Mathematical impact of SIR network model on varying size of the human population

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Abstract: This manuscript concerns mathematical modeling and simulation of SIR network in a heterogeneous population with imperfect vaccination. In this work, a modified susceptible- infected-recovered system that includes a homogeneous network is modelled in the form of differential equations. The nominal analytical result of SIR concentration can be obtained using the HAM for different values of relevant parameters. The result of the analysis is compared with the numerical and previous results from an existing work in literature.

Key words: Mathematical modelling; Asymptotic tool; Simulations; Birth and Death rate

1. Introduction

The study of SIR model network deals with the factors responsible for the spread of disease over space and time. [1] did many moved mathematical arguments in the theory of epidemic during 1900-1930. They found that if the disease was above threshold size of susceptibility, the spread of disease would occur in the population. The spread of infection with different and causing factors is modeled to eliminate the risk of the epidemic [2–4]. Many research attempts were made on the dynamics of the nonlinear model to control the incidence rate [5–7]. The global dynamics of an SEIS epidemic model was utilized to know about transport related infection and exposure [8, 9]. Recently SIR network model has been used to assess the spread of disease with imperfect vaccination in a heterogeneous population. The paper aims to explain the spread of disease under existence and non-existence of limit cycles with the global steady-state model and the result of SIR network in the heterogeneous population were simulated. This paper is orderly explained as below, secondly combination SIR epidemic model, thirdly non-perturbation analysis of non-disease equilibrium. Fourthly, the results are analyzed using asymptotic tools. Fifthly, the numerical analyses are done with same sufficient conditions. Sixthly, the results are discussed with numerical simulation.

2. Mathematical problem formulation

The non-linear differential equation describing the SIR network with the heterogeneous population with imperfect vaccination can be represented as[9]:

$$\frac{dS}{dt} = (1-p)bN - \beta <k> SI/N - (\mu + \upsilon)S + \varepsilon R \tag{1}$$

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$$\frac{dI}{dt} = \beta < k > SI/N + \sigma\beta < k > IR/N - (\mu + \sigma + k)I \tag{2}$$

$$\frac{dR}{dt} = kI + \beta bN + \varepsilon - \mu R - \sigma\beta < k > IR/N - \varepsilon R \tag{3}$$

where S is susceptible, I is infectious, R is the recovered,α is the disease introduced mortality rate, b is the population's natural birth rate, μ is the population natural death rate $< k >$ is the average network connectivity.The disease distribution of three category transmission is illustrated in Figure 1. SIRS model with homogeneous networks by considering two hypotheses is established:

1.Homogeneity: Each network node has the same degree $k_i \approx < k >, < k >$ as the average network connectivity that ignores the heterogeneity of node degrees.

2. Homogenic mixture: Infection strength is proportional to population density. The differential equation of the total population (1) shall be:

$$\frac{dN}{dt} = \frac{d}{dt}(S + I + R) = bN - \mu N - \alpha I \tag{4}$$

The non-linear differential equation is formulated to form with dimension-less variables as below,

$$x = S/N, y = I/N, z = R/N \tag{5}$$

$$\frac{dx}{dt} = (1 - p)b - \beta < k > xy - (b + v)x + \varepsilon z + \alpha xy \tag{6}$$

$$\frac{dy}{dt} = \beta < k > xy + \sigma\beta < k > yz - (b + \alpha + k)y + \alpha y^2 \tag{7}$$

$$\frac{dz}{dt} = ky + pb + vx - bz - \sigma\beta < k > yz - \varepsilon z + \alpha yz \tag{8}$$

where x, y, z is the concentration of the populations, It can easily be checked with $x + y + z = 1$ and

$$\frac{dx}{dt} + \frac{dy}{dt} + \frac{dz}{dt} = b - b(x + y + z) - \alpha y + \alpha y(x + y + z) = 0 \tag{9}$$

The initial conditions are provided

$$x(0) = 0.01, y(0) = 0.99, z(0) = 0 \tag{10}$$

3. Asymptotic Method Problem Result

HAM is a non- perturbative analytical method to obtain infinite power series solutions in the fields of science and engineering. It has an ability to adjust and convergent the solution with control parameters in nonlinear differential forms[10–16]. HAM is a good technique easy to handle and gives accurate results.

4. Analytical expression of concentrations of susceptible, infectious and recovered

The normalized concentrations of the susceptible, infectious and recovered are presented in Equations (6)(7)(8) defines the initial value problem [9]. [10–16] method is used to provide approximate solutions to non - linear Equations(6)(7)(8).(Appendix A), we can derive the solution of susceptible, infectious and recovered by solving the Equations (6)(7)(8). The analytical expression of dimensionless concentrations is of the solution form:

$$x(t) = 0.01e^{-(b+v)t} + [\frac{h(1-p)b}{b+v} - \frac{\beta <k> h0.01*0.99}{-(b+\alpha+\eta)} - \frac{0.01*0.99\alpha h}{(b+\alpha+\eta)}]e^{-(b+v)t} - (1+h)(b+v)0.01e^{-(b+v)t}t$$
$$- \frac{h(1-p)b}{b+v} + \frac{\beta <k> h0.01*0.99e^{-(2b+v+\alpha+\eta)t}}{-(b+\alpha+\eta)} - \frac{\alpha h0.01*0.99e^{-(2b+v+\alpha+\eta)t}}{-(b+\alpha+\eta)} - \frac{\varepsilon h(b+\varepsilon)t}{b+v}$$

$$(11)$$

$$y(t) = 0.99e^{-(b+\alpha+\eta)t} + [\frac{0.01*0.99\beta <k> h}{-(b+v)} + \frac{(0.99)^2\alpha h}{-(b+\alpha+\eta)}]e^{-(b+\alpha+\eta)t} - (1+h)$$
$$*0.99e^{-(b+\alpha+\eta)t}(b+\alpha+\eta)t + (1+h)0.99e^{-(b+\alpha+\eta)t}t - \frac{\beta <k> h*0.01e^{-(b+v)t}*0.99e^{-(b+\alpha+\eta)t}}{-(b+v)}$$
$$- \frac{\alpha h[0.99e^{-(b+\alpha+\eta)t}]^2}{-(b+\alpha+\eta)} + 6\beta <k> *0.99e^{-(b+\alpha+\eta)t}(b+\varepsilon)t^2h$$

$$(12)$$

$$z(t) = -(b+\varepsilon)t + [\frac{0.99h\eta}{\varepsilon-\alpha-\eta} + \frac{pbh}{b+\varepsilon} + \frac{0.01vh}{\varepsilon-v} + (1+h)]e^{-(b+\varepsilon)t}$$
$$- \frac{0.99h\eta e^{-(b+\alpha+\eta)t}}{\varepsilon-\alpha-\eta} - \frac{pbh}{b+\varepsilon} - \frac{0.01vhe-(b+v)t}{\varepsilon-\alpha-\eta} - (1+h) - b(1+h)t - c(1+h)t$$
$$- \frac{0.99\sigma\beta <k> e^{-(b+\alpha+\eta)t}(b+\varepsilon)th}{\varepsilon-\alpha-\eta} + \frac{0.99\alpha e^{-(b+\alpha+\eta)t}(b+\varepsilon)th}{\varepsilon-\alpha-\eta}$$

$$(13)$$

5. Numerical Analysis

In this section, we will implement the differential equations solution (11)(12)(13). Parameters used in the model will be selected as shown in Table 1. The previous reference parameters as shown in the table were utilized for analysis.. Numerically, nonlinear differential equations(6)(7)(8) could be solved to get an initial condition with the help of function pdex in MATLAB. The simulation results for various parameters were compared with dimension-less concentrations of susceptible, infectious and recovered results. Satisfactory results are observed. Appendix C&D denote Mat lab program.

6. Result and Discussions

Equations (11)(12)(13)represent the new and closed analytical notation of susceptible, infectious and recovered concentration for all experimental values of parameters.Figure 2 and Figure 3 denote susceptible concentration increases from initial values gradually and attains the steady-state value for all time and parameters value. Infectious concentration variation with respect to time for different parameters, infectious gradually decreases from its initial value and reaches the steady-state value and the recovered concentration increases absurdly and reaches a maximum and steady-state value. Our analytical expression gives excellent agreement with the numerical solution. Moreover, the analytical expression is compared with the numerical result in Table 2,

Table 3,Table 4 for experimental values of $p = 0.5, b = 0.011, \beta = 0.2, < k >= 6, \upsilon = 0.73, \varepsilon = 0.05, \alpha = 0.06. \sigma = 0.05, k = 0.073$

7. Vaccination and changing size of population

Effect of vaccination ratio in the size of the population was predicted. HAM is used to analyse the non-differential equations by solving the approximate analytical solutions. The analytical result is useful to understand the effect of the model. This solution procedure can easily be extended to all types of combined non - linear equation system with different complex boundary conditions in biological processes. This analytical result helps to better understand the model. Through numerical experiments, we have been able to gain further insight into the thresholds for the extinction of diseases that can contribute to the critical knowledge of disease control.

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Appendix A

Results of HAM analysis

The common solution of nonlinear differential equations is represented in equations (11)(12)(13) using asymptotic tools. The homotopy is formulated to find the solution of eqn. (11) as below.

$$(1-p)(\frac{dx}{dt} + (b+v)x) = ph(\frac{dx}{dt} - (1-p)b + \beta < k > xy + (b+v)x - \varepsilon z - \alpha xy) \tag{14}$$

The initial approximate solution of (14) is represented as (15).

$$x = x_0 + px_1 + p^2 x_2 + \ldots \tag{15}$$

The main homotopy parameter p is primarily introduced in this method with the range of $0-1$. If the equation becomes in a linear form if it transforms into a numerical form. Collecting the coefficient for the above equations, we obtain

$$(1-p)\Big(\frac{d(x_0 + px_1 + p^2 x_2 + \ldots) + (b+v)(x_0 + px_1 + p^2 x_2 + \ldots)}{dt}\Big)$$

$$= ph\Big(\frac{d(x_0 + px_1 + \ldots)}{dt} - (1-p)b + \beta < k > (x_0 + px_1 + \ldots)(y_0 + py_1 + \ldots) +$$

$$(b+v)(x_0 + px_1 + \ldots) - \varepsilon(z_0 + pz_1 + \ldots) - \alpha(x_0 + px_1 + \ldots)(y_0 + py_1 + \ldots)\Big) \tag{16}$$

Comparing similar power coefficients of p , we have

$$P^0 : \frac{dx_0}{dt} + (b+v)x_0 = 0 \tag{17}$$

$$P^1 : \frac{dx_1}{dt} + (b+v)x_1 = (1+h)\frac{dx_0}{dt} + (1+h)(b+v)x_0 - h(1-p)b + \beta < k > x_0 y_0 h - \varepsilon z_0 h - \alpha x_0 y_0 h \tag{18}$$

Solving the Equations(17) and (18):

$$x_0(t) = 0.01 e^{-(b+v)t} \tag{19}$$

$$x_1(t) = \Big[\frac{h(1-p)b}{b+v} - \frac{\beta < k > h0.01*0.99}{-(b+\alpha+\eta)} - \frac{0.01*0.99\alpha h}{(b+\alpha+\eta)}\Big] e^{-(b+v)t}$$

$$-(1+h)0.01e^{-(b+v)t}(b+v)t + (1+h)(b+v)0.01e^{-(b+v)t} - \frac{h(1-p)b}{b+v}$$

$$+\frac{\beta < k > h0.01*0.99e^{-(2b+v+\alpha+\eta)t}}{-(b+\alpha+\eta)} - \frac{\alpha h0.01*0.99e^{-(2b+v+\alpha\eta)t}}{-(b+\alpha+\eta)} - \frac{\varepsilon h(b+\varepsilon)t}{b+\varepsilon} \tag{20}$$

Few iterative processes, the approximate solution of equation(11) could be obtained. Based on HAM procedure, the approximate solution can be concluded as below form.

$$x(t) \cong x_0(t) + x_1(t) \tag{21}$$

After put equation(19)and equation(20)in equation(21) the approximate solution can be described in equation(11) in the text as a approximate solution. Similarly, we get the approximate analytical solutions is in the form described in (12)(13).

Appendix B

Convergent region of h

The auxiliary parameter h represents a different level of convergence and accuracy in the equation(11). Distribution of U and U_1 against h is the convergence region for the respective function. The common region between $u(t)$ and its derivatives is known as the overall convergence region. The h-curves of $u(0.5)$ and u' (0.5) are traced in Figure 4 (a) and (b) respectively to study the influence of h on the convergence of the solution. These figures clearly indicate that the valid h region is around $-1 < h < 0.8$. Similarly, the value of the convergence control parameter h can be found for different values of constant parameters.

Appendix C

MATLAB programme for the numerical solution of non - linear differential equations(6)(7)(8)

```
function main
options= odeset ('RelTol',1e-6,'Stats','on');
r=0.01;
m=0.99;
n=0
Xo = [r, m, n];
tspan = [0,500];
xspan = [0,1];
tic
[t, X] = ode45(@TestFunction, tspan, Xo, options);
toc
figure
plot(t,X(:,1),t,X(:,2),t,X(:,3))
ylabel('x')
xlabel('t')
return
function[dx_dt] = TestFunction(t, x)
k=6;
b=0.011;
p=0.5;
alpha=0.06;
v=0.73;
B=0.2;
l=0.073;
A=0.05;
e=0.05;
dx_dt(1) =(1-p)*b-B*k*x(1)*x(2)-(b+v)*x(1)+e*x(3)+alpha*x(1)*x(2);
```

dx_dt(2) =B*k*x(1)*x(2)+A*B*k*x(2)*x(3)-(b+alpha+l)*x(2)+alpha*(x(2))^2;

dx_dt(3) =l*x(2)+p*b+v*x(1)-b*x(3)-A*B*k*x(2)*x(3)-e*x(3)+alpha*x(2)*x(3);

dx_dt = dx_dt';

return

Appendix D

MATLAB programme for the numerical solution of non - linear differential equations (6)(7)(8)

```
function main
options= odeset('RelTol',1e-6,'Stats','on');
r=0.99;
m=0.01;
n=0
Xo = [r, m, n];
tspan = [0,300];
xspan = [0,1];
tic
[t, X] = ode45(@TestFunction, tspan, Xo, options);
toc
figure
plot(t,X(:,1),t,X(:,2),t,X(:,3))
ylabel('x')
xlabel('t')
return
function [dx_dt]= TestFunction(t,x)
k=6;
b=0.011;
p=0.3;
alpha=0.06;
v=0.27;
B=0.2;
l=0.073;
A=0.1;
e=0.05;
dx_dt(1) =(1-p)*b-B*k*x(1)*x(2)-(b+v)*x(1)+e*x(3)+alpha*x(1)*x(2);
dx_dt(2) =B*k*x(1)*x(2)+A*B*k*x(2)*x(3)-(b+alpha+l)*x(2)+alpha*(x(2))^2;
dx_dt(3) =l*x(2)+p*b+v*x(1)-b*x(3)-A*B*k*x(2)*x(3)-e*x(3)+alpha*x(2)*x(3);
dx_dt = dx_dt';
return
```

Figure 1. Schematic disease distribution of three categories susceptible individuals (S),infectious individuals (I) and recovered individuals (R).
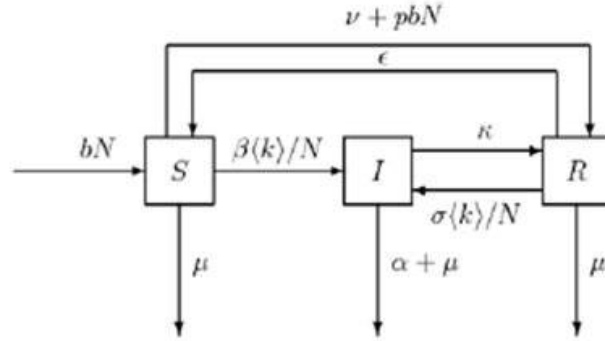

Figure 2. Parameter experimental value susceptible individuals (S) infectious individuals (I) and recovered persons (R).
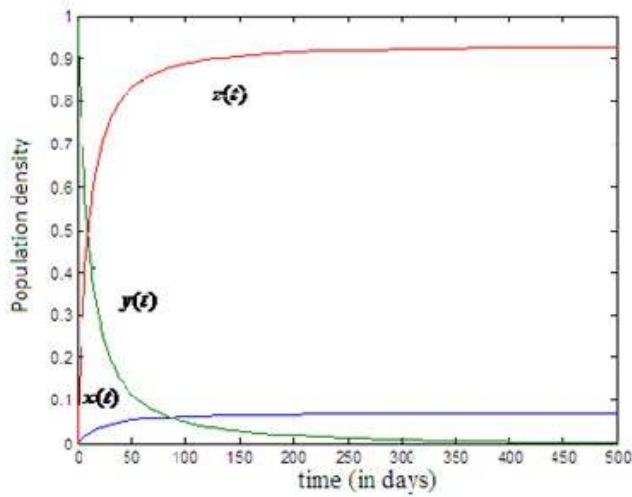
Figure 3. The concentration of susceptible, infectious and recovered population versus the time in days with experimental values of parameters. The curves are plotted for using the equations(11)(12)(13) (—).
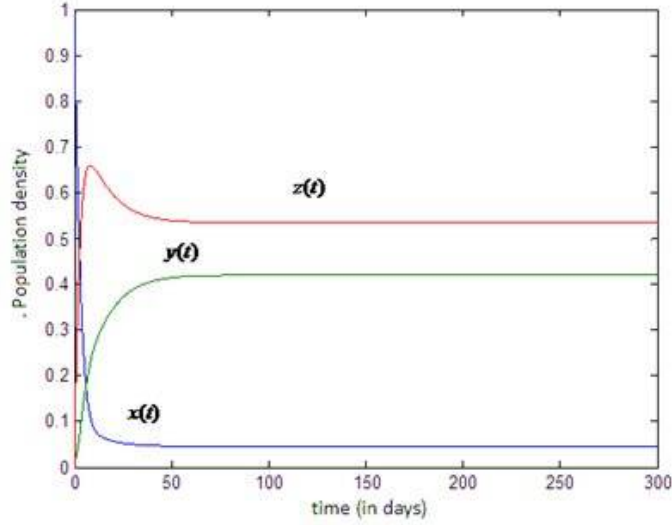

Figure 4. Convergence region h curves.
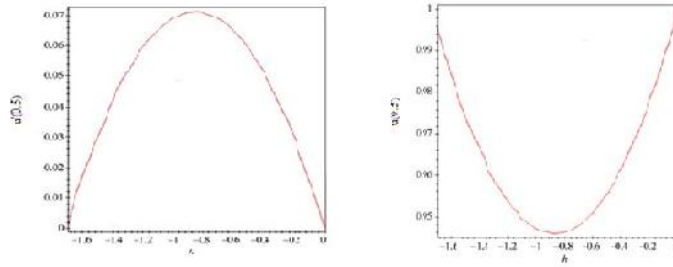
Table 1. Value of Parameters in simulation analysis.

Parameter	Value	Data Source
b	0.012	[10]
p	0.950	[11]
α	0.000	[12]
υ	0.270	[15]
β	0.060	[13]
σ	0.010	[11]
ϵ	0.050	[14]
K	0.073	[9]
$< k >$	6.000	[9]

Table 2. Comparison of analytical result with numerical result concentration $x(t)$ for the parameter value.

t	Numerical simulation	Analytical solution using HAM	Error (%)
0	0.010	0.010	0.000
50	0.054	0.055	0.183
100	0.062	0.061	1.726
150	0.066	0.065	0.214
200	0.067	0.067	0.179
250	0.068	0.068	0.219
300	0.069	0.068	0.219
350	0.069	0.070	0.948
400	0.069	0.069	0.000
450	0.069	0.069	0.000
500	0.070	0.070	0.115

Table 3. Comparison of analytical result with numerical result concentration $y(t)$ for the parameters value.

t	Numerical simulation	Analytical solution using HAM	Error (%)
0	0.990	0.990	0.000
50	0.115	0.115	0.087
100	0.050	0.049	0.202
150	0.029	0.029	0.347
200	0.019	0.019	0.000
250	0.013	0.013	0.752
300	0.010	0.010	0.101
350	0.008	0.008	0.130
400	0.006	0.006	0.000
450	0.004	0.004	0.000
500	0.004	0.003	0.299

Table 4. Comparison of analytical results with numerical result concentration for the parameter's value.

t	Numerical simulation	Analytical solution using HAM	Error (%)
0	0.000	0.000	0.000
50	0.831	0.831	0.012
100	0.888	0.887	0.113
150	0.906	0.905	0.022
200	0.914	0.914	0.011
250	0.919	0.919	0.011
300	0.922	0.922	0.011
350	0.924	0.924	0.000
400	0.925	0.925	0.000
450	0.926	0.926	0.000
500	0.927	0.926	0.000