



Variational Iteration Method for Solving HIV/AIDS Epidemic Model

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ABSTRACT

In this paper, a deterministic model on the transmission dynamics of Hiv/Aids was presented. Variational Iteration Method (VIM) was employed to attempt the series solution of the model. The validity of the VIM in solving the model was established by using the computer in-built classical fourth-order Runge-Kutta method. The comparison between Variational Iteration Method solution and Runge-Kutta (RK4) were performed which were found to be efficient, accurate and rapidly convergence.

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INTRODUCTION

Acquired immunodeficiency syndrome (AIDS) is a chronic disorder triggered by the human immunodeficiency virus (HIV) that is possibly life threatening. HIV interferes with the body's capacity to combat the disease causing organisms by damaging the immune system. Because of its universal threat to humanity, the research of HIV/AIDS transmission dynamics has been of excellent concern to mathematicians and biologists. Mathematical models have become significant instruments for evaluating the spread and control of HIV/AIDS as they provide brief and long-term HIV and AIDS forecast. Arazoza, and Lounes (2002). HIV can be transmitted between injecting drug users if the drug equipment (needles, syringes or rinsing water) is contaminated by HIV-infected fluids (usually blood) and is then reused by another person without first sterilizing it. Mother to child transmission of HIV is also possible. According to the UNICEF, nine out of every 10 children under the age of 15 become infected with HIV every year because their mothers are HIV positive. This is known as "mother to child transmission" of HIV. In 2001 alone, 710,000 children under 15 contracted HIV while in their mother's womb, during childbirth or through breastfeeding. Srinivasa Rao, (2003). 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 value 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 value 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 way 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. (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 methods 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 by Udoy et al (2015). This model was solved by Peter and Akinduko, (2018) using Differential Transform

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Method. In this paper we solved the same model using VIM and to verify the validity of VIM in solving the model using computer in-built Maple 18

FORMULATION OF THE MODEL

The total sexually-active population at time t , is denoted by $N(t)$. This population is subdivided into four classes, namely susceptible class $S(t)$, the infected Carrier individuals who do not know that they are infected with the disease $I_1(t)$, the infected individuals who are aware that they are infected with the disease $I_2(t)$, and that

$$\begin{aligned} \frac{dS}{dt} &= \Pi - (\beta_1 I_1 + \beta_2 I_2)S - \mu S \\ \frac{dI_1}{dt} &= (\beta_1 I_1 + \beta_2 I_2)S - \omega I_1 - \delta_1 I_1 - \mu I_1 \\ \frac{dI_2}{dt} &= \omega I_1 - \delta_2 I_2 - \mu I_2 \\ \frac{dA}{dt} &= \delta_1 I_1 + \delta_2 I_2 - (\mu + d)A \end{aligned} \tag{1}$$

VARIATIONAL ITERATION METHOD

To illustrate the basic idea of variational iteration method, Abbasbandy and Shivanian, $Ny + Ly = g(x)$ **(2)**

Where N is a non-linear operator, L is a linear operator and $g(x)$ is a non-homogenous term

$$y_{n+1}(x) = y_n(x) + \int_0^x \lambda \{Ly_n(s) + N\tilde{y}_n(s) - g(s)\} ds \tag{3}$$

Where λ is a Lagrangian multiplier which can be expressed as:

$$\lambda(\eta) = \frac{(-1)^n}{(n-1)!} (\eta - t)^{n-1} \tag{4}$$

where n is the highest order of the differential equation. Subject to the initial conditions $S_0=3000, I_0=200, R_0=10$

Solution of the Model Using Variational Iteration Method

We present the analysis of the system of equations governing the model using variational

classical fourth-order Runge-Kutta method as a base

of the AIDS populations $A(t)$. It is assumed that individuals are recruited at a constant rate Π into the susceptible class $S(t)$ also, individuals can be infected with HIV following the force of infection at the rate λ , where $\lambda = \beta_1 I_1 + \beta_2 I_2$. We adopt the mathematical model of Udo et al (2015) by solving the model by Differential Transform Method. The model is governed by the following system of ordinary differential equations

(1999), Abdou and Soliman (2005), and Akinboro et al. (2014) gave the analysis of VIM as follows: Given the general differential equation of the form:

of the differential equations. The construction of correctional function for the equation is given as:

iteration method. Following the same approach as in Momani and Abuasad (2006), we obtain the correctional function as:

$$\begin{aligned} S_{n+1}(t) &= S_n(t) - \int_0^t \{S_n'(x) - \Pi + \tilde{S}_n(x)(\beta_1 \tilde{I}_1(x) + \beta_2 \tilde{I}_2(x)) + \mu \tilde{S}_n(x)\} dx \\ I_{1n+1}(t) &= I_1(t) - \int_0^t \{I_1'(x) + \tilde{S}_n(x)(\beta_1 \tilde{I}_1(x) + \beta_2 \tilde{I}_2(x)) + \omega \tilde{I}_1(x) + \delta_1 \tilde{I}_1(x) + \mu \tilde{I}_1(x)\} dx \\ I_{2n+1}(t) &= I_2(t) - \int_0^t \{I_2'(x) - \omega \tilde{I}_1(x) + \delta_2 \tilde{I}_2(x) + \mu \tilde{I}_2(x)\} dx \\ A_{n+1}(t) &= A_n(t) - \int_0^t \{A_n'(x) - \delta_1 \tilde{I}_1(x) - \delta_2 \tilde{I}_2(x) + (\mu + d) \tilde{A}(x)\} dx \\ R_{n+1}(t) &= R_n(t) - \int_0^t \{R_n'(x) - \epsilon \tilde{T}_n(x) + \mu \tilde{R}_n(x)\} dx \end{aligned}$$

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Subject to the initial conditions $S(0) = 2000$, $I_1(0) = 1000$, $I_2(0) = 800$, $A(0) = 400$.

Using the initial conditions and the parameter values in the table and with the help of Maple 18, we obtain the iterated values for each compartment

Hence, when $k = 4$ the solution to the system (1) in closed form is obtained as

$$S(t) = \sum_{n=0}^k S(k)t^k = 2000 - 1.116000040t - 8.749664400t^2 + 1.166176695t^3 + 1.161453044t^4 + \dots$$

$$I_1(t) = \sum_{n=0}^k I_1(k)t^k = 1000 + 1.118399980t - 1.97536800t^2 - 1.166176589t^3 - 6.949824085t^4 + \dots$$

$$I_2(t) = \sum_{n=0}^k I_2(k)t^k = 800 + 597.89400t + 5.031639885t^2 - 73017.95663t^3 - 2.623896595t^4 + \dots$$

$$A(t) = \sum_{n=0}^k A(k)t^k = 400 + 1019.981200t + 3.915559658t^2 + 62473.23157t^3 - 2.040809761t^4 + \dots$$

Table 1: Parameters values for model

Parameter	Description	Values
Π	Recruitment rate	4000 Assumed
β_1	Transmission rate of HIV in $I_1(t)$ class	0.28 Chavez, C (2004).
β_2	Transmission rate of HIV in $I_2(t)$ class	0.35 Sarah. A (2011).
δ_1	Transfer rate between $I_1(t)$ and A .	0.74 Lawi et al (2011).
δ_2	Transfer rate between $I_2(t)$ and A .	0.4 Udoy S. Basak et al (2015).
ω	Transfer rate between $I_1(t)$ and $I_2(t)$	0.9 Sarah. A (2011).
μ	Natural mortality rate	0.00002 Assumed
d	Disease induced death tare	0.000027 Assumed

NUMERICAL SIMULATION AND GRAPHICAL ILLUSTRATION OF THE MODEL

We present the numerical simulation which demonstrate the analytical results for the proposed HIV/AIDS model. This is achieved by using some set of parameter values given in the table (2) and whose source are mainly from literature and well as assumptions. We considered different initial conditions for the human populations.

$S(0) = 2000$, $I_1(0) = 1000$, $I_2(0) = 800$, $A(0) = 400$. The VIM is demonstrated against mapple in-buit fourth order Runge-Kutta Procedure for the solution of the model. Figs 1 to 4 show the combined plots of the solutions of $S(t)$, $I_1(t)$, $I_2(t)$ and $A(t)$ by VIM and RK4

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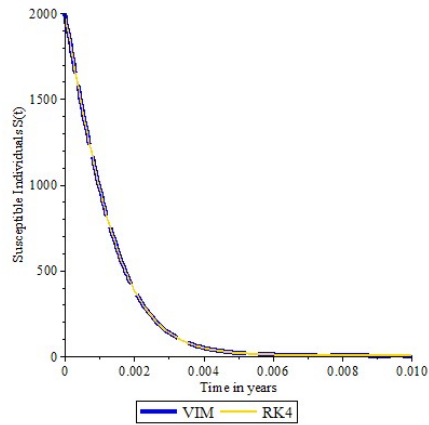


Fig. 1: Solution of Susceptible Population by VIM and RK4

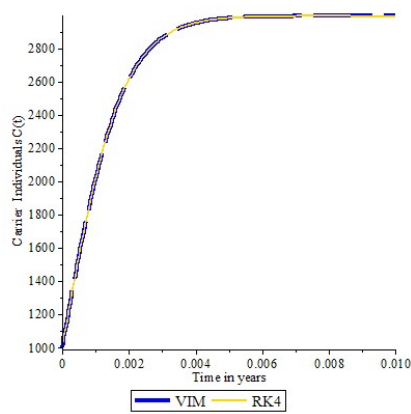


Fig. 2: Solution of Infected Carrier Population by VIM and RK4

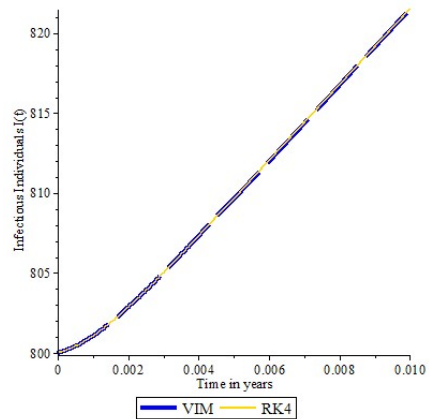


Fig. 3: Solution of Infected Population by VIM and RK4

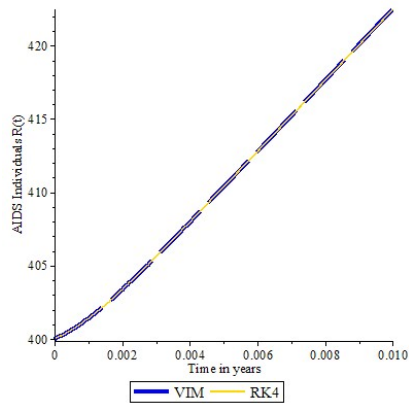


Fig. 4: Solution of Aids Population by VIM and RK4

DISCUSSION OF RESULTS FOR VARIATIONAL ITERATION METHOD

We demonstrate the numerical simulation which illustrate the analytical results for the analysis of Hiv/Aids model. This is achieved by using some set of parameter values given in the table (1) whose source are mainly from literature and well as assumptions. Figs (1) to (4) show the combined plots of the solutions of $S(t)$, $I_1(t)$, $I_2(t)$ and $A(t)$ by VIM and RK4. 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 from our analysis follows the same pattern and behaviour. This shows that Variational Iteration Method is suitable and efficient to conduct the analysis of Hiv/Aids model.

CONCLUSION

Variational Iteration method (VIM) has been successfully applied to solve for the series solution of the HIV/AIDS Epidemic Model with given initial conditions. Numerical simulations were carried out to compare the results obtained by Variational Iteration Method with the result of classical fourth-order Runge-Kutta method. We obtained the same result with (Peter and Akinduko, 2018). It can be concluded that this method is very powerful and efficient in obtaining numerical solutions for the analysis of modern epidemics.

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