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Full Length Research Article

SEMI ANALYTIC METHOD FOR SOLVING INFECTIOUS DISEASE MODEL

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ABSTRACT
In this paper, we present a deterministic model that captures the essential dynamics of infectious diseases. Differential Transform Method (DTM) is applied to attempt the series solution of the model. The efficiency of the DTM in solving the model is confirmed by classical fourth-order Runge-Kutta method implemented in Maple 18. The comparisons between the DTM and Runge-Kutta (RK4) solutions were made and there exists positive correlation between the results obtained by the two methods. The outcome of comparison between the DTM and RK4 validates the potential of the DTM in coping with the analysis of modern epidemics.

Keywords: Infectious Disease, Differential Transform Method, Runge-Kutta Method.

INTRODUCTION

A disease is a malfunctioning of any part of the body. Onyebuchi-Chukwu (2013) asserted that a disease is any deviation from or an interruption of the normal structure or function of any part of the body, organ or system that is manifested by a characteristic set of symptoms and signs and whose etiology, pathology and prognosis may be known or unknown. A disease may be infectious or non-infectious. A disease is infectious if it can spread from person to person. Infectious diseases have been occurring in human population right from the pre-Stone Age and the menace of these diseases is not only a major cause of death and misery to man but also has the potential to jeopardize the social and economic stability (Mark & Rohni, 1996). The outbreak of infectious diseases often leads to the enormous expenditure on healthcare delivery in relation to the disease control and management. The evidence of economic implication of infectious diseases was the outbreak of measles in Italy between 2002 and 2003 which brought about the hospitalization of over 5 000 patients and the overall treatment outlay of between 17.6 million Euro and 22.0 million Euro (Alonso-Quesada & Delasen, 2008). Also, the outbreak of measles in California in 2008 resulted in the treatment cost of $10 376 or $177 000 per case (Fred *et al.,* 2014).

Every year, millions of human beings suffer or die of various infectious diseases globally (D'Agata *et al.,* 1993). Infectious diseases have tremendous influence on human life and the entire human race has been frustrated by different types of contagious diseases such as Polio, SARS, Cholera, Leprosy, Meningitis, H5N1, HIV/AIDS, Small pox, Chicken pox, Monkey pox, Ebola, Lassa fever and so on (Squires & Tappenden, 2011). Many a time the propagation of an infectious disease can be instantaneous to the degree that within few days it spreads at an unimaginable rate.

For instance, in an English boarding school with a total of 763 boys, there was an outbreak of influenza from January 22 to February 4 1978. A total of 512 boys were put to bed during the epidemic that seems to have started from a single boy (Abramson, 2011).

Infectious diseases have various attributes which make their elimination or control procedures differ from one another. For example, H5N1 can be contained via behavioural changes of the susceptible in the population whereas, other diseases like small pox and polio have been eliminated in various parts of the globe as a result of the preventive and control systems instituted by organizations like WHO, UNICEF and many government agencies (Daley & Gani, 2005). A good number of infectious diseases which are vaccine preventable have specific ways of management. For instance, every effort to contain measles and small pox is anchored on immunization of the susceptible individuals. These efforts have recorded positive result for small pox whose global eradication was declared on December 9, 1979, two years after the last case in Somalia (Ayoade *et al.,* 2017). Unfortunately, unlike small pox, the battle to eradicate other infectious diseases that have similar characteristics with small pox e.g. measles has not been won rather the disease continues to pose itself as one of the global health issue of all time (Edward *et al.,* 2014).

The outbreak and spread of diseases have been questioned and studied for many years. Controlling infectious diseases has been an increasing complex issue in recent years (Keeling & Danon, 2009). The ability to make predictions about diseases could enable scientists to evaluate inoculation or isolation plans and may have a significant effect on the mortality of a particular epidemic (Naresheta, 2008). The modeling of infectious diseases is a tool which has been used to study the mechanism by which disease spread, to predict the future course of an outbreak and to evaluate strategies to control the epidemic (Bell & Dominici, 2010). A mathematical model is described by Neilan *et al.* (2010) as the representation of the real world characterized by the use of mathematics to represent the parts of the real world that are of interest and the relationship between those parts. Patz *et al.* (1996) argued that models can be used to inform policy decisions by synthesizing a diverse range of evidence within a coherent and explicit framework. In developing a model, modelers do adopt mathematics concepts to characterize the real life situations and in the process, they arrive at equations which are generally nonlinear because occurrences in real life are mostly nonlinear.

When the equations are formulated, the next step is how to solve the equations. Generally, the solutions of nonlinear equations through the traditional theory of mathematics are not easy if not impossible. Hence, modelers do employ one numerical method or the other to obtain the solutions of these nonlinear equations. Differential transform method is one of the notable semi-numeric-analytic methods for obtaining approximate analytic series solutions to nonlinear problems. Zhou applied the differential transform method for the first time in 1986 to solve problems on

electric circuit (Hussin *et al.,* 2010). Since then the method has gained popularity and received considerable amount of interest of the scientists globally. It was employed to obtain the solution of quadratic Riccati differential equation by Biazar & Eslami (2010), Lane-Emden type equation by Arikoglu & Ozkol (2007) and boundary layer equation in a finite domain by Oderinu *et al.* (2018). Differential transform method had also been applied in Biomathematics on several occasions. It was applied by Akinboro *et al*. (2014) to solve an epidemic model, by Chakraborty *et* al. (2017) to solve a model which described the transmission dynamics of computer virus, by Peter & Ibrahim (2017) and Peter *et al.* (2018) to obtain the solutions of typhoid fever models, and also by Peter & Akinduko (2018) to solve HIV/AIDS model and by Lawal *et al.* (2018) to solve cholera model.

The introduction of the differential transform method has been advantageous in that the rigorous and laborious massive computational work, round off errors, linearization and perturbation are overcome. In the light of this, we formulate a basic compartmental mathematical model and employ the differential transform method to obtain the solutions of the model.

MATERIALS AND METHODS

A compartmental model is adopted to analyze the transmission dynamics of disease in a human population. The model is divided into subpopulations based on the epidemiological status of individuals in the population. The susceptible population is generated from the daily recruitment of birth at the rate β. It is increased as a result of loss of immunity after recovery and vaccination at the rate σ and decreases due to vaccination and natural death at the rate ρ and μ respectively. The infectious class is generated at the rate α when there is interaction between the susceptible and the infectious individuals. The infectious class however reduces through the recovery from infection and the disease induced death at the rates γ and δ respectively. Furthermore, the Recovery subclass is generated from vaccinated susceptible subpopulation and recovered infected individuals at the rate ρ and γ respectively. They are reduced due to loss of immunity from recovery and natural death at the rate γ and μ respectively**.** To indicate this mathematically, we have:

$$\frac{dS}{dt} = \beta - \alpha SI - (\rho + \mu)S + \sigma R \qquad (1)$$

$$\frac{dI}{dt} = \alpha SI - (\gamma + \delta + \mu)I \qquad (2)$$

$$\frac{dR}{dt} = \gamma I - (\mu + \sigma)R + \rho S \qquad (3)$$

The Differential Transform Method

The process involved in DTM is as follows: Given an arbitrary function of x, suppose $y(x)$ is a non-linear funtion of x, then $y(x)$ can be expanded in a Taylor series about a point $x = 0$ as

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

Thus,the differential Transform of $y(x)$ is given as:

$$Y(k) = \frac{1}{k!}\left[\frac{d^k}{dx^k} y(x)\right]_{x=0}$$

and the inverse differential Transform is given as

$$y(x) = \sum_{k=0}^{\infty} Y(k)x^k$$

Some of the operational properties of the DTM are outlined in table 1 while table 2, the initial values assigned to each parameter and their sources to conduct the simulation are presented. In table 1, $c(x)$ and *d(x)* are arbitary functions with transforms $C(k)$ and $D(k)$ respectively.

Table 1: Basic operation properties of the DTM

S/No	Original Function	Transformed Function
1	$y(x) = c(x) \pm d(x)$	$Y(k) = C(k) \pm D(k)$
2	$y(x) = \alpha c(x)$	$Y(k) = \alpha C(k)$, α is a constant
3	$y(x) = \frac{dc(x)}{dx}$	$Y(k) = (k+1)C(k+1)$
4	$y(x) = \frac{d^2c(x)}{dx^2}$	$Y(k) = (k+1)(k+2)C(k+2)$
5	$y(x) = \frac{d^n c(x)}{dx^n}$	$Y(k) = (k+1)(k+2)\cdots(k+n)C(k+n)$
6	$y(x) = 1$	$Y(k) = \delta(k)$
7	$y(x) = x$	$Y(k) = \delta(k-1)$, δ is the Kronecker delta
8	$y(x) = e^{(\lambda x)}$	$Y(k) = \frac{\lambda^k}{k!}$
9	$y(x) = c(x)d(x)$	$Y(k) = \sum_{n=0}^{k} D(n)C(k-n)$
10	$y(x) = (1+x)^n$	$Y(k) = \frac{n(n-1)(n-2)\cdots(n-k+1)}{k!}$

NUMERICAL SIMULATION AND GRAPHICAL ILLUSTRATION OF THE RESULTS

In this section, we present the numerical simulation which demonstrates the analytical results for the infectious disease model. This is achieved by using the set of parameter values given in Table 2 which are derived from the literature as well as assumptions. We considered the following initial conditions for the different compartments. $S(0) = 300$, $I(0) = 200$, $R(0) = 100$. Using the operational properties (1), (2), (3) and (6) in Table 1 and applying them to the system of differential equations (1) – (3), we obtain the following system of transformed equations:

$$S(k+1) = \frac{1}{k+1}[\beta b(k,0) - \alpha \sum_{l=0}^{k} S(l)I(k-l) - (\rho + \mu)S(k) + \sigma R(k)]$$

$$I(k+1) = \frac{1}{k+1}[\alpha \sum_{l=0}^{k} S(l)I(k-l) - (\gamma + \delta + \mu)I(k)]$$

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$$R(k+1)=\frac{1}{k+1}[\gamma I(k)-(\mu+\sigma)R(k)+\rho S(k)]$$

Applying the initial conditions for the state variables together with the values of the parameters in table 2 and the computation at k = *6* for the above equations, the 6th terms approximations to the solutions of *S(t), I(t),* and *R(t)* in a closed form are determined with the help of mathematical software (Maple18) as follows:

$$S(t)=\sum_{n=0}^{k}S(k)t^k=3000+9.9982944001E5t-2.849606446E5t^2+21242.56063t^3$$
$$-3.024139142E7t^4+6.000217282E6t^5-5.542837547E9t^6+...$$

$$I(t)=\sum_{n=0}^{k}I(k)t^k=200+57.4000t+1.099894753E5t^2+10668.28948t^3$$
$$+3.023938248E7t^4-4.143376832E6t^5+5.542515808E9t^6+...$$

$$R(t)=\sum_{n=0}^{k}R(k)t^k=100+98.5600t+1.649709422E5t^2-32320.80299t^3$$
$$+1976.338874t^4-1.935462713E6t^5+3.309772042E5t^6+...$$

The DTM is demonstrated against the Maple 18 fourth order Runge-Kutta procedure to investigate the degree of accuracy of the method (i.e. DTM). Fig (1) , Fig (2) and Fig (3) show the combined plots of the solutions of $S(t)$, $I(t)$ and $R(t)$ by the DTM and RK4

Table 2: Parameters Values for the Model

Description	Parameter	Initial Value	Source
rate of loss of immunity after recovery	σ	0.44	Estimated
rate of recovery from infection	γ	0.01	Mushayaba (2011)
disease induced death rate	δ	0.013	Adetunde (2008)
natural death rate	μ	0.02	Assumed
contact rate	α	0.0011	Assumed
vaccination rate	ρ	0.33	Lauria et al (2009)
recruitment rate	β	10^5	Assumed

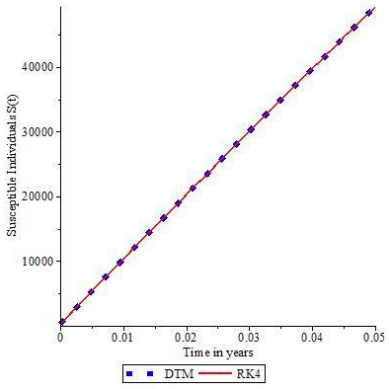

Fig1: Solution of Susceptible Population by DTM and RK4

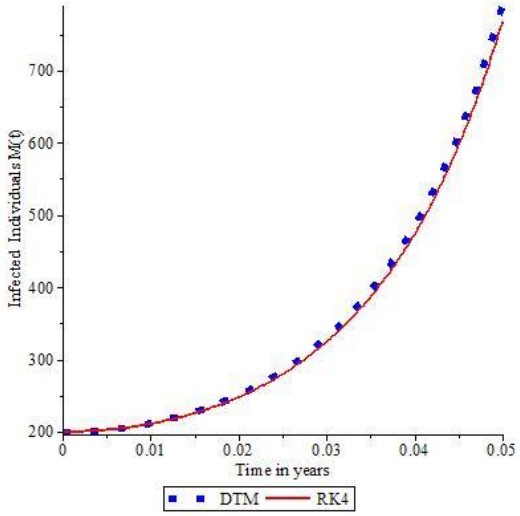

Fig2: Solution of Infected Population by DTM and RK4

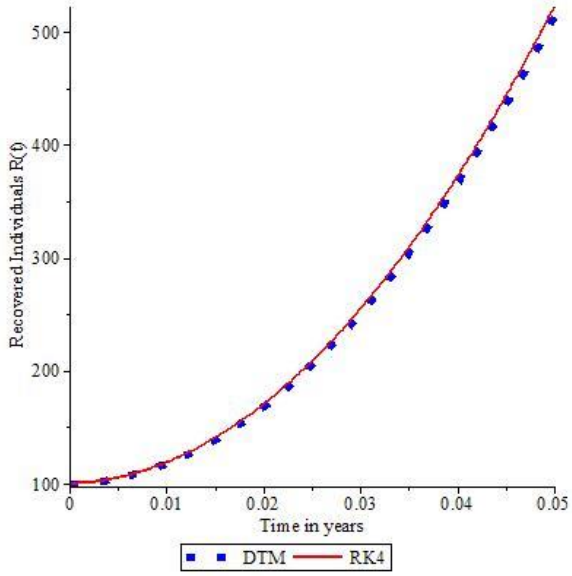

Fig3: Solution of Recovered Population by DTM and RK4

DISCUSSION OF RESULTS

Figures 1, 2, and 3 show the outcome of the comparison between the solutions of the proposed model by using the DTM and RK4. The figures demonstrate the existence of positive correlation between the solutions the two methods as the two curves follow the same pattern and behaviour in each case. The superb convergence of the solutions of the DTM with that of RK4 indicates that the DTM obtained the reliable and accurate results for the model.

Conclusion

A deterministic model is formulated to analyze the transmission dynamics of infectious disease. Taking the initial conditions from the literature as well as assumption, the DTM is applied straight

away to obtain the solutions of the model without linearization or perturbation. The reliability and accuracy of the DTM is examined when the results obtained by it are compared with the results obtained by using the Runge-Kutta method; the outcome of which is displayed graphically. Going by the outcome of our simulations, we conclude that the DTM is a powerful technique which can be used to obtain the approximate accurate series solutions for the epidemic models designed in terms of ordinary differential equations

Contribution of authors

A. F Adebisi and A. B Ganiyu designed the model, O. J. Peter wrote the code and did the computation; A. A. Ayoade and T.A Ayoola wrote the introduction and proofread the manuscript. O. E Faniyi anchored the revisions and approved the article submission.

Conflict of Interest

The authors declare no conflict of interest

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