Application of Differential Transform for Solving Typhoid Fever Model

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ABSTRACT

The authors of this paper have developed a mathematical model on the transmission dynamics of typhoid fever using the concept of differential equation. Differential Transform Method (DTM) is employed to attempt the series solution of the model. The validity of the DTM in solving the model is established by classical fourth-order Runge-Kutta method implemented in Maple 18. The comparison between DTM solution and Runge-Kutta(RK4) was performed. The results obtained confirm the accuracy and potential of the DTM to cope with the analysis of modern epidemics.

(Keywords: typhoid fever, differential transform method, DTM, Runge-Kutta method, mathematical biology, disease transmission, mathematical modeling)

INTRODUCTION

Typhoid fever is a life-threatening infection caused by the bacterium *Salmonella typhi*. It is usually spread through contaminated food or water. Once *Salmonella typhi* bacteria are ingested, they multiply and spread into the bloodstream (Kariuki, 2004).

Urbanization and climate change have the potential to increase the global burden of typhoid. In addition, increasing resistance to antibiotic treatment is making it easier for typhoid to spread in communities that lack access to safe drinking water or adequate sanitation.(Moffact, 2014).

Typhoid bacteria are passed in the feces and urine of infected individuals. People become

infected after eating food or drinking beverages that have been handled by a person who is infected or by drinking water that has been contaminated by sewage containing the bacteria.

Once the bacteria enter the body they travel in the human intestines, and then enter to the bloodstream. They enter to the blood through lymph nodes, gallbladder, spleen, liver, etc. Abdominal pain, fever and general ill feeling are the symptoms of this disease. High fever (103°F, or 39.5 C) or higher and severe diarrhea occur as the disease gets worse (Mushayabasa, *et al.*. 2014; Mushayabasa, 2012). According to estimates in the literature, 21.6 million people worldwide were sick with typhoid fever in 2001, contributing to 216,500 deaths (WHO, 2004).

Many computational mathematicians find it important and fascinating to model the transmission and spread of typhoid illness. In the past, the main focus of the research of infectious diseases has also been on how they affect the human population (Watson and Edmunds, 2015).

Typhoid fever has recently been linked to a significant number of deaths in the urban and peri-urban population. For instance, some community-based studies from South Asia, where rates reach 500–1000 cases per 100,000 inhabitants and the incidence rate seems to be high among young children (Mushayabasa, *et al.*, 2013).

When dealing with large populations, as in the case of typhoid fever, compartmental mathematical models are used. In the deterministic model, individuals in the population

are assigned to different subgroups, each representing a specific stage of the epidemic.

Mathematical models are used in science and engineering to help understand complex systems and optimize industrial processes. There are numerous examples of the fruitful application of mathematical principles to problems in typhoid vaccines and in the recent years, there have been increasing interests in applying the transmission models.

Various studies including mathematical model of spread of typhoid fever, dynamic model for analyzing and predicting process of typhoid fever among others have been conducted by many researchers globally. For instance, according to Peter, *et al.* (2017) constructed mathematical model of the type PSITR in which added a recovered compartment in which all treated individuals recovered but after some time the recovered individuals lose immunity and return back to susceptible class.

Several authors have also worked in this area, and few among them are Lauria, *et al.* (2009) and Nithiri, *et al.* (2016). In Lauria, *et al.* (2009) an optimization model for reducing typhoid cases in developing countries without increasing public spending; Nithiri, *et al.* (2016) mathematical modelling of typhoid fever disease incorporating protection against the disease. Thus, in this work, the test for the existence and uniqueness of solution for the model using Lipschitz condition and compute the basic reproduction number necessary for the disease control.

The concept of the differential transform was first proposed by Zhou (1986) and its main applications therein are to solve both linear and nonlinear initial value problems in electric circuit analysis. Differential Transform Method (DTM) is proved to be an excellent tool to investigate analytical and numerical solutions of nonlinear ordinary differential equations.

The concept of differential transformation is briefly presented and some well-known properties of this DTM are rewritten in more generalized forms. The DTM is one of the semi-analytical methods commonly used for solving ordinary and partial differential equations in the forms of polynomials as approximations of exact solution. DTM has been used by many researchers to solve various problems (Peter, *et al.*, 2017, 2018; Abioye, *et al.*, 2018).

In this study, we employ the Differential Transformation Method (DTM) to the model developed by (Victor, *et al.*, 2022). In order to illustrate the accuracy of the DTM, the obtained results are compared with classical fourth-order Runge-Kutta Method.

MODEL FORMULATION

The compartment used in this model consists of three classes, namely;

- Susceptible class S(t): these are individuals who are susceptible to the disease or are prove to the disease.
- Infected I(t): these are individuals who are infected with the disease and are capable of transmitting the disease to those in the susceptible class.
- 3) Recovered class R(t): these are who have recovered from the disease.

Recruitment rate to susceptible class is either by immigration or by birth at a rate (π). Susceptible individuals get infected through interaction with the infected individuals at a rate (β), γ represent rate of recovery from infection. In each of the classes, individual can die naturally at a rate (μ), the disease induced death rate is given as (δ), the above illustration can be represented by the system of differential-equations given below:

$$\frac{dS}{dt} = \pi - \beta SI - \mu S \tag{1}$$

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

$$\frac{dR}{dt} = \gamma I - \mu R \tag{3}$$



Figure 1: The Model's Flow Diagram.

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Variable	Description	
S(t)	Susceptible class at time t	
l(t)	Infected individual at time t	
R(t)	Recovered individuals at time t	
Parameter	Description	
π	Recruitment rate	
β	Force of infection	
μ	Natural death rate	
δ	Disease induced death rate	
γ	Recovered rate	

METHODOLOGY

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

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

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:

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

Table 3 gives some operational properties of DTM.In the table, c(x) and d(x) are arbitrary functions with transforms C(k) and D(k) are the transformed functions, respectively.

S/No	Original Function	Transformed Function
1	$y(x) = c(x) \pm d(x)$	$Y(k) = C(k) \pm D(k)$
2	$y(x) = \alpha c(x)$	$Y(k) = \alpha C(k), \ lpha$ is a constant
3	$y(x) = \frac{dc(x)}{dx}$	Y(k) = (k+1)C(k+1)
4	$y(x) = \frac{d^2 c(x)}{dx^2}$	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	$y(x) = (1+x)^n$	$Y(k) = \frac{n(n-1)(n-2)\cdots(n-k+1)}{k!}$

 Table 2: Basic Operation Properties of the DTM.

Solution of the Model

In this section, we apply the steps involved in differential transform method to model (1) as follows.

Using the operational properties (1), (2), (3) and (6) in Table 1 and applying them to the systyem of differential equations in (1) we obtain the following system of transformed equations below:

$$S(k+1) = \frac{1}{k+1} [\theta b(k,0) - \sum_{l=0}^{k} S(l) (\beta I_{e}(k-l)) - \mu S(k)]$$

$$I(k+1) = \frac{1}{k+1} \left[\sum_{l=0}^{k} S(l) (\beta I(k-l)) - K_1 I(k) \right]$$

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

where,

 $K_1 = \mu + \delta + \gamma$

Subject to the initial conditions S(0) = 60, I(0) = 20, R(0) = 10. Using the initial conditions and the parameter values in the table and with the help of Maple 18, obtain the following expansion below.

Hence,

$$S(t) = \sum_{n=0}^{k} S(k)t^{k} = 60 + \dots$$
$$I(t) = \sum_{n=0}^{k} R(k)t^{k} = 20 + \dots$$
$$R(t) = \sum_{n=0}^{5} R(k)t^{k} = 10 + \dots$$

NUMERICAL SIMULATION AND GRAPHICAL **ILLUSTRATION OF MODEL**

In this section, we present the numerical simulation which demonstrate the analytical results for the proposed typhoid carrier individual in model (1). This is achieved by using the set of parameter values given in the Table which are derived from literature and well as assumptions .

We considered the following initial conditions for the different compartments. S(0) = 60, I_c0 = 40, I(0) = 20, R(0) = 10. The DTM is demonstrated against Maple 18's fourth order Runge-Kutta procedure for the solution of typhoid carrier individuals in Model (1).

Figures (2) to (5) shows the combined plots of the solutions of S(t), $I_c(t)$ I(t) and R(t) by DTM and RK4.

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Figure 2: Solution of Susceptible Population by DTM and RK4.



Figure 3: Solution of Infected Population by DTM and RK4.



Figure 4: Solution of Recovered Population by DTM and RK4.

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CONCLUSION

We solved the model developed by (Victor, *et al.*, 2022) by DTM. Numerical simulations were carried out to compare the results obtained by Differential Transform Method with the result of classical fourth-order Runge-Kutta method. The results of the simulations were displayed graphically.The results obtained confirm the accuracy and potential of the DTM to cope with the analysis of modern epidemics.

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SUGGESTED CITATION

Victor, A.A., A.O. Yekeen, M.L. Olaosebikan, N.H. Sayeed, M.T. Raji, N.M. Momoh, and K.M. Adeyemo. 2023. "Application of Differential Transform for Solving Typhoid Fever Model". *Pacific Journal of Science and Technology*. 24(1): 124-130.

Pacific Journal of Science and Technology