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Research Article

Theoretical Model for the Control of Lassa Fever and Transmission Using Homotopy Perturbation Method

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Abstract

A mathematical model for the dynamics of Lassa fever transmission and control is presented. The model is a modified form of the traditional SIR model for infectious disease. We employed the modified Homotopy perturbation method to solve and analyze the transmission of the SIR model of this disease. For all time values, the analytical expression of the population of the susceptible group S(t), the infected group I(t), and the recovered group R(t) is derived. The impact of various parameters is addressed. The numerical simulation is carried out using MATLAB and compared with our analytical results.

Keywords: Mathematical Modeling, Nonlinear Differential Equations, Lassa Fever, SIR Model, Numerical Simulation, Homotopy Perturbation Method.

1. Introduction

Lassa fever is a zoonotic (animal-borne) acute viral illness. The disease originated in Nigeria in the 1950s, and It is widespread in parts of West Africa, including Sierra Leone, Liberia, Guinea[1,2]. It is an agent that causes infection to human with high death rates. The incubation period of Lassa fever ranges from 6–21 days. The disease's symptoms generally appear with fever, general fatigue, and malaise as the first signals. Headache, sore throat, muscle pain, chest pain, nausea, vomiting, diarrhoea, cough, and abdominal pain may occur within a few days. Facial swelling, lung problems, leakage from the lips, nose, vaginal or gastrointestinal tract, and low blood pressure can occur in extreme situations [3].

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Lassa fever is modelled by system of nonlinear equations. Mathematical modelling has been one of the most effective methods for studying and controlling infectious diseases. According to Laarabi et al. [4], mathematical modelling has a significant value in understanding the underpinning mechanisms that affect disease transmission and propose control strategies. Bernoulli and Blower [5] state that mathematical models provide conceptual results such as thresholds, simple reproductive numbers, contact numbers, and replacement numbers. Modelling

infectious disease transmission helps researchers to evaluate the efficacy of control measures and establish more efficient strategies to prevent disease spread in the future.

In this paper, we apply the homotopy perturbation method to investigate the solution of the control of a mathematical model of Lassa fever proposed by Durojaye et al.[6], considering different parameters. We stated the SIR model of Lassa fever as proposed by Durojaye et al. deals with the analysis of numerical simulation applied to a system of ordinary differential equations. We presented the numerical results of the model with respect to various reproductive numbers using MATLAB ode 45.

2. Mathematical Formulation of the Problem

The dynamics of the population infected by an infectious disease is traditionally described mathematically by the system of differential equations. The SIR epidemic model, where the population divided into three groups: the susceptible group, denoted by S(t), the infected group, denoted by I(t), and the recovered group, denoted by R(t). The total population is assumed constant during the short period of time under study, this is given by

$$N = S(t) + I(t) + R(t) \tag{1}$$

A major strategy to control infectious diseases is through vaccination. Now our idea is to study the effect of vaccination on Lassa fever disease. In this section, we improve the SIR model described in equation and present the system of equations that describe the Susceptible-Infectious-Recovery (SIR) model with vaccination as [6]:

$$\frac{dS}{dt} = -\beta S(t)I(t) - \nu S(t) \tag{5}$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \mu I(t) \tag{6}$$

$$\frac{dR}{dt} = \mu I(t) + \nu S(t) \tag{7}$$

Initial conditions are

$$S(0) = 0.5, I(0) = 0.3226, R(0) = 0.1774$$
 (8)

Where β the rate of infection, μ is is the rate of recovery, and ν is the percentage of individuals vaccinated every day.

3. Approximate Analytical Expression of Susceptible Human, Exposed Human and Infected Human Using Homotopy Perturbation Method

Nonlinear equations play a significant role in modelling the many problems in physics, biology and engineering. Recently the nonlinear equations are solved by semi-analytical methods like the Adomian decomposition method [7], homotopy perturbation method [8], new iterative method[9], differential transform method[10], Green's function iterative method [11,12], Agbari-Ganji method[13] and Taylor series method[14], among others. Among the methods mentioned above, the homotopy perturbation method is very simple in its principles and application to solve nonlinear differential equations.

The Homotopy Perturbation method first proposed by et al. [15] has been demonstrated to be an effective technique in deducing analytical solutions of non-linear differential equations in a hierarchical manner [16,17]. The basic concept of Homotopy Perturbation method is given in Appendix A.

By solving Eqs. (5)-(7) using the homotopy perturbation method (Appendix B), we obtain the analytical expression of population of susceptible group S(t), the infected group I(t), and the recovered group R(t) as follows:

$$S(t) = 0.5e^{-\nu t} + \frac{0.1613\beta}{\mu} \left(1 - e^{\mu t} \right) \left(e^{-t(\mu + \nu)} \right)$$

$$I(t) = 0.3226e^{-\mu t} + \frac{0.1613\beta}{\nu} \left(e^{\nu t} - 1 \right) \left(e^{-t(\mu + \nu)} \right)$$

$$R(t) = \frac{1}{\nu \mu} \left[\nu e^{-\nu t} \left(0.1613\beta - 0.5\mu \right) - 0.4839\mu e^{-\mu t} + 0.1613\beta \left(e^{-t(\mu + \nu)} \right) \left(\mu - \nu \right) + \nu \mu \right]$$

$$(11)$$

4. Numerical Simulation

We simulate the SIR model with vaccination in order to predict the evolution of every group of individuals in case of vaccination. We consider different rates of vaccinations and their effect on the curve of every group. We adopt the data in [6] taking S(0) = 0.5, I(0) = 0.3226, R(0) = 0.1774, $\beta = 0.5$ and $\mu = 0.7$, $\nu = 0.1$. This gives $R_0 = 0.71$ such that $R_0 < 1$. The analytical results are compared with simulation results the following figures 1-2 and Tables 1-3. Satisfactory agreements is noted.

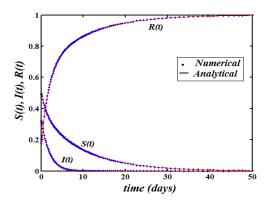


Fig. 1. Comparison of S(t), I(t) and R(t) with simulation results for several values of parameters $\beta = 0.5$, $\mu = 0.7$ and $\nu = 0.1$. Here $R_0 = \frac{\beta}{\mu} = 0.71$.

5. Result and Discussion

Equation 9 to 11 are the new simple expression of the population of susceptible group (t), the infected group (t), and the recovered group R(t). Figs.1 describe the comparison of numerical and analytical expression of populations in SIR models. The figure is inferred that susceptible and infected people are decreasing function whereas recovered group (t) is increasing function. The susceptible population reaches the minimum value when

$$\begin{array}{l} t_s = \ \log \; \{ \; 0.1613\beta \, (\mu + v) \, / \, v \; \mu \, (0.1613 \; \beta - 0.5 \; \mu) \; \} \\ \text{Similarly, the infected population reaches the lowest value when} \\ t_I = \ \log \; \{ 0.1613\beta \, (\mu + v) \, / \, v \mu \, (0.3226v + 0.1613 \; \beta) \; \} \\ \text{The recovered group} \; (\textit{t}) \; \text{reaches the maximum when} \\ t_R = \; (0.1613 \; \beta \; \mu^2 - 0.3226 \; \beta \; v^2 + 0.5 \; \mu \; v^2 + 0.4839 \; \mu^2 \;) \, / \, (\mu \; \beta \; v^2 (0.1613) - 0.5 \; \mu^2 v^2 - 0.4839 \; \mu^2 v) \end{array}$$

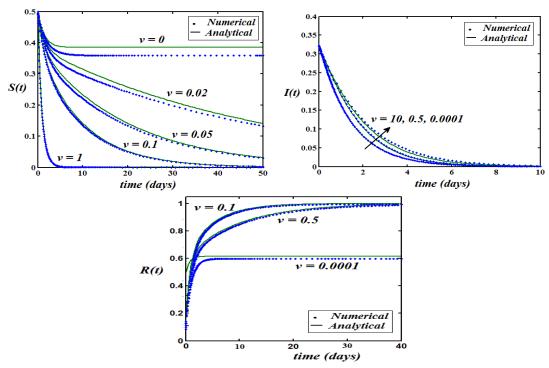
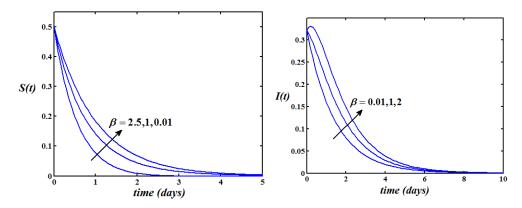


Fig. 2. Comparison of S(t), I(t) and R(t) with simulation results for several values of parameters v and for some fixed values of $\beta = 0.5$, $\mu = 0.7$. Here $R_0 = \frac{\beta}{\mu} = 0.71$.

Figs (2) represent the population of S(t), I(t) and R(t) for various values of vaccination. From the figure 2 (a,b), it is inferred that an increase in vaccination leads to decrease in both susceptible group S(t) and the infected group I(t). From Figure 2(c), it is observed that an increase in vaccination number results in a increasing in recovered group (t).



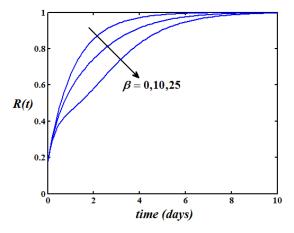


Fig. 3. Plot of S(t), I(t) and R(t) with simulation results for several values of parameters $\mu = 0.7, \nu = 1$.

The S(t), I(t) and R(t) profiles for different values of the β (rate of infection) are displays in the Figs. 3(a-c). From this figure we observe that the S(t), and R(t) is decreased by increasing the rate of infection. Also I(t) increase when rate of infection in increases.

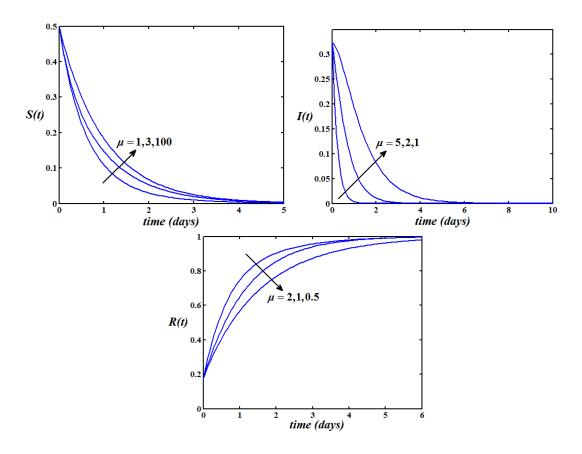


Fig. 4.Plot of S(t), I(t) and R(t) with simulation results for several values of parameters $\beta = 2$, v = 1

The effect of different values of rate of recovery μ for S(t), I(t) and R(t) is shown in Fig. 4(a-c). From these figures it is observed that an increase in μ leads to decrease in I(t) and increase in S(t) and R(t).

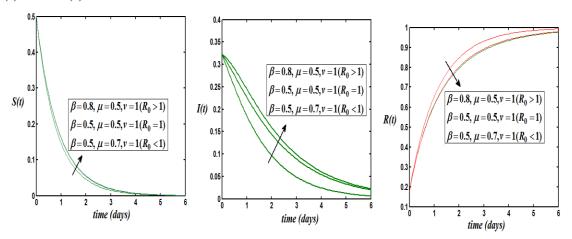


Fig. 5. Plot of S(t), I(t) and R(t) for several values of parameters β , μ

The capacity of any infectious disease to infiltrate a community is one of the most severe worries about it. Many epidemiological models feature a disease-free equilibrium (DFE), which is the point at which the population remains disease-free. The fundamental reproductive number R0 is typically used as a threshold parameter in these models. The basic reproductive number is a crucial notion in mathematical biology. It is described as the average number of secondary infections generated by a single infectious individual throughout their transferrable life. For the SIR model with vital dynamics, Ro is defined as

$$R_0 = \frac{\beta}{\mu}$$

where β is the rate of infection and μ is the rate of recovery. It is a basic parameter that affects disease propagation and is related to long-term behaviors as well as the degree of immunization required for eradication.

Fig. 5 shows the effect of reproductive number on the S(t), I(t) and R(t) for several values of parameters β , μ . If $R_0 < 1$, each individual produces, less than one new infected individual, and the disease cannot invade the population and hence the disease dies out. If $R_0>1$, each individual produces more than one new infected individual and hence the disease is able to invade the susceptible population and invasion is always possible.

6. Conclusion

In this study, we successfully solved the model of Lassa fever virus that arises from the ODE system using the h

Homotopy Perturbation method. The analytical expression of the population of susceptible group (t), the infected group (t), and the recovered group R(t), are obtained for all values time. The effect

of various parameter on S(t), I(t) and R(t) are discussed. Also, our analytical results are compared with simulation results, and satisfactory agreement is noted.

Nomenclature

Symbol	Name
S	The susceptible group
I	The infected group
R	The recovered group
β	Rate of infection
μ	Rate of recovery
v	Percentage of individuals vaccinated every day
t	Time

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Table 1. Comparison of our analytical expression of S with the numerical result for various values of the parameter μ and some fixed values parameter $\beta = 0.5, \mu = 0.7$ using Eqn. (9). Here $R_0 = \frac{\beta}{\mu} = 0.71$.

	v = 0			v = 0.05			v = 0.1	-		v = 1			
z	Nume rical Result	Our Eq.(15)	% of devia tion	Nume rical Result	Our Eq.(15)	% of deviat ion	Num erical Resul t	Our Eq.(1 5)	% of deviati	Nume rical Result	Our Eq.(1 5)	% of deviat ion	
0	0.500 0	1.00	0.00	0.500 0	0.50 00	0.00	0.500	0.500	0.00	0.500 0	0.500	0.00	
2	0.411 2	0.41 32	0.49	0.370 8	0.37 39	0.83	0.332	0.329 7	0.78	0.055 9	0.056	0.54	
4	0.379 8	0.38 79	2.13	0.315 4	0.32 08	1.70	0.252 6	0.254 7	0.82	0.007 2	0.007	0.87	
6	0.377 9	0.38 65	2.28	0.278 9	0.28 63	2.67	0.210 1	0.204	2.87	0.001 0	0.001	1.25	
8	0.374 8	0.38 52	2.78	0.247 8	0.25 42	0.00	0.169 1	0.164	2.83	0.000 1	0.000	0.60	
1	0.369 8	0.38 49	4.08	0.229	0.23 34	1.85	0.139 6	0.134	3.86	0.000	0.000	2.29	
	Average error: 1.	-	centage	Average percentage error: 1.18			Average percentage error:1.86			Average percentage error:0.98			

	v = 0				v = 0.05			v = 0.1				v = 1				
t	Numer	Our	%	of	Numer	Our	%	of	Numer	Our	%	of	Nume	Our	%	of
	ical	Eq.(1	dev	iat	ical	Eq.(1	dev	iat	ical	eq.(dev	/iat	rical	eq.(1	dev	/iat
	Result	6)	ion	L	Result	6)	ion		Result	16)	ion	L	Result	6)	ion	

0	0.3226	0.322 6	0.00	0.3226	0.322 6	0.00	0.3226	0.32 26	0.00	0.322 6	0.32 26	0.00
2	0.1024	0.104 7	2.24	0.1059	0.104 7	1.14	0.0830	0.08 15	1.76	0.096 7	0.09 73	0.55
4	0.0396	0.039	0.86	0.0289	0.028 1	2.81	0.0205	0.02 01	1.67	0.024 4	0.02 47	1.14
6	0.0132	0.012 9	2.14	0.0080	0.007 9	1.17	0.0052	0.00 50	3.87	0.006	0.00 60	0.75
8	0.0036	0.003 6	0.50	0.0019	0.001 8	3.22	0.0012	0.00 12	1.31	0.001 5	0.00 15	1.74
1 0	0.0010	0.001	0.32	0.0004	0.000 4	3.25	0.0003	0.00 03	0.51	0.000 4	0.00 04	1.04
	Average percentage error: 1.01			Average percentage error:1.93			Average percentage error:1.52			Average percentage error: 0.87		

Table 2. Comparison of our analytical expression of I with the numerical result for various values of the parameter μ and some fixed values parameter $\beta = 0.5$, $\mu = 0.7$ using Eqn. (10). Here $R_0 = \frac{\beta}{\mu} = 0.71$.

Table 3. Comparison of our analytical expression of R with the numerical result for various values of the parameter μ and some fixed values parameter $\beta=0.5, \mu=0.7$ using Eqn. (11). Here $R_0=\frac{\beta}{\mu}=0.71$.

	v = 0			v = 0.05			v = 0.1			v = 1			
t	Numer	Our	% of	Numer	Our	% of	Numeri	Our	% of	Numeri	Our	% of	
	ical	Eq.(deviat	ical	Eq.(1	deviat	cal	Eq.(1	deviat	cal	Eq.(1	deviat	
	Result	17)	ion	Result	7)	ion	Result	7)	ion	Result	7)	ion	
0	0.1774	0.17 74	0.00	0.1774	0.17 74	0.00	0.1774	0.17 74	0.00	0.1774	0.17 74	0.00	
2	0.4776	0.46 75	2.12	0.5081	0.50 87	0.12	0.5379	0.54 61	1.52	0.8473	0.85 23	0.59	
4	0.5661	0.56 90	0.51	0.6529	0.64 18	1.70	0.7113	0.70 16	1.37	0.9684	0.97 02	0.18	
6	0.6096	0.60 14	1.35	0.7169	0.70 26	2.00	0.7833	0.77 76	0.73	0.9930	0.99 33	0.03	
8	0.6307	0.61 12	3.09	0.7470	0.73 86	1.12	0.8332	0.82 41	1.09	0.9984	0.99 86	0.02	
1 0	0.6301	0.61 41	2.54	0.7783	0.76 57	1.62	0.8643	0.85 76	0.77	0.9996	0.99 60	0.36	
	Average	per	centage	Average percentage			Average percentage			Average percentage			
	error: 1.	60		error :1.09			error : 0.91			error : 0.21			

Appendix A: Basic concept of homotopy perturbation method (HPM)

To illustrate the basic ideas of this method, we consider the following nonlinear functional equation:

$$A(U) - f(r) = 0, \quad r \in \Omega$$
(A1)

With the following boundary condition:

$$B\left(u, \frac{\partial u}{\partial n}\right) = 0, \quad r \in \Gamma, \tag{A2}$$

where Ais a general functional operator, B a boundary operator, f(r) is a known analytical function and Γ is the boundary of the domain Ω . The operator A can be decomposed into two operators Land N, where Lis linear, and N is nonlinear operator.

Eqn. (19) can be, therefore, written as follows:

$$L(U) + N(U) - f(r) = 0.$$
 (A3)

Using the homotopy technique, we construct a homotopy $U(r, p): \Omega \times [0,1] \to R$, which satisfies:

$$H(U, p) = (1 - p)[L(U) - L(U_0)] + p[A(U) - f(r)] = 0, \ p \in [0, 1], \ r \in \Omega,$$
 (A4)

or

$$H(U, p) = L(U) - L(U_0) + pL(U_0) + p[N(U) - f(r)] = 0,$$
 (A5)

where $p \in [0,1]$ is an embedding parameter, u_0 is an initial approximation for the solution of Eqn. (SA2), which satisfies the boundary conditions. Obviously, from Eqns. (A4) and (A5) we will have:

$$H(U,0) = L(U) - L(U_0) = 0,$$
 (A6)

$$H(U,1) = A(U) - f(r) = 0.$$
 (A7)

The changing values of p from zero to unity are just that of U(r, p) from $u_0(r)$ to u(r). In topology, this is called homotopy. According to HPM, we can first use the embedding parameter pas a small parameter and assume that the solution of Eqns. (A4) and (S5) as a power series in p:

$$V = U_0 + pU_1 + p^2U_2 + \dots$$
 (A8)

Setting p = 1, results in the approximation to the solution of Eqn. (A8)

$$U = \lim_{p \to 1} V = U_0 + U_1 + U_2 + \dots$$
 (A9)

The combination of the perturbation method and the homotopy method is called the homotopy perturbation method (HPM), which has eliminated limitations of the traditional perturbation techniques. The series Eqn. (A9) is convergent for more cases.

Appendix B: Analytical solution on nonlinear Eqns. (11)-(13) using homotopy perturbation method (HPM).

Consider the differential equation

$$\frac{dS}{dt} = -\beta S(t)I(t) - \nu S(t)$$
(B1)

$$\frac{dI}{dt} = \beta S(t)I(t) - \mu I(t)$$
(B2)

$$\frac{dR}{dt} = \mu I(t) + vS(t)$$
(B3)

The initial conditions are

$$S(0) = 0.5, I(0) = 0.3226, R(0) = 0.1774$$
 (B4)

The homotopy form the Eqns. (B1)-(B3) can be constructed as follows:

$$\left(1 - p\right)\left(\frac{dS}{dt} + vS(t)\right) + p\left(\frac{dS}{dt} + \beta S(t)I(t) + vS(t)\right) = 0$$
(B5)

$$(1-p)\left(\frac{dI}{dt} + \mu I(t)\right) + p\left(\frac{dI}{dt} - \beta S(t)I(t) + \mu I(t)\right) = 0$$
(B6)

where p is the embedding parameter and $p \in [0,1]$, The approximate solution of (B5) and (B6) are

$$S = S_0 + pS_1 + p^2S_2 + \dots$$
 (B7)

$$I = I_0 + pI_1 + p^2I_2 + \dots$$
 (B8)

Substituting Eqns. (B7) and (B8) into (B5) and (B6), gives the following result.

$$(1-p)\left(\frac{d}{dt}\left(S_{0}+pS_{1}+p^{2}S_{2}+...\right)+v\left(S_{0}+pS_{1}+p^{2}S_{2}+...\right)\right) + p\left(\frac{d}{dt}\left(S_{0}+pS_{1}+p^{2}S_{2}+...\right)+\beta\left(S_{0}+pS_{1}+p^{2}S_{2}+...\right)I(t)+v\left(S_{0}+pS_{1}+...\right)\right)=0$$
(B9)

$$(1-p)\left(\frac{d}{dt}(I_0+pI_1+p^2I_2+...)+\mu(I_0+pI_1+p^2I_2+...)\right) + p\left(\frac{d}{dt}(I_0+pI_1+...)-\beta(S_0+pS_1+...)(I_0+pI_1+...)+\mu(I_0+pI_1+...)+\mu(I_0+pI_1+...)\right) = 0$$
(B10)

Comparing the coefficients of like powers of p in Eqn. (B9) gives:

$$p^{0}: \frac{dS_{0}}{dt} + vS_{0} = 0 {(B11)}$$

$$p^{1}: \frac{dS_{1}}{dt} + vS_{1}(t) + \beta S_{0}(t)I_{0}(t) = 0$$
(B12)

The initial conditions are,

$$S_0(t=0) = 0.5, S_1(t=0) = 0$$
 (B13)

The solution of the Eqns. (B11) and (B12) are given by

$$S_0 = 0.5 e^{-vt} ag{B14}$$

$$S_1 = \frac{0.1613\beta}{\mu} \left(1 - e^{\mu t} \right) \left(e^{-t(\mu + \nu)} \right)$$
 (B15)

Comparing the coefficients of like powers of p in Eqn. (B10) gives:

$$p^{0}: \frac{dI_{0}}{dt} + \mu I_{0}(t) = 0$$
(B16)

$$p^{1}: \frac{dI_{1}}{dt} + \mu I_{1}(t) - \beta S_{0}(t)I_{0}(t) = 0$$
(B17)

The initial conditions are,

$$I_0(t=0) = 0.3226, I_1(t=0) = 0$$
 (B18)

The solution of the Eqns. (B16) and (B17) are given by

$$I_0(t) = 0.3226e^{-\mu t} \tag{B19}$$

$$I_1(t) = \frac{0.1613 \,\beta}{v} \left(e^{vt} - 1 \right) \left(e^{-t(\mu + v)} \right) \tag{B20}$$

The concentration can be obtained by solving the (B3) as follows:

$$R(t) = \frac{1}{v\mu} \left[v e^{-vt} \left(0.1613\beta - 0.5\mu \right) - 0.4839\mu e^{-\mu t} + 0.1613\beta \left(e^{-t(\mu + v)} \right) \left(\mu - v \right) + v\mu \right]$$
 (B21)

With the use of these two iterations only, we obtain an approximate solution for the concentration given by

$$S(t) \approx S_0 + S_1 = 0.5e^{-\nu t} + \frac{0.1613\beta}{\mu} \left(1 - e^{\mu t} \right) \left(e^{-t(\mu + \nu)} \right)$$
 (B22)

$$I(t) \approx I_0 + I_1 = 0.3226 e^{-\mu t} + \frac{0.1613 \,\beta}{v} \left(e^{vt} - 1 \right) \left(e^{-t(\mu + v)} \right)$$
 (B23)

$$R(t) \approx \frac{1}{v\mu} \left[v e^{-vt} \left(0.1613\beta - 0.5\mu \right) - 0.4839\mu e^{-\mu t} + 0.1613\beta \left(e^{-t(\mu+v)} \right) (\mu-v) + v\mu \right]$$
 (B24)

Appendix B. Matlab program for the numerical solution of differential Eqns. (11) – (13)

```
function graphmain3
options = odeset('RelTol',1e-6,'stats','on');
X0=[0.5;0.3226;0.1774];
tspan=[0,100];
tic
[t,X]=ode45(@TestFunction,tspan,X0,options);
toc
figure
hold on
plot(t,X(:,1),'*');
plot(t,X(:,2),'.');
plot(t,X(:,3),'+');
legend('x1','x2','x3','x4')
ylabel('x')
xlabel('t')
return
```

Theoretical Model for the Control of Lassa Fever and Transmission Using Homotopy Perturbation Method

```
\begin{split} & \text{function } [dx\_dt] = TestFunction(t,x) \\ & b = 0.5, v = 0.1, m = 0.7; \\ & dx\_dt(1) = -(b*x(1)*x(2) + v*x(1)); \\ & dx\_dt(2) = b*x(1)*x(2) - m*x(2); \\ & dx\_dt(3) = m*x(2) + v*x(1); \\ & dx\_dt = dx\_dt'; \\ & \text{return} \end{split}
```