Science World Journal Vol 13(No 2) 2018
www.scienceworldjournal.org
ISSN 1597-6343

Full Length Research Article

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

Peter O. J[1*], Afolabi, O. A[2], Oguntolu F. A[3], Ishola C. Y[4], Victor, A. A[5]

[1, 2, 5] Department of Mathematics, University of Ilorin, Ilorin, Kwara State, Nigeria.
[3]Department of Mathematics, Federal University of Technology, Minna, Nigeria
[4]Department of Mathematics, National Open University of Nigeria Jabi, Abuja, Nigeria

[1]peterjames4real@gmail.com, [2]afolabiahmed79@gmail.com, [3]festus.tolu@futminna.edu.ng, [4]cishola@noun.edu.ng, [5]adekunlevictora@yahoo.com

*Corresponding author: peterjames4real@gmail.com. Phone: +2348033560280

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 andFalkow, 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 these includes (Adetunde, 2008), (Date *et al*, 2015), (Cvjetanovic *et al*, 2014), (Kalajdzievska, 2011), (Lauria *et al* 2009), (Moatlhodl 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 δ. The Infected carrier and infected individuals both excrete bacteria into the environment. However, the rate of excretion by the infectious group ε_2 is higher than that of the carrier group ε_1 this is because infectious carrier do not show any signs of infection. The constant recruitment rate into the susceptible human is represented by θ , while the natural death rate of human is represented by μ .

Model Equations

From the assumptions, descriptions of the model, we formulate

the following system of differential equations

$$\left.\begin{aligned}
\frac{dS}{dt} &= \theta - \mu_1 S - \lambda S \\
\frac{dIc}{dt} &= \rho\lambda S - (\mu_2 + \varepsilon_1) I_c \\
\frac{dI}{dt} &= (1-\rho)\lambda S - (\mu_3 + \delta + \varepsilon_2) I \\
\frac{dR}{dt} &= \delta I - \mu_4 R \\
\frac{dW}{dt} &= \varepsilon_1 I_c + \varepsilon_2 I - \mu_b W
\end{aligned}\right\} \quad (1)$$

$$\lambda = \beta_1 I_c + \beta_2 I + \beta_3 W$$

Substituting the value of force of infection

$$\left.\begin{aligned}
\frac{dS}{dt} &= \theta - \mu_1 S - S(\beta_1 I_c + \beta_2 I + \beta_3 W) \\
\frac{dIc}{dt} &= \rho S(\beta_1 I_c + \beta_2 I + \beta_3 W) - (\mu_2 + \varepsilon_1) I_c \\
\frac{dI}{dt} &= (1-\rho) S(\beta_1 I_c + \beta_2 I + \beta_3 W) - (\mu_3 + \delta + \varepsilon_2) I \\
\frac{dR}{dt} &= \delta I - \mu_4 R \\
\frac{dW}{dt} &= \varepsilon_1 I_c + \varepsilon_2 I - \mu_b W
\end{aligned}\right\} \quad (2)$$

Table 1: Description of Variables and Parameters for Model

Variables	Description
$S(t)$	susceptible individuals at time t
$Ic(t)$	carrier infectious individuals at time t
$I(t)$	infectious individuals at time t
$R(t)$	recovered individuals at time t
$W(t)$	environmental bacteria concentration,
Parameters	**Interpretation**
θ	recruitment rate of susceptible individuals
μ_1	natural death rate
μ_2	natural rate for I_c class and disease induced death rate
μ_3	natural death rate for I class and disease induced death rate
μ_b	natural death rate of bacteria
μ_4	natural death rate
ε_1	bacteria sheeding rate for I_c
ε_2	bacteria sheeding rate for I
ρ	probability that newly infected individuals are asymtomatic/carrier
β_1	transmission rate between S and I_c
β_2	transmission rate between S and I
β_3	transmission rate between S and W
δ	recovery rate for infectious class
λ	force of infection

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:

$$y_{n+1}(x) = y_n(x) + \int_0^x \lambda\{Ly_n(s) + N\tilde{y}_n(s) - g(s)\}ds \quad (4)$$

Where λ is a Lagragian multiplier which can be express as:

$$\lambda(\eta) = \frac{(-1)^n}{(n-1)!}(\eta - t)^{n-1} \quad (5)$$

where n is the highest order of the differential equation.
Subject to the initial conditions S_0=60, Ic_0=40, I_0=20, R_0=10, W(0)=200.

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:

$$\begin{aligned}
S_{n+1}(t) = S_n(t) - \int_0^t \{S_{n'}(x) - \theta + \mu_1 \tilde{S}_n(x) + \tilde{S}_n(x)(\beta_1 \tilde{I}c_n(x) \\
+ \beta_2 \tilde{I}_n(x) + \beta_3 \tilde{W}_n(x)\}dx \\
Ic_{n+1}(t) = Ic_n(t) - \int_0^t \{Ic_{n'}(x) - \rho S_n(x)(\beta_1 \tilde{I}c_n(x) \\
+ \beta_2 \tilde{I}_n(x) + \beta_3 \tilde{W}_n(x) + (\mu_2 + \varepsilon_1)\tilde{I}c_n(x)\}dx \\
I_{n+1}(t) = I_n(t) - \int_0^t \{I_{n'}(x) - (1-\rho)\tilde{S}_n(x)(\beta_1 \tilde{I}c_n(x) \\
+ \beta_2 \tilde{I}_n(x) + \beta_3 \tilde{W}_n(x) + (\mu_3 + \delta + \varepsilon_2)\tilde{I}_n(x)\}dx \\
R_{n+1}(t) = R_n(t) - \int_0^t \{R_{n'}(x) - \delta \tilde{I}_n(x) + \mu_4 \tilde{R}_n(x)\}dx \\
W_{n+1}(t) = W_n(t) - \int_0^t \{W_{n'}(x) - \varepsilon_1 \tilde{I}c_n(x) - \varepsilon_2 \tilde{I}_n(x) \\
+ \mu_b \tilde{W}_n(x)\}dx
\end{aligned}$$

Subject to the initial conditions S_0=60, Ic_0=40, I_0=20, R_0=10, W(0)=200. Using the initial conditions and the parameter values in the table and with the help of Mapple 18, we obtain the iterated values for each compartment.

$$\begin{aligned}
S(t) = 60 + 9.9981148001E5t - 1.570768935E6t^2 \\
+ 4.719980973E5t^3 - 5.622348246E9t^4 \\
+ 1.165524202E10t^5 - 1.405574263E13t^6 \\
+ 4.748083674E13t^7 - 3.003632145E13t^8
\end{aligned}$$

$$\begin{aligned}
I_c(t) = 40 + 66t + 7.498713600E5t^2 - 3.487984559E5t^3 \\
+ 2.811218064E9t^4 - 6.085091149E9t^5 \\
+ 7.028058272E12t^6 - 2.374023676E12t^7 \\
+ 1.501819281E13t^8
\end{aligned}$$

$$I(t) = 20 + 61t + 7.498469350E5t^2 - 5.612502025E5t^3 + 2.811369197E9t^4 - 6.562908640E9t^5 + 7.028405241E12t^6 - 2.373989970E13t^7 + 1.501825235E13t^8$$

$$R(t) = 10 + 13.58000000t + 21.91082000t^2 + 1.874606966E5t^3 - 1.118892677E5t^4 + 4.216098798E8t^5 - 3.061495037E8t^6 - 2.973999923E8t^7 - 5.253487415E7t^8$$

$$W(t) = 200 + 24t + 28.33000000t^2 + 2.249572427E5t^3 - 1.055985140E5t^4 + 5.059401508E8t^5 - 3.673794045E8t^6 - 3.568799909E8t^7 - 6.304184899E7t^8$$

RESULTS

Numerical simulation which illustrate the analytical results for the proposed Model was demostrated. 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. $S(0) = 60, I_c(0) = 40, \quad I(0) = 20, R(0) = 10$ and that of bacterial populations $W(t) = 200$ The VIM is demostrated against mapple buit-in fourth order Runge-Kutta Procedure for the solution of the model. Figure (1) to (5) shows the combined plots of the solutions of $S(t), I_c(t), I(t), R(t)$ and $W(t)$ by VIM and RK4

Table 2: Parameters values for model

Parameter	Initial Value	Source
μ_2	0.2	Assumed
μ_1	0.142	Mushayabasa, (2011)
μ_3	0.2	Assumed
μ_4	0.142	Mushayabasa, (2011)
ρ	0.5	Assumed
β_1	0.02	Assumed
β_2	0.01	Assumed
β_3	0.01	Assumed
δ	0.75	Assumed
θ	10^6	Lauria *et al.*,(2009)
ε_1	0.4	Estimated
ε_2	0.5	Estimated
μ_b	0.01	Mushayabasa, (2017)

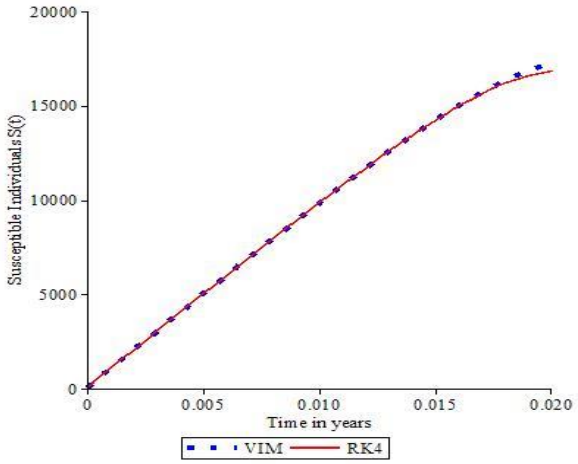

Figure 1: Solution of Infected Population by VIM and RK4

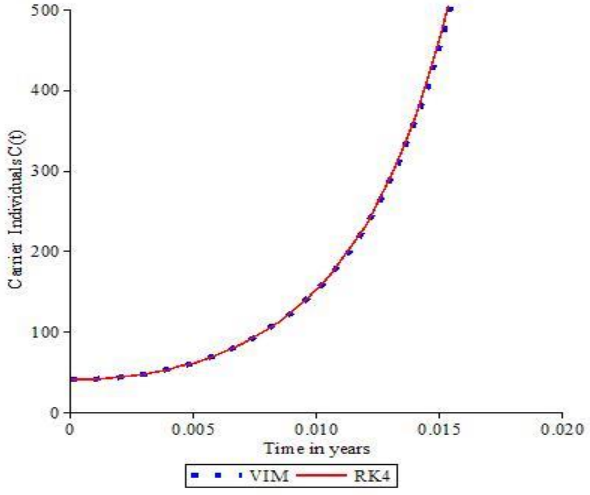

Figure 2: Solution of Infected Population by VIM and RK4

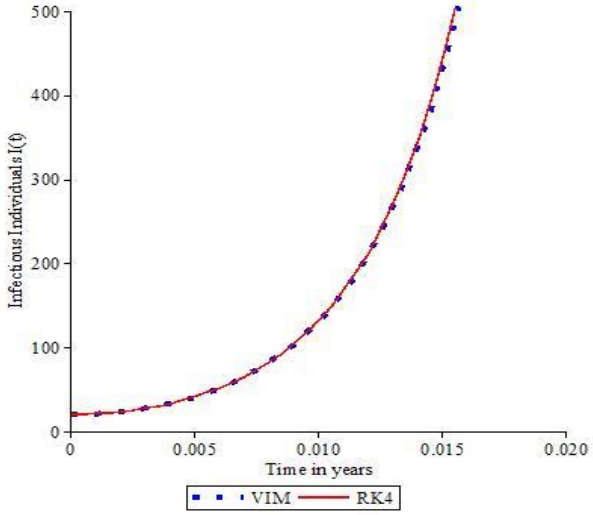

Figure 3: Solution of Recovered Population by VIM and RK4

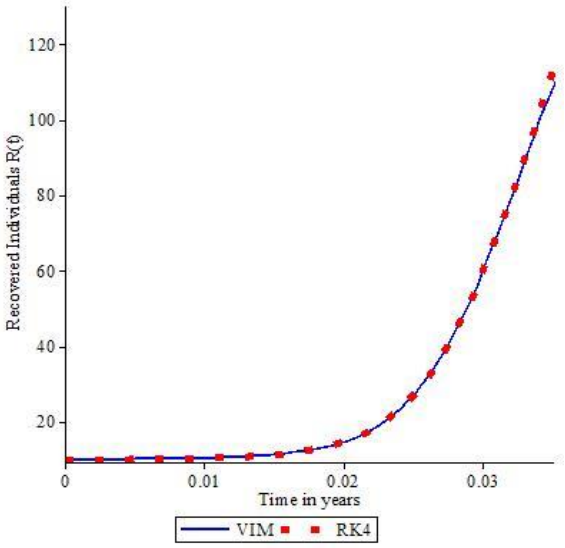

Figure 4: Solution of Infected Population by VIM and RK4

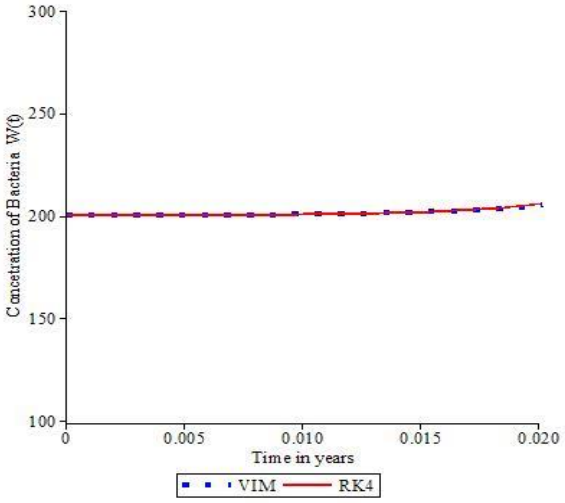

Figure 5: Solution of Concentration Bacteria Population by VIM and RK4

DISCUSSION

The solutions obtained by using Variational Iteration Method with given initial conditions compared favourably with the solution obtained by using classical fouth-order Runge-Kuta method. The solutions of the two methods follows 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

Abbasbandy, E & Shivanian, E. (2009). Application of the variational iteration method for systemof nonlinear Volterra'sintegro-differential equations, Mathematical and Comp. Applic., Vol 14, Issue2, Pg 147-158

Abdou, M . A & Soliman, A. A (2005), Variational iteration method for solving Burger's and coupled Burger's bequation,J.Comp.Appl.Math., Vol 181, Issue 2, 245-251

Adetunde, I. A. (2008). Mathematical models for the dynamics of typhoid fever in kassena-nankana district of upper east region of Ghana. J. Modern Math Stat.,Vol 2, Pg 45-49

Akinboro, F. S., Alao, S., & Akinpelu, F. O. (2014). Numerical solution of SIR model using differential transformation method and variational iteration method. General Mathematics Notes, Vol 22, No. 2, Pg 82-92.

Anderson, R. M,, and May, R. M. (1991). Infectious diseases of humans: dynamics and control. Jama the Journal of the American Medical Association, 268(23), 33-81.

Cvjetanovic, B., Grab, B & Uemura, K.(2014). Epidemiological model of typhoid fever and its use in the planning and evaluation of antityphoid immunization and sanitation programmes, Bull. Org. Mond. Sante (45), 53-75.

Date, K. A., Bentsi-Enchill, A., Marks, F., Fox, K. (2015). Typhoid fever vaccination strategies, Vaccine 33, Pg 55-61.

He, J. H (1999), Variational iteration method a kind of nonlinear analytical technique: Some examples, Int. J. Nonlinear Mech., Vol.34, Pg 669-708.

Ibrahim, M. O Peter, O. J. OGWUMU O. D and Akinduko, O.B. (2017) On the Homotopy Analysis Method for PSTIR Typhoid Model. Transactions of the Nigerian Association of Mathematical Physics Vol.4, Pg 51-56

Kalajdzievska, D. (2011). "Modeling the Effects of Carriers on the Transmission Dynamics of Infectious Diseases", Math Biosci Eng., Vol.8, Issue 3, Pg 711-722.

Kariuki,C. (2004). Characterization of Multidrug-Resistant Typhoid Outbreaks in Kenya, J. C. Micbol. Vol. 42 Issue 4, Pg 1477-1482.

Kariuki, S., Gilks, C Revathi, G and Hart, C. A. (2000). Genotypic analysis of multidrug-resistant Salmonella enterica Serovar Typhi, Kenya,Emerg. Infect.Vol 6, Pg 649-651.

Lauria, D. T. Maskery, B. Poulos, C and Whittington, D. (2009). "An optimization model for reducing typhoid cases in developing countries without increasing public spending," Vaccine, 27(10), 1609-1621.

Lawi (2011). Mathematical Model for Malaria and Meningitis Co-infection among Children. Applied Mathematics Sciences, Vol.5 (47), Pg 2337-2359.

Lifshitz, E. I. (1996) Travel trouble: typhoid fever-A case presentation and review. J. Am Coll Health. 45(3), 99-105

Momani, S,Abuasad, S (2006), Application of He's variational iteration method toHelmholtz equation, Chaos, Solitons& Fractals., 27: 1119- 1123strategies in microbial pathogenesis, Nature, 430, 250-256

Moatlhodl, K. and Gosaamang, R. (2017). Mathematical Analysis of Typhoid Infection with Treatment. Journal of Mathematical Sciences: Advances and Applications. 40(1), 75-91

Moffact,N. (2014). Mathematical Model and Simulation of the Effects of Carriers on the Transmission Dynamics of Typhoid Fever. Transactions on Computer Science Engineering and its Applications (CSEA), Vol2, Issue3,

Pg 14-20.

Muhammad, A. K., Muhammad, P.Saeed I., Ilyas, K., Sharidan S and Taza, G., (2015). Mathematical Analysis of Typhoid Model with Saturated Incidence Rate Advanced Studies in Biology, Vol 7 Issue 2,Pg 65 - 78.

Mushayabasa, S. (2011). Impact of vaccines on controlling typhoid Journal of modern mathematics and Statistics 5(2), 54-59.

Mushayabasa, S. (2017). Typhoid with saturated incidence rate and treatmenteffect", World Academy of Science, Engineering and Technology, International Journal of Sciences: Basic and Applied Research (IJSBAR). 32(1), 151-168

Naresh, R. Pandey, S. and Misra, A. K. (2008), "Analysis of a Vaccination Model for Carrier Dependent Infectious Diseases with Environmental Effects", Nonlinear Analysis: Modelling and Control, 13, 331-350

Nthiiri, J. K (2016). Mathematica modelling of typhoid fever disease incorporating protection against infection British Journal of mathematics and computer science 14(1), 1-10.

Peter, O. J, Ibrahim, M. O.,Akinduko O. B. and Rabiu, M.(2017)Mathematical Model for the Control of Typhoid Fever IOSR Journal of Mathematics Vol.13Issue 4, Pg 60-66

Peter, O. J & Ibrahim, M. O. (2017). Application of Differential Transform Method in Solving a Typhoid Fever Model. International Journal of Mathematical analysis and Optimization. Vol 1, Issue 1, Pg 250-260

Roumagnac, P., Weill F. X., Dolecek C., Baker, S., Brises S., Chinh, N. T., Le TA, Acosta,C. J., Farrar, J., Dougan G., Achtman M., (2006). Evolutionary history of Salmonella typhi, Science, 314, Pg 1301-1304.

Van den Driessche, P and Watmough, J. (2002). "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission", Mathematical Biosciences, Vol 180 (1-2), Pg29-48,

Watson, C. H., and Edmunds, W. J. (2015) Review of typhoid fever transmission dynamic models and economic evaluations of vaccination.Vaccine 33, 42-54. http://dx.doi.org/10.1016/j. vaccine.2015.04.013