

**Article Citation Format**

Bashiru K.A & Olayiwola M.O. (2019); Variational Iteration Method for the Numerical Simulation of HIV Epidemic.  
Journal of Advances in Mathematical & Computational Sciences  
Vol. 7, No. 1. Pp 21-30

**Article Progress Time Stamps**

Article Type: Research Article  
Manuscript Received 19<sup>th</sup> Dec. 2018  
Review Type: Blind  
Final Acceptance: 7<sup>th</sup> January, 2019  
Article DOI: [dx.doi.org/10.22624/AIMS/MATHS/V7N1P3](https://doi.org/10.22624/AIMS/MATHS/V7N1P3)

## Variational Iteration Method for the Numerical Simulation of HIV Epidemic

**Bashiru K.A<sup>1</sup> & Olayiwola M.O.<sup>2</sup>**

<sup>1,2</sup>Department of Mathematical Sciences  
Faculty of Basic and Applied Sciences  
College of Science, Engineering and Technology  
Osun State University  
Osogbo, Nigeria.

**E-mail:** <sup>1</sup>olayiwola.oyedunsi@uniosun.edu.ng

**Phone:** +2348131109234

### ABSTRACT

In this paper, a variational iteration method is used for the simulation of HIV model. The results obtained are in agreement with the existing results. This shows that VIM is a powerful computational tool for the solution of the model. The result also shows that as the rate of treatment increases, the disease dies out.

**Keyword:** - Variational iteration method, HIV, AIDS, Lagrange multiplier.

### 1. INTRODUCTION

The human immune deficiency virus (HIV) infection which can lead to acquired immune deficiency syndrome (AIDS) has become a serious infectious disease in the entire world especially in developing countries. It is a deadly disease, which breaks down the body's immune system leaving the victim vulnerable to a host of life threatening opportunistic infectious, neurological disorders or unusual malignancies [1]. Mathematical models for the spread of the HIV/AIDS epidemic have been studied extensively since the first case were recognized in the late 80's [2-5]. Many of these models often lead to non-linear differential equations. Mathematical models based on the underlying transmission mechanism of HIV might help the medical and scientific community understand better how the disease spreads in the community. Even though the actual data needed for the models might not be accurate or even unavailable, such modelling is still vital in investigating how changes in the various assumptions and parameter value affect the course of the epidemic [6]. Therefore, by developing such models, we can evaluate the potential effectiveness of different approaches to bring the epidemic under control.

At times numerical solution may be resorted to when analytical methods to solve a resulting differential equation is not available. Common analytical procedures linearize the system or assume that non-linearities are relatively insignificant. Such procedures change the actual problem to make it tractable by the conventional methods, as a result the problem being solved is no longer a proper representation of the physical problem whose solution is desired [7].

## 2. HIV EPIDEMIC MODEL

System of differential equations plays important roles in the biological modeling. In this section, we present the system of ordinary differential equations that describe the HIV/AIDS transmission model. Considering the classical assumption of [8 - 19], we formulate a compartmental model to describe the transmission of HIV/AIDS Epidemic. It is assumed that the total population ( $N$ ) is divided into four (4) compartments; Susceptible ( $S$ ), Infected ( $I$ ), Treatment ( $T$ ), and Aids ( $A$ ).

We assumed that the susceptible class ( $S$ ) become Infected via sexual contacts with Infected person which may also lead to birth of infected children. It is also assumed that a fraction of newborns are infected at birth, hence are directly recruited into the infected class at with rate of  $\gamma\xi$ . we do not consider direct recruitment of the other infected person except through Mother - to - Child transmission. The infected moves to join treatment class at the rate  $\sigma_2$ , while others with serious infection moves directly to AIDS class at the rate  $\sigma_1$ . The AIDS class reduces as a result of natural death and disease induced death at the rate of  $\mu$  and  $\alpha$  respectively.

This is described Mathematically as:

$$\left. \begin{aligned} \frac{ds}{dt} &= \psi N - \frac{\beta SI}{N} - \mu S \\ \frac{dI}{dt} &= \gamma\xi I + \frac{\beta SI}{N} - (\mu + \sigma_1 + \sigma_2)I \\ \frac{dT}{dt} &= \sigma_2 I - \mu T + VA \\ \frac{dA}{dt} &= \sigma_1 I - (V + (\alpha + \mu))A \end{aligned} \right\} 1$$

Where the variables  $S_{(t)}$ ,  $I_{(t)}$ ,  $T_{(t)}$  and  $A_{(t)}$  are functions of time  $0 \leq t < \alpha$ .  
 $\psi = N \times \text{birth rate} \times \text{infant survival rate} \times \text{migration}$ .



Infant survival rate = 0.92. (1 - infant mortality rate) ,Infant mortality rate is 75 per 1000 population (NDHS 2010), Birth rate = 0.027, Migration = 1.065 [8]

$$\psi = 162.245 \times 0.027 \times (1-0.75) + 1.065 = 5.12$$

Natural death rate ( $\mu$ ):=0.3

This was estimated using the life expectancy for a Nigerian at birth who was 47.7 years old.

**Table 1: Definition of the parameters.**

No.	Symbols	Description
1	S	Susceptible
2	I	Infected
3	T	Treatment
4	$\psi$	Recruitment rate to susceptible
5	$\beta$	The contact rate of the epidemic
6	$\mu$	Natural death rate
7	N	Total number of population
8	$\gamma$	Rate of infected new born baby
9	$\xi$	The fraction of infected newborn
10	V	Rate of movement from AIDS class to treatment
11	$\sigma_1$	Rate of movement from infected class to AIDS
12	$\sigma_2$	Rate to movement from infected class to treatment
13	$\alpha$	Disease - induced death rate
14	A	AIDS

**Table 2: Assumed values of the used parameters..**

Parameters notation	Assumed values
$\beta$	0.2
$\xi$	0.02
$\gamma$	0.04
$\sigma_1$	0.07
$\sigma_2$	0.06
$\alpha$	0.02

## 2.1 Steady State and Stability of the equilibrium point.

In this sub section, the local stability of the disease - free equilibrium and reproductive number of the system (1) will be discussed.

It is very obvious that the system (1) exhibit the disease free equilibrium given by  $E_0(S, I, T, A) = \left(\frac{\psi}{\mu}, 0, 0, 0\right)$  and the reproductive number  $R_0 = \frac{\beta\psi}{(\mu + \sigma_2 + \sigma_1 - \gamma\xi)\mu N}$ .

### Proposition 1

If  $R_0 < 1$ , then the disease free equilibrium ( $E_0$ ) is locally asymptotically stable.

Proof.

By linearization, the system (1) gives the following jacobian matrix ;

$$p(\lambda) = \begin{bmatrix} -(\mu + \lambda) & -\frac{\beta\psi}{\mu N} & 0 & 0 \\ 0 & \frac{\beta\psi}{\mu N} - (\mu + \sigma_1 + \sigma_2 - \gamma\xi) - \lambda & 0 & 0 \\ 0 & \sigma_2 & -(\mu + \lambda) & V \\ 0 & \sigma_1 & 0 & -(V + \alpha + \mu + \lambda) \end{bmatrix} \quad (2)$$

The eigenvalues of (2) are

$$-(\mu + \lambda) \left[ \left( \frac{\beta\psi}{\mu N} - (\mu + \sigma_1 + \sigma_2 - \gamma\xi) - \lambda \right) (\mu + \lambda) (V + \alpha + \mu + \lambda) - 0 \right] \quad (3)$$

Simplifying (3) we obtained

$$\lambda_1 = -\mu, \quad \lambda_2 = \frac{\beta\psi}{\mu N} - (\mu + \sigma_1 + \sigma_2 - \gamma\xi), \quad \lambda_3 = -\mu, \quad \lambda_4 = -(V + \alpha + \mu) \quad (4)$$

It can be seen clearly from (4) that

$$\frac{\beta\psi}{(\mu + \sigma_2 + \sigma_1 - \gamma\xi)\mu N} < 1 \quad (5)$$

$$\text{Let } R_0 = \frac{\beta\psi}{(\mu + \sigma_2 + \sigma_1 - \gamma\xi)\mu N}$$

Therefore  $R_0 < 1$ , Since all the parameters are non - negative, this proves the proposition.

### 3. THE VARIATION ITERATION METHOD

The basic idea of the He's Variational Iteration Method (VIM) [9-12], can be explained by considering the following nonlinear partial differential equations

$$Lu + Nu = g(x) \tag{6}$$

Where  $L$  is the linear operator,  $N$  is the nonlinear operator and  $g(x)$  is the inhomogeneous term.

According to the method, the corresponding variational iteration method for solving (6) is given as:

$$u_{n+1}(x) = u_n(x) + \int_0^x \lambda(s) \left[ Lu_n(s) + Nu_n(s) - g(s) \right] ds, \tag{7}$$

where  $\lambda$  is a Lagrange multiplier which can be identified optimally by variational iteration method. The subscript  $n$  denote the  $n$ th approximation,  $u_n$  is considered as a restricted variation i.e  $\delta u_n = 0$ . The successive approximation  $u_{n+1}, n \geq 0$  of the solution  $u$  can be easily obtained by determine the Lagrange multiplier and the initial guess  $u_0$ , consequently, the solution is given by  $u = \lim_{n \rightarrow \infty} u_n$ .

Many authors [14 - 18] have used and confirmed the efficiency of the VIM.

### 4. SOLUTION TO HIV MODEL USING VIM

In this section, we present the VIM for the solution of systems of ordinary differential equations that described the model as stated in (1). According to the method, we can construct the correction functional as below:

$$\left. \begin{aligned} S_{n+1}(t) &= S_n(t) + \int_0^t \lambda_1(\tau) \left[ S_n^1(\tau) - \psi N + \frac{\beta S_n(\tau) I_n(\tau)}{N} + \mu S_n(\tau) \right] d\tau \\ I_{n+1}(t) &= I_n(t) + \int_0^t \lambda_2(\tau) \left[ I_n^1(\tau) - \gamma \xi I_n(\tau) - \frac{\beta S(\tau) I_n(\tau)}{N} + I_n(\tau) (\mu + \sigma_1 + \sigma_2) \right] d\tau \\ T_{n+1}(t) &= T_n(t) + \int_0^t \lambda_3(\tau) \left[ T_n^1(\tau) - \sigma_2 I_n(\tau) + \mu T_n(\tau) + VA_n(\tau) \right] d\tau \\ A_{n+1}(t) &= A_n(t) + \int_0^t \lambda_4(\tau) \left[ A_n^1(\tau) - \sigma_1 I_n(\tau) + A_n(\tau) (V + \alpha + \mu) \right] d\tau \end{aligned} \right\} \tag{8}$$

Where  $\lambda_i, i = 1 \dots 4$  are general Lagrange Multipliers,  $\tilde{S}_n, \tilde{I}_n, \tilde{T}_n,$  and  $\tilde{A}_n$  denote restricted variations i.e.  $\delta \tilde{S}_n, \delta \tilde{I}_n, \delta \tilde{T}_n,$  and  $\delta \tilde{A}_n = 0$

Making equation (6) the correction functional  $\lambda$  is stationery when:

$$\left. \begin{aligned} \partial S_{n+1}(t) &= \partial S_n(t) + \partial \int_0^t \lambda_1(\tau) \left[ S_n^1(\tau) - \psi \mid + \frac{\beta S_n(\tau) I_n(\tau)}{N} + \mu S_n(\tau) \right] d\tau \\ \partial I_{n+1}(t) &= \partial I_n(t) + \partial \int_0^t \lambda_2(\tau) \left[ I_n^1(\tau) - \gamma \xi I_n(\tau) - \frac{\beta S(\tau)_n I_n(\tau)}{N} + I_n(\tau) (\mu + \sigma_1 + \sigma_2) \right] d\tau \\ \partial T_{n+1}(t) &= \partial T_n(t) + \partial \int_0^t \lambda_3(\tau) \left[ T_n^1(\tau) - \sigma_2 I_n(\tau) + \mu T_n(\tau) + V A_n(\tau) \right] d\tau \\ \partial A_{n+1}(t) &= \partial A_n(t) + \partial \int_0^t \lambda_4(\tau) \left[ A_n^1(\tau) - \sigma_1 I_n(\tau) + A_n(\tau) (V + \alpha + \mu) \right] d\tau \end{aligned} \right\} 9$$

Solving equation (7), the Lagrange multipliers  $\lambda_i, i = 1 \dots 4 = -1$ .

Given the initial values of

$$S_0(t) = 158.806$$

$$I_0(t) = 1.793$$

$$T_0(t) = 1.449$$

$$A_0(t) = 0.217$$

### 5. RESULTS AND DISCUSSION

Considering [14 - 18], we solve the system of equation (1) by implementing the idea of He’s iteration method numerical scheme. While varying the parameter ( $\sigma_2$ ) value.

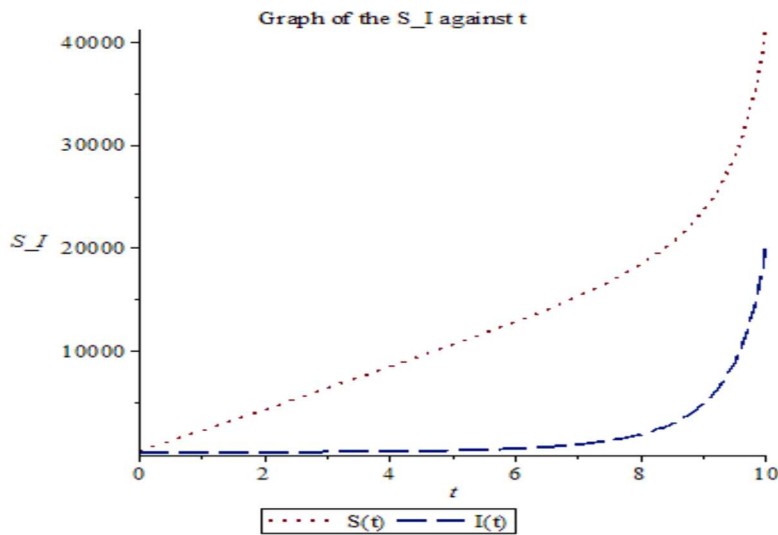


Fig.1: Graph of the Susceptible and Infected individuals when  $\sigma_2 = 0.025$  and other parameters remain constant.

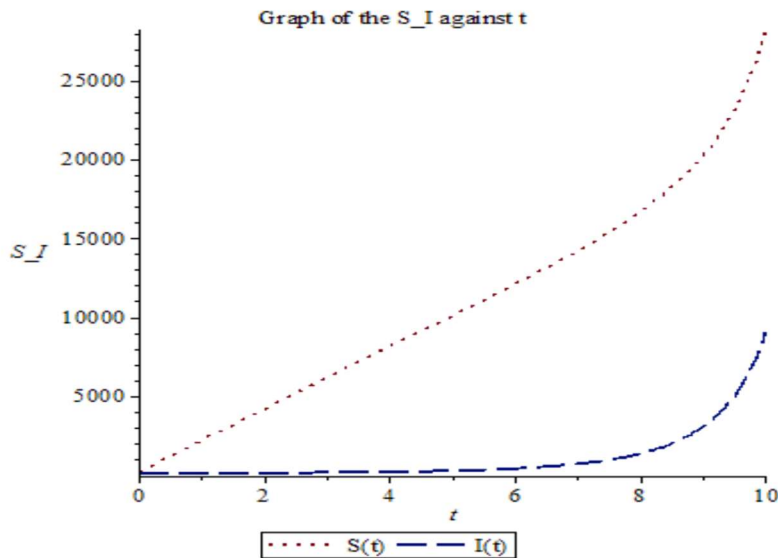


Fig.2: Graph of the Susceptible and Infected individuals when  $\sigma_2 = 0.05$  and other parameters remain constant.

Generally, we observed that as the value of the rate at which people move from infected class to treatment increases the infected class decreases, this is evident from figure.1 - figure.4. It can be seen from figure.1 when  $\sigma_2 = 0.025$  the infected population is 2500 at time ( $t = 8$ ) and when  $\sigma_2 = 0.05$  from figure 2 the infected population reduces to 1000 at time ( $t = 8$ ).

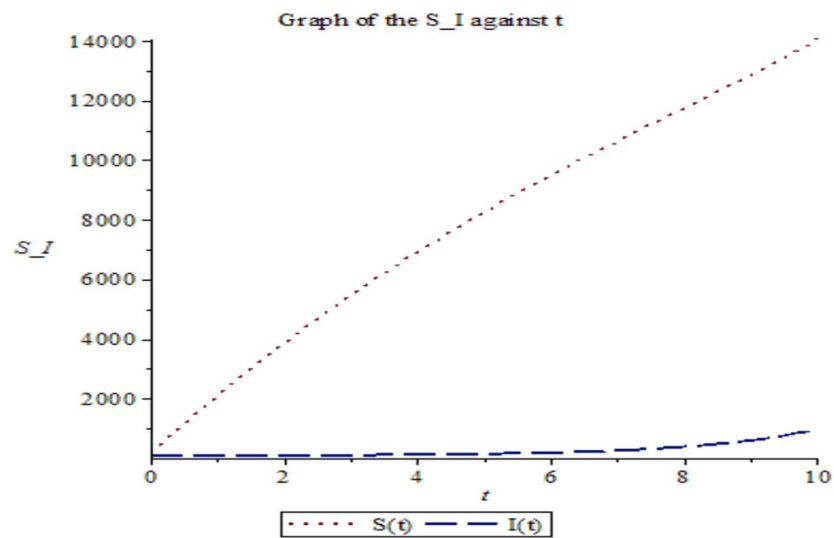


Fig.3: Graph of the Susceptible and Infected individuals when  $\sigma_2 = 0.075$  and other parameters remain constant.

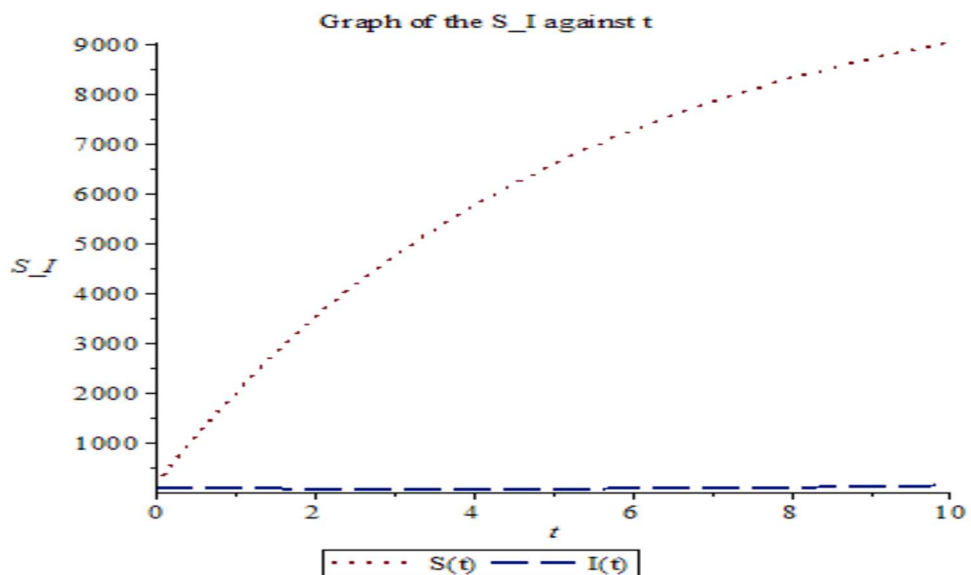


Fig.4: Graph of the Susceptible and Infected individuals when  $\sigma_2 = 0.1$  and other parameters remain constant.





Also it was observed from figure 3 and figure 4, that as  $\sigma_2$  increases from 0.075 the infected class reduces drastically towards equilibrium level. The reduction could be as a result of aggressive awareness campaign on HIV/AIDS Treatment through the Television, Radio, Social Media and during antenatal program for pregnant women. Also the sermon on fornication and adultery from religion leaders which bring the reduction in the number of sexual partners.

## 6. CONCLUSION .

In this research paper, numerical solution of HIV/AIDS Epidemic model was presented using the scheme of Variational Iteration Method (VIM). The simulation was carried out and the result was presented graphically. It was observed that as the rate of treatment is increases the infected population reduces this show that treatments play a vital role in eradication of HIV/AIDS. If the government can intensify more effort on the coverage area of the treatment and its awareness the HIV/AIDS Epidemic will go to extinction. The results also justified the conclusion that the variational iteration method is a powerful tool for solving system of differential equations that modeled epidemiological diseases that arises in the real life situation. This is also evident since results obtained are in good agreement with those that are available in the literatures.

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