinear initial value problems in electric circuit analysis. DTM uses the Taylor series for the solution of differential equations through a semi-analytical numerical method. The DTM replaces the procedure of obtaining a solution for any given differential equation of Taylor series expansion and may help to solve various other types of differential equations. In this method, it is possible to obtain greater accuracy in the numerical solution of differential equations.

Rapid spreading of the infectious disease to a large number of people within a short period of time is known as an epidemic. The first epidemiological model published by Daniel Bernoulli in 1763, that aimed to demonstrate the graft with animate virus obtained directly from a patient with a temperate case of smallpox in which this might to increase the population and reduce the death rate. In 1761, D'Alembert defined applicable alternative method for non-infectious diseases and infectious diseases to dealing with competing hazards of death. These examples and many others, such as the methods proposed by Daniel Bernoulli provide some prediction knowledge regarding smallpox (Hethcote, 1989). For instance, the average of age expectancy increases from 26 years 7 months until 29 years 9 months after the universal inoculation versus smallpox (Bernoulli & Blower, 2004).

The first mathematical model of epidemiology can be traced back to Bernoulli in 1763 and the modern modeling proposed by Kermack and McKendrick (1927). There are two main epidemic models: the SIS model and the SIR model. In the SIS model, it is more likely to catch the disease and be influenced by it. In addition to that it is ineffective by the disease. In other words, 'S' refers to the susceptible component, while 'I' refers to this component when it is ineffective. However, the disease can take two forms, the first is SIS where the disease goes through the process of being susceptible then infective and goes back to be a susceptible component. However, in the SIR model, 'R' refers to a recovery state. Nevertheless, in the SIR case, the disease goes from being susceptible, followed by being infected, and after that the disease can be removed by recovery or death or even by developing immunity against the disease, unlike the SIS model where the disease can go back to the susceptible component. This usually happens when the susceptible component cannot produce immunity against the reinfection. These models can be applied in the case of the bacterial or Helminth agents, disease, and similarly in most of the sexually transmitted disease. These models were felicitous in predicting the behavior of propagation, very similar to that spotted in many recorded epidemics (Brauer & Castillo-Chavez, 2001).

1.3 Problem Statement

Certain epidemiology models have been solved by DTM. See the works by Batiha and Batiha (2011a) and Akinboro, Alao and Akinpelu (2014). The former considered the numerical solution of SIR model without vital dynamics using DTM. The latter considered the numerical solution of SIR model with vital dynamics using DTM. However, to the best of our knowledge, SIS model without vital dynamics and SI model with vital dynamics are not solved by DTM yet. So, this study focused on finding semi-analytic solutions of the SIS model without vital dynamics and SI model with vital dynamics using DTM.

SIS model without vital dynamics returns the infective to the susceptible class on recovery because the diseases confer no immunity against reinfection. The SIS model without vital dynamics is as follows:

$$\begin{cases} s'(t) = -rs(t)i(t) + \alpha i(t), \\ i'(t) = rs(t)i(t) - \alpha i(t), \end{cases} \tag{1.3.1}$$

subject to the initial conditions:

$$i(0) = I_0,\ s(0) = S_0 \tag{1.3.2}$$

where s is the susceptible fraction of the population, i is the infected fraction of the population, r is the infectivity coefficient and α is the recovery coefficient, while $I_0 > 0,\ r > 0,\ \alpha > 0,\ S_0 > 0$.

In the SI model with vital dynamics, the infectives donot recover. This model also assumed that births and natural deaths occur at equal rates and that all newborns are susceptible. Individuals are removed by death from the susceptible and the infective classes. The said model is as follows:

$$\begin{cases} s'(t) = -\beta s(t) i(t) - \mu s(t) + \mu, \\ i'(t) = \beta s(t) i(t) - \mu i(t), \end{cases} \tag{1.3.3}$$

subject to the initial conditions:

$$s(0) = S_0,\ i(0) = I_0, \tag{1.3.4}$$

where β is the infectivity coefficient, μ is the births and natural deaths rate, s is the susceptible fraction of the population and i is the infected fraction of the population, while $\mu > 0,\ \beta > 0, S_0 > 0, I_0 > 0$.

Important: For the rest of the dissertation, SIS model without vital dynamics as shown in Eq. (1.3.1) and Eq. (1.3.2) is referred as **SIS model**; while SI model with vital dynamics as shown in Eq. (1.3.3) and Eq. (1.3.4) is referred as **SI model**.

1.4 Research Objectives

The aim of this study is to solve the SIS model and SI model using Differential Transformation Method (DTM) by achieving the following objectives:

1. To study DTM and its properties.
2. To derive the solutions of SIS and SI models using DTM.
3. To study the convergence of the solutions given by DTM.
4. To compare the results generated by DTM with the exact solutions of SIS and SI models.

1.5 Scope of the Study

The scope of this study is to present semi-analytical solutions for systems of differential equations, namely the SIS and SI models using the DTM. The study starts by presenting the idea of DTM and its properties. Later, it is used to derive the solutions of SIS and SI models. The solutions give an overview to understand the SIS and SI epidemic models about the diseases which are spread by direct person-to-person contact in a population.

1.6 Significance of the Study

In this study, DTM is used to solve the SIS and SI epidemic models. DTM produced good results that are very close to the exact solution, and in some cases DTM gives the exact solution. Therefore, the accurate values of $s(t)$ and $i(t)$ are highly essential in biology and epidemiological field to control of the spread of diseases.

1.7 Conclusion

This chapter quickly warps up the general introduction, research background, problem statement, research objectives, scope of the research, significance of the study, and outlines the strategy adopted by the research. In the second chapter, brief literature reviews on DTM and epidemic models will be discussed.

CHAPTER 2

LITERATURE REVIEW

2.1 Introduction

In this chapter, a literature review of differential transformation method (DTM), SIS and SIR epidemic models have been discussed.

2.2 Differential Transformation Method (DTM)

The differential equation (DE) is an important field in mathematics and it has many applications in physics, engineering, chemical, biological, and many more. Moreover, there are many types of differential equations such as first order DE, second order DE, higher order DE, homogeneous DE, non-homogeneous DE and so on. Therefore, there are many methods to solve a differential equation such as separable method, Laplace method, series method and etc. to solve DE. Therefore, series solution and Taylor series established a differential transformation method.

The linear and non-linear initial value problems can be solving using DTM which is part of electric circuit analysis (Zhou, 1986). This method formulates a numerical technique which is known to be semi-analytical and it works on the basis of Taylor series that resolves the issues of polynomial differential equations. The high-order Taylor series method depends upon symbolic computation of essential derivatives of data function which differentiate it from DTM. The Taylor series method is time-consuming especially in the case of higher order equations. On the other hand, DTM provides iterative process for the solution of differential equations in the form of analytical Taylor series. For the solution of different types of differential equations, DTM is effective and efficient. Additionally, DTM also solves linear and non-linear boundary-value problems (Chen & Liu, 1998).

DTM has been used to solve initial value problems, and approximate the solution of linear and non-linear initial value problems by DTM of fixed grid size presented by Jang, Chen and Liy (2000). Hassan (2007) compared the DTM with the Adomain decomposition method for solving linear and non-linear initial value problem Hassan (2008) used DTM to solve systems of linear and non-linear differential equations and the results of DTM are in a good agreement with Runge–Kutta method and exact solution. The exact solution of SIS and SI epidemic models are obtained using the direct integration tools (Shabbir, Khan, & Sadiq, 2010). Moreover, the differential transformation method was extended to singularly perturbed Volterra integral equations and accurately solved some examples of singular perturbed Volterra equations (Doğan, Ertürk, Momani, Akın, & Yıldırım, 2011).

The DTM has been generalized to solve higher order linear boundary value problems (Hussin, Kilicman, & Mandangan, 2010). Additionally, it is important to check the accuracy of solutions generated by DTM. Hussin et al. (2010) showed that the solution of the DTM is accurate and efficient.

The DTM can also be applied to find the numerical solution of higher order homogeneous and non- homogeneous ordinary differential equations. Furthermore, the DTM is capable to diminish the size of the calculation when finding the numerical solution of differential equation, and the numerical solution found is closed to the exact solution or sometimes it gives the exact solution (Batiha & Batiha, 2011b). The hyperbolic telegraph equation was solved by DTM, and exact solutions of this equation were obtained (Soltanalizadeh, 2011).

DTM is used to solve fourth order parabolic partial differential equations and the DTM has given the exact solution of this equation (Soltanalizadeh & Branch, 2012). Furthermore, DTM was used to solve the one dimensional planar Bratu problem (Hassan & Ertürk, 2007). DTM also applied to the generalized Burgers-Huxley equation (Biazar & Mohammadi, 2011). Likewise, DTM was used to obtain approximate solutions for the El Nino Southern Oscillation (ENSO) model. Efficiency, accuracy and error rates of the solutions are compared with the analytical solution, and solutions generated by variational iteration method and Adomain decomposition mehod (Gubes, 2013).

2.3 Epidemic Models

The epidemic model was generalized by several scholars such as Kermack and McKendrick (1927) and Severo (1969). In the same way, Liu, Hethcote and Levin (1987) showed an important result concerning non-linear incidence rates in their equations. In addition, the convergent series solutions for SIR and SIS models have been obtained by Khan, Mohapatra, Vajravelu and Liao (2009) by using the homotopy analysis method. Many researchers have considered these models by using stability, bifurcation theory, Poincaré-Bendixson type theorems, index and topological concepts (Diekmann, Heesterbeek, & Metz 1990; Murray, 1993). In addition, modeling human mobility responses to the large scale spreading of infectious diseases (Meloni, Perra, Gómez, Moreno, & Vespignani, 2011). However, Holme and Liljeros (2014) investigated two canonical models of infectious disease epidemiology in the SIS and SIR models. Besides, Krobenikov and Maini (2004) used Lyapunov functions for the SIS and SIR models as to introduce global stability of the endemic equilibrium states. Moreover, Yicang and Liu (2003) studied the dynamical behavior of the SIS model and showed that the disease free periodic solution is stable if $R_0 > 0$ and unstable when $R_0 < 0$, where R_0 is the basic reproductive number.

Katriel (2012) formulated an epidemic SIS model with individual susceptibility distributed according to a discrete or continuous probability function to assess the generality of such hypothesis in order to attack rates in an epidemic SIR model with heterogeneity introduces an ordering among susceptibility distributions with the same mean, analogous to that considered. The expected correlation between variance and prevalence does not always hold since both the discrete and continuous frameworks can be finite. For continuous distributions, the results are based on numerical studies with the beta distribution. On the other hand, for discrete distributions this fact is demonstrated analytically (Margheri, Rebelo, & Gomes, 2015).

Moreover, in the network structure, the theory of epidemic outbursts introduced by Tagore (2015), which is exclusively for the scale of free networks. Furthermore, the development of epidemics penetrates in the scientific community because it applies in the actual network world on the large scale. It will be easy for the reader to find out the solution of issues that relates to epidemics such as propagation. The next objective is to explain the SIS and SIR models and their implications by using the developing strategies to analyze the reason of damage on the free scale network.

The SIR model for general infectious dynamics was solved by the homotopy perturbation method (HPM). Computer software was used to obtain the graphical profiles of the three compartments while varying some salient parameters. The analysis revealed that the efforts at eradication or reduction of disease prevalence must always match or even supersede the infection rate (Abubakar, Akinwande, Jimoh, Oguntolu, & Ogwumu, 2013).

SIR models without and with vital dynamics were considered in Batiha and Batiha (2011a) and Akinboro et al. (2014), respectively. They have solved the said models using DTM. Both of them found out that DTM is efficient, accurate and comparable to variational iteration method, Adomian decomposition method and homotopy perturbation method (HPM). To the best of our knowledge, SIS model without vital dynamics and SI model with vital dynamics are not solved by DTM yet.

2.4 Conclusion

This chapter incorporates the reviews of DTM, and the SIS and SIR epidemic models; furthermore, stating the current efforts to solve SIS and SIR epidemic models. In the following chapter, research methodology will state the main definitions and theorems of DTM, listing the equations of SIS and SI epidemic models, and explain