Modification in the Logistic Growth due to Chronic Infectious Disease

Nareshkumar C. Chavda[1]
Assistant Professor, Government Engineering College, Dahod
Email: nareshc.chavda@gmail.com
Ashish A Prajapati[2]
Assistant Professor, Government Engineering College, Dahod
Email: ashishprajapati14@gmail.com
Ramesh S Damor[3]
L. D. College of Engineering, Ahmedabad
Email : rameshsvnit2010@gmail.com

Abstract

A new generalized version of logistic growth is proposed to study the dynamics of logistically growing population with a chronic infection in the population. A modification is made due to the change in the birth and death rates in the infectious population with chronic disease. A nonlinear mathematical model is proposed for each of the cases when growth rate (birth minus death rate) in the infected class is positive and negative. There are three nonnegative equilibrium points out of which two are boundary equilibrium points in which there is no disease and the endemic equilibrium in which disease remains present. The local as well as global stability depends on the basic reproduction number R_0. The disease free equilibrium is globally stable if basic reproduction number is smaller than one. The endemic equilibrium point exists and become globally stable when basic reproduction number exceeds one.

Keywords: Logistic growth; carrying capacity; infectious disease; basic reproduction number; stability.

DOI Number: 10.48047/nq.2016.14.3.888 **NeuroQuantology 2016; 14(3):647-661**

1. Introduction

The logistic growth model for self limiting population growing with constant intrinsic growth rate (birth – death) and carrying capacity K is given by

$$\frac{dN}{dt} = g\left(1-\frac{N}{K}\right)N$$

In the presence of a chronic disease, the birth rate decreases and death rate increases. These changes play a vital role in the dynamics of population that cannot be ignored in case of diseases such as HIV and TB. So, let us divide the total population of interest in two different classes: susceptible class S without infection and the other class I with infection. Clearly, these two classes are mutually disjoint classes and they together include total population N. Let $S(t)$ be the total number of individuals susceptible to disease and $I(t)$ be the total number of individuals infected with the disease. If the large number of individuals is infected with disease for a long time then it is necessary to consider different growth rates for the two classes of susceptible and infective because of the changes in birth and death rates due to the disease. Let $g_0 = B_0 - D_0 > 0$ and $g_1 = B_1 - D_1 > 0$ be the positive constants. Here, B_0 and D_0 are the birth and death rates in susceptible class while B_1 and D_1 are the birth rate and death rate respectively in infected class. In case of no vertical transmission, it is assumed that infectives give birth to susceptible. Then in the isolated compartments, the dynamics of S and I is governed by the following two equations respectively

$$\frac{dS}{dt} = (B_0 - D_0)S\left(1-\frac{S+I}{K}\right) + B_1 I\left(1-\frac{S+I}{K}\right), \frac{dI}{dt} = -D_1 I\left(1-\frac{S+I}{K}\right)$$

Or $$\frac{dN}{dt} = \left(g_0 S + g_1 I\right)\left(1-\frac{N}{K}\right)$$

However, in case of vertical transmission, the infectives give birth to infectives. Accordingly the dynamics is governed by

$$\frac{dS}{dt} = (B_0 - D_0)S\left(1-\frac{S+I}{K}\right), \frac{dI}{dt} = (B_1 - D_1)I\left(1-\frac{S+I}{K}\right)$$

Or $$\frac{dN}{dt} = \left(g_0 S + g_1 I\right)\left(1-\frac{N}{K}\right)$$

In a chronic case the birth rate in the infectives can go at the extent to zero, while the death rate increases in the infected class. Accordingly, it is possible that g_1 is negative. In such a case, decay in infected class will be proportional to the number of persons in the class and the self limiting process is meaningless. The logistic growth for infectives is not considered:

Or $$\frac{dN}{dt} = g_0 S\left(1-\frac{N}{K}\right)+g_1 I$$

As per the report of World Health Organization(WHO) TB is the seventh most morbidity – causing disease in the world and will remain on the same position up to 2020. It is the second largest cause of death from an infectious agent after HIV/AIDS in developing countries. The World Health Organization (2009) reported 9.3 million incident cases and 1.8 million TB-related deaths worldwide in 2007 alone. It is responsible for approximately 1.6 million deaths each year [1-12]. So to study the dynamics of logistically growing population it is necessary to study the effects and future of such diseases like tuberculosis, HIV and some other infectious diseases in human population. Also, the disease may come into a child by birth and this may also play a vital role to change the population-disease dynamics. It is observed that if sufficient care/treatment is not taken HIV/AIDS comes into a child by birth while some other infection may not come into a child by birth.

This study is restricted for the case of no vertical transmission (Applicable for TB in the human population) so it can be assumed that new borne in any of the two classes is without disease and hence all births increase the population of the susceptible class. Before proceeding further, it is necessary to specify certain required assumptions for the construction of the Mathematical model.

Based on epidemiological status, the population is divided into two disjoint classes: susceptible and infected. Let S and I be the number of persons in class susceptible class and infected class respectively. Let the total population size $N = S + I$. It is assumed that disease transmission occurs via random mixing between members in the susceptible class and infected class. We denote the sufficient contact rates for the disease by α. Some members of infected class are also cured and recovered at a rate L and become susceptible again. Let D_0 be the natural death rate in the population and D_1 be the increased death rate due to the disease. Let B_0 be the natural birth rate in the susceptible class and B_1 be the decreased birth rate due to the disease in infected class. All parameters are assumed to

be nonnegative. Keeping these assumptions in mind let us come back to equation (2.2) in case of $g_1 > 0$ and to equation (2.3) in case of $g_1 < 0$ to proceed further in the direction of constructing a model for each of the cases. In equation (2.2), the term $B_0\left(1-\frac{N}{K}\right)S$ is for new births in the susceptible class. So it is in the dynamics of susceptible while the term $B_1\left(1-\frac{N}{K}\right)I$ shows birth in the infective class. But because of no vertical transmission these new borne are not infective but they are susceptible so this term will be a part of the equation showing the growth of susceptible. While the term $D_0\left(1-\frac{N}{K}\right)S$ shows the deaths in the infected class. The term αSI showing spread of infection. The term LI is because of treatment, infective are treated and cured at the rate of L and they become susceptible again at the rate of L.

Mathematically, for $g_0 > 0$ and $g_1 > 0$

$$\frac{dS}{dt} = \left(1-\frac{N}{K}\right)\left(B_0 S + B_1 I\right) + LI - \alpha SI - \left(1-\frac{N}{K}\right)D_0 S \tag{2.4}$$

$$\frac{dI}{dt} = \alpha SI - LI - \left(1-\frac{N}{K}\right)D_1 I \tag{2.5}$$

It is clear that sum of these two equations (2.4) and (2.5) shows growth of the total population.

Now, for case of $g_0 > 0$ and $g_1 < 0$

$$\frac{dS}{dt} = \left(1-\frac{N}{K}\right)B_0 S + B_1 I + LI - \alpha SI - \left(1-\frac{N}{K}\right)D_0 S \tag{2.6}$$

$$\frac{dI}{dt} = \alpha SI - LI - D_1 I \tag{2.7}$$

For non-dimensional form of the system, defining dimensionless state variables and parameters as

$$n = \frac{N}{K},\ s = \frac{S}{K},\ i = \frac{I}{K},\ t = g_0 T,\ \gamma = \frac{L}{g_0}, a = \frac{\alpha K}{g_0},\ b_0 = \frac{B_0}{g_0},\ b_1 = \frac{B_1}{g_0}$$

Clearly, $b_0 - d_0 = 1$

$$\frac{ds}{dt} = \left(1-n\right)\left(s + b_1 i\right) + \gamma i - asi \tag{2.8}$$

$$\frac{di}{dt} = asi - \gamma i - d_1\left(1-n\right)i \tag{2.9}$$

Using the fact that $n = s + i$ the system (2.8) and (2.9) can be written as

$$\frac{ds}{dt} = (1 - s - i)(s + b_1 i) + \gamma i - asi \tag{2.10}$$

$$\frac{di}{dt} = asi - \gamma i - d_1 (1 - s - i) i \tag{2.11}$$

Similarly for $g_0 > 0$ and $g_1 < 0$

$$\frac{ds}{dt} = (1 - s - i) s + b_1 i + \gamma i - asi \tag{2.12}$$

$$\frac{di}{dt} = asi - \gamma i - d_1 i \tag{2.13}$$

2.1. Preliminary analysis.

In this section, it is proved that all solutions of the system (2.10) to (2.11) or system (2.12) to (2.13) with positive initial data will remain positive for all $t > 0$.

Theorem 2.1 The solution $(s(t), i(t))$ of the model is bounded for both the cases

(A) $g_0 > 0$ and $g_1 > 0$ (B) $g_0 > 0$ and $g_1 < 0$.

Proof: Case (A) $g_0 > 0$ and $g_1 > 0$

Adding equation (2.10) and (2.11) and using the fact

$$\frac{dn}{dt} = (1 - n)(s + (b_1 - d_1) i)$$

Taking $g = \max(1, (b_1 - d_1))$

$$\frac{dn}{dt} \le g (1 - n)(s + i)$$

$$\frac{dn}{dt} \le g (1 - n) n$$

Clearly, $\limsup_{t \to \infty} n(t) \le 1$ (2.14)

Thus, the solution of the system (2.10)-(2.11) is bounded.

Case (B) $g_0 > 0$ and $g_1 < 0$

Adding equation (2.12) and (2.13) and using the fact

$$\frac{dn}{dt} = (1-n)\,s + (b_1 - d_1)i$$
$$\leq (1-n)\,(s)$$
$$\leq (1-n)\,(n)$$

Clearly, $\limsup_{t\to\infty} n(t) \leq 1$ (2.15)

This completes the proof of the theorem.

Lemma 1 For $s(0) = s_0 > 0,\ i(0) = i_0 > 0$, the solution $(s(t),\ i(t))$ of the system (2.10) - (2.11) or (2.12) - (2.13) remains in the non-negative quadrant for all $t > 0$.

The proof is straight forward application of Nagumo's theorem.

3. Equilibrium points and stability analysis

In this section, equilibrium points are obtained and their stability are checked

3.1. Equilibrium points.

The system (2.10) - (2.11) has three non-negative equilibrium points namely,

(1) The disease free equilibrium points $E_0(0,\ 0)$ existence of E_0 is obvious.

(2) The disease free equilibrium points $E_{01}(1, 0)$ existence of E_{01} is obvious.

(3) The endemic equilibrium point $E_0(\frac{\gamma}{a},\ 1-\frac{\gamma}{a})$, exists when

$$R_0 = \frac{\gamma}{a} > 1. \qquad (3.1)$$

Here, the threshold quantity R_0 is the basic reproduction number for the system (2.10)-(2.11).

The model (2.12) - (2.13) has three non-negative equilibrium points namely,

(1) The disease free equilibrium points $P_0(0,\ 0)$ P_0 existence of P_0 is obvious.

(2) The disease free equilibrium points $P_{01}(1,\ 0)$ P_{01} existence of P_{01} is obvious

(3) The endemic equilibrium point $P_{01}(\bar{s},\ \bar{i})$, with

$$\bar{s} = \frac{d_1+\gamma}{a},\ \bar{i} = \frac{(a-d_1-\gamma)(d_1+\gamma)}{a\left((d_1+\gamma)-a(b_1-d_1)\right)}.$$

The point $P_{01}(\bar{s},\ \bar{i})$ exists if

$$R_{01} = \frac{a}{d_1 + \gamma} > 1 \tag{3.2}$$

Here, the threshold quantity R_{01} is the basic reproduction number for the system (2.12)-(2.13).

3.2. Local stability of the equilibrium points

Theorem 3.1A For the system (2.12)-(2.13),

(i) The equilibrium point $E_0(0, 0)$ is a saddle point.

(ii) The equilibrium point $E_{01}(1,0)$ is locally asymptotically stable if $R_0 < 1$.

(iii) The equilibrium point $E_1(\frac{\gamma}{a}, 1-\frac{\gamma}{a})$ is locally asymptotically stable if $R_0 > 1$.

Proof: (i) The variation matrix of the system (2.10)-(2.11) is computed around E_0 as,

$$M(E_0) = \begin{bmatrix} 1 & b_1 + \gamma \\ 0 & -(d_1 + \gamma) \end{bmatrix}$$

The eigenvalues are $1, -(d_1 + \gamma)$.

Therefore, the point $E_0(0, 0)$ is a saddle point.

(ii) The variation matrix of the system (2.12)-(2.13) is computed around E_{01} as,

$$M(E_{01}) = \begin{bmatrix} -1 & -(\alpha + 1 - \gamma) \\ 0 & \alpha - \gamma \end{bmatrix}$$

The eigenvalues are $-1,\ \alpha - \gamma$ which are negative when $R_0 = \frac{\alpha}{\gamma} < 1$.

Thus, it is clear that E_{01} is locally asymptotically stable (LAS) provided $R_0 < 1$ (basic reproductive number associated with the disease is less than one) and the disease dies out and under this condition the other equilibrium point E_1 does not exist. Hence, the disease free equilibrium E_{01} is locally asymptotically stable if $R_0 < 1$.

To determine the local stability of $E_1(\frac{\gamma}{a}, 1-\frac{\gamma}{a})$, the following variation matrix of the system (2.13)-(2.14) is computed around E_1 as

$$M(E_1)=\begin{bmatrix} -\dfrac{\alpha^2-\alpha(b_1-\gamma)+\gamma(1-b_1)}{\alpha} & \dfrac{-b_1(\alpha-\gamma)+\gamma}{\alpha} \\ \dfrac{(\alpha-\gamma)(\alpha+d_1)}{\alpha} & \dfrac{-d_1(\alpha-\gamma)}{\alpha} \end{bmatrix}$$

The characteristic equation corresponding to the above matrix is given by

$$\lambda^2+\left(\frac{\alpha^2+\alpha(b_1-d_1-\gamma)+(1-b_1+d_1)\gamma}{\alpha}\right)\lambda+\frac{(\alpha-\gamma)(\alpha(b_1-d_1)+(1-b_1+d_1)\gamma)}{\alpha}=0$$

The eigenvalues of the matrix are

$$-(\alpha-\gamma),\ (b_1-d_1)\left(-1+\frac{\gamma}{\alpha}\right)-\frac{\gamma}{\alpha}$$

Clearly, the eigenvalues are negative when basic reproductive number $R_0>1$.

Thus, it is clear that E_1 is locally asymptotically stable (LAS) provided $R_0>1$. The basic reproductive number associated with the disease exceeds more than one and thus the disease will persist in the population and under this condition the other equilibrium point E_0 is unstable. Thus, the endemic equilibrium is locally asymptotically stable if it exists. □

Theorem 3.1B For the system (2.13)-(2.14)

(i) The equilibrium point $P_0(0,\ 0)$ is a saddle point.

(ii) The equilibrium point $P_{01}(1,0)$ is locally asymptotically stable if $R_{01}<1$.

(iii) The equilibrium point $P_1(\bar{s},\ \bar{i})$ is locally asymptotically stable if $R_{01}>1$.

Proof: (i) Proof is same as the proof of (i) of (3.1A)

(ii) The variation matrix of the system (2.13)-(2.14) is computed around P_{01} as

$$M(P_{01})=\begin{bmatrix} -1 & -(\alpha+1-b_1-\gamma) \\ 0 & \alpha-d_1-\gamma \end{bmatrix}$$

The characteristic equation corresponding to the above matrix is given by

$$\lambda^2+(1+d_1+\gamma-\alpha)\lambda+(d_1+\gamma-\alpha)=0.$$

The eigenvalues are $-1,\ \alpha-d_1-\gamma$ which are negative when $R_{01}=\dfrac{\alpha}{d_1+\gamma}<1.$

Hence, the equilibrium point P_{01} is locally asymptotically stable (LAS) provided $R_{01}<1$ (basic reproductive number associated with the disease is less than one) and thus the disease dies out and

under this condition the other equilibrium point P_{01} does not exist. Thus, the disease free equilibrium P_{01} is locally asymptotically stable if $R_{01}<1$ and it is unstable if $R_{01}<1$.

(iii) The variation matrix of the system (2.13)-(2.14) is computed around the point $P_1(\bar{s},\bar{i})$ is

$$M(P_1)=\begin{bmatrix} -\dfrac{\alpha^2(b_1+\gamma)-\alpha(2b_1-d_1+\gamma)(d_1+\gamma)+(d_1+\gamma)^2}{\alpha\left((d_1+\gamma)-\alpha(b_1-d_1)\right)} & \dfrac{\left(\alpha(b_1-d_1)-d_1-\gamma\right)}{\alpha} \\ \dfrac{(\alpha-d_1-\gamma)(d_1+\gamma)}{\alpha\left((d_1+\gamma)-\alpha(b_1-d_1)\right)} & 0 \end{bmatrix}$$

The characteristic equation corresponding to the above matrix is given by

$$\lambda^2+a_0\lambda+a_1=0;$$

$$a_0=\frac{\alpha^2(b_1+\gamma)-\alpha(2b_1-d_1+\gamma)(d_1+\gamma)+(d_1+\gamma)^2}{\alpha\left((d_1+\gamma)-\alpha(b_1-d_1)\right)}>0,\ a_1=\frac{(\alpha-d_1-\gamma)^2(d_1+\gamma)}{\alpha}.$$

Clearly, the eigenvalues are negative or with real part negative, when basic reproductive number $R_{01}=\dfrac{\alpha}{d_1+\gamma}>1.$ This indicates that the endemic equilibrium point is locally asymptotically stable whenever it exists. This means the disease will persist in the population and under this condition the other equilibrium point P_{01} is unstable. □

3.3 Global stability analysis

To show the global stability behavior of the equilibrium points, the bounds of dependent variables are required. For this we find the region of attraction stated in form of following lemma.

Lemma 1 For the each system (2.11)-(2.12) and (2.13)-(2.14), the set $\Delta=\{(s,i):0<s+i\le 1\}$ is a region of attraction.

Proof: The proof is obvious from the result (2.15) and (2.16).

Theorem 3.2 There does not exist any periodic solution in the region Δ for each of the system (2.11)-(2.12) or the system (2.13)-(2.14).

Proof: Define $V(s,i)=\dfrac{\partial}{\partial s}g(s,i)F(s,i)+\dfrac{\partial}{\partial i}g(s,i)F(s,i)$

where, $F(s,i)=(1-s-i)(s+b_1i)+\gamma i-asi$, $G(s,i)=asi-\gamma i-(1-s-i)(d_1i)$ and $g(s,i)=\dfrac{1}{si}$

This implies $V(s,i)=-\dfrac{i(b_1+\gamma)+s^2}{s^2i}<0$.

Hence, by Dulac's criterion (Theorem 4.8 [10]), there is no periodic orbit of the system (2.11)-(2.12). This also can be proved easily for the system (2.13)-(2.14). □

Since there is no periodic solution in the region Δ and the disease free equilibrium point is the only locally stable equilibrium point in the sub region $R_0 < 1$ of region Δ therefore, the point is globally asymptotically stable if $R_0 < 1$ Similarly, it is clear that the locally asymptotically stable equilibrium point is globally asymptotically stable if $R_0 > 1$.

Exactly similar arguments prove that the points P_{01} and P_1 of the system (2.13)-(2.14) are globally stable if $R_0 < 1$ and $R_0 > 1$ respectively.

4. Numerical Simulations

We give here numerical simulation to support the analytical results.

For this, we use MATLAB 7 with the parameters value used by [6]

$$B_0 = 0.52,\ D_0 = 0.02,\ g_0 = 0.5, \alpha = 1, L = 0.2$$

With the arbitrary value for,

the case (A) $B_1 = 0.42,\ D_1 = 0.12,\ g_1 = 0.3$ and for the case (B) $B_1 = 0.27,\ D_1 = 0.32,\ g_1 = -0.05$

The non- dimensional parameters have the following values

Case (A) $b_0 = 1.04,\ d_0 = 0.04,\ b_1 = 0.84,\ d_1 = 0.24,\ a = 2, \gamma = 0.4$

Case (B) $b_0 = 1.04,\ d_0 = 0.04,\ b_1 = 0.54,\ d_1 = 0.64,\ a = 2, \gamma = 0.4$

Clearly, the basic reproduction number for the case (A) $R_0 = 5 > 1$ for the case (B) $R_0 = 2.94 > 1$ The endemic equilibrium point for these values of parameters are computed as

Case (A) $E_0(\frac{\gamma}{a}, 1-\frac{\gamma}{a}) = (0.2, 0.8)$) Case (B) $P_{01}(\bar{s}, \bar{i}) = (0.403,\ 0.52)$

The eigenvalues or real parts of eigenvalues corresponding to the endemic equilibrium point are given by,

Case (A) -1.6, -0.68 Case (B) -0.62, -0.62

Since all the eigenvalues or real parts of the eigenvalues are negative, the endemic equilibrium is locally asymptotically stable. Also, for this system locally asymptotically stable equilibrium point is globally stable. So the endemic equilibrium point is globally stable. Now if we increase the value of γ which is directly proportional to recovery rate then the basic reproduction number becomes smaller and smaller. So we need to increase the recovery rate by finding tuberculosis invective and treating them with

effective treatment available. We have shown the effect of recovery rate in the Table 1. The higher values of recovery rate leads to reduce the disease.

Table 1.

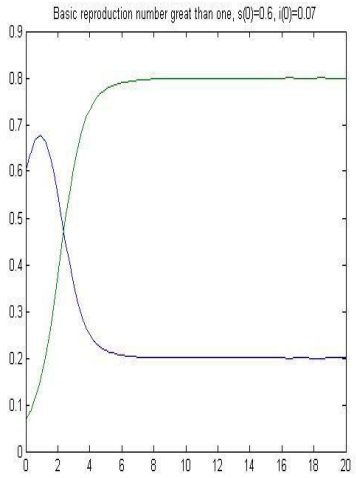
Effect of γ on basic reproduction number ($a = 2$)

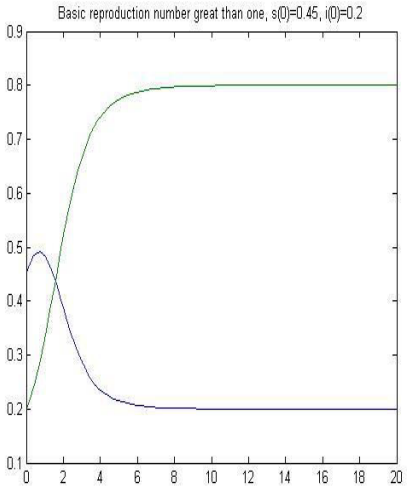
γ	0.5	1	1.5	2.0	2.5
R_0	4	2	1.33	1.0	0.8
s*	0.25	0.5	0.75	1.0	1.0
I*	0.75	0.5	0.25	0.0	0.0

The computer simulations are performed for many different initial values but two figures for two different initial conditions are shown for each of the cases (A) and (B) when $R_0 > 1$ and also two figures are considered for the both cases when $R_0 < 1$

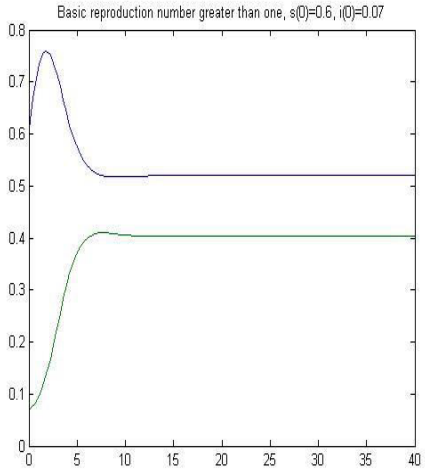
When R_0>1($a = 2,\ b_0 = 1.04,\ d_0 = 0.04,\ b_1 = 0.84,\ d_1 = 0.24,\ a = 2, \gamma = 0.4$)

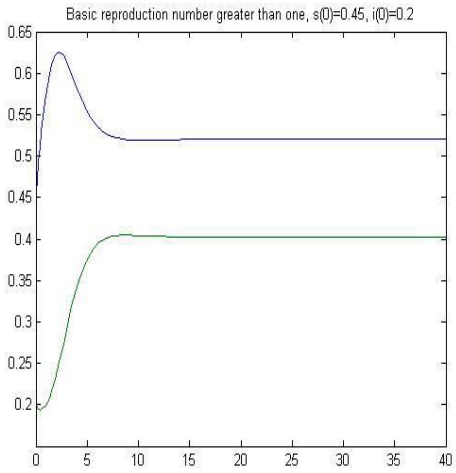
Case (A) s(0)=0.6 and i(0)=0.07 s(0)=0.45 and i(0)=0.2





Case (B) s(0)=0.6 and i(0)=0.07 s(0)=0.45 and i(0)=0.2

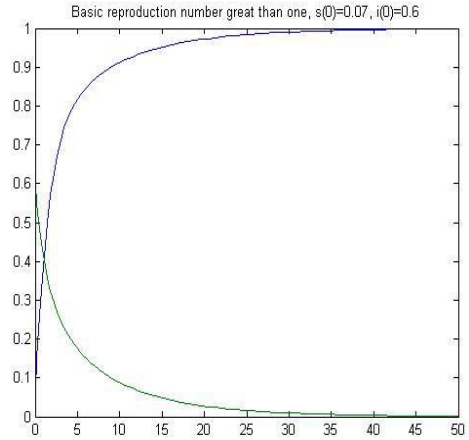


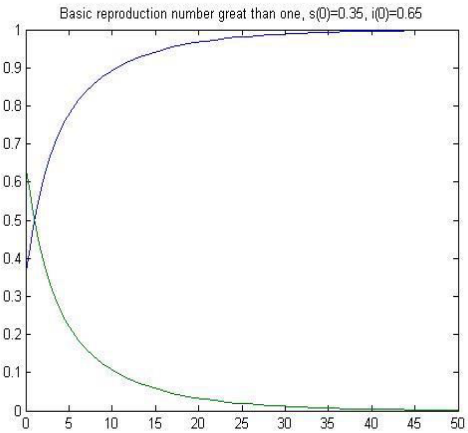


The above four figures support the analytical result that the endemic equilibrium point is globally stable. Because if we start from anywhere in the region, solution approaches to the endemic equilibrium point when the basic reproduction number exceed unity. Even if the initial value is far away from the equilibrium point then also solution approaches to the endemic equilibrium point when basic reproduction number is more than 1.

Now if $R_0 < 1$ ($a = 0.5,\ b_0 = 1.04,\ d_0 = 0.04,\ b_1 = 0.84,\ d_1 = 0.24,\ a = 2, \gamma = 0.4$) then the eigenvalues are -1, -0.01

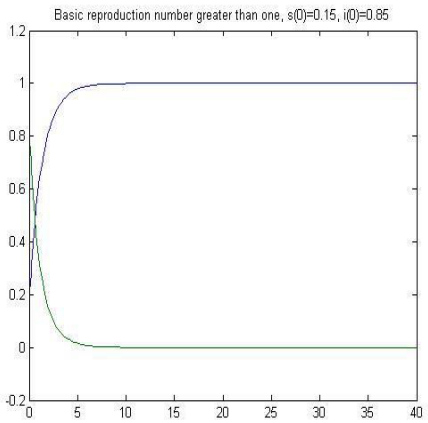
Case (A) s(0)=0.07 and i(0)=0. 6 s(0)=0.45 and i(0)=0.2

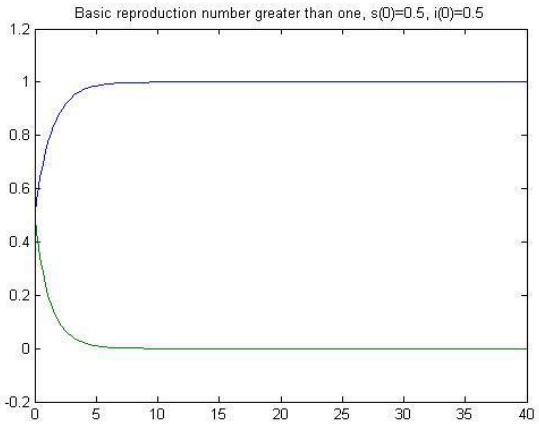




If $R_0 < 1$ ($a = 0.6,\ b_0 = 1.04,\ d_0 = 0.04,\ b_1 = 0.84,\ d_1 = 0.24,\ a = 2, \gamma = 0.4$) then the eigenvalues are -1, -0.74

Case (B) s(0)=0.15 and i(0)=0. 7 s(0)=0.15 and i(0)=0.85





When the basic reproduction number is less than one the solution approaches to disease free equilibrium for any initial start which establishes the global stability of disease free equilibrium point. At the time of numerical simulation initial value is taken with zero susceptible and total population is infected then also solution approaches to disease free equilibrium point when $R_0 < 1$. Thus, it can be seen from all these figures that for any initial start, the solution curves tend to disease free equilibrium or endemic equilibrium point depending on the basic reproduction number.

5. Conclusion and Summary

In this paper, a nonlinear mathematical model is derived and analyzed to study the effect of chronic infectious disease in a logistically growing population. The model gets two different forms depending on the difference of birth rate and death rate in the infected subpopulation. For each of the two systems equilibrium points are obtained and their stability results are obtained which depends on the basic reproduction number. We have found a threshold parameter R_0 which is if less than one, the diseases die out and when $R_0 > 1$ the infection will be present in the population. The disease free equilibrium point always exist while the endemic equilibrium exists only when $R_0 > 1$. Each equilibrium point is locally asymptotically stable as well as globally asymptotically stable depending on the threshold parameter R_0. If infected people are treated and cured at higher rate in such a manner that R_0 becomes smaller. The most important result is that the system (2.11)-(2.12) is generalization of the logistic growth equation given by Verhulst. If the birth rate and death rates are same for each compartment then this is exactly similar to logistic equation. The system (2.11)–(2.12) can be generalized as given in the system (5.1) if i_k represents one or more diseases in the population and can transmit the disease i_k only.

$$\frac{ds}{dt} = \left(1 - s - \sum_{k=1}^{m} i_k\right)\left(s + \sum_{k=1}^{m} b_k i_k\right) + \gamma i - \sum_{k=1}^{m} (a_k s i_k)$$
$$\frac{di_k}{dt} = a_k s i_k - \left(1 - s - \sum_{k=1}^{m} i_k\right)(d_k i_k) \qquad k = 1, 2, ..., m \tag{5.1}$$

Similarly, the system (2.12) –(2.13) can be generalized as (5.2) if $b_k - d_k < 0$ for each k

$$\frac{ds}{dt} = \left(1 - s - \sum_{k=1}^{n} i_k\right)(s) + \sum_{k=1}^{n} b_k i_k + \gamma i - \sum_{k=1}^{m} (a_k s i_k)$$
$$\frac{di_k}{dt} = a_k s i_k - (d_k i_k) \qquad k = 1, 2, ..., n \tag{5.2}$$

The system (5.1) and (5.2) together can be combined as final system as

$$\frac{ds}{dt} = \left(1 - s - \sum_{k=1}^{m+n} i_k\right)\left(s + \sum_{k=1}^{m+n} b_k i_k\right) + \gamma i - \sum_{k=1}^{m} (a_k s i_k)$$
$$\frac{di_k}{dt} = a_k s i_k - \left(1 - s - \sum_{k=1}^{m} i_k\right)(d_k i_k) \qquad k = 1, 2, ..., m \tag{5.3}$$
$$\frac{di_k}{dt} = a_k s i_k - (d_k i_k) \qquad k = m, m+1, ..., n$$

Where, $b_k - d_k > 0$ and $b_k - d_k < 0, k = m+1,\ m+2, ..., n$.

Here, the system (5.3) can get different forms according to the vertical transmission of the some diseases i_k for some k. These forms are easy to be visualized.

References

[1] World Health Organization (2010). The HIV- TB Reports.

[2] B. M. Murphy, B. H. Singer, D. Kirschner, On treatment of tuberculosis in heterogeneous populations, Journal of Theoretical Biology 223 (2003) 391–404.

[3] World health report 2001: global tuberculosis control. Technical Report, World Health Organization.

[4] B. Song, C. Castillo-Chavez, J. P. Aparicio, Tuberculosis models with fast and slow dynamics: the role of close and casual contacts, Mathematical Biosciences 180 (2002) 187–205.

[5] Brian M. Murphy, Benjamin H. Singer, Shoana Anderson, Denise Kirschner, Comparing epidemic tuberculosis in demographically distinct heterogeneous populations, Mathematical Biosciences 180 (2002) 161–185.

[6] C. Castillo-Chavez, Z. Feng, Global stability of an age-structure model for TB and its applications to optimal vaccination Strategies, Mathematical Biosciences 151 (1998) 135-154.

[7] D. Okuonghae, S.E.Omosigho, Analysis of a mathematical model for tuberculosis: What could be done to increase case detection, Journal of Theoretical Biology 269 (2011) 31–45

[8] R.W. West, J.R. Thompson, Modeling the impact of HIV on the spread of Tuberculosis in the United States, Math. Biosc. 143 (1) (1997) 35_60.

[9] S. Bowong, J. J. Tewa, Mathematical analysis of a tuberculosis model with differential infectivity, Commun Nonlinear Sci Numer Simulat 14 (2009) 4010–4021.

[10] G. Birkhoff, G.C. Rota, Ordinary Differential Equations, Ginn, 1982.

[11] J.D. Murray, Mathematical Biology: An Introduction.

[12] F. Brauer, C. Castillo-Chavez, Mathematical Models in Population Biology and Epidemiology, Springer-Verlag, New York, 2001.

[13] L.C.M. Miranda, C.A.S. Lima, On the logistic modeling and forecasting of volutionary processes: Application to human population dynamics.