

APPROXIMATE SERIES SOLUTION OF EBOLA VIRUS DISEASE MODEL USING HOMOTOPY ANALYSIS METHOD

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Abstract

Ebola virus disease (EVD) is a deadly disease that has become a global concern, especially in the Sub-Saharan Africa where the disease is endemic. In this paper, a nonlinear deterministic model of EVD with control measures is proposed. The existence of disease-free equilibrium of EVD model was established. Furthermore, the effective reproduction number that governs the spread of the disease was computed and its threshold property discussed. A non-perturbation method used to get series solution to nonlinear problems, homotopy analysis method (HAM) was applied to the EVD model. The result demonstrates the series solution of EVD model and the convergence region of applying HAM.

Keywords: *Ebola virus disease, homotopy analysis method, effective reproduction number, disease-free equilibrium, endemic equilibrium.*

1. Introduction

Ebola virus disease (EVD) is a deadly disease caused by Ebola virus. The virus is one of the thirty (30) known viruses that cause Viral Hemorrhagic Fevers (VHFs). It belongs to family of filoviruses (Brooks *et al.*, 2007). The filoviridae family includes three genera, Ebolavirus, Marburgvirus and most recent cuevavirus (Ghazanfar *et al.*, 2015).

The virus was named after a small river near the Catholic Mission in Yambuku, Zaire where the first outbreak was recorded in 1976. After the first outbreak of EVD, there have been more than twenty-five (25) epidemics of Ebola virus with 2014 epidemic in West African being the highest epidemic of 28,608 cases and 11,306 deaths as of March 24, 2016 (WHO, 2016).

Ebola virus is introduced into human population via close contact with body fluids of an infected non-human primate found ill or dead. The virus then spread through direct contact with blood and bodily fluids of an infected person and with objects, surfaces, and materials (needles, beddings, and clothing) contaminated with those fluids. These put the health-care givers and family members of an infected person at high risk of contracting the virus. Ebola virus is also transmitted through direct contact with the dead bodies of an infected person or by semen of men who recovered for as long as seven weeks after recovery (Maryland Department of Health & Mental Hygiene, 2002). According to PAHO/WHO (2014), the incubation period of the virus is usually varies from 2 to 21 days but most people show symptoms from 7 to 10 days after exposure to the virus with onset of influenza-like symptoms (WHO, 2014a; ECDC, 2014).

There is no approved medication or licensed vaccine for Ebola virus since the natural host is still unknown. It is speculated that bat and bush meat may be the host (Leach and Scoones, 2013). This makes it difficult to implement policy on how to control or eliminate viral reservoirs transmission in human population (Sullivan *et al.*, 2003). Supportive therapies are used to treat infected person. There are some experimental therapies such as antiviral drug and vaccine under trial (Bishop, 2015; WHO, 2014b).

Many mathematical models have been developed to analyse the spread of EVD and how to halt its further spread (Legrand *et al.*, 2007; Okeke *et al.*, 2014; Madubueze *et al.*, 2017). Some of these mathematical models are describe using nonlinear system of ordinary differential equations and it is difficult to obtain analytic solution of them due to the presence of nonlinearity in them (Brauer).

There are many methods to solve nonlinear problems, methods such as Homotopy perturbation method (HPM), Adomian decomposition method (ADM) but Homotopy analysis method (HAM) is a unified method for both perturbation and non-perturbation methods (Liao, 2003, 2004). It is one of the most powerful non-perturbation used to get series solution to nonlinear problems and is applicable to both strong and weak nonlinear problems. This method is based on a fundamental concept of topology (Rani *et al.*, 2016). HAM has advantages of controlling and adjusting the convergence region and rate of approximation series where necessary. It is independent of small physical parameters and provide a freedom of choosing initial approximation solution, auxiliary linear operator, auxiliary function and auxiliary parameter. This help to ensure the convergence of the series solution. HAM has been applied to cholera, Ebola virus disease, Tuberculosis and HIV models in order to get analytic solutions (Atangana and Goufo, 2014; Muthuramalingam *et al.*, 2014; Oghre and Madubueze, 2013).

In this paper, HAM is applied to EVD model proposed by Madubueze *et al.* (2016). This paper is organized as follows: Section 2 is the presentation of the EVD model with control measures. Section 3 is the model analysis of the EVD model. We highlighted the basic ideals of HAM in section 4. While Section 5 illustrates the application of HAM to EVD model, results and discussion in order to show the convergence and validity of the method. Section 6 contains the conclusion.

2. Model Description

The system of ordinary differential equations for transmission dynamics of EVD with control measures are as follows:

$$\frac{dS}{dt} = \Lambda - \frac{\beta SI}{N} + \sigma Q + \theta T - \mu S - c_1 S, S(0) = S_0 \quad (1)$$

$$\frac{dQ}{dt} = \varepsilon + c_1 S - \sigma Q - \varphi Q - \mu Q, Q(0) = Q_0 \quad (2)$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - (\mu + \alpha + d)I - c_2 I, I(0) = I_0 \quad (3)$$

$$\frac{dT}{dt} = \alpha I + \varphi Q + c_2 I - \mu T - \theta T, T(0) = T_0 \quad (4)$$

where, all parameters of the model and S_0, Q_0, I_0 , and T_0 are positive constants with exception of Ebola induce death, d , which is nonnegative. The total population size, $N(t)$, at time t is given by $N(t) = S(t) + Q(t) + I(t) + T(t)$.

The Table 1 gives all the parameters and state variables used in the model.

Table 1: Model parameters

Parameter	Description
$S(t)$	Total number of susceptible individuals at any time t ;
$Q(t)$	Total number of quarantined individuals at time t ;
$I(t)$	Total number of infected individuals at time t ;
$T(t)$	Total number of individuals undergoing treatment at time t ;
β	Disease transmission rate
c_2	Contact tracing rate for infected individuals
c_1	Contact tracing rate for exposed susceptible individuals
d	Ebola induced death rate for infected class
Λ	Immigration rate from non-Ebola affected populations
σ	Rate at which quarantined individuals who did not develop symptoms of infection return to susceptible class
θ	Rate at which individuals under treatment recover and become susceptible again
ε	Immigration rate from Ebola affected populations
μ	Natural death rate for all classes
φ	Rate for identifying the infected persons in the quarantined class
α	Rate for identifying the infected persons in the infected class

3. Model Analysis

3.1. Invariant Region

The EVD model will be analyzed in a validity region in order to show that it is biological meaningful and the region is feasible for human population. Thus, lead to theorem 1;

Theorem 1: The EVD model has solutions which are contained in the region $\Omega = \left\{ (S, Q, I, T) \in \mathbb{R}_+^4 : N \leq \frac{\varepsilon + \Lambda}{\mu} \right\}$.

Proof. Adding the right hand sides of (1)-(4)

$$\frac{dN}{dt} = \varepsilon + \Lambda - \mu N - dI,$$

Since $I(t) \leq N(t)$

$$\frac{dN}{dt} \leq \varepsilon + \Lambda - \mu N. \tag{5}$$

By using a standard comparison theorem with the initial condition, $N(0) = N_0$, we obtain from (5) that

$$N(t) \leq \frac{\varepsilon + \Lambda}{\mu} + \left[N_0 - \frac{\varepsilon + \Lambda}{\mu} \right] e^{-\mu t}. \tag{6}$$

The population size, $N(t) \rightarrow \frac{\varepsilon + \Lambda}{\mu}$, as $t \rightarrow \infty$ in (6), which implies that $0 \leq N(t) \leq \frac{\varepsilon + \Lambda}{\mu}$. If $N_0 < \frac{\varepsilon + \Lambda}{\mu}$ then as $t \rightarrow \infty$, the trajectories approach $\frac{\varepsilon + \Lambda}{\mu}$; If $N_0 > \frac{\varepsilon + \Lambda}{\mu}$, the solution $N(t)$ decrease to $\frac{\varepsilon + \Lambda}{\mu}$ as $t \rightarrow \infty$. In either case the solution approaches $N(t) = \frac{\varepsilon + \Lambda}{\mu}$ as $t \rightarrow \infty$. Hence, the feasible

solution set of the EVD model enters the region $\Omega = \left\{ (S, Q, I, T) \in \mathbb{R}_+^4 : N \leq \frac{\varepsilon + \Lambda}{\mu} \right\}$, which is a positively invariant set. According to Hethcote (2000), the EVD model is biologically meaningful and epidemiologically well posed in the region Ω .

3.2. Equilibrium States and Stability

The disease – free equilibrium (DFE) state, E_0 , is a steady state solution where there is no EVD in the population (that is $I = 0$). This is given as

$$E_0 = (S^0, Q^0, I^0, T^0) = \frac{\Lambda}{\mu}.$$

We have non-zero disease-free equilibrium (NDFE) state, E_0^1 , which is calculated by setting the derivatives of the EVD model of equations (1) – (4) to zero and solve the resultant equations simultaneously for $I = 0$. This is given as

$$E_0^1 = (S^1, Q^1, I^1, T^1) = \left[\frac{\Lambda f g + g \sigma \varepsilon + \theta \varphi \varepsilon}{\mu g f + c_1 \varphi \mu + g c_1 \mu'}, \frac{\Lambda g c_1 + g c_1 \varepsilon + g \mu \varepsilon}{\mu g f + c_1 \varphi \mu + g c_1 \mu'}, 0, \frac{\Lambda \varphi c_1 + \varphi c_1 \varepsilon + \mu \varphi \varepsilon}{\mu g f + c_1 \varphi \mu + g c_1 \mu'} \right] \quad (7)$$

where $f = \sigma + \varphi + \mu$, $g = \theta + \mu$, $h = \mu + \alpha + d_1 + c_2$.

In order to examine the stabilities of the DFE and NDFE, we first compute the effective reproduction numbers R_e . The effective reproduction number, R_e , is defined as the average number of new infections generated by a typical infectious individual introduced in a population where control measures are introduced. When $R_e < 1$, it means that EVD can be eliminated from the population in the presence of control measures. However, when $R_e > 1$, it implies that EVD will persist in the population where interventions are implemented. R_e are computed using next generation method described by Driessche and Watmough (2002). Based on the notations in Driessche and Watmough (2002), the effective reproduction number is given by $R_e = \rho(GU^{-1})$; where ρ is the spectral radius of the matrix, GU^{-1} .

From the EVD model, $F = \frac{\beta SI}{N}$ is the rate of new Ebola virus in compartment I while $V = hI$ is the transfer of individuals in and out of the compartment I by all other means except new infection.

The associated generation matrices G and U , can be found from F and V by taking the partial derivatives of F and V with respect to infected compartment I at DFE, E_0 . That is $G = \frac{\beta S^0}{N^0}$ are the rate of new infection at DFE E_0 , and NDFE, E_0^1 respectively. $U = h$ is the remaining transition terms at DFE, E_0 , and $N^0 = S^0 + Q^0 + T^0$. It follows that the effective reproduction number at DFE and are given by

$$R_e = \rho(GU^{-1}) = \frac{\beta}{h}$$

while the effective reproduction number, R_e^* , at NDFE, E_0^1 is given as

$$R_e^* = \rho(GU^{-1}) = \frac{\beta}{h} \left[\frac{\Lambda f g + g \sigma \varepsilon + \theta \varphi \varepsilon}{\Lambda f g + g \sigma \varepsilon + \theta \varphi \varepsilon + \Lambda g c_1 + g c_1 \varepsilon + g \mu \varepsilon + \Lambda \varphi c_1 + \varphi c_1 \varepsilon + \mu \varphi \varepsilon} \right].$$

According to Driessche and Watmough (2002), the DFE, E_0 and NDFE, E_0^1 are locally asymptotically stable if $R_e, R_e^* < 1$ and unstable if $R_e, R_e^* > 1$.

The Endemic Equilibrium (EE) state, E_1 , is a steady state solution where the disease persists in the population (that is $I \neq 0$). This is computed by setting the derivatives of the EVD

model to zero and solve the resultant equations simultaneously for $I \neq 0$. This gives $E_1 = (S^*, Q^*, I^*, T^*)$,

$$\text{where } S^* = \frac{Ch(\Lambda fg + \varepsilon g \sigma + \varepsilon \theta \varphi)}{AD(R_e^* - 1) + BC}, Q^* = \frac{D(\varepsilon \mu c_1 + \varepsilon \mu \alpha + \varepsilon g \mu + \varepsilon g d_1)(R_e^* - 1) + Ch(\Lambda g c_1 + \varepsilon g \mu + \varepsilon g c_1)}{AD(R_e^* - 1) + BC}, I^* = \frac{D(\Lambda fg + \varepsilon g \sigma + \varepsilon \theta \varphi)(R_e^* - 1)}{AD(R_e^* - 1) + BC}, T^* = \frac{D(\Lambda \alpha f + \Lambda f c_2 + \varepsilon \sigma \alpha + \varepsilon h \varphi + \varepsilon \sigma c_2)(R_e^* - 1) + Ch(\Lambda \varphi c_1 + \varepsilon \mu \varphi + \varepsilon h c_1)}{AD(R_e^* - 1) + BC}$$

$$A = f(\alpha \mu + \mu c_2 + \mu g + g d_1); \quad B = \sigma + \mu^2 \varphi + \mu^3 + \mu \theta \sigma + \mu \theta \varphi + \mu^2 \phi + \mu \varphi c_1 + \mu^2 c_1 + \theta c_1 \mu.$$

$$C = \Lambda f g + g \sigma \varepsilon + \theta \varphi \varepsilon + \Lambda \alpha f + \Lambda f c_2 + \alpha \varepsilon \sigma + \varepsilon h \varphi + \sigma \varepsilon c_2 + \varepsilon(\alpha \mu + \mu c_2 + \mu g + g d_1),$$

$$D = h(\Lambda f g + g \sigma \varepsilon + \theta \varphi \varepsilon + \Lambda g c_1 + g c_1 \varepsilon + g \mu \varepsilon + \Lambda \varphi c_1 + \varphi c_1 \varepsilon + \mu \varphi \varepsilon).$$

Theorem 2: The EVD model has one unique (positive) endemic equilibrium, given by E_1 , whenever $R_e^* > 1$.

4. Basic Ideas of Homotopy Analysis Method

Consider a nonlinear equation of the form

$$M[u(t)] = 0 \tag{8}$$

where M is a nonlinear operator, t denotes the time. Let $u_0(t)$ denotes an initial approximation of $u(t)$ and L denotes an auxiliary linear operator, Liao (1997) constructs the zero-order deformation equation.

$$(1 - p)L[\phi(t; p) - u_0(t)] = phH(t)M(t; p) \tag{9}$$

where $p \in [0, 1]$ is the embedding parameter, $h \neq 0$ is a nonzero auxiliary parameter, $H(t) \neq 0$ is a nonzero auxiliary function.

When $p = 0$ and $p = 1$, the zero-order deformation equations becomes

$$\phi(t; 0) = u_0(t) \tag{10}$$

and

$$\phi(t; 1) = u(t) \tag{11}$$

Thus, as p increases from 0 to 1, the solution $\phi(t; p)$ varies continuously from the initial approximation $u_0(t)$ to the exact solution $u(t)$. Expanding $\phi(t; p)$ by Taylor's series in power series of p by using (10), we have

$$\phi(t; p) = u_0(t) + \sum_{m=1}^{\infty} u_m p^m \tag{12}$$

where

$$u_m(t) = \frac{1}{m} \frac{\partial^m \phi(t; p)}{\partial p^m} \text{ at } p = 0 \tag{13}$$

Equation (13) is the m th-order deformation derivatives.

If the auxiliary linear operator L , the initial approximation $u_0(t)$, the auxiliary parameter h and the auxiliary function $H(t)$ are properly chosen so that

- i. the solution $\phi(t; p)$ of the zero-order deformation equation (9) exists for all $p \in [0, 1]$,
- ii. the m th-order deformation derivatives (13) exists for all $m = 1, 2, 3, \dots$,
- iii. the series (12) converges at $p = 1$.

Then, we have based on these conditions (i) – (iii) that the series solution is given by

$$u(t) = u_0(t) + \sum_{m=1}^{\infty} u_m(t) \tag{14}$$

Define the vector

$$\vec{u}_m(t) = \{u_0(t), u_1(t), \dots, u_m(t)\} \quad (15)$$

According to the definition (13), the governing equation can be derived from the zero-order deformation equation (9). Differentiating (9) m times with respect to the embedding parameter, p , then setting $p = 0$ and finally dividing by $m!$, we obtain the so called m th-order deformation equation

$$L[u_m(t) - \chi_m u_{m-1}(t)] = hH(t)Q_m(\vec{u}_{m-1}(t)) \quad (16)$$

where

$$Q_m(\vec{u}_{m-1}(t)) = \frac{1}{(m-1)!} \frac{\partial^{m-1} N[\phi(t;p)]}{\partial p^{m-1}} \quad \text{at} \quad p = 0 \quad (17)$$

and

$$\chi_m = \begin{cases} 0, & m \leq 1 \\ 1, & m > 1 \end{cases} \quad (18)$$

According to (17), the right hand side of (16) depends only on $u_{m-1}(t)$. Thus, we can easily obtain the series $u_1(t), u_2(t), \dots$ by solving the linear m th order deformation equation (16) using symbolic computational software such as Matlab, Maple or Mathematica.

5. Application of HAM to EVD Model

For easy implementation of HAM to the EVD model, we normalized the population of each class, that is, $s = \frac{S}{N}, q = \frac{Q}{N}, i = \frac{I}{N}, h = \frac{T}{N}$ and let $a = \frac{\Lambda}{N}$ and $b = \frac{\epsilon}{N}$ such that $s(t) + q(t) + i(t) + h(t) = 1$.

This leads to the following system of differential equations for EVD model.

$$\frac{ds}{dt} = a - (a + b)s - \beta si + \sigma q + \theta h - c_1 s + ds, s(0) = s_0 \quad (19)$$

$$\frac{dq}{dt} = b - (a + b)q + c_1 s - \sigma q - \varphi q + dq, q(0) = q_0 \quad (20)$$

$$\frac{di}{dt} = \beta si - (a + b)i - (\alpha + d)i - c_2 i + di^2, i(0) = i_0 \quad (21)$$

$$\frac{dh}{dt} = \alpha i + \varphi q + c_2 i - (a + b)h - \theta h + di, h(0) = h_0 \quad (22)$$

We apply HAM to the transformed EVD model of equations (19) – (22) in order to find the approximate series solution of the model. Let $\phi_i = (t, p), i = 1, 2, 3, 4$ be function of time, t and $p \in [0, 1]$, the embedding parameter. We define the following nonlinear operators

$$M_1[\phi_1, \phi_2, \phi_3, \phi_4] = \frac{\partial \phi_1(t,p)}{\partial t} - a + (a + b)\phi_1(t, p) + \beta \phi_1(t, p)\phi_3(t, p) + c_1 \phi_1(t, p) - d\phi_1(t, p)\phi_3(t, p) - \theta \phi_4(t, p) - \sigma \phi_2(t, p)$$

$$M_2[\phi_1, \phi_2, \phi_3, \phi_4] = \frac{\partial \phi_2(t,p)}{\partial t} - b + (a + b)\phi_2(t, p) - c_1 \phi_1(t, p) + (\varphi + \sigma)\phi_2(t, p) - d\phi_3(t, p)\phi_2(t, p)$$

$$M_3[\phi_1, \phi_2, \phi_3, \phi_4] = \frac{\partial \phi_3(t,p)}{\partial t} - \beta \phi_1(t, p)\phi_3(t, p) + (\alpha + c_2 + d)\phi_3(t, p) + (a + b)\phi_3(t, p) - d\phi_3^2(t, p)$$

$$M_4[\phi_1, \phi_2, \phi_3, \phi_4] = \frac{\partial \phi_4(t,p)}{\partial t} - \varphi \phi_2(t, p) - (\alpha + c_2)\phi_3(t, p) + \theta \phi_4(t, p) + (a + b)\phi_4(t, p) - d\phi_1(t, p)\phi_3(t, p)$$

The auxiliary linear operators are given by

$$L_l = \frac{\partial \phi_l}{\partial t} \quad (23)$$

$$L_2 = \frac{\partial \phi_2}{\partial t} \tag{24}$$

$$L_3 = \frac{\partial \phi_3}{\partial t} + \phi_3 \tag{25}$$

$$L_4 = \frac{\partial \phi_4}{\partial t} \tag{26}$$

with the property that

$$L_1(c_1) = 0; \quad L_2(c_2) = 0, \quad L_3(c_3 e^{-t}) = 0; \quad L_4(c_4) = 0. \tag{27}$$

Here $c_i, (i = 1,2,3,4)$ are integral constants to be determined.

Let $h_i \neq 0$, and $H_i \neq 0, i = 1,2,3,4$ denote the non-zero auxiliary parameters and nonzero auxiliary functions respectively. We then construct the following zeroth – order deformation equations given by

$$(1 - p)L_1[\phi_1(t, p) - s_0(t)] = ph_1H_1(t)M_1[\phi_1(t, p)] \tag{28}$$

$$(1 - p)L_2[\phi_2(t, p) - q_0(t)] = ph_2H_2(t)M_2[\phi_2(t, p)] \tag{29}$$

$$(1 - p)L_3[\phi_3(t, p) - i_0(t)] = ph_3H_3(t)M_3[\phi_3(t, p)] \tag{30}$$

$$(1 - p)L_4[\phi_4(t, p) - h_0(t)] = ph_4H_4(t)M_4[\phi_4(t, p)] \tag{31}$$

subject to the initial conditions

$$\phi_1(t, 0) = s_0(t); \phi_2(t, 0) = q_0(t); \phi_3(t, 0) = i_0(t); \phi_4(t, 0) = h_0(t).$$

From (28)-(31), we have when $p = 0$ that

$$\phi_1(t, 0) = s_0(t), \phi_2(t, 0) = q_0(t), \phi_3(t, 0) = i_0(t), \phi_4(t, 0) = h_0(t) \tag{32}$$

and when $p = 1$

$$\phi_1(t, 1) = s(t)$$

$$\phi_2(t, 1) = q(t)$$

$$\phi_3(t, 1) = i(t)$$

$$\phi_4(t, 1) = h(t)$$

Hence, as the embedding parameter, p increases from 0 to 1, $\phi_i(t, p), i = 1,2,3,4$ varies from initial approximation, $s_0(t), q_0(t), i_0(t), h_0(t)$ to the exact solution, $s(t), q(t), i(t), h(t)$.

Expanding $\phi_i(t, p), i = 1,2,3,4$ with respect to p by using the Taylor's theorem and imploring equations (32), we have

$$\phi_1(t, p) = s_0(t) + \sum_{m=1}^{+\infty} s_m(t)p^m \tag{33}$$

$$\phi_2(t, p) = q_0(t) + \sum_{m=1}^{+\infty} q_m(t)p^m \tag{34}$$

$$\phi_3(t, p) = i_0(t) + \sum_{m=1}^{+\infty} i_m(t)p^m \tag{35}$$

$$\phi_4(t, p) = h_0(t) + \sum_{m=1}^{+\infty} h_m(t)p^m \tag{36}$$

where,

$$s_m(t) = \frac{1}{m!} \frac{\partial^m \phi_1(t, p)}{\partial p^m} \Big|_{p=0}$$

$$q_m(t) = \frac{1}{m!} \frac{\partial^m \phi_2(t, p)}{\partial p^m} \Big|_{p=0}$$

$$i_m(t) = \frac{1}{m!} \frac{\partial^m \phi_3(t, p)}{\partial p^m} \Big|_{p=0}$$

$$h_m(t) = \frac{1}{m!} \left. \frac{\partial^m \phi_4(t,p)}{\partial p^m} \right|_{p=0}$$

with initial approximations,

$$s_0(t) = 0.994, q_0(t) = 0.003, i_0(t) = 0.002e^{-t}, h_0(t) = 0.001. \quad (37)$$

If the nonzero auxiliary parameters h_1, h_2, h_3, h_4 and auxiliary parameters $H_1(t), H_2(t), H_3(t), H_4(t)$ are properly chosen in such a way that these series (33) – (36) converge at $p = 1$, we have

$$s(t) = s_0(\square) + \sum_{m=1}^{+\infty} s_m(t) \quad (38)$$

$$q(t) = q_0(t) + \sum_{m=1}^{+\infty} q_m(t) \quad (39)$$

$$i(t) = i_0(t) + \sum_{m=1}^{+\infty} i_m(t) \quad (40)$$

$$h(t) = h_0(t) + \sum_{m=1}^{+\infty} h_m(t) \quad (41)$$

Equations (38) – (41) are called the homotopy series solution for $s(t), q(t), i(t)$ and $h(t)$. Getting the m th-order deformation equations, we define the vectors

$$\vec{s}_m(t) = \{s_0(t), s_1(t), \dots, s_m(t)\}$$

$$\vec{q}_m(t) = \{q_0(t), q_1(t), \dots, q_m(t)\}$$

$$\vec{i}_m(t) = \{i_0(t), i_1(t), \dots, i_m(t)\}$$

$$\vec{h}_m(t) = \{h_0(t), h_1(t), \dots, h_m(t)\}$$

Differentiating the zeroth - order deformation equations (28)-(31) m times with respect to p , divide by $m!$ and finally set $p = 0$. We obtain the m th-order deformation equation given as

$$L_1[s_m(t) - \chi_m s_{m-1}(t)] = h_1 H_1(t) R_m(\vec{s}_{m-1}(t)), \quad m = 1, 2, \dots, n \quad (42)$$

$$L_2[q_m(t) - \chi_m q_{m-1}(t)] = h_2 H_2(t) R_m(\vec{q}_{m-1}(t)), \quad m = 1, 2, \dots, n \quad (43)$$

$$L_3[i_m(t) - \chi_m i_{m-1}(t)] = h_3 H_3(t) R_m(\vec{i}_{m-1}(t)), \quad m = 1, 2, \dots, n \quad (44)$$

$$L_4[h_m(t) - \chi_m h_{m-1}(t)] = h_4 H_4(t) R_m(\vec{h}_{m-1}(t)), \quad m = 1, 2, \dots, n \quad (45)$$

with initial conditions

$$s_m(0) = 0, \quad q_m(0) = 0, \quad \square_m(0) = 0, \quad h_m(0) = 0.$$

Taking the inverse auxiliary linear operator of both sides of (42) – (45), we have

$$s_m(t) = \chi_m s_{m-1}(t) + L_1^{-1}[h_1 H_1(t) R_m(\vec{s}_{m-1}(t))] + c_1, \quad (46)$$

$$q_m(t) = \chi_m q_{m-1}(t) + L_2^{-1}[h_2 H_2(t) R_m(\vec{q}_{m-1}(t))] + c_2, \quad (47)$$

$$i_m(t) = \chi_m i_{m-1}(t) + L_3^{-1}[h_3 H_3(t) R_m(\vec{i}_{m-1}(t))] + c_3 e^{-t}, \quad (48)$$

$$h_m(t) = \chi_m h_{m-1}(t) + L_4^{-1}[h_4 H_4(t) R_m(\vec{h}_{m-1}(t))] + c_4, \quad (49)$$

Let $h_1 = h_2 = h_3 = h_4 = h^*$ for simplicity. Then from the definition of our auxiliary linear operator of each functions in (23)-(26), we have

$$L_1^{-1} = \int_0^t (\cdot) dr, \quad L_2^{-1} = \int_0^t (\cdot) dr, \quad L_3^{-1} = e^{-t} \int_0^t e^r (\cdot) dr, \quad L_4^{-1} = \int_0^t (\cdot) dr \quad (50)$$

and $H_1(t), H_2(t), H_3(t)$ and $H_4(t)$ by the rule of coefficient ergodicity are given as

$$H_1(t) = 1, \quad H_2(t) = 1, \quad H_3(t) = e^{-t}, \quad H_4(t) = 1. \quad (51)$$

Therefore, substituting $h_1 = h_2 = h_3 = h^*$ and equations (50) and (51) in equations (46)-(49), we have

$$s_m(t) = \chi_m s_{m-1}(t) + h^* \int_0^t R_m(\vec{s}_{m-1}(r)) dr + c_1 \tag{52}$$

$$q_m(t) = \chi_m q_{m-1}(t) + h^* \int_0^t R_m(\vec{q}_{m-1}(r)) dr + c_2 \tag{53}$$

$$i_m(t) = \chi_m i_{m-1}(t) + h^* e^{-t} \int_0^t e^r R_m(\vec{i}_{m-1}(r)) dr + c_3 e^{-t} \tag{54}$$

$$h_m(t) = \chi_m h_{m-1}(t) + h^* \int_0^t R_m(\vec{h}_{m-1}(r)) dr + c_4 \tag{55}$$

with

$$R_m(\vec{s}_{m-1}(r)) = s'_{m-1}(r) - a + (a + b)s_{m-1} + \beta \sum_{n=0}^{m-1} s_n i_{m-1-n} + c_1 s_{m-1} - \theta h_{m-1} - \sigma q_{m-1} - d \sum_{n=0}^{m-1} s_n i_{m-1-n} \tag{56}$$

$$R_m(\vec{q}_{m-1}(r)) = q'_{m-1}(r) - c_1 s_{m-1} + (a + b)q_{m-1} - b + (\varphi + \sigma)q_{m-1} - d \sum_{n=0}^{m-1} q_n i_{m-1-n} \tag{57}$$

$$R_m(\vec{i}_{m-1}(r)) = i'_{m-1}(r) - \beta \sum_{n=0}^{m-1} s_n i_{m-1-n} + (\alpha + c_2 + d_1)i_{m-1} + (a + b)i_{m-1} - d \sum_{n=0}^{m-1} i_n i_{m-1-n} \tag{58}$$

$$R_m(\vec{h}_{m-1}(r)) = h'_{m-1}(r) - \varphi q_{m-1} - (\alpha + c_2)i_{m-1} + \theta h_{m-1} + (a + b)h_{m-1} - d \sum_{n=0}^{m-1} h_n i_{m-1-n} \tag{59}$$

Using the initial approximations given in equation (37) and the parameter values in Table 2, we obtain successively for $m = 1, 2, \dots$, the solutions of equations (52) – (55) together with (56) – (59) as

$$\begin{aligned} s_1(t) &= 0.994 + (0.0000258111 - 0.000258111 e^{-t} + 0.0594876t)h^* \\ q_1(t) &= 0.003 + (1.80992 \times 10^{-7} e^{-t} - 1.80992 \times 10^{-7} - 0.0592695t)h^* \\ i_1(t) &= 0.002 e^{-t} + (6.03306 \times 10^{-8} e^{-3t} - 0.00199597 + 0.00199591 e^{-2t})h^* \\ h_1(t) &= 0.001 + (0.00026166 e^{-t} - 0.00026166 - 0.000218385t)h^* \end{aligned}$$

$$\begin{aligned} s_2(t) &= 0.994 + (0.000516223 - 0.000516223 e^{-t} + 0.118975t)h^* + (-2.59524 \times 10^{-9} e^{-3t} - 0.000128758 e^{-2t} + (7.73069 \times 10^{-6} - 0.0000154471t)e^{-t}) + \\ &0.00320278t^2 + 0.059511604t + 1.210309732 \times 10^{-4})h^{*2} \end{aligned}$$

$$\begin{aligned} q_2(t) &= 0.003 + (-3.61984 \times 10^{-7} + 3.61984 \times 10^{-7} e^{-t} - 0.118539t)h^* + (1.81989 \times 10^{-12} e^{-3t} + 9.03164 \times 10^{-8} e^{-2t} + (-0.0000190858 - 3.57576 \times 10^{-6}t)e^{-t}) - \\ &0.00566879t^2 - 0.059285223t + 1.899556768 \times 10^{-5})h^{*2} \end{aligned}$$

$$\begin{aligned} i_2(t) &= 0.002 e^{-t} + (1.20661 \times 10^{-7} e^{-3t} + 0.00399182 e^{-2t} - 3.991946022 \times 10^{-3} e^{-t})h^* + (1.81989 \times 10^{-12} e^{-5t} + 1.40566 \times 10^{-7} e^{-4t} + 0.00199371 e^{-3t} - \\ &(0.00197277 - 0.000019036t)e^{-2t}) - 0.0000210771 e^{-t})h^{*2} \end{aligned}$$

$$h_2(t) = 0.001 + (0.000523321e^{-t} - 0.00043677t - 0.000523321)h^* + (2.63102 \times 10^{-9}e^{-3t} + 0.000130571e^{-2t} - (7.75669 \times 10^{-6} + 1.31753 \times 10^{-8}t)e^{-t} + 0.00246601t^2 - 2.283828579 \times 10^{-4}t - 1.223390082 \times 10^{-4})h^{*2}$$

and so on. Therefore, the n^{th} -order approximate series solution for $s(t)$, $q(t)$, $i(t)$ and $h(t)$ that converges for any valid region of h^* is given by

$$s(t) \approx \sum_{m=0}^n s_m(t)$$

$$q(t) \approx \sum_{m=0}^n q_m(t)$$

$$i(t) \approx \sum_{m=0}^n i_m(t)$$

$$h(t) \approx \sum_{m=0}^n h_m(t).$$

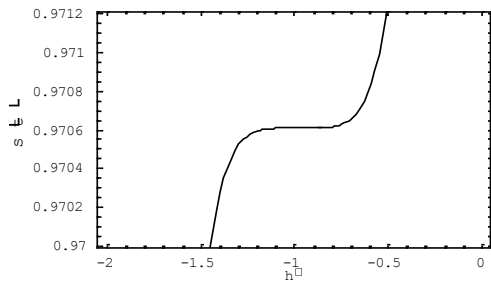
5.1 Results and Discussion

In this section, HAM is applied to transformed EVD model of equations (19) – (22) using the initial conditions and parameters values in Table 2. The symbolic software MATHEMATICA is used to carry out the algorithm of HAM. The importance of the auxiliary parameter, h^* in adjusting and controlling the convergence region of the obtained series solution is described in this section. We plot the 5th order approximation solutions of $s(t)$, $q(t)$, $i(t)$ and $h(t)$ against h^* at $t = 0$ to get the convergence region of h^* . This is presented graphically in Figure 1. The convergence region is the line segment nearly parallel to the horizontal axis in these curves as shown in Figure 1. Therefore from Figure 1(a – d), the valid region of h^* is $-1.3 < h^* < -0.7$. This means that any value of h^* chose within this valid region will ensure convergence of the resulted series solutions. The Figure 2 demonstrates the effect of h^* on the approximation series solution. The different values of h^* is chosen within the valid region, $-1.3 < h^* < -0.7$, the convergence rate of the approximate series solution differs except the prevalence of disease, $i(t)$. Here; they converge at the same rate (see Figure 2(c)). Furthermore, Figure 3 is the 4th order approximation solution of the transformed EVD model when $h^* = -1$. This is equivalent to the series solution obtained by using Homotopy perturbation Method as proved by Liao (2003).

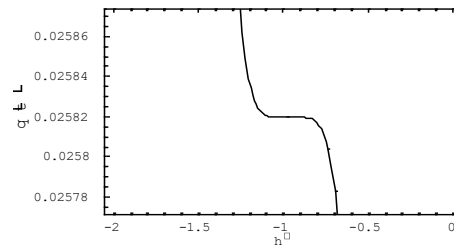
Table 2: Initial conditions and Parameter values

Parameter	Value (day) ⁻¹	Source	Parameter	Value (day) ⁻¹	Source
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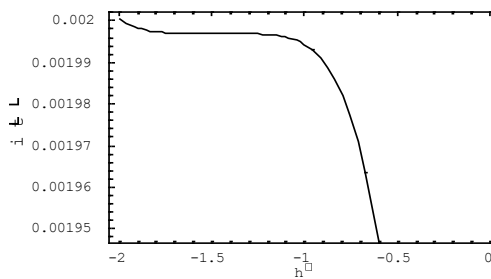
$s(0)$	0.994	Estimated	ϕ	0.0314862	„
$q(0)$	0.003	„	d	0.0301653	„
$i(0)$	0.002	„	σ	0.047619	„
$h(0)$	0.001	„	c_1	0.06	Estimated
β	0.160	Rivers et al.	c_2	0.07	„
α	0.0608	(2014)	b	0.0000227	„
φ	0.08333	„	a	0.000096	„
		„			



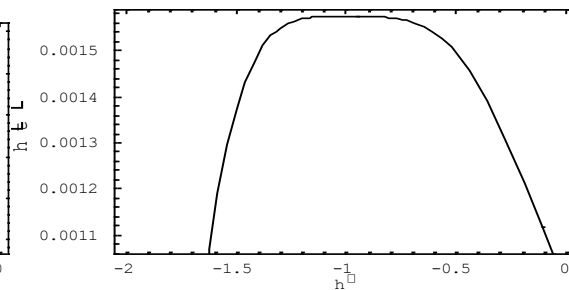
(a)



(b)



(c)



(d)

Figure 1: 5th order approximation solutions of $s(t)$, $q(t)$, $i(t)$ and $h(t)$ against h^* at $t = 0$.

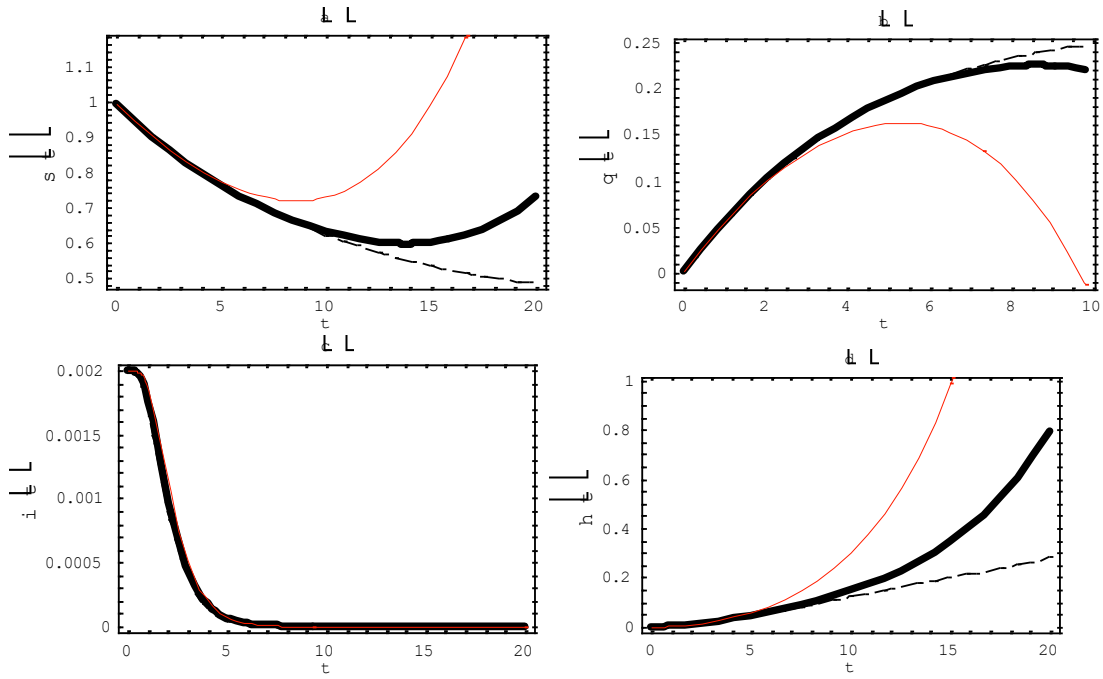


Figure 2. The 4th order HAM approximation solution for EVD transformed model. Dashed line: $h^* = -0.8$, thick line: $h^* = -1$ and hue line: $h^* = -1.2$.

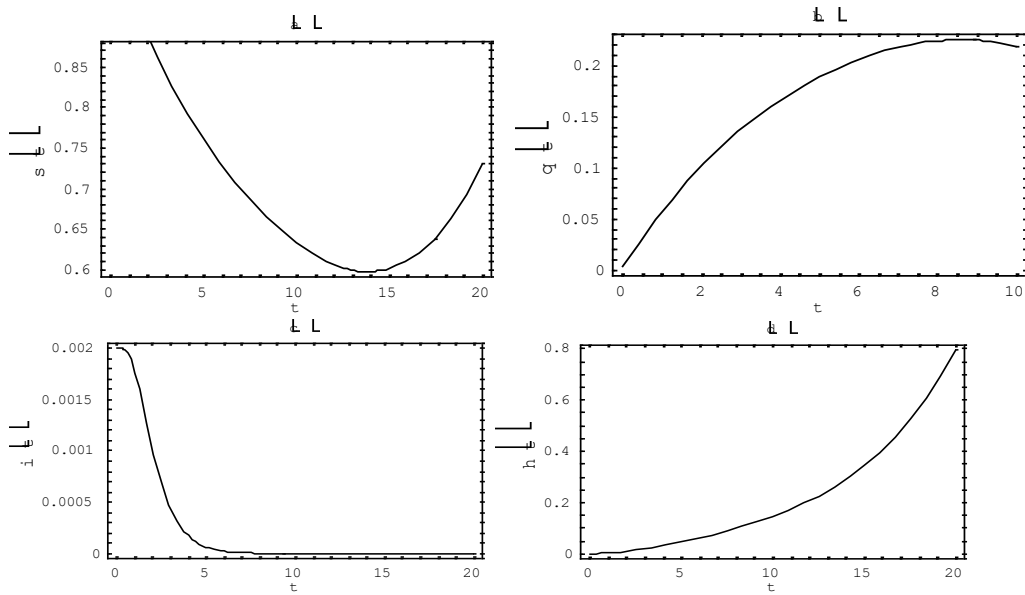


Figure 3: The 4th order HAM approximation solution for EVD transformed model when $h^* = -1$.

7. Conclusion

A deterministic model for the transmission dynamics of EVD is presented in this paper. The model proved to be epidemiologically and mathematically well posed in an invariant region. The basic analysis of an epidemic model such as the computation of effective reproduction numbers, the existence and stability of the disease-free and endemic equilibrium states are determined. The EVD model was further transformed into proportions in which we applied HAM to the transformed EVD model to get the approximate series solution. The importance of choosing from the valid region, a proper value of auxiliary parameter for adjusting and controlling the convergence region was discussed. From the results, HAM was shown to be a viable method for solving nonlinear problems such as mathematical model of EVD.

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