**SOLUTION OF A DETERMINISTIC MATHEMATICAL MODEL OF TYPHOID FEVER BY VARIATIONAL ITERATION METHOD**

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**ABSTRACT**

The aim of this paper is to apply Variational Iteration Method (VIM) to solve typhoid fever model for a given constant population. This mathematical model is described by nonlinear first order ordinary differential equations. First, we find the solution of this model by using Variational Iteration Method (VIM). In order to show the efficiency of the method we compare the solutions obtained by VIM and RK4. The validity of the VIM in solving the model is established by using the computer in-built classical fourth-order Runge-Kutta method. We illustrated the profiles of the solutions of each of the compartments, from which we speculate that the VIM and RK4 solutions agreed well.

**Keywords:** Typhoid Fever, Variational Iteration Method, Runge-Kutta Method.

**INTRODUCTION**

Typhoid fever is one of the infectious disease which is endemic in most part of the world. It is systemic infection caused by Salmonella enterica serotype typhi (S typhi). It is spread through contaminated food, water or drink. Merrell and Falk, 2004).

Typhoid fever infects 21 million people and kills 200,000 worldwide every year. Asymptomatic carriers are believed to play a major role in the evolution and global transmission dynamics of Typhoid fever, and their presence greatly hinders the eradication of Typhoid fever using treatment and vaccination. (Naresh et al., 2008).

“Typhoid fever has continue to be a health problem in developing countries where there is poor sanitation, poor standard of personal hygiene and prevalence of contaminated food. It is endemic in many parts of the developing world, illness do occur around the world in span of a day”. (Lifshitz, 1996).

Several mathematical models on the transmission dynamics of typhoid fever disease have been developed includes (Adetunde, 2008), (Date et al, 2015), (Cvetanovic et al, 2014), (Kalajdzievska, 2011), (Lauria et al 2009), (Moathold and Gosaamang, 2017), (Moffact, 2014), (Muhammad, et al 2015), (Mushayabasa, 2011), (Mushayabasa, 2017), (Nthiiri, 2016), (Virginia et al, 2014), (Watson and Edmunds, 2015), (Peter and Ibrahim, 2017), (Ibrahim et al, 2017) but none has incorporated both direct and indirect transmission dynamics in typhoid fever. We will like to complement and extend the existing works in the literature. We assume the existence of both direct transmission of typhoid from infected individuals to susceptible and indirect transmission of bacteria from the environment to the susceptible individuals.

The aim of this paper is to present the application of Variational Iteration Method to the proposed model and to verify the validity of Variational Iteration Method in solving the model using computer in-built Maple 18 classical fourth-order Runge-Kutta method as a base.

“the concept of variational iteration method was first proposed by (He, 1998), VIM which is a modified general Lagrange multiplier method (Abbasbandy and Shivanian, 2009), (Abdou and Soliman, 2005), (Momani and Abuasad, 2006) has been shown to solve effectively, easily and accurately, a large class of nonlinear problems with approximations which converge quickly to accurate solutions. In this study, we employ the Variational Iteration Method (VIM) to the system of non-linear differential equations which describe our model and approximating the solutions in a sequence of time intervals. In other to illustrate the accuracy of the VIM, the obtained results are compared with classical fourth-order Runge-Kutta Method.

**MATERIALS AND METHODS**

The model subdivides the human population into four compartments: susceptible S(t), infected I(t), infected carrier Ic(t), and recovered R(t). The model assume direct transmission of typhoid from infected individuals to susceptible individuals. However, typhoid is largely contacted from environmental bacteria through contaminated water or food and drinks and transmission of typhoid through. To incorporate this real biological phenomenon, we consider an additional compartment, W(t), which represents bacteria in the environment. We assume that susceptible individuals get infected with typhoid fever at a rate proportional to the susceptible population, Individuals in the infected class, can recover from typhoid at the rate $\delta$. The infected carrier and infected individuals both excrete bacteria into the environment. However, the rate of excretion by the infectious group $\varepsilon_2$ is higher than that of the carrier group $\varepsilon_1$ this is because infectious carrier do not show any signs of infection. The constant recruitment rate into the susceptible human is represented by $\theta$, while the natural death rate of human is represented by $\mu$.

**Model Equations**

From the assumptions, descriptions of the model, we formulate the following system of nonlinear differential equations which represents the mathematical model of typhoid fever as:

$$\frac{dS}{dt} = \frac{\theta}{\mu} - \beta S I - \gamma S$$

$$\frac{dI}{dt} = \beta S I - \gamma I - \delta I$$

$$\frac{dIc}{dt} = \gamma S - \gamma I - \delta Ic$$

$$\frac{dR}{dt} = \delta I$$

where $S$, $I$, $Ic$, and $R$ represent the susceptible, infected, infected carrier, and recovered population, respectively; $\beta$, $\gamma$, $\delta$, and $\mu$ are the parameters representing transmission rate, natural death rate, recovery rate, and recruitment rate, respectively.
the following system of differential equations

\[
\begin{align*}
\frac{dS}{dt} &= \theta - \mu_s S - \lambda S \\
\frac{dI_c}{dt} &= \rho \lambda S - (\mu_c + \epsilon_1) I_c \\
\frac{dI}{dt} &= (1 - \rho) \lambda S - (\mu_i + \delta + \epsilon_2) I \\
\frac{dR}{dt} &= \delta I - \mu_R R \\
\frac{dW}{dt} &= \epsilon_1 I_c + \epsilon_2 I - \mu_W W
\end{align*}
\]

(1)

Substituting the value of force of infection

\[
\lambda = \beta_1 I_c + \beta_2 I + \beta_3 W
\]

Solution of the Model Using Variational Iteration Method

We present the analysis of the system of equations governing the model using variation iteration method. In this section, following the same approach (Momani, and Abuasad, 2006), we obtain the correctional function as:

\[
S_{n+1}(t) = S_n(t) - \int_0^t S_n(x) - \theta - \mu_s S_n(x) + \delta_n(x) dx + \beta_1 \tilde{I}_n(x) + \beta_2 \tilde{W}_n(x)
\]

(2)

Subject to the initial conditions \( S(0) = 60, I_c(0) = 40, I(0) = 20, R(0) = 10, W(0) = 200 \).

Variational Iteration Method

To illustrate the basic idea of variational iteration method, (Abbasbandy, and Shivanian 1999), (Abdou and Soliman 2005; Akinboro et al., 2014) gave the analysis of VIM as follows: Given the general differential equation of the form:

\[ Ny + Ly = g(x) \]

Where \( N \) is a non-linear operator, \( L \) is a linear operator where \( g(x) \) is a non-homogenous term of the differential equations. The construction of correctional function for the equation is given as:

\[ y_{n+1}(x) = y_n(x) + \int_0^x \lambda[M y_n(s) + N y_n(s) - g(s)] ds \]

(4)

Where \( \lambda \) is a Lagragian multiplier which can be express as:

\[ \lambda(\eta) = \left( \frac{(-1)^n}{(n-1)!} \right) (\eta-t)^{n-1} \]

(5)

where \( n \) is the highest order of the differential equation.

Table 1: Description of Variables and Parameters for Model

<table>
<thead>
<tr>
<th>Variables</th>
<th>Description</th>
<th>Parameters</th>
<th>Interpretation</th>
</tr>
</thead>
<tbody>
<tr>
<td>( S(t) )</td>
<td>Susceptible individuals at time ( t )</td>
<td>( \theta )</td>
<td>Recruitment rate of susceptible individuals</td>
</tr>
<tr>
<td>( I_c(t) )</td>
<td>Infected individuals at time ( t )</td>
<td>( \mu_s )</td>
<td>Natural death rate</td>
</tr>
<tr>
<td>( I(t) )</td>
<td>Infected individuals at time ( t )</td>
<td>( \mu_c )</td>
<td>Natural rate of infected in I class disease induced death rate</td>
</tr>
<tr>
<td>( R(t) )</td>
<td>Recovered individuals at time ( t )</td>
<td>( \mu_i )</td>
<td>Natural death rate of I class disease induced death rate</td>
</tr>
<tr>
<td>( W(t) )</td>
<td>Environmental bacteria concentration</td>
<td>( \mu_W )</td>
<td>Natural death rate of bacteria</td>
</tr>
<tr>
<td>( \rho )</td>
<td>Probability that newly infected individuals are asymtomatic carriers</td>
<td>( \delta )</td>
<td>Recovery rate for infectious class</td>
</tr>
</tbody>
</table>

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\[
I(t) = 20 + 6t + 7.498469350E5t^2 - 5.612502025E5t^3 \\
+ 2.811369197E9t^4 - 6.562908640E9t^5 \\
+ 7.028405241E12t^6 - 2.373989970E13t^7 \\
+ 1.501825235E13t^8
\]

\[
R(t) = 10 + 13.580000000t + 21.910820000t^2 + 1.874606966E5t^3 \\
- 1.118892677E5t^4 + 4.216098798E5t^5 \\
- 3.061495037E8t^6 - 2.977399923E8t^7 \\
- 5.253487415E7t^8
\]

\[
W(t) = 200 + 24t + 28.330000000t^2 + 2.249572427E5t^3 \\
- 1.055985140E5t^4 + 5.059401508E5t^5 \\
- 3.673794045E8t^6 - 3.568799909E8t^7 \\
- 6.304184899E7t^8
\]

RESULTS

Numerical simulation which illustrate the analytical results for the proposed Model was demonstrated. This is achieved by using some set of values given in the table (2) below and whose source are mainly from literature and well as assumptions. We considered different initial conditions for the human populations. 

\[
S(0) = 60, I_x(0) = 40, I(0) = 20, R(0) = 10
\]

and that of bacterial populations \( W(t) = 200 \) The VIM is demonstrated against maple built-in fourth order Runge-Kutta Procedure for the solution of the model. Figure (1) to (5) shows the combined plots of the solutions of \( S(t), I_x(t), I(t), R(t) \) and \( W(t) \) by VIM and RK4

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Initial Value</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \mu_2 )</td>
<td>0.2</td>
<td>Assumed</td>
</tr>
<tr>
<td>( \mu_3 )</td>
<td>0.142</td>
<td>Mushayabasa, (2011)</td>
</tr>
<tr>
<td>( \mu_4 )</td>
<td>0.2</td>
<td>Assumed</td>
</tr>
<tr>
<td>( \mu_5 )</td>
<td>0.142</td>
<td>Mushayabasa, (2011)</td>
</tr>
<tr>
<td>( \rho )</td>
<td>0.5</td>
<td>Assumed</td>
</tr>
<tr>
<td>( \beta_1 )</td>
<td>0.02</td>
<td>Assumed</td>
</tr>
<tr>
<td>( \beta_2 )</td>
<td>0.01</td>
<td>Assumed</td>
</tr>
<tr>
<td>( \beta_3 )</td>
<td>0.01</td>
<td>Assumed</td>
</tr>
<tr>
<td>( \delta )</td>
<td>0.75</td>
<td>Assumed</td>
</tr>
<tr>
<td>( \theta )</td>
<td>( 10^9 )</td>
<td>Laursen et al.,(2009)</td>
</tr>
<tr>
<td>( \varepsilon_1 )</td>
<td>0.4</td>
<td>Estimated</td>
</tr>
<tr>
<td>( \varepsilon_2 )</td>
<td>0.5</td>
<td>Estimated</td>
</tr>
<tr>
<td>( \mu_6 )</td>
<td>0.01</td>
<td>Mushayabasa, (2017)</td>
</tr>
</tbody>
</table>
The solutions obtained by using Variational Iteration Method with given initial conditions compared favourably with the solution obtained by using classical fourth- order Runge-Kutta method. The solutions of the two methods follow the same pattern and behaviour. This shows that Variational Iteration Method is suitable and efficient to conduct the analysis of typhoid models.

Conclusion
We present a deterministic model on the analysis of direct and indirect transition dynamics of typhoid fever model. Variational Iteration Method is employed to attempt the series solution of the model. Numerical simulations were carried out to compare the results obtained by VIM with the result of classical fourth-order Runge-Kutta method. The results of the simulations were displayed graphically. Based on the results obtained from this study, we may conclude that VIM is very effective in predicting the solution of modern epidemics.

REFERENCES
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