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VARIATIONAL ITERATION METHOD FOR SOLVING NONLINEAR HIV/AIDS MODEL

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ABSTRACT

Semi-analytical tools present an alternative means of solving system of nonlinear differential equations that ordinarily do not have an exact solution.Thus, in this study, Variational Iteration Method (VIM) which is one of the semi-analytical method was used to solve the system of nonlinear ordinary differential eqautions arising from the Mathematical model of HIV/AIDS with consideration of effect of immigrants into a hyper-mixed population. Positivity of solution, equilibria states and reproduction number of the model were all calculated. Series solution of the transformed model was obtained and graphs were plotted. The graphs were compared with the result obtained when using Runge-Kutta order 4 and a reliably accurate result was obtained

Keywords*: Nonlinear, Semi-analytical method,VIM,Hyper-mixed populationandSeries-solution*

1.0 INTRODUCTION

Clinically, lot of efforts have been devoted to the study of the class of virus causing HIV ad how to eradicate (or reduce) their multiplying effect once they enter the bloodstream of an infected person. However, from all the result obtained so far, there's no established medication that has been scientifically proven to eliminate this virus from the body. Thus, the quest for effective solution for this menace is still ongoing with no end visibly in sight. For an infection with multiple pathway, which include vertical (mother-child at birth), use of unsterilized sharp objects and sexual activities (among same sex, opposite sex, animal-man etc.), blood transfusions, tissue transplantation, medical procedures thatinvolve unsterilized cutting or piercing; and experiencing accidental needle stick injuries, including among health workers (Avert, 2018), more has to be done to curtail the spread of this infection. According to CDC (2019), the presence of HIV in human renders the immune system vulnerable to external attacks which are called opportunistic infections (such can include Tuberculosis, incessant malaria, HBV etc.). Among several authors that worked on HIV/AIDS dynamics is Temesgen and Semu (2018) where they discussed control strategy for TB-HIV co-infection withconsideration of behavioral adjustment and they agreed that applying both preventive andcurative measures brings optimal economic and epidemiological gain.

Thus, the quest for means of reducing the spread of this infection fuel this research work.

Mathematical modeling is a fast growing field of applied Mathematics where physical problems are written as a form of system of equations (Differential Equations such as ODE, PDE;

Algebraic equations and so on). Due to the complexity of most physical problems, the resultingmathematical equations obtained are non-linear in nature, hence, exact (or analytic) solution of theresulting governing equations may not exist. The system of equations can be analyzed qualitatively with the help of some standard theorem and principles or

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quantitatively with the helpof numerical tools (analysis) using numerical data from the appropriate sources. Simulation ofthe model equations give insight into the likely future pattern of the systems been modeled.

Furthermore, Mathematical epidemiology is an applied field of Mathematics that deals withthe study of incidence and distribution of new cases of infection, analysis and possibility of itscontrol. A dynamical system of the disease under study is presented in a system of differentialequations (either as ODE or PDE) and the system analyzed qualitatively and numerically

2.0 Model Formulation

Thus in this work, the effect of an event gathering that bring different categories of people into a population on the transmission dynamics of HIV/AIDS was considered. The motivation for consideration of immigrant on the transmission dynamics of HIV/AIDS emanate from the alarm raised by BBC before the popular FIFA 2010 world cup about the risk of potential surge (increase) in HIV/AIDS patients after the tournament (Dawson, 2010). It was gathered that the population of HIV/AIDS infective could increase astronomically both in the host country and visiting countries after the event if proper control is not in place. Hence, this work extend the model of Naresh et al., (2009) by assuming the total population is N at any time t, recruitment intothe host community by birth at the rate π and there is an immigrants at the rate $Q_i$into eachi^{th} compartment respectively. The total population was subdivided into six compartments to accommodate the different stages of progression of the virus namely, the Susceptible compartment (S), the exposed compartment (E), the HIV infective at asymptomatic stage (I_1), theHIV infective at symptomatic stage (I_2), the full blown AIDS compartment (A) and the Treatment compartment. The force of infection of the disease is given asψ and depends upon many factors that include effective contact rate $\beta_i$of susceptible with infected classes through sexualactivities, exposure to unscreened blood transfusion, contaminated sharp object etc. Rate ofprogression to asymptomatic or symptomatic stage is given as $\xi_i$and may be a function ofearly screening, early therapeutic treatment etc. Natural death occur at the same rate across all compartments at the rate μ and HIV/AIDS induced death occurred at the rate $\delta_i$acrossinfected compartments with high viral load. Progression from compartments I_i to full blownAIDS is at the rate $\sigma_i$and the treated individuals from each categories are taken as $\omega_i$which is taken to be a function of availability of fund for treatment and effectiveness of treatment amongothers. The diagrammatic representation of the model developed is given in figure below:

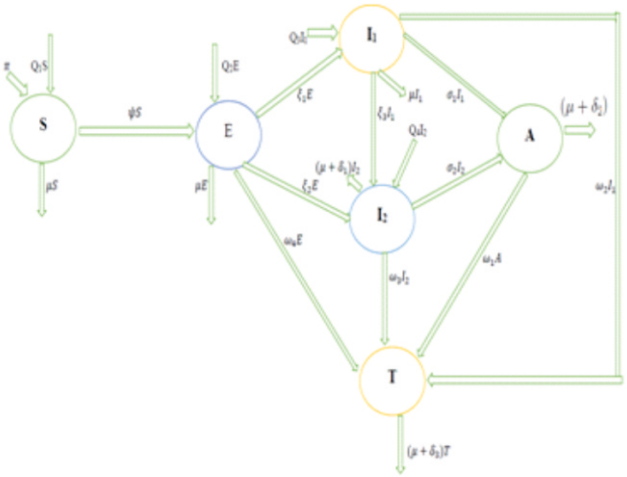

Figure 1: Flow Chart of the Extended Model

The system of equation governing the model is given as:

$$\begin{aligned}
\frac{dS}{dt} &= \pi + Q_1 S - (\mu + \psi)S \\
\frac{dE}{dt} &= Q_2 E + \psi S - (\mu + \xi_1 + \xi_2 + \omega_4)E \\
\frac{dI_1}{dt} &= Q_3 I_1 + \xi_1 E - (\mu + \sigma_1 + \omega_2 + \xi_3)I_1 \\
\frac{dI_2}{dt} &= Q_4 I_2 + \xi_3 I_1 + \xi_2 E - (\mu + \sigma_2 + \omega_3 + \delta_1)I_2 \qquad (1) \\
\frac{dA}{dt} &= \sigma_1 I_1 + \sigma_2 I_2 - (\mu + \omega_1 + \delta_2)A \\
\frac{dT}{dt} &= \omega_2 I_1 + \omega_3 I_2 + \omega_1 A + \omega_4 E - (\mu + \delta_3)T
\end{aligned}$$

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Where the force of infection ψ is given as:

$$\psi = \beta_1 E + \beta_2 I_1 + \beta_3 I_2 + \beta_4 A + \beta_5 T \qquad (2)$$

Some basic assumptions were made in this course of formulating the model, most of which are:

a. The population is an open one and access is non-restricted
b. Sensitivity to testing distinguish compartment E from I_i
c. Viral count distinguish compartment $I_1$from I_2
d. The AIDS compartment are taken to be sexually inactive in the population, however they influence the transmission rate of HIV minimally by other means like vertical and/or use of needle or clipper etc.
e. Sensitization leads to early detection and hence early treatment
f. HAART reduces the viral load of the disease and hence people in E and I_1 compartments who can afford the drug will remain in those compartments till they die naturally
g. Effective curative drug for HIV/AIDS is assumed at the moment to be unavailable.

The definition of parameters used in the model and there meaning together with values used to obtain the iteration are presented in the table below:

Table 1: Model Parameters and Description

Parameter	Description	Value
ψ	Force of Infection	Estimated
β_i	Effective contact rate	Varied(Mukandavire *et al.,* 2009)
δ_i	Induced death rate	0.1 (Mohammed *et al.,* 2013)
ω_i	Screening rate	Assumed
Q_i	Immigrant rate	Varied
ξi	Progression rate	Assumed
σ_i	Deterioration rate	Varied
μ	Natural death rate	Assumed
π	Recruitment rate	Assumed
S	Susceptible class	700 (hypothetical)
E	Exposed class	100 (Assumed)
I_1	Asymptomatic HIV	125 (Assumed)
I_2	Symptomatic HIV	75 (Assumed)
A	AIDS class	65 (Assumed)
T	Treatment class	35 (Assumed)

3.0 Methodology

He (1998) introduced a Variational approach to nonlinear problems and its application where he presented a Variational Iteration Method to construct an iterative solution of a nonlinear system based on correction functional that include a generalized Lagrange multiplier. He (1999)proposed VIM using variational theory to choose the value of the Lagrange multipliers so thateach improves the accuracy of the solution. The initial approximation usually includes unknown coefficient which can be determined to satisfy any initial or boundary condition(s) given. VIMhas gained wide usage as Abbasbandy and Shivanian (2009) applied VIM to solve nonlinear Volterra's Integro-differential equations, Momani and Abuasad (2006) solved Helmholtz equation with VIM etc.

He (1998, 1999) gave the analysis of the variational iteration method as discussed by Akinboro *et al*.,(2014) 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 and $g(x)$ is a non-homogenous term of the DE. The construction of the correctional function for the equation is given as:

$$y_{n+1} = y_n(x) + \int_0^x \lambda \left\{ L y_n(s) + N\overline{y}_n(s) - g(s) \right\} ds$$

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

$$\lambda(\eta) = \frac{(-1)^n}{(n-1)!}(\eta) - x^{n-1}$$

where n is the highest order of the differential coefficient. The highest order derivative in this model is one, hence, $n = 1$.

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4.0 Result and Discussion

Setting the total population at any time *t* to *N(t),* thus,

$$N(t) = S(t) + E(t) + I_1(t) + I_2(t) + A(t) + T(t) \quad (3)$$

For computational effectiveness, let

$$\begin{aligned} k_2 &= \mu + \xi_1 + \xi_2 + \omega_4 \\ k_3 &= \mu + \sigma_1 + \omega_2 + \xi_3 \\ k_4 &= \mu + \delta_1 + \sigma_2 + \omega_3 \\ k_5 &= \mu + \delta_2 + \omega_1 \\ k_6 &= \mu + \delta_3 \end{aligned} \quad (4)$$

System of equation (1) becomes

$$\begin{aligned} \frac{dS}{dt} &= \pi + Q_1 S - (\mu + \psi)S \\ \frac{dE}{dt} &= Q_2 E + \psi S - k_2 E \\ \frac{dI_1}{dt} &= Q_3 I_1 + \xi_1 E - k_3 I_1 \\ \frac{dI_2}{dt} &= Q_4 I_2 + \xi_3 I_1 + \xi_2 E - k_4 I_2 \\ \frac{dA}{dt} &= \sigma_1 I_1 + \sigma_2 I_2 - k_5 A \\ \frac{dT}{dt} &= \omega_2 I_1 + \omega_3 I_2 + \omega_1 A + \omega_4 E - k_6 T \end{aligned} \quad (5)$$

4.1 Positivity of Solution of Model

Adding the system of equation (5) together to obtain:

$$\begin{aligned} \frac{dN(t)}{dt} &= \pi + Q_1 S + Q_2 E + Q_3 I_1 + Q_4 I_2 \\ &\quad - \mu N - \delta_1 I_2 - \delta_2 A - \delta_3 T \end{aligned} \quad (6)$$

Assuming that the sum of total recruitment rate π and immigration rate Q_i is denoted as Qthen (6) becomes:

$$\begin{aligned} \frac{dN(t)}{dt} &= Q - \mu N - \delta_1 I_2 - \delta_2 A - \delta_3 T \quad (7) \\ \frac{dN(t)}{dt} &\le Q - \mu N \\ \frac{dN(t)}{dt} &+ \mu N \le Q \end{aligned}$$

Solving (7) by using integrating factor with initial condition $N(0)=N_0$to obtain

$$N(t) \le \frac{Q}{\mu} + \left(N_0 - \frac{Q}{\mu} \right) e^{-\mu t} \quad (8)$$

Theresult in (8) is a positively invariant set and attracting with respect to the basic model equation. As time ***t*** approaches infinity, the closed set ***D*** depicting the region where the model equation is epidemiologically well posed and mathematically meaningful is thus derived as

$$D = \left\{ (S, E, I_1, I_2, A, R) \in R_+^6 : N(t) \le \frac{Q}{\mu} \right\} \quad (9)$$

4.2 Equilibria Points of the Model

The system of equation (1) for the model exhibits two equilibria points which are known respectively as the Disease Free Equilibrium (DFE denoted as P_0) and the Endemic Equilibrium (EE denoted as P^*) points which are respectively given as:

$$P_0 = (S_0, E_0, I_{1,0}, I_{2,0}, A_0, T_0) = \left(\frac{\pi}{\mu - Q_1}, 0, 0, 0, 0, 0 \right)$$

and

$$P^* = (S^*, E^*, I_1^*, I_2^*, A^*, T^*)$$

$$S^* = \frac{(k_2 - Q_2)(k_3 - Q_3)(k_4 - Q_4)k_5 k_6}{D}$$

$$E^* = \frac{\pi}{(k_2 - Q_2)} - (Q_1 - \mu)\left[\frac{(k_3 - Q_3)(k_4 - Q_4)k_5 k_6}{D} \right]$$

$$I_1^* = \frac{\xi_1}{(k_3 - Q_3)} \left(\frac{\pi}{(k_2 - Q_2)} - (Q_1 - \mu)\left[\frac{(k_3 - Q_3)(k_4 - Q_4)k_5 k_6}{D} \right] \right)$$

$$I_2^* = \frac{\xi_2}{(k_4 - Q_4)} \left(\frac{\pi}{(k_2 - Q_2)} - (Q_1 - \mu)\left[\frac{(k_3 - Q_3)(k_4 - Q_4)k_5 k_6}{D} \right] \right)$$

$$A^* = \frac{\xi_2}{k_5} \left(\frac{\pi}{(k_2 - Q_2)} - (Q_1 - \mu)\left[\frac{(k_3 - Q_3)(k_4 - Q_4)k_5 k_6}{D} \right] \right)$$

$$T^* = \frac{\xi_1}{k_6} \left(\frac{\pi}{(k_2 - Q_2)} - (Q_1 - \mu)\left[\frac{(k_3 - Q_3)(k_4 - Q_4)k_5 k_6}{D} \right] \right)$$

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Where

$$D = k_5 k_6 (k_4 - Q_4)\left[\beta_1 (k_3 - Q_3) + \beta_2 \xi_1\right] +$$
$$\beta_3 y_3 k k k_6 (\ _3 - Q_3) +$$
$$(k_3 - Q_3)(k_4 - Q_4)\left[\beta_4 y_2 k_6 + \beta_5 y_1 k_5\right]$$

4.3 Model Reproduction Number (R_0)

This is defined as the number of secondary case(s) generated by an infected individual introduced into a susceptible population. The model reproduction number (R_0) of the model was obtained as:

$$R_0 = \frac{S_0(\beta_1 k_6 + \beta_5 \omega_4)}{k k (\ _2 - Q_2)} \qquad (10)$$

4.4 Semi-Analytic Solution of the Model Equation using Variational Iteration Method

Following the method established by He (1998) and adopted by Akinboro *et al.,* (2014), the correctional function for the system of equation (1) was obtained as:

$$S_{n+1} = S_n(t) - \int_0^t \left\{ \begin{array}{l} S'_n(s) - Q_1 \overline{S}_n(s) + \mu \overline{S}_n(s) + \\ \overline{S}_n(s)\left(\begin{array}{l} \beta_1 \overline{E}_n(s) + \beta_2 \overline{I}_{1n}(s) \\ + \beta_3 \overline{I}_{2n}(s) + \beta_4 \overline{A}_n(s) \\ + \beta_5 \overline{T}_n(s) \end{array} \right) \end{array} \right\} ds$$

$$E_{n+1} = E_n(t) - \int_0^t \left\{ \begin{array}{l} E'_n(s) - Q_2 \overline{E}_n(s) + k_2 \overline{E}_n(s) - \\ \overline{S}_n(s)\left(\begin{array}{l} \beta_1 \overline{E}_n(s) + \beta_2 \overline{I}_{1n}(s) \\ + \beta_3 \overline{I}_{2n}(s) + \beta_4 \overline{A}_n(s) \\ + \beta_5 \overline{T}_n(s) \end{array} \right) \end{array} \right\} ds$$

$$I_{1,n+} = I_{1,n}(t) - \int_0^t \left\{ \begin{array}{l} I'_{1,n}(s) - Q_3 \overline{I}_{1,n}(s) - \xi_1 \overline{E}_n(s) \\ + k_3 \overline{I}_{1,n}(s) \end{array} \right\} ds$$

$$I_{2,n+} = I_{2,n}(t) - \int_0^t \left\{ \begin{array}{l} I'_{2,n}(s) - Q_4 \overline{I}_{2,n}(s) - \xi_2 \overline{E}_n(s) \\ -\xi_3 \overline{I}_{1,n}(s) + k_4 \overline{I}_{2,n}(s) \end{array} \right\} ds$$

$$A_{n+1} = A_n(t) - \int_0^t \left\{ \begin{array}{l} A'_n(s) - \sigma_1 \overline{I}_{1,n}(s) - \sigma_2 \overline{I}_{2,n}(s) \\ + k_5 \overline{A}_n(s) \end{array} \right\} ds$$

$$T_{n+1} = T_n(t) - \int_0^t \left\{ \begin{array}{l} T'_n(s) - \omega_4 \overline{E}_n(s) - \omega_3 \overline{I}_{2,n}(s) \\ -\omega_2 \overline{I}_{1,n}(s) - \omega_1 \overline{A}_n(s) + k_5 \overline{T}_n(s) \end{array} \right\} ds \qquad (11)$$

With initial conditions: S(0) =700, E(0) =100, $I_1(0)$ =125, $I_2(0)$ =75, A(0) = 65, T(0) =35 and N(0) = 1100. Using the above initial conditions together with the parameter value in table 1 to perform iterations for the transformed model, the series solution for each compartment is given as:

$$S(t) = 700 + 2015.796401\ t + 1209.343199\ t^2 + 257.952378523\ t^3 + 20735551\ t^4 + 0.8899271114\ t^5 + O(t \geq 6)$$

$$E(t) = 100 + 33.20359908\ t + 2.411804319\ t^2 + 0.096911281110\ t^3 + 008188216789\ t^4 + 0.001036943968\ t^5 + O(t \geq 6)$$

$$I_1(t) = 125 + 6.0\ t + 0.4151764082\ t^2 + 0.010768313960\ t^3 + 0002042168189\ t^4 + 0.00001057192901\ t^5 + O(t \geq 6)$$

$$I_2(t) = 75 + 106.50\ t - 10.32730742\ t^2 + 0.7777360144\ t^3 - 0.01533307107\ t^4 + 0.0003794834524\ t^5 + O(t \geq 6)$$

$$A(t) = 65 - 4.650\ t + 12.84093750\ t^2 - 1.181702934\ t^3 + 0.04305647463\ t^4 - 0.0005729595246\ t^5 + O(t \geq 6)$$

$$A(t) = 65 - 4.650\ t + 12.84093750\ t^2 - 1.181702934\ t^3 + 0.04305647463\ t^4 - 0.0005729595246\ t^5 + O(t \geq 6)$$

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$$T(t) = 35+34.350000t+2.060081758t^2 -0.01370946818t^3 + 0.00005283461328t^4 + 0.00004995891901t^5 + O(t \geq 6) \quad (12)$$

4.5 Numerical Simulation of Result

The numerical simulation of the series result in equation (12) is presented below:

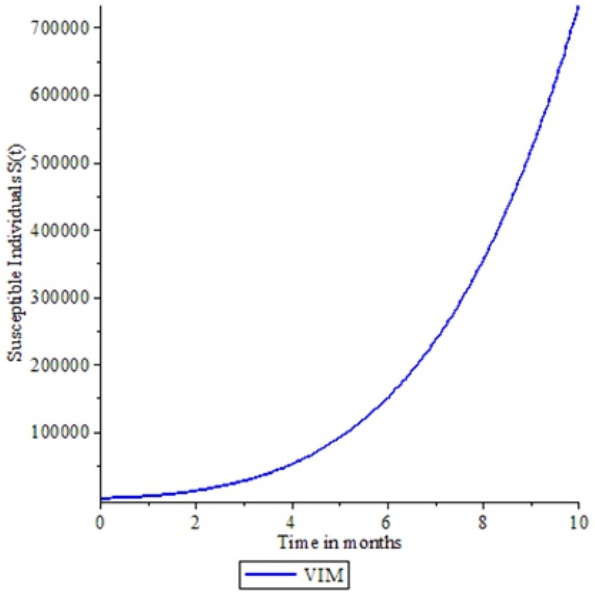

Figure 2: VIM solution for Susceptible class

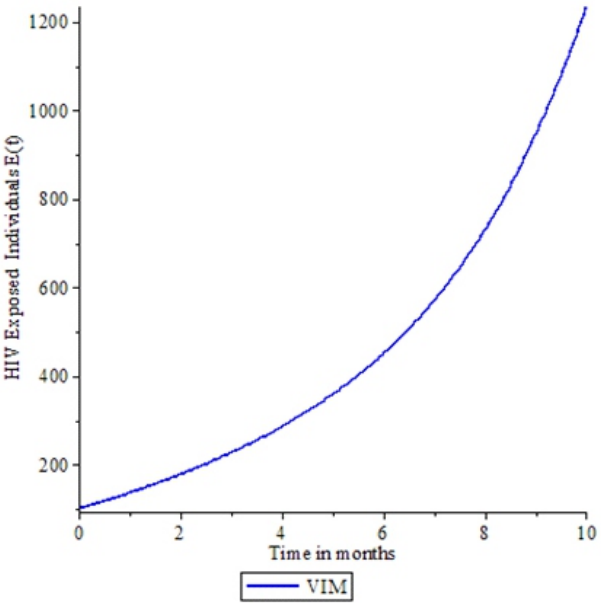

Figure 3: VIM solution for Exposed class

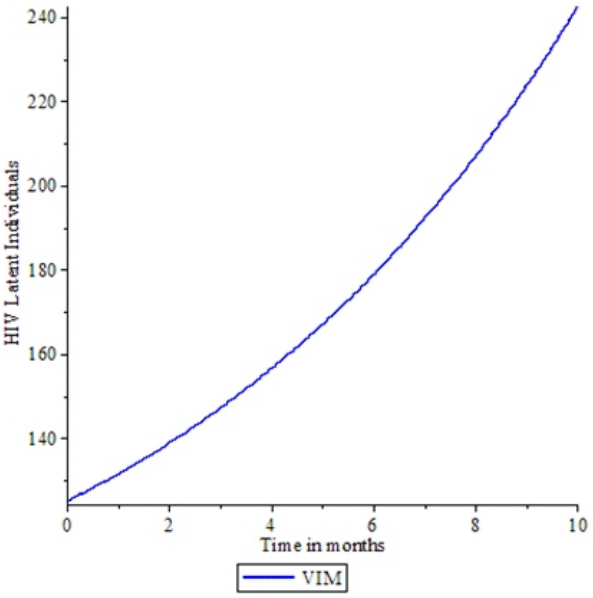

Figure 4: VIM solution for HIV Asymptomatic class

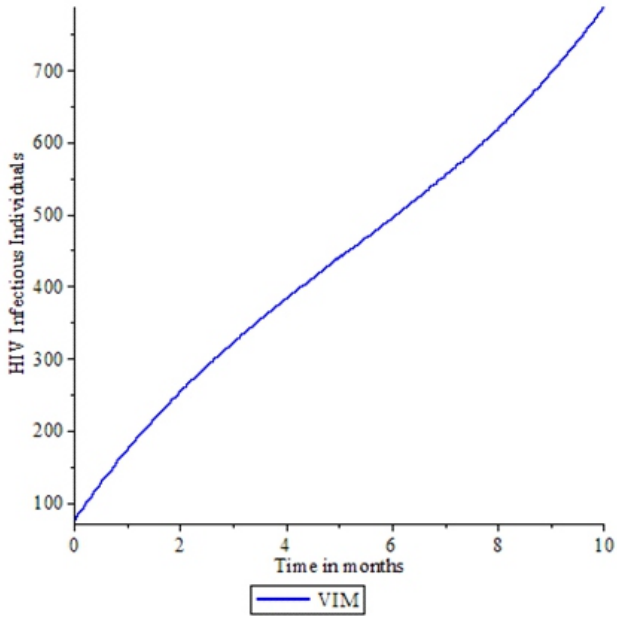

Figure 5: VIM solution for HIV Symptomatic class

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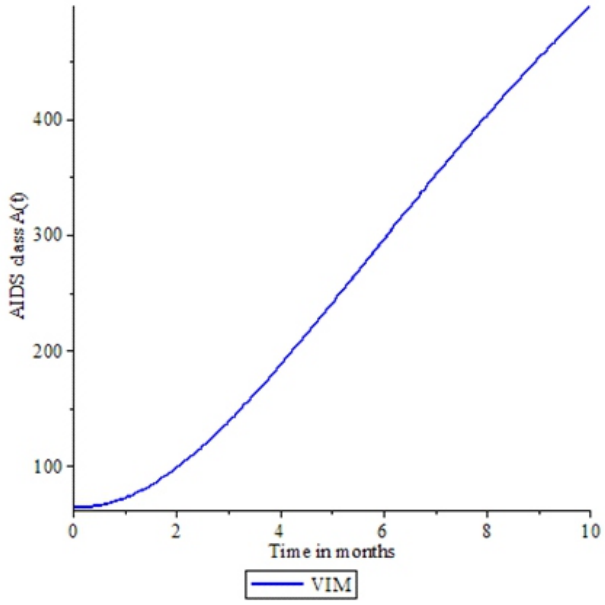

Figure 6: VIM solution for AIDS class

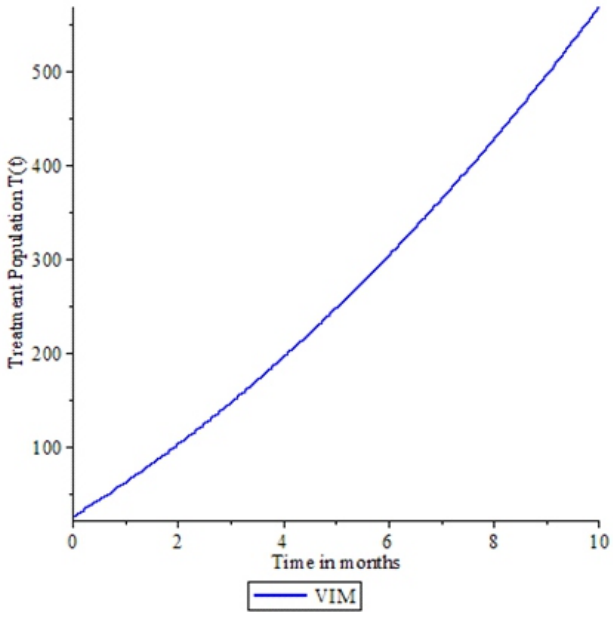

Figure 7: VIM solution for Treatment class

The result obtained for the solution of the model using variational iteration method was compared with Runge-Kutta order 4 (which is in-built in Maple 18) to obtain the following results.

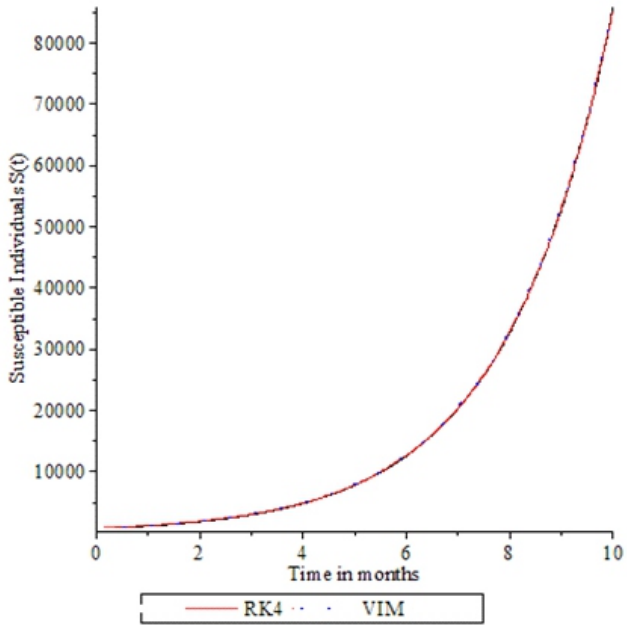

Figure 8: VIM and RK4 solution for Susceptible class

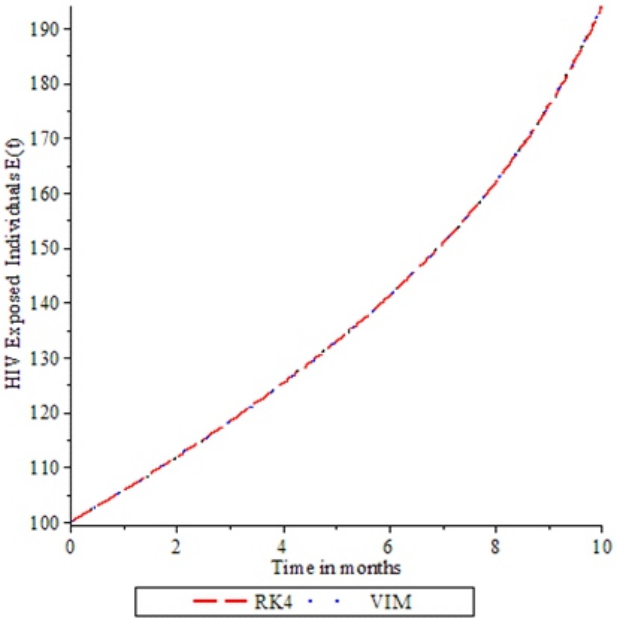

Figure 9: VIM and RK4 solution for Exposed class

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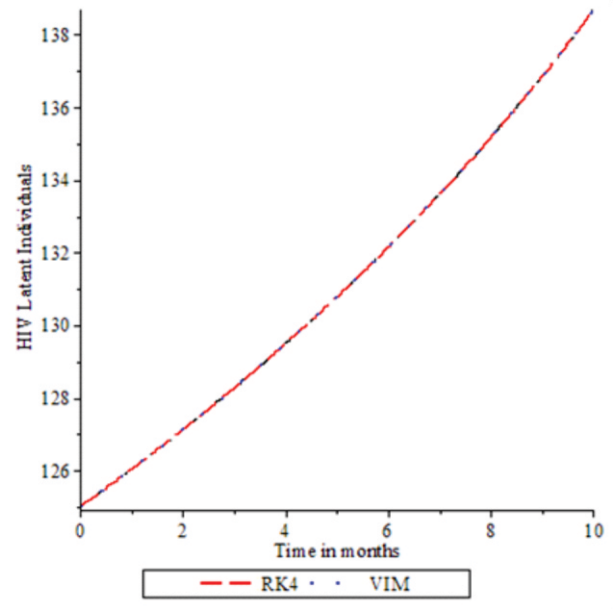


Figure 10: VIM and RK4 solution for HIV Asymptomatic class

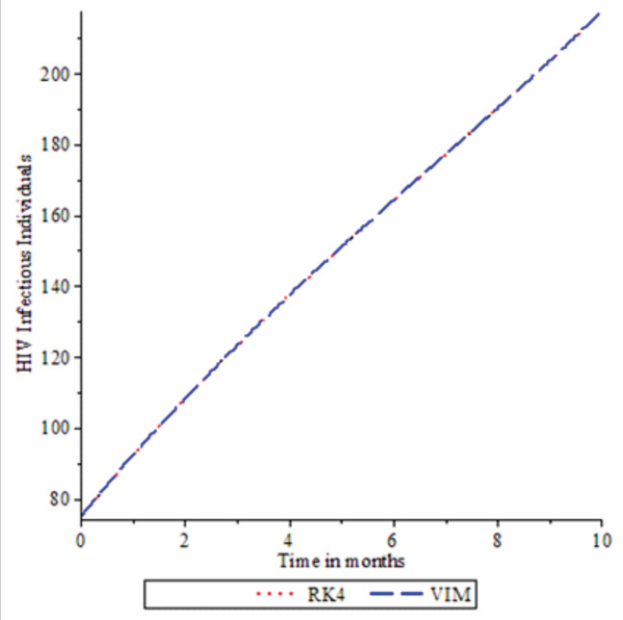
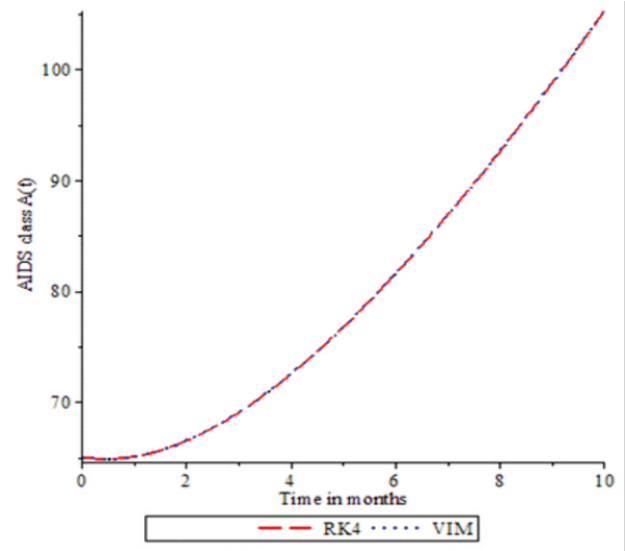


Figure 11: VIM and RK4 solution for HIV Symptomatic class



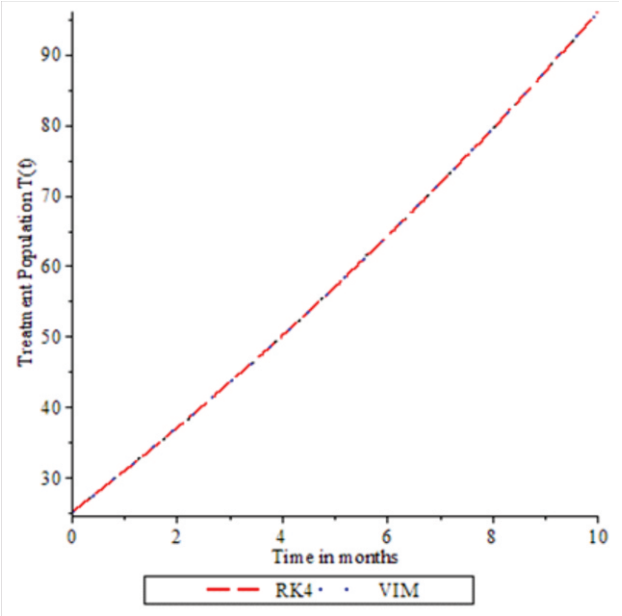


Figure 13: VIM and RK4 solution for Treatment class

Table of Results for VIM and RK4 Solutions of the Model

In this section, the table of result for the semi-analytic method used (VIM) and the standard Runge-Kutta order 4 numerical scheme was presented for comparison for some of the compartments to show the accuracy of VIM to solve system of non-linear differential equations. As obtained from the tables below, it can be deduced that VIM gives a good approximation of solution to any non-linear system of differential equations.

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Table 2: Result comparison for susceptible class

Time	VIM	RK4	Error
0	700	700	0
1	1042.42286066096	1042.422860	$6.60957994114142 \times 10^{-7}$
2	1377.89734397931	1377.897344	$2.06928234547377\times 10^{-8}$
3	1706.49450493028	1706.494505	$6.97159521223512 \times 10^{-8}$
4	2028.29268769545	2028.292686	0.00000169544887285156
5	2343.37801410365	2343.378015	$8.96352503332309\times 10^{-7}$

Table 3: Result comparison for Exposed class

Time	VIM	RK4	Error
0	100	100	0
1	145.188720565781	145.1887102	.0000103657811791891
2	164.913198142217	164.9131697	0.0000284422174843257
3	173.634577944712	173.6345494	0.0000285447124213078
4	177.621182029619	177.6211491	0.0000329296190102468
5	179.586277117134	179.5862449	0.0000322171336222254

5.0 Conclusion

In this work, the effect of immigrants on the overall prevalence of HIV/AIDS in a society serves as a basis for the model formulation. The system of equations governing the model was tested for positivity of solution and found to be both epidemiologically well posed and mathematically meaningful. The disease free equilibrium of the model as well as its infection persistent equilibrium states were both computed. The threshold parameter R_0 (which indicate subsequent infection from a single infected individual) was obtained. The solution of the non-linear differential equation was obtained by using the semi-analytical tool Variational Iteration Method (VIM) which was first propounded by He (1998). The numerical simulation of the result was done and the accuracy of the method was compared with standard Runge-Kutta order 4 method. From the analysis, it was observed that infected immigrants play a vital role in the transmission dynamics of the HIV infection because DFE obtained depend on Q (immigration rate). Also, from the result of the R_0 obtained, it is obvious to see that the same Q also appears in the result, which implies that the eradication or reduction in the spread of the infection has to do largely about effective screening of all immigrants so as to ascertain the status of the individual entering the population. The result obtained for the numerical simulation of both VIM and RK4 indicate that VIM provide a reliable means of solving non-linear system of ordinary differential equation.

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