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The Mathematical Analysis of Hepatitis B Virus Using Homotopy Analysis Method (Ham)

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ABSTRACT: *In this paper, we developed the model of Hepatitis B Virus as SVEACR model and determined the qualitative properties (that is, boundedness and positivity) of the model. The steady states of the model were determined (disease-free and endemic steady states). The Model Basic Reproduction Number was calculated and the disease-free equilibrium was established to be locally asymptotically stable. Global Stability of the Disease-free equilibrium and Endemic Equilibrium were proved to be stable. This was followed Sensitivity Analysis and discussion of Results. Solution of the SVEACR Model by Homotopy Analysis Method (HAM) as obtained. A simulation solution was obtained and this was followed by Summary, Conclusion and Recommendations*

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I. INTRODUCTION

The establishment and spread of Hepatitis B Virus is a complex phenomenon with many interacting factors, e.g., the environment in which the pathogen and hosts are situated, the population(s) it is exposed to, and the intra and inter-dynamics of the population it is exposed to. The role of mathematical epidemiology is to model the establishment and spread of diseases. A predominant method of doing so, is to use the notion of abstracting the population into compartments under certain assumptions, which represent their health status with respect to the pathogen in the system. One of the cornerstone works to achieve success in this method was done by Kermack and McKendrick in the early 1900s, Kermack and McKendrick (1927).

Most of the models in mathematical epidemiology are compartmental models, with the population being divided into compartments with the assumptions about the nature and time rate of transfer from one compartment to another. In several works, any compartment model can be adopted, for example SIR, SIS, SEIR, SEIS, MSEIR, MSEIRS models and so on.

Many authors used the SIR and SEIR model to analyze the behavior of dynamics of computer virus Grassberger (2002), Han and Tan (2010), Ren et al. (2012) and Zhu et al (2012). Also Momoh et al. (2015) presented the application of the Homotopy Analysis method for solving the SEIR models of epidemics. Awawdeh et al. (2009) proposed the solutions of the SIR models of epidemics also using the Homotopy Analysis Method, Following the trend of evolving models to describe transmission dynamics, Ibrahim and Egbetade (2013) proposed the Homotopy Analysis Method for an SEIR Tuberculosis Model. Subsequently, we consider that most of these models developed so far have systems of non-linear ordinary differential equations describing its dynamics. Hence, to solve these systems, many authors have employed the use of linearization, perturbation, massive computation and transformations in which a few new solutions of the non-linear problem are neglected. A lot of work has been done on the application of HAM in different aspect of mathematical modeling. In the works by Momoh et al (2015), Awawdeh et al. (2009), Ibrahim and Egbetade (2013), considerable effort has been made in demonstrating the accuracy and convergence of HAM. In the referred works, it has been established that HAM converges faster and it is more accurate in solving non-linear ODEs. In this work, our aim is to divide the population into six compartments, that is, SVEACR, formulate the model and seek to use HAM to solve the formulated SVEACR epidemic model. An example is tested, and the obtained results suggest that HAM provides a useful analytic tool to investigate highly non-linear problems with multiple solutions and singularity in epidemic models. In our work, we seek to extend the model in the work of Muhammad et al (2013) to the field of Epidemiology, particularly on Hepatitis B Virus with the migration effect and considering the bilinear incidence rate factor which is the measure of the risk that an individual develops a new condition within a specified period of time. Furthermore, solving the six systems of non-linear differential equations, we employed the use of the Homotopy Analysis Method instead of using linearization and perturbation methods. We also investigate the accuracy of the Homotopy Analysis Method for solving the problem. Other papers that are consulted are: Ukobasi et al (2017), Omame et al (2017), Van den Driesshe (2002), WHO (2008), Kane (1995) and Candotti et al (2006).

1.1 Flow Diagram of the Model

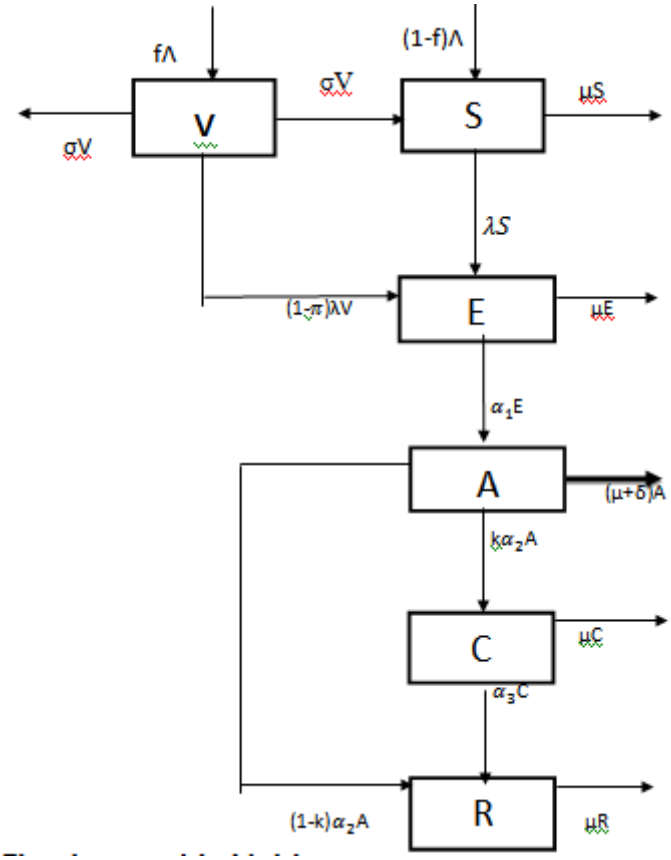


Fig. 1: Flow diagram of the Model

1.2 Symbols and Parameters

Table 1 below is the symbols and parameters used in the models.

Table 1: Symbols and Description of Model Parameters

Symbol and Parameters	Description
S(t)	The number of susceptible individuals at time t
V(t)	The number of vaccinated individuals at time t
E(t)	The number of exposed individuals at time t
A(t)	The number of acutely infected individuals at time t
C(t)	The number of infectious individuals at time t
R(t)	The number of recovered individuals at time t
β	Contact rate
π	Vaccine efficacy
Λ	Recruitment rate
δ	Disease induced death rate for acute individuals
μ	Birth rate and Death rate
$\frac{dS}{dt} = \frac{\beta(A+\eta C)}{N}$	Rate of transmission coefficient
σ	Waning vaccine rate
F	Fraction of infected individuals
k	Proportion rate of acute individuals to carrier stage
α_1	Progression rate from exposed to acute
α_2	Progression rate from acute to carrier stage
α_3	Recovery rate of individuals in carrier stage
η	Modification parameter

Where $\lambda = \frac{\beta(A+\eta C)}{N}$

1.3 Mathematical Formulation

In this work, we consider the mathematical model of an SVEACR epidemic model of an Hepatitis B Virusby Muhammad et al (2013) with bilinear incidence rate.

$$\left.\begin{aligned}
\frac{dS}{dt} &= (1-f)\Lambda + \sigma V - (\mu+\lambda)S \\
\frac{dV}{dt} &= f\Lambda - \sigma V - (1-\pi)\lambda V - \mu V \\
\frac{dE}{dt} &= \lambda S + (1-\pi)\lambda V - (\mu+\alpha_1)E \\
\frac{dA}{dt} &= \alpha_1 E - (\alpha_2 + \mu + \delta)A \\
\frac{dC}{dt} &= k\alpha_2 A - (\mu+\alpha_3)C \\
\frac{dR}{dt} &= \alpha_3 C + (1-K)\alpha_2 A - \mu R
\end{aligned}\right\} \quad (1)$$

Where $S(t)$,V(t), $E(t)$,A(t), C(t), R(t) denote the number of susceptible individuals, vaccinated individual, exposed individuals but not yet infectious, infected but not infectious individuals, infected and infectious individuals at time t, respectively, and R(t)represents the total population of recovered individuals at time t. And Λ is the recruitment rate of the population, β is the disease transmission coefficient, μ is the natural death rate of the population, δ is the disease induced death of infectious individuals, and k, σ ,α_1,α_2,α_3 , η,and π are the state transition rates. We suppose that the recovered individuals have gained permanent immunity and can no longer be infected while the vaccinated-treated

The total number of population N at time t is given by

N(t) = S(t)+V(t)+E(t)+A(t)+C(t)+R(t).

1.4 Boundedness

Theorem 1: The closed set $D = \left\{ \left(S(t),V(t),E(t),A(t),C(t),R(t)\right) \in \Re_+^6 : N \le \frac{\Lambda}{\mu} \right\}$ is positively invariant and attractsall positive solutions of the model.

Proof: For boundedness we add all the equation of our model, that is,

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dV}{dt} + \frac{dE}{dt} + \frac{dA}{dt} + \frac{dC}{dt} + \frac{dR}{dt}$$

$$\frac{dN}{dt} = (1-f)\Lambda + \sigma V - (\mu+\lambda)S + f\Lambda - \sigma V - (1-\pi)\lambda V - \mu V + \lambda S + (1-\pi)\lambda V - (\mu+\alpha_1)E + \alpha_1 E -$$

$$(\alpha_2 + \mu + \delta)A + k\alpha_2 A - (\mu+\alpha_3)C + \alpha_3 C + (1-K)\alpha_2 A - \mu R = \Lambda - \lambda N$$

$$\frac{dN}{dt} + \mu N. \le \Lambda$$

Integrating both sides using an integrating factor $e^{\mu t}$ we have,

$$\frac{d}{dt}(e^{\mu}N) = \Lambda e^{\mu t} dt \Rightarrow e^{\mu} N \le \frac{\Lambda}{\mu} e^{\mu t} + c \Rightarrow N \le \frac{\Lambda}{\mu} + ce^{-\mu t}$$

Therefore the closed set $D=\left\{\left(S(t),V(t),E(t),A(t)+C(t)+R(t)\right)\in\Re_+^6 : N\le\frac{\Lambda}{\mu}\right\}$ is positively invariant and attractsall positive solutions of the model.

Therefore, the total population N may vary with time t. In the absence of disease, the total population size $N(t)$ converges to the equilibrium$\frac{\Lambda}{\mu}$. From epidemiological consideration, we study our system (3.1) in the closed feasible region:

$$\Omega=\left\{(S,V,E,A,C,R)\ \le S+V+E+A+C+R\le\frac{\Lambda}{\mu}\right\}$$

1.5 Positivity of Solutions

We show that all the variables in the model equation are non-negative.

Let the initial data for the model (1) be$S(0)>0,V(0)>0,E(0)>0,A(0)>0,C(0)>0,R(0)>0$.. Then, the solutions

$(S(t),V(t),E(t),A(t),C(t),R(t))$of the model (2.1) with positive initial data, will remain positive for all time $t>0.$

1.6 Steady State of the Model

At the steady state$\frac{dS(t)}{dt}=\frac{dV(t)}{dt}=\frac{dE(t)}{dt}=\frac{dA(t)}{dt}=\frac{dC(t)}{dt}=\frac{dR(t)}{dt}=0$

Hence

$$\begin{gathered}(1-f)\Lambda+\sigma V-\lambda S-\mu S=0\\ f\Lambda-\sigma V-(1-\pi)\lambda V-\mu V=0\\ \lambda S+(1-\pi)\lambda V-(\mu+\alpha_1)E=0\\ \alpha_1E-(\alpha_2+\mu+\delta)A=0\\ k\alpha_2A-(\mu+\alpha_3)C=0\\ \alpha_3C+(1-k)\alpha_2A-\mu R=0\end{gathered}\qquad(2)$$

Solving the equation above we have;

$$\left.\begin{aligned}S^0&=\frac{(1-f)\Lambda+\sigma V^0}{\lambda+\mu}\\ V^0&=\frac{f\Lambda}{\sigma+(1-\pi)\lambda+\mu}\\ E^0&=\frac{\lambda S(1-\pi)\lambda V^0}{(\mu+\alpha_1)}\\ A^0&=\frac{\alpha_1E^0}{\alpha_2+\mu+\delta}\\ C^0&=\frac{k\alpha_2A^0}{\mu+\alpha_3}\\ R^0&=\frac{\alpha_3C^0+(1-k)\alpha_2A^0}{\mu}-\end{aligned}\right\}\qquad(3)$$

The equilibrium points occur at,

$$\xi\left(S^0,V^0,E^0,A^0,C^0,R^0\right)\left(\frac{(1-f)\Lambda+\sigma V^0}{\lambda+\mu},\frac{f\Lambda}{\sigma+(1-\pi)\lambda+\mu},\frac{\lambda S(1-\pi)\lambda V^0}{(\mu+\alpha_1)},\frac{\alpha_1E^0}{\alpha_2+\mu+\delta},\frac{k\alpha_2A^0}{\mu+\alpha_3},\frac{\alpha_3C^0+(1-k)\alpha_2A^0}{\mu}\right)$$

The disease-free equilibrium is $\xi\left(S^0,0,0,0,0,0\right)\left(\frac{(1-f)\Lambda+\sigma V^0}{\lambda+\mu},0,0,0,0,0\right)$ while the Endemic equilibrium is

$$\xi\left(0,V^0,E^0,A^0,C^0,R^0\right)\left(\frac{(1-f)\Lambda+\sigma V^0}{\lambda+\mu},\frac{f\Lambda}{\sigma+(1-\pi)\lambda+\mu},\frac{\lambda S(1-\pi)\lambda V^0}{(\mu+\alpha_1)},\frac{\alpha_1 E^0}{\alpha_2+\mu+\delta},\frac{k\alpha_2 A^0}{\mu+\alpha_3},\frac{\alpha_3 C^0+(1-k)\alpha_2 A^0}{\mu}\right)$$

1.7 The Model Basic Reproduction Number

The local stability is established by using the next generation operator method on the system.

The basic reproduction number $\Re_0$ is defined as the effective number of secondary infections caused by an infected individual during his/her entire period of infectiousness (Van den Driesshe and Watmough (2002)). This definition is given for the models that represent spread of infection in a population. It is obtained by taking the largest (dominant) eigenvalue or spectral radius of

$\rho\left(F_i V^{-1}\right)$

Where $F_i=\left[\frac{\partial f_i(E^0)}{\partial X_j}\right]$ and $V_i=\left[\frac{\partial v_i(E^0)}{\partial X_j}\right]$

f_i is the rate of appearance of new infection in compartment i and $v_i=v_i^-\ -v_i^+$

v_i^- is the transfer of individuals out of the disease compartment E,A,C,

v_i^+ is the rate of transfer into compartment E,A,C by any other means,

E^0 is the disease free equilibrium

By linearization approach, the associated matrices at disease free equilibrium are f_i and v_i respectively.

The infected compartments are E, A and C, hence a straightforward calculation gives

$f_i=\begin{pmatrix}\lambda S+(1-\pi)\lambda V\\0\\0\end{pmatrix}, v_i=\begin{pmatrix}(\mu+\alpha_1)E\\(\mu+\delta+\alpha_2)A-\alpha_1 E\\(\mu+\alpha_3)C-k\alpha_2 A\end{pmatrix}$ then

We have;

$$F_i(E^0)=\begin{pmatrix}0&\frac{\beta(\sigma+\mu+\mu f\pi)}{\sigma+\mu}&\frac{\beta\eta(\sigma+\mu+\mu f\pi)}{\sigma+\mu}\\0&0&0\\0&0&0\end{pmatrix},\quad V_i(E^0)=\begin{pmatrix}\mu+\alpha_1&0&0\\-\alpha_1&(\mu+\delta+\alpha_2)&0\\0&-k\alpha_2&\mu+\alpha_3\end{pmatrix}$$

$$V^{-1}=\begin{pmatrix}\frac{1}{\mu+\alpha_1}&0&0\\\frac{1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\alpha_1)}&\frac{1}{\mu+\delta+\alpha_2}&0\\\frac{k\alpha_1\alpha_2}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\mu+\alpha_3)}&\frac{k\alpha_2}{(\mu+\delta+\alpha_2)(\mu+\alpha_3)}&\frac{1}{\mu+\alpha_3}\end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} \frac{[\beta(\sigma+\mu+\mu f\pi)]\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\sigma+\mu)} + \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]k\alpha_1\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\mu+\alpha_3)(\sigma+\mu)} & \frac{[\beta(\sigma+\mu+\mu f\pi)](\mu+\alpha_1)(\mu+\alpha_2)}{\sigma+\mu} + \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]k\alpha_2}{(\sigma+\mu)(\mu+\delta+\alpha_2)(\mu+\alpha_3)} & \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]}{(\mu+\alpha_3)(\sigma+\mu)} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

The basic reproduction number is given by $\rho(FV^{-1})$, i.e the highest eigenvalue of FV^{-1}

$$|FV^{-1} - \lambda I| = 0$$

$$\begin{pmatrix} \frac{[\beta(\sigma+\mu+\mu f\pi)]\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\sigma+\mu)} + \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]k\alpha_1\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\mu+\alpha_3)(\sigma+\mu)} - \lambda & \frac{[\beta(\sigma+\mu+\mu f\pi)](\mu+\alpha_1)(\mu+\alpha_2)}{\sigma+\mu} + \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]k\alpha_2}{(\sigma+\mu)(\mu+\delta+\alpha_2)(\mu+\alpha_3)} & \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]}{(\mu+\alpha_3)(\sigma+\mu)} \\ 0 & -\lambda & 0 \\ 0 & 0 & -\lambda \end{pmatrix}$$

Hence

$$\lambda^2\left[\frac{[\beta(\sigma+\mu+\mu f\pi)]\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\sigma+\mu)} + \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]k\alpha_1\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\mu+\alpha_3)(\sigma+\mu)} - \lambda\right] = 0$$

$$\lambda_2 = \frac{[\beta(\sigma+\mu+\mu f\pi)]\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\sigma+\mu)} + \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]k\alpha_1\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\mu+\alpha_3)(\sigma+\mu)}$$

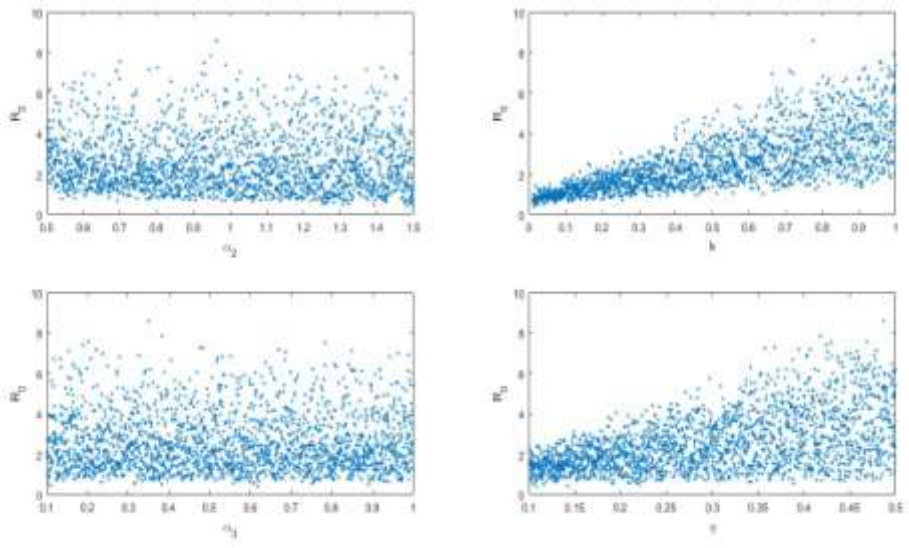
Thus, the Eigen values are;

Therefore, the basic reproduction number

$$\Re_0 = \frac{[\beta(\sigma+\mu+\mu f\pi)]\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\sigma+\mu)} + \frac{[\beta\eta(\sigma+\mu+\mu f\pi)]k\alpha_1\alpha_1}{(\mu+\alpha_1)(\mu+\delta+\alpha_2)(\mu+\alpha_3)(\sigma+\mu)}$$

Theorem 2.2: The disease-free equilibrium of the model (1) is locally asymptotically stable when $R_0<1$ and unstable when $R_0>1$.

II. SENSITIVITY ANALYSIS



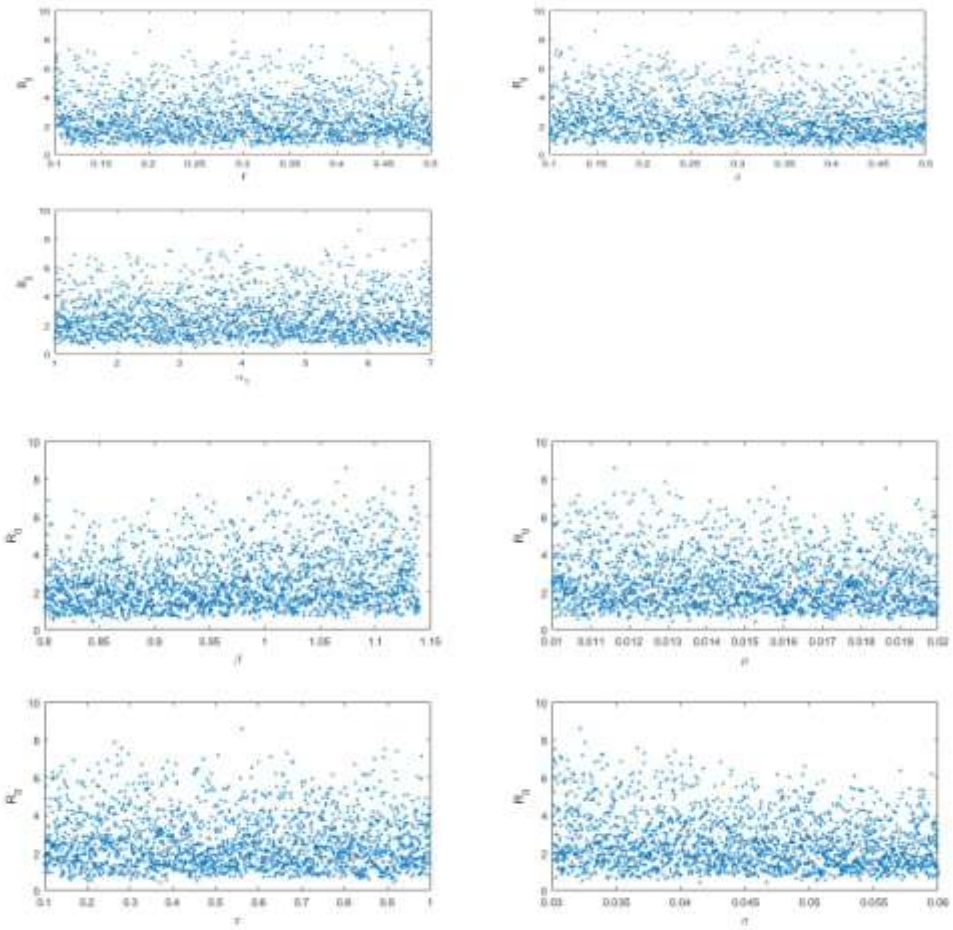


Fig. 2: Graphs of the sensitivity analysis showing the parameters varying with the basic reproduction

2.1 Discussion of Result

The model has eleven parameters and uncertainties are expected to arise in estimation of the values used in the numerical simulations, hence, the need for the sensitivity analysis. We perform Latin Hypercube Sampling (LHS) and partial rank correlation coefficient(PRCC) on the model

Using the reproduction number as the response function, the top ranked parameters are shown in Table 2 below

Table 2: PRCC values for the parameters of the model using the reproduction number (R_0) as response function.

Parameters	**PRCC** (R_0)
β	0.9149
δ	0.9002
α_3	0.0136
K	-0.0307
μ	-0.0452
π	-0.6274
Λ	-0.0325
α_1	0.8357
α_2	-0.9836
η	0.0099
f	-0.0334

A parameter is said to be significant if its PRCC values $|P| \geq 0.5$ from the table 3.8. the most significant parameters are β, δ, π, α_1 and α_2 where β andδ are positively correlated. This means if there is an increase in β andδ, it will also result in an increase in the disease burden in the population.π, α_1 *and* α_2 are negatively correlated. This means that if there is an increase in π, α_1 and α_2, it would result in a decrease in the disease burden in the population.In the next section, we describe the basic concept of Homotopy analysis method and then use it to solve equation (2.1).

III. BASIC IDEA OF HOMOTOPY ANALYSIS METHOD

In this section, we apply the homotopy analysis method to the problem (1). Consider the following equation:

$$N\left[\vartheta(t)\right]=0 \tag{4}$$

Where N is a nonlinear operator, t denotes the independent variable. $\vartheta(t)$ is an unknown function. Let $\vartheta_0(t)$ denote an initial guess of the exactsolution $\vartheta(t)$, $h\neq 0$ an auxiliary parameter, $H(t)\neq 0$ an auxiliary function, and L an auxiliary linear operator with the property $L\left[\vartheta(t)\right]=0$ when $\vartheta(t)=0$.

Then using $\rho\left[0,1\right]$ as an embedding parameter, we construct such a Homotopy

$$(1-\rho)L[\phi(t;\rho)-\vartheta_0(t)]-\rho hH(t)N[\phi(t;\rho)]=\hat{H}[\phi(t;\rho);\vartheta_0(t),H(t),h,\rho] \tag{5}$$

We have freedom to choose the initial guess $\vartheta_0(t)$, the auxiliary linear operator L, the non-zero auxiliary parameter h, and the auxiliary function $H(t)$.

Equating the Homotopy (3.8.2) to zero, i.e,

$$\hat{H}\left[\phi(t;\rho);\vartheta_0(t),H(t),h,\rho\right]=0$$

We have the so-called zero order deformation equation

$$(1-\rho)L\left[\phi(t;\rho)-\vartheta_0(t)\right]=\rho hH(t)N\left[\phi(t;\rho)\right] \tag{6}$$

When $\rho=0$, the zero-order deformation equation (5) becomes

$$\phi(t;0)=\vartheta_0(t), \tag{7}$$

And when $\rho=1$, since $h\neq 0$ and $H(t)\neq 0$, the zero-order deformation equation (5) becomes

$$\phi(t;1)=\vartheta(t) \tag{8}$$

Based on (4.4) and (4.5), as the embedding parameter ρ increases from 0 to 1 $\phi(t;\rho)$ varies continuously from the initial approximation $\vartheta_0(t)$ to the exact solution $\vartheta(t)$

Expanding $\phi(t;\rho)$ in Taylor series with respect to ρ, we have

$$\phi(t;\rho)=\vartheta_0(t)+\sum_{m=1}^{\infty}\vartheta_m(t)\,p^m \tag{9}$$

Where

$$\vartheta_m(t)=\frac{1}{m!}\frac{\partial^m\phi(t;\rho)}{\partial p^m}\bigg|_{p=0} \tag{10}$$

If the auxiliary linear operator, the initial guess, the auxiliary parameter h, and the auxiliary function are properly chosen so that

a. The solution $\phi(t;\rho)$ of the zero-order deformation equation (6) exists for all $\rho\left[0,1\right]$

b. The deformation derivative $\dfrac{\partial^m\phi(t;\rho)}{\partial p^m}\bigg|_{p=0}$ exist for $m=1,2.....$

c. The power series (4.6) $\phi(t;\rho) = \vartheta_0(t) + \sum_{m=1}^{\infty} \vartheta_m(t)\, p^m$ converges at $\rho = 1$.

Then, we have under these assumptions the solution series.

$$\phi(t;1) = \vartheta_0(t) + \sum_{m=1}^{\infty} \vartheta_m(t)\, p^m \qquad (11)$$

According to equation (4.7), the governing equation can be deduced from the zero-order deformation equation (4.3). Define the vector

$$\vec{\varphi}_m = \{\vartheta_0(t), \vartheta_1(t), \vartheta_2(t), ..., \vartheta_n(t)\} \qquad (12)$$

Differentiating the zero-order deformation equation (6) m times with respect to ρ, then dividing by $m!$ and finally setting $\rho = 0$, we have the so-called m^{th} order deformation equation.

$$L\left[\vartheta_m(t) - \chi_m \vartheta_{m-1}(t)\right] = hH(t)\Re_m\left(\vartheta_{m-1}(t)\right) \qquad (13)$$

Where

$$\Re_m\left(\vartheta_{m-1}(t)\right) = \frac{1}{(m-1)!}\frac{\partial^{m-1} N\left[\phi(t;\rho)\right]}{\partial \rho^{m-1}} \qquad (14)$$

and

$$\chi_m = \begin{cases} 0, & m \le 1 \\ 1, & m > 1 \end{cases}$$

It should be emphasized that $\vartheta_0(t)$ for $m \ge 1$ is governed by linear equation (10) with the linear boundary conditions that comes from the original problem, which can be solved easily using symbolic computation software such as; Maple, MATLAB or MATHEMATICA.

3.1 Solution of the SVEACR Model by Homotopy Analysis Method (HAM)

In order to explicitly construct approximate non-perturbative solutions of the system described by equations (1), we employ the concept of Homotopy analysis method.

The advantage of this method is that it provides a direct scheme for solving the problem. To apply the Homotopy analysis method, we choose;

$S_0(t) = N_S, V_0(t) = N_V, E_0(t) = N_E, A_0(t) = N_A, C_O(t) = N_C$ *and* $R_0(t) = N_R$ Initial approximationof $S(t)$, V(t), E(t), A(t), C(t) *and* R(t). Let $p \in [0,1]$ be the so-called embedding parameter. The HAM is based on the kind of continuous mappings.

$$S(t) \to \emptyset_1(t;p)$$
$$V(t) \to \emptyset_2(t;p)$$
$$E(t) \to \emptyset_3(t;p)$$
$$A(t) \to \emptyset_4(t;p)$$
$$C(t) \to \emptyset_5(t;p)$$
$$R(t) \to \emptyset_6(t;p)$$

such that, as the embedding parameter p increases from 0 to $1, \phi_i(t;p)$ varies from the initial approximation to the exact solution. To ensure this, choose such auxiliary linear operators as

$$L_i\left[\phi_i(t;p)\right] = \frac{\partial \phi_i(t;p)}{\partial t},\ i = 1,2,3,4,5$$

With the property

$$L_i\left[C_i\right] = 0$$

where C_i are integral constants. We define the nonlinear operators;

$$N_1[\emptyset_i(t;p)] = \frac{\partial \emptyset_i(t;p)}{\partial t} + (1-f)\Lambda - \sigma\emptyset_2(t;p) + \lambda\emptyset_1(t;p) + \mu\emptyset_1(t;p)$$
$$N_2[\emptyset_i(t;p)] = \frac{\partial \emptyset_i(t;p)}{\partial t} - f\Lambda + \sigma\emptyset_2(t;p) + (1-\pi)\lambda\emptyset_2(t;p) + \mu\emptyset_2(t;p)$$
$$N_3[\emptyset_i(t;p)] = \frac{\partial \emptyset_i(t;p)}{\partial t} - \lambda\emptyset_1(t;p) - (1-\pi)\lambda\emptyset_2(t;p) + (\mu+\alpha_1)\emptyset_3(t;p)$$
$$N_4[\emptyset_i(t;p)] = \frac{\partial \emptyset_i(t;p)}{\partial t} - \alpha_1\emptyset_3(t;p) + (\alpha_2+\mu+\delta)\emptyset_4(t;p)$$
$$N_5[\emptyset_i(t;p)] = \frac{\partial \emptyset_i(t;p)}{\partial t} - k\alpha_2\emptyset_4(t;p) + (\mu+\alpha_3)\emptyset_5(t;p)$$
$$N_6[\emptyset_i(t;p)] = \frac{\partial \emptyset_i(t;p)}{\partial t} - \alpha_3\emptyset_5(t;p) + (1-k)\alpha_2\emptyset_4(t;p) + \mu\emptyset_6(t;p)$$

Let $h_i \neq 0$ and $H_i(t) \neq 0$ denote the so-called auxiliary parameter and auxiliary function, respectively. Using the embedding parameter ρ, we construct a family of equations

$$(1-\rho)L[\phi_1(t;\rho) - S_0(t)] = \rho h_1 H_1(t) N_1[\phi_1(t;\rho)]$$
$$(1-\rho)L[\phi_2(t;\rho) - V_0(t)] = \rho h_2 H_2(t) N_2[\phi_2(t;\rho)]$$
$$(1-\rho)L[\phi_3(t;\rho) - E_0(t)] = \rho h_3 H_3(t) N_3[\phi_3(t;\rho)]$$
$$(1-\rho)L[\phi_4(t;\rho) - A_0(t)] = \rho h_4 H_4(t) N_4[\phi_4(t;\rho)]$$
$$(1-\rho)L[\phi_5(t;\rho) - C_0(t)] = \rho h_5 H_5(t) N_5[\phi_5(t;\rho)]$$
$$(1-\rho)L[\phi_6(t;\rho) - R_0(t)] = \rho h_6 H_6(t) N_6[\phi_6(t;\rho)]$$

Subject to the initial conditions

$$\phi_1(0;\rho) = S_0, \phi_2(0;\rho) = V_0, \phi_3(0;\rho) = E_0, \phi_4(0;\rho) = A_0, \phi_5(0;\rho) = C_0, \phi_6(0;\rho) = R_0$$

By Taylor's theorem, we expand $\phi_i(t;\rho)$ by a power series of the embedding parameter ρ as follows

$$\phi_1(t;p) = S_0(t) + \sum_{m=1}^{\infty} S_m(t)\, p^m$$
$$\phi_2(t;p) = V_0(t) + \sum_{m=1}^{\infty} V_m(t)\, p^m$$
$$\phi_3(t;p) = E_0(t) + \sum_{m=1}^{\infty} E_m(t)\, p^m$$
$$\phi_4(t;p) = A_0(t) + \sum_{m=1}^{\infty} A_m(t)\, p^m$$
$$\phi_5(t;p) = C_0(t) + \sum_{m=1}^{\infty} C_m(t)\, p^m$$
$$\phi_6(t;p) = R_0(t) + \sum_{m=1}^{\infty} R_m(t)\, p^m$$

Where

$$S_m(t) = \frac{1}{m!}\frac{\partial^m \emptyset_1(t;\rho)}{\partial p^m}\Big|_{p=0}$$
$$V_m(t) = \frac{1}{m!}\frac{\partial^m \emptyset_2(t;\rho)}{\partial p^m}\Big|_{p=0}$$
$$E_m(t) = \frac{1}{m!}\frac{\partial^m \emptyset_3(t;\rho)}{\partial p^m}\Big|_{p=0}$$
$$A_m(t) = \frac{1}{m!}\frac{\partial^m \emptyset_4(t;\rho)}{\partial p^m}\Big|_{p=0}$$
$$C_m(t) = \frac{1}{m!}\frac{\partial^m \emptyset_5(t;\rho)}{\partial p^m}\Big|_{p=0}$$
$$R_m(t) = \frac{1}{m!}\frac{\partial^m \emptyset_6(t;\rho)}{\partial p^m}\Big|_{p=0}$$

From the so-called m^{th} order deformation equation (3.8.10) and (3.8.11), we have

$$L[S_m(t) - \chi_m S_{m-1}(t)] = h_1 H_1(t)\Re_m\left(S_{m-1}(t)\right)$$
$$L[V_m(t) - \chi_m V_{m-1}(t)] = h_1 H_1(t)\Re_m\left(V_{m-1}(t)\right)$$
$$L[E_m(t) - \chi_m E_{m-1}(t)] = h_1 H_1(t)\Re_m\left(E_{m-1}(t)\right)$$
$$L[A_m(t) - \chi_m A_{m-1}(t)] = h_1 H_1(t)\Re_m\left(A_{m-1}(t)\right)$$
$$L[C_m(t) - \chi_m C_{m-1}(t)] = h_1 H_1(t)\Re_m\left(C_{m-1}(t)\right)$$
$$L[R_m(t) - \chi_m R_{m-1}(t)] = h_1 H_1(t)\Re_m\left(R_{m-1}(t)\right)$$
$$S_m(0) = 0, \quad V_m(0) = 0, \; E_m(0) = 0, \quad A_m(0) = 0, \; C_m(0) = 0, \quad R_m(0) = 0$$

By the h −curves, it is reasonable to use $h_i = -1$. Using $H_i(t) = 1$ Hence the solution of the m^{th} order deformation equation of equations (17)-(22) for

$m \geq 1$ and using $h = -1$ and $H(t) = 1$ is given by;

$$S_m(t) = \chi_m S_{m-1}(t) - \int_0^t \left[\frac{dS_{m-1}(t)}{dt} - (1-f)\Lambda + \sigma V - \lambda S_{m-1}(t) - \mu S_{m-1}(t)\right] dt$$
$$V_m(t) = \chi_m V_{m-1}(t) - \int_0^t \left[\frac{dS_{m-1}(t)}{dt} - f\Lambda + \sigma V_{m-1} + (1-\pi)V_{m-1} + \mu V_{m-1}\right] dt$$
$$E_m(t) = \chi_m E_{m-1}(t) - \int_0^t \left[\frac{dE_{m-1}(t)}{dt} - \lambda S_{m-1}(t) - (1-\pi)\lambda V_{m-1}(t) + (\mu + \alpha_1)E_{m-1}(t)\right] dt$$
$$A_m(t) = \chi_m A_{m-1}(t) - \int_0^t \left[\frac{dA_{m-1}(t)}{dt} - \alpha_1 E_{m-1}(t) + (\alpha_2 + \mu + \delta)A_{m-1}(t)\right] dt$$
$$C_m(t) = \chi_m C_{m-1}(t) - \int_0^t \left[\frac{dC_{m-1}(t)}{dt} - k\alpha_2 A_{m-1}(t) + (\mu + \alpha_3)C_{m-1}(t)\right] dt$$
$$R_m(t) = \chi_m R_{m-1}(t) - \int_0^t \left[\frac{dR_{m-1}(t)}{dt} - \alpha_3 C_{m-1}(t) + (1-k)\alpha_2 A_{m-1}(t) + \mu R_{m-1}(t)\right] dt$$

3.2 Numerical Results and Discussion

For numerical results, we consider the following values for the parameters involved in the model.

Table 3: Parameter values for the series solutions

Variables and Parameters	Values	**Units**	**References**
S	1, 000	$Year^{-1}$	Assumed
V	800	$Year^{-1}$	Assumed
E	70	$Year^{-1}$	Assumed
A	70	$Year^{-1}$	Assumed
C	85	$Year^{-1}$	Assumed
R	10	$Year^{-1}$	Assumed
μ	0.0143	$Year^{-1}$	Muhammad Altaf Khan,(2013)
π	0.5	$Year^{-1}$	Assumed
Λ	100	$Year^{-1}$	Assumed
β	1.1387	$Year^{-1}$	Suxia Zhang and Yicang Zhou (2011)
σ	0.045	$Year^{-1}$	Assumed
δ	0.3	$Year^{-1}$	Assumed
f	0.3	$Year^{-1}$	Muhammad A. K. (2013)
α_1	6.0	$Year^{-1}$	Muhammad A. K.(2013)
α_2	0.885	$Year^{-1}$	Suxia Z.and Yicang Z. (2011)
K	0.6	$Year^{-1}$	Assumed
α_3	0.34	$Year^{-1}$	Muhammad A. K. (2013)
η	0.3	$Year^{-1}$	Assumed

For high accuracy of results, we use Maple 17 computation software to find the approximate series solution for S(t), V(t), E(t), A(t), C(t), and R(t)up to fifth iteration.

The $1^{st}, 2^{nd}, 3^{rd}, 4^{th}$ and 5^{th} iterations forS(t) , V(t), E(t), A(t), C(t), and R(t) are calculated and the 5^{th} iteration graphed and presented as below;

1^{st} *Iteration*

$$S_1(x,t) = \sum_{m=0}^{1} S_m(t) = 1000 + 38.26223587t$$

$$V_1(x,t) = \sum_{m=0}^{1} V_m(t) = 800 - 38.81510565t$$

$$E_1(x,t) = \sum_{m=0}^{1} E_m(t) = 70 - 346.1881302t$$

$$A_1(x,t) = \sum_{m=0}^{1} A_m(t) = 70 + 336.0490000t$$

$$C_1(x,t) = \sum_{m=0}^{1} C_m(t) = 85 + 36.81570000t$$

$$R_1(x,t) = \sum_{m=0}^{1} R_m(t) = 10 + 3.977000000t$$

2^{nd} *Iteration*

$$S_2(x,t) = \sum_{m=0}^{2} S_m(t) = 1000 + 38.26223587t - 2.169239032t^2$$

$$V_2(x,t) = \sum_{m=0}^{2} V_m(t) = 800 - 38.81510565t + 1.669415998t^2$$

$$E_2(x,t) = \sum_{m=0}^{2} E_m(t) = 70 - 346.1881302t + 1041.543412t^2$$

$$A_2(x,t) = \sum_{m=0}^{2} A_m(t) = 70 + 336.0490000t - 1240.076174t^2$$

$$C_2(x,t) = \sum_{m=0}^{2} C_m(t) = 85 + 36.81570000t + 89.22100950t^2$$

$$R_2(x,t) = \sum_{m=0}^{2} R_m(t) = 10 + 3.977000000t - 53.25043955t^2$$

3^{rd} *Iteration*

$$S_3(x,t) = \sum_{m=0}^{3} S_m(t) = 1000 + 38.26223587t - 2.169239032t^2 + 0.7402104060t^3$$

$$V_3(x,t) = \sum_{m=0}^{3} V_m(t) = 800 - 38.81510565t + 1.669415998t^2 - 0.4786709927t^3$$

$$E_3(x,t) = \sum_{m=0}^{3} E_m(t) = 70 - 346.1881302t + 1041.543412t^2 - 2088.075286t^3$$

$$A_3(x,t) = \sum_{m=0}^{3} A_m(t) = 70 + 336.0490000t - 1240.076174t^2 + 2578.827942t^3$$

$$C_3(x,t) = \sum_{m=0}^{3} C_m(t) = 85 + 36.81570000t + 89.22100950t^2 - 219.4934828t^3$$

$$R_3(x,t) = \sum_{m=0}^{3} R_m(t) = 10 - 1.333000000t - 0.28614545t^2 - 0.1625376133t^3$$

4^{th} *Iteration*

$$S_4(x,t) = \sum_{m=0}^{4} S_m(t) = 1000 + 38.26223587t - 2.169239032t^2 + 0.7402104060t^3 - 0.1792009814t^4$$

$$V_4(x,t) = \sum_{m=0}^{4} V_m(t) = 800 - 38.81510565t + 1.669415998t^2 - 0.4786709927t^3 + 0.001029368592\ t^4$$

$$E_4(x,t) = \sum_{m=0}^{4} E_m(t) = 70 - 346.1881302t + 1041.543412t^2 - 2088.075286t^3 + 3139.578468\ t^4$$

$$A_4(x,t) = \sum_{m=0}^{4} A_m(t) = 70 + 336.0490000t - 1240.076174t^2 + 2578.827942t^3 - 3905.310018t^4$$

$$C_4(x,t) = \sum_{m=0}^{4} C_m(t) = 85 + 36.81570000t + 89.22100950t^2 - 219.4934828t^3 + 342.3394092\ t^4$$

$$R_4(x,t) = \sum_{m=0}^{4} R_m(t) = 10 - 1.333000000t - 0.28614545\mathrm{t}^2 - 0.1625376133\mathrm{t}^3 - 246.8826378\mathrm{t}^4$$

5^{th} *Iteration*

$$\mathrm{S}_5(\mathrm{x},\mathrm{t}) = \sum_{\mathrm{m}=0}^{5} \mathrm{S}_\mathrm{m}(\mathrm{t}) = 1000 + 38.26223587\mathrm{t} - 2.169239032\mathrm{t}^2 + 0.7402104060\mathrm{t}^3 - 0.1792009814\mathrm{t}^4 + 0.00003354166494\ \mathrm{t}^5$$

$$\mathrm{V}_5(\mathrm{x},\mathrm{t}) = \sum_{\mathrm{m}=0}^{5} \mathrm{V}_\mathrm{m}(\mathrm{t}) = 800 - 38.81510565\mathrm{t} + 1.669415998\mathrm{t}^2 - 0.4786709927\mathrm{t}^3 + 0.001029368592\ \mathrm{t}^4 - 0.1770902710\mathrm{t}^5$$

$$\mathrm{E}_5(\mathrm{x},\mathrm{t}) = \sum_{\mathrm{m}=0}^{5} \mathrm{E}_\mathrm{m}(\mathrm{t}) = 70 - 346.1881302\mathrm{t} + 1041.543412\mathrm{t}^2 - 2088.075286\mathrm{t}^3 + 3139.578468\ \mathrm{t}^4 - 3650.661564\mathrm{t}^5$$

$$\mathrm{A}_5(\mathrm{x},\mathrm{t}) = \sum_{\mathrm{m}=0}^{5} \mathrm{A}_\mathrm{m}(\mathrm{t}) = 70 + 336.0490000\mathrm{t} - 1240.076174\mathrm{t}^2 + 2578.827942\mathrm{t}^3 - 3905.310018\mathrm{t}^4 + 4578.709196\ \mathrm{t}^5$$

$$\mathrm{C}_5(\mathrm{x},\mathrm{t}) = \sum_{\mathrm{m}=0}^{5} \mathrm{C}_\mathrm{m}(\mathrm{t}) = 85 + 36.81570000\mathrm{t} + 89.22100950\mathrm{t}^2 - 219.4934828\mathrm{t}^3 + 342.3394092\ \mathrm{t}^4 - 414.7439240\mathrm{t}^5$$

$$\mathrm{R}_5(\mathrm{x},\mathrm{t}) = \sum_{\mathrm{m}=0}^{5} \mathrm{R}_\mathrm{m}(\mathrm{t}) = 10 - 1.333000000\mathrm{t} - 0.28614545\mathrm{t}^2 - 0.1625376133\mathrm{t}^3 - 246.8826378\mathrm{t}^4 + 300.4811134\ \mathrm{t}^5$$

In this work, we consider an HBV with the following basic behaviour in a population. At the beginning, the number ofSusceptible, Vaccinated, Exposed, Acute-Infected, Carriers (infected) and Recovered individuals are given as S(0) = 1,000, V(0) = 800, E(0) = 70, A(0) = 70 ,

C(0) = 85, R(0) = 10 respectively. Other parameter values in this simulation are as given in Table (4.1) above. When all other parameters do not vary and we obtain $\Re_0 = 1.96 > 1$, Observe that the number of the

infected population do not die out between 0 and$\frac{\Lambda}{\mu}$, epidemic persists.We change π,$\alpha_1$andα_2 from 0.5, 6, 0.885 to 0.9, 7, 1.48 respectively, hence$\Re_0 = 0.889 < 1$, the epidemic will gradually fizzle out. The tendency of the epidemic propagation is depreciating. In the long run, the whole population is in the vaccinated state. In order to effectively defend individuals against this epidemic, we must adopt some feasible methods to decrease the rate of infection or increase the following parametersα_1, α_2, α_3, σ and π to guarantee the basic reproduction number $\Re_0 < 1$.

IV. SUMMARY, CONCLUSION AND RECOMMENDATIONS

4.1 Summary

Our work proposed a mathematical model which incorporates vaccination of Hepatitis B virus. We formulated a flow diagram for our model and thereby formulated a non-linear differential equation. Firstly, we show that the population classes are non-negative and then obtain the basic reproduction number using the next generation matrix. Next, with the help of the reproduction number, we prove the stability of disease-free equilibrium. When the reproduction number is less than or equal to one, our model has only a disease free equilibrium which is globally stable, which implies the disease dies out eventually; when the reproduction number is larger than one, it implies that the disease persists in the whole population and tends to a steady state. Finally, simulation results are given to verify our conclusions.

4.2 Conclusion

We see that the results obtained from the analysis using Math-lab and Maple is such that if there is an increase in β andδ, it will also result in an increase in the disease burden in the population.π, α_1 and α_2 are negatively correlated. This means that if there is an increase in π, α_1 and α_2, it would result in a decrease in the disease burden in the population.

It is also well-known that nonlinear ordinary differential equations (ODEs) are difficult to solve than linear ODEs, especially by means of analytic methods. From our numerical example, we demonstrated the ability of HAM to converge very fast, we saw that the HAM converges in just few iterations. For the accuracy of the method, it has been established by Liao, S. J. We can then conclude that HAM is very efficient and accurate in solving SVEAVR model.

4.3 Recommendatons

Globally, diseases have been the major problem to human health, which contributes to the high mortality rate in the world today. Also it thrives in the context of poverty, the costs of seeking accurate diagnosis and treatment can be considerable for low-income household. Infected individuals face substantial cost before diagnosis in that they often consult several public and private providers before and in the process of being diagnosed. Hence, in view to these, we therefore recommend that;

1. The Government, non-governmental organizations and stakeholders should help in creatingawarenessbecause prevention is better than cure.
2. Infectious individual should be referred to necessary places for proper treatment to avoid spread of disease.
3. Individuals should shun un-prescribed drug usage, as this will have another side effect.

For the eradication of this disease, we also recommend that the rate of infected individual should be considered more important than that of the susceptible and exposed populations, as the increase in its rate contributes to a significant decrement in the infected population.

Also the rate at which vaccination strategy is been carried out should be more focused on the infected individuals compared to those who are susceptible or exposed to the disease. This is because high rate of vaccination of individuals reduces the infected population and the rate of the vaccination of infected population is of more significant.

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