Approximate Solution of Typhoid Fever Model by Variational Iteration Method

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ABSTRACT

In this paper, a deterministic mathematical model involving the transmission dynamics of typhoid fever is presented and studied. Basic idea of the disease transmission using compartmental modeling is discussed. 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 the model by using Variation Iteration Method (VIM). The validity of the VIM in solving the model is established by classical fourth-order Runge-Kutta method (RK4) implemented in Maple 18. In order to show the efficiency of the method we compare the solutions obtained by VIM and RK4. 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 a serious and life-threatening bacterial infection that is attributed to the bacterium *Salmonella Typhi*. It is one of the water-borne diseases whose mode of transmission is primarily ingestion of contaminated water or food. An individual suffering from typhoid may develop headache, nausea, abdominal pain, fatique, constipation or diarrhea. There may be rash in some infected persons and serious complication may be experienced in severe cases which may result in death. Treatment for typhoid is straightforward and can be completed with appropriate antibiotics though the treatment is complicated nowadays due to high rate of cases of resistance to various types of antibiotics. Typhoid fever is one of the diseases that cannot be cured once and for all. Numerous studies have shown that typhoid patients can transmit typhoid infection to other people after they have got over all the symptoms of typhoid fever. (Gasem et al., 2001), (Vollaard, et al., 2004).

Available data had it that about 11 – 20 million people suffer from typhoid and an average of 161 000 deaths is attributed to typhoid every year. Typhoid fever bacteria (*Salmonella Typhi)* survive in poor communities. Also, individuals living in areas whose hygiene conditions are despicable. Typhoid fever is not a new disease in human history and the emergence and reemergence of the disease has made it popular among researchers. Several approaches have directed to proffer solutions to the severity of the disease in recent time.

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(Hosoglu, et al., 2006). Several mathematical models have been developed on the transmission dynamics of typhoid fever, these includes, (Adetunde, 2008; Cvjetanovic et al, 2014; Kalajdzievska, 2011; Lauria et al 2009; Moatlhodl & Gosaamang, 2017; Chamuchi et al, 2014; Muhammad, et al 2015; Mushayabasa, 2011; Nthiiri, 2016; Virginia et al, 2014; Watson & Edmunds, 2015; Peter, et al 2017; Peter, et al 2017). In this paper, we extend previous efforts by introducing a model that includes educated infected and uneducated infected class.

The interpretations of the real-life situations have lead mathematicians to the formulation of nonlinear differential equations. Real life situations are communicated when the equations in which they are transformed into are solved. Variational iteration method (VIM) is one of the promising techniques of solving nonlinear differential equations. (Lu, 2007) demonstrated the applicability of the VIM for solving a nonlinear system of second-order boundary values problems. Lu gave numerous examples and concluded that the VIM was a new approach to obtain an analytical approximation to both linear and nonlinear second-order boundary values problems without linearization or discretization. Besides, exact solutions can be derived by using only one iteration with the help of the VIM. Also, (Batiha, et al 2007) applied the VIM to solve general Riccati differential equations in a direct without restrictive assumptions or transformations. They concluded the VIM is very powerful and efficient in finding analytical as well as numerical solutions for wide classes of linear and nonlinear differential equations. The analytical treatment of the linear and nonlinear systems of partial differential equations was investigated by (Wazwaz, 2007). The author discovered that the VIM reduces not only the size of the computation but also the difficulty of handling nonlinear terms. The efficiency of the VIM to solve system of nonlinear Volterra's integro-differential equations has also been appraised by (Abbasbandy and Shivanian 2009).

Variational iteration method (VIM) has a place in population dynamics and epidemiology and has been applied by a good number of researchers. (Yuliyanto and Mungkasi 2017) investigated the dynamical model of two species coexisting under mutualism, parasitism and competition conditions. Their results showed that the VIM is a reliable technique for obtaining the solutions of the population dynamics models of two species accurately. (Peter et al, 2018) applied Variational Iteration Method (VIM) to solve typhoid fever model for a given constant population. The mathematical model is described by nonlinear first order ordinary differential equations of this model by using Variational Iteration Method (VIM). The results obtained were compared with the solutions obtained by RK4 which is implemented in maple 18. The solution of the two method was in good agreement.

Akinboro et al, (2017) study the application of differential transformation method and variational iteration method in finding the approximate solution of Epidemiology (SIR) model. The result revealed that both methods are in complete agreement, accurate and efficient for solving systems of ODE.

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

FORMULATION OF THE MODEL

This section describes the formulation of the model. We develop a deterministic compartmental typhoid transmission model. The human population $N(t)$ divided into six sub-populations namely; protected, $P(t)$, susceptible, $S(t)$, uneducated infectious, $Iu(t)$, educated

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infectious $Ie(t)$, treated $T(t)$ and recovered individuals, $R(t)$. Individuals are recruited into the susceptible population by either immigration or birth at the rate Λ .Susceptible individuals acquire typhoid infection at per capita rate λ. We assume that proportion α progress to educated infectious class, while the compliment $1-\alpha$ progress to uneducated infectious compartment.Susceptible individuals received vaccination to protect themselves against infection at the rate τ . Since vaccine wanes with time, then after its expiry, the protected individuals return back to susceptible class at the rate ω. We assume that an individuals in each compartment may undergo a natural death at the rate μ. Let β_1, β_2, and β_3 be transmission rates for uneducated infectious, educated infectious and treated individuals respectively then the susceptible population S(t), is exposed to force of infection denoted by $\lambda = \beta_1 I_u + \beta_2 I_e + \beta_3 T$ Detailed description of parameters is shown in Table 1 while the compartmental flow diagram of the model is shown in Figure 1.

Model Assumptions

1. Recovered individuals may become susceptible again at the rate ω , this is due to the fact that typhoid does not confer permanent immunity on recovery
2. Susceptible individuals receive vaccination to protect themselves against infection at the rate τ
3. A susceptible individual can be infected through a direct contact with educated infected or uneducated infected
4. All parameters are non-negative
5. All treated individuals recovered

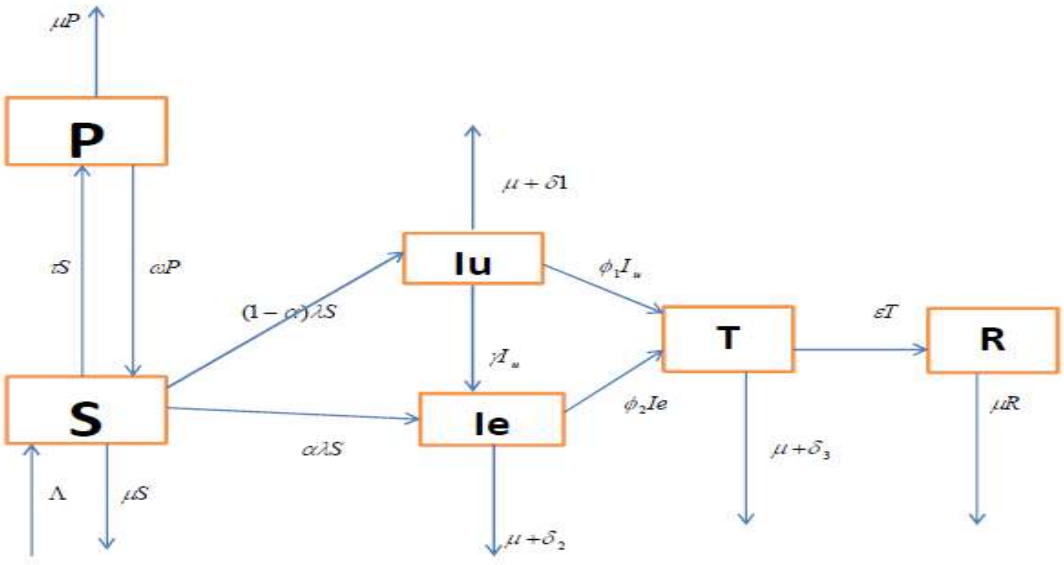

Figure 1: Pictorial Representation of Model

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$$\left.\begin{aligned}
\frac{dP}{dt} &= \tau S - (\mu + \omega)P \\
\frac{dS}{dt} &= \Lambda - \lambda S + \omega P - (\tau + \mu)S \\
\frac{dIu}{dt} &= (1-\alpha)\lambda S - (\mu + \delta_1 + \phi_1 + \gamma)I_u \\
\frac{dIe}{dt} &= \alpha\lambda S - (\mu + \delta_2 + \phi_2)I_e + \gamma Iu \\
\frac{dT}{dt} &= \phi_1 I_u + \phi_2 I_e - (\mu + \delta_3 + \varepsilon)T \\
\frac{dR}{dt} &= \varepsilon T - \mu R
\end{aligned}\right\} \quad (1)$$

Where the force of infection λ is given as:

$$\lambda = \beta_1 I_u + \beta_2 I_e + \beta_3 T \quad (2)$$

Substituting the value of force of infection

$$\left.\begin{aligned}
\frac{dP}{dt} &= \tau S - (\mu + \omega)P \\
\frac{dS}{dt} &= \Lambda - (\beta_1 I_u + \beta_2 I_e + \beta_3 T)S + \omega P - (\tau + \mu)S \\
\frac{dIu}{dt} &= (1-\alpha)(\beta_1 I_u + \beta_2 I_e + \beta_3 T)S - (\mu + \delta_1 + \phi_1 + \gamma)I_u \\
\frac{dIe}{dt} &= \alpha S(\beta_1 I_u + \beta_2 I_e + \beta_3 T) - (\mu + \delta_2 + \phi_2)I_e + \gamma I_u \\
\frac{dT}{dt} &= \phi_1 I_u + \phi_2 I_e - (\mu + \delta_3 + \varepsilon)T \\
\frac{dR}{dt} &= \varepsilon T - \mu R
\end{aligned}\right\} \quad (3)$$

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Table 1: Description of Variables and Parameters of the Model

Variables	**Description**
$P(t)$	protected individuals at time t
$S(t)$	susceptible individuals at time t
Iu	uneducated infectious individuals at time t
Ie	educated infectious individuals at time t t
T	treated individuals at time t t
$R(t)$	recovered individuals at time t
Parameters	**Interpretation**
Λ	recruitment rate of susceptible individuals
μ	natural death rate
δ_1	disease induced death rate for I_u class
δ_2	disease induced death rate for I_e
δ_3	disease induced death rate for T
ϕ_1	treatment rate for I_u
ϕ_2	treatment rate for I_e
ω	waning rate of vaccine
ε	rate of recovery from treatment
γ	rate of educating or counseling uneducated infected
τ	rate of vaccinating individual in the susceptible class
β_1	transmission rate between S and I_u class
β_2	transmission rate between S and I_e class
β_3	transmission rate between S and T class

Variational Iteration Method

To illustrate the basic concept of variational iteration method,He (1998, 1998), (Abdou & Soliman, 2005) gave the analysis of VIM as follows: Given the general differential equation of the form:

$$Ny + Ly = g(x) \tag{4}$$

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

$$y_{n+1}(x) = y_n(x) + \int_0^x \lambda\{Ly_n(s) + N\tilde{y}_n(s) - g(s)\}ds \tag{5}$$

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

$$\lambda(\eta) = \frac{(-1)^n}{(n-1)!}(\eta - t)^{n-1} \tag{6}$$

where n is the highest order of the differential equation

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SOLUTION OF MODEL EQUATIONS BY VARIATIONAL ITERATION METHOD

We present the analysis of the system of equations governing the model using variation iteration method in this section.:

$$
\begin{aligned}
P_{n+1}(t) &= P_n(t) - \int_0^t \{P_{n'}(x) - \tau\widetilde{S}_n(x) + (\mu+\omega)\widetilde{P}_n(x)\}dx \\
S_{n+1}(t) &= S_n(t) - \int_0^t \{S_{n'}(x) - \Lambda + \widetilde{S}_n(x)(\beta_1\widetilde{I}u_n(x) + \beta_2\widetilde{I}e_n(x) + \beta_3\widetilde{T}_n(x)) - \omega\widetilde{P}_n(x) + (\tau+\mu)\widetilde{S}_n(x)\}dx \\
Iu_{n+1}(t) &= Iu_n(t) - \int_0^t \{Iu_{n'}(x) - (1-\alpha)\widetilde{S}_n(x)(\beta_1\widetilde{I}u_n(x) + \beta_2\widetilde{I}e_n(x) + \beta_3\widetilde{T}_n(x)) \\
&\quad + (\mu+\delta_1+\phi_1+\gamma)\widetilde{I}u_n(x)\}dx \\
Ie_{n+1}(t) &= Ie_n(t) - \int_0^t \{Ie_{n'}(x) - \alpha\widetilde{S}_n(x)(\beta_1\widetilde{I}u_n(x) + \beta_2\widetilde{I}e_n(x) + \beta_3\widetilde{T}_n(x)) \\
&\quad + (\mu+\delta_2+\phi_2)\widetilde{I}e_n(x) - \gamma\widetilde{I}u_n(x)\}dx \\
T_{n+1}(t) &= T_n(t) - \int_0^t \{T_{n'}(x) - \phi_1\widetilde{I}u_n(x) - \phi_2\widetilde{I}e_n(x) + (\mu+\delta_3+\phi_2+\varepsilon)\widetilde{T}_n(x)\}dx \\
R_{n+1}(t) &= R_n(t) - \int_0^t \{R_{n'}(x) - \varepsilon\widetilde{T}_n(x) + \mu\widetilde{R}_n(x)\}dx
\end{aligned}
\tag{7}
$$

Subject to the initial conditions $P(0)=100$, $S(0)=200$, $I_u(0)=140$, $I_e(0)=120$, $T(0)=80$, $R(0)=60$. 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 compartments

$$P(t) = 100 - 44.2060t - 2175.731800t^2 - 56687.71841t^3 - 2.27568225098E6t^4 + 092828054E8t^5 + ..$$

$$S(t) = 200 - 43798.40000t - 1.698452544E6t^2 + 9.108991502E8t^3 + 7.267992427E10t^4 - 2.180764807E13t^5 + ...$$

$$I_u(t) = 140 + 43468.7200\ 0t + 1.69817007\ 6E6t^2 - 9.05051270\ 3E8t^3 - 7.18647038\ 8E10t^4 + 2.166934658E13t^5 + ...$$

$$I_e(t) = 120 + 338.760000\ 0t + 25353.8758\ 4t^2 - 6.23584674\ 2E10E6t^3 - 6.57591629\ 3E8t^4 + 1.484376144E11t^5 + ...$$

$$T(t) = 80 - 7.7600000t + 924.4323600t^2 + 24437.07634t^3 - 9.521970628E6t^4 - 6.196543924E8t^5 + ..$$

$$R(t) = 60 + 23.48000000t - 3.219080000t^2 + 121.5433116t^3 + 2484.392845t^4 - 7.618269290E5t^5 + ...$$

NUMERICAL SIMULATION AND GRAPHICAL ILLUSTRATION OF THE MODEL

We demonstrated the numerical simulation which illustrate the analytical results for the proposed model . This is achieved by using some set of parameter 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. $P(0)=100$, $S(0)=200$, $Iu(0)=140$, $Ie(0)=120$, $T(0)=80$ and $R(0)=20$. The VIM is demostrated against mapple buit-in fourth order Runge-Kutta Procedure for the solution of typhoid model .Fig (2) to (7) shows the combined plots of the solutions of $P(t)$ $S(t)$, $I_u(t)$ $I_e(t)$ and $R(t)$ by VIM aand RK4

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Table 2: Parameters values of the model

Parameter	Initial Value	Source
Λ	200	Assumed
μ	0.142	Mushayabasa, (2011)
ε	0.4	Kariuki, C. (2004)
γ	0.6	Assumed
ω	0.5	Assumed
τ	0.1	Estimated
α	0.0072	Assumed
β_1	1.5	Kalajdzievska, D. (2011),
β_2	0.05	Assumed
β_3	0.05	Assumed
δ	0.075	Assumed
ϕ_1	0.04	Estimated
ϕ_2	0.3	Estimated

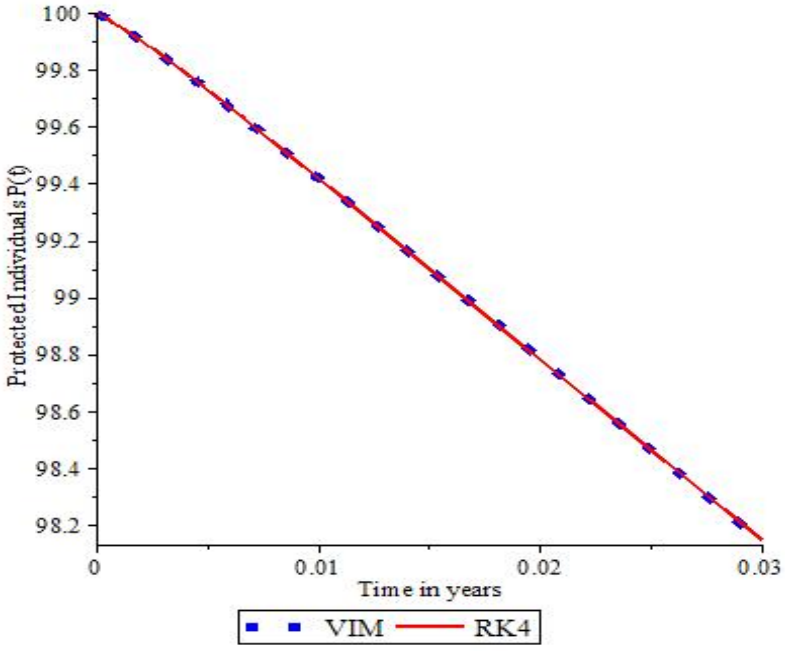

Figure 2: Solution of protected Population by VIM and RK4

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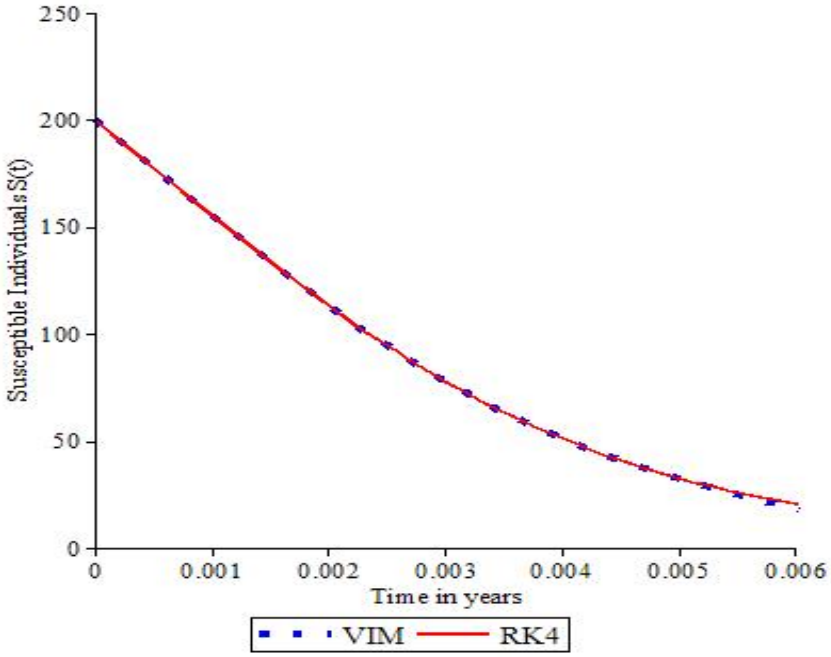

Figure 3: Solution of Susceptible Population by VIM and RK4

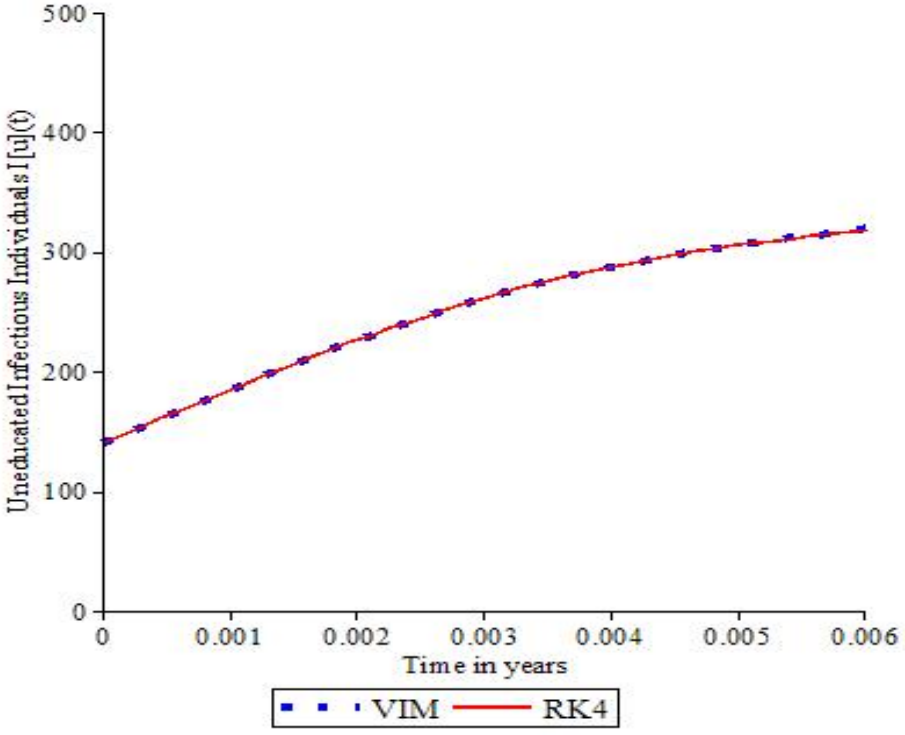

Figure 4: Solution of Uneducated Infected Population by VIM and RK4

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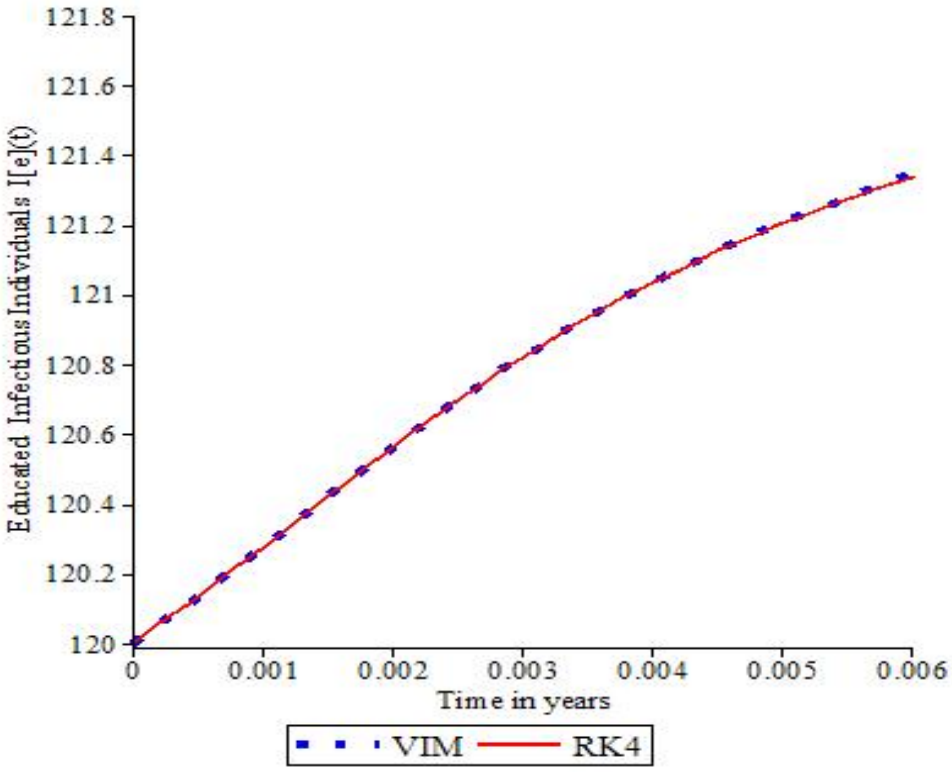

Figure 5: Solution of Educated Infected Population by VIM and RK4

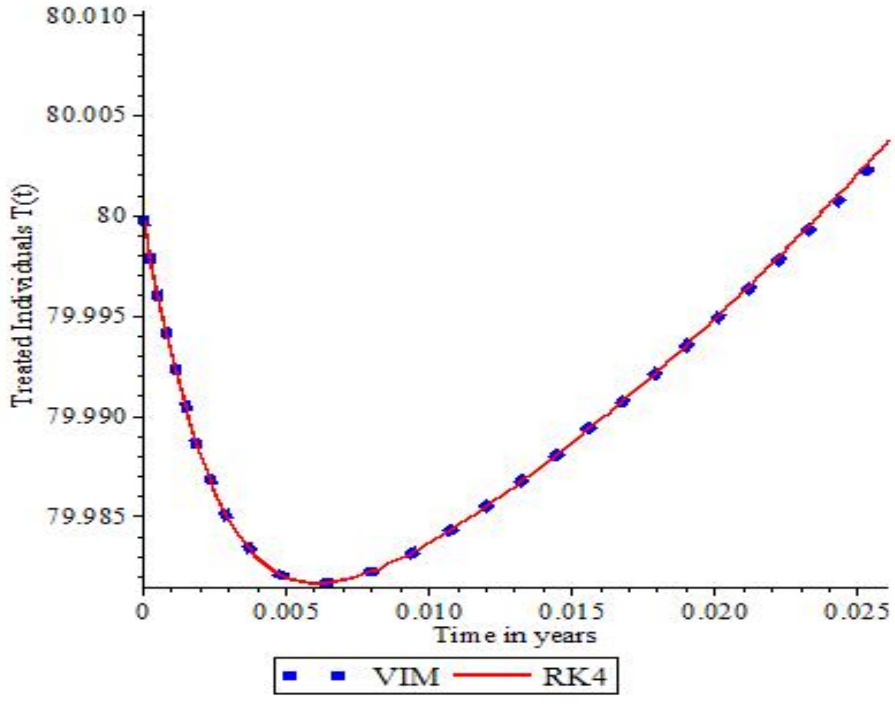

Figure 6: Solution of Treated Population by VIM and RK4

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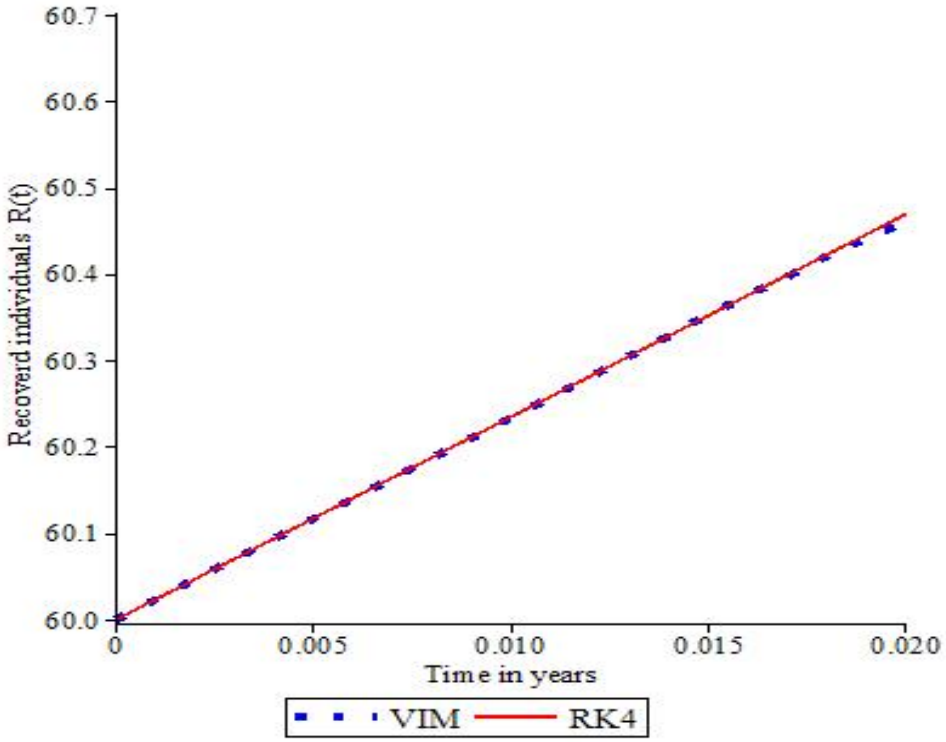

Figure 7: Solution of Recovered Population by VIM and RK4

DISCUSSION

It is obvious from the graphical displays that the results attained with the VIM compared favourably with the solution obtained by the classical fourth-order Runge-Kutta method. The outcome of the two approaches follows the same direction and pattern which vindicates the suitability of the VIM in solving typoid fever models.

CONCLUSION

In the study,we have investigated via a deterministic mathematical modelon the transmission dynamics of typhoid fever. The variational iteration approach has been employed to approximately solve the system of nonlinear equations of typhoid fever disease dynamic. Numerical studies of the results were conducted and the results obtained by using the VIM were compared with that of the classical fourth-order Runge-Kutta method. The outcomes of the comparisons were displayed graphically. Based on the outcome of the comparisons, we conclude that the VIM is suitable to conduct the analysis of modern epidemics.

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