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Effects of density dependent migration on the spread of infectious diseases: A Mathematical Model

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ABSTRACT

In this paper, an SIS Mathematical model is proposed and analyzed by considering population density dependent migration. It is assumed that the disease is transmitted by direct contact of susceptibles and infectives with immigration and emigration dependent contact rate. The equilibrium analysis of the model is conducted by using the stability theory of ordinary differential equation and simulation. The model analysis shows that the spread of infectious disease increases as therate of immigration increasesbut its spread decreases as emigration rate increases and also if non-emigrating population density increases then infective population increases. The simulation study also confirms these analytical results.

KEW WORDS: Epidemiology, mathematical modelling, Density dependent migration, stability.

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Efectos de la migración dependiente de la densidad en la propagación de enfermedades infecciosas: un modelo matemático

RESUMEN

En este artículo se propone y analiza un modelo matemático SIS considerando la migración dependiente de la densidad de población. Se supone que la enfermedad se transmite por contacto directo de susceptibles e infecciosos con la tasa de contacto dependiente de inmigración y emigración. El análisis de equilibrio del modelo se realiza utilizando la teoría de la estabilidad de la ecuación diferencial común y la simulación. El análisis del modelo muestra que la propagación de enfermedades infecciosas aumenta a medida que aumenta la tasa de inmigración, pero su propagación disminuye a medida que aumenta la tasa de emigración y también si aumenta la densidad de población no emigrante, entonces aumenta la población infecciosa. El estudio de simulación también confirma estos resultados analíticos.

PALABRAS CLAVE: Epidemiología, modelación matemática, migración dependiente de la densidad, estabilidad.

Introduction

Epidemiology is the study of patterns, causes, and effects of health and disease conditions in a population. It provides critical support for publiche alth by identifying risk factors for disease and targets for preventive medicine. Epidemiology has helped develop methodology used in clinical research and public health studies. Major areas of epidemiological study include disease etiology, disease break, disease surveillance, and comparison of treatment effects such as in clinical trials. Epidemiologists gather data and apply a broad range of biomedical and psychosocial theories to generate theory, test hypotheses, and make educated, informed assertions as to which relationships are causal and in which way. For example, many epidemiological studies are aimed at revealing unbiased relationships between exposure to smoking, biological agents, stress, or chemicals to mortality and morbidity. In the identification of causal relationship between these exposures and outcome epidemiologists use statistical and mathematical tools.

In the age of globalization due to emigration from one geographic location to another location, the spread of infectious disease is measure concern for the human or animal

living. The density dependent dispersal movements play a key factor in the fate of epidemic outbreaks occurring within spatially distributed populations.

It is well established that the immigration is a very important factor to bring in a new disease or to spread of old disease that is present in community therefore in most of countries, apart from other disease related factors, the immigration is restricted and whenever it is allowed then lot of immunization process is applied. It is well known that migration effect the spread of disease but the number of people living in the habitat (non-emigrating population density) must also play a very important role in the spread of disease. The spread of infectious diseases in human population depend upon various factors including densities of susceptibles and infectives, their variable contact rate (Greenhalgh & Das, 1992), density population migration Linda (Q Gao & Herbert H W(1992), human carrying capacity of habitat and non-emigrating population of the habitat etc. Many infectious diseases transmit through the direct contact of susceptibles and infectives such as H1N1, tuberculosis, influenza, conjunctivitis, AIDS, Hepatitis and typhoid fever (Zhou & Hethcote, 1994; May & Anderson,1979). The most of the research related to the spread of infectious diseases is a constant immigration dependent (Last, 2001; Hsu & Zee, 2004) but density dependent migration (variable immigration and emigration) [Linda Q Gao & Herbert H W(1992] is also plays very important role in the spreading of infectious diseases. There are two aspect of migration process as immigration and emigration. The following two important aspects has been found missing.

(i) Thepopulation density of community under consideration (non-emigrating population) where the disease is spreading.
(ii) Human carrying capacity of habitat.

In the past, mathematical models have been used to study the spread of infectious diseases by taking the rate of contact between susceptible and infective as a constant (Hethcote,1979 & 1991; May & Anderson,1988; Singh et al,2003 &2015; Shukla et al,

2004). But population density dependent rate of contact plays an important role in the spread of infectious diseases (Greenhalgh,1990; Lee & Maa, 2002; Linda & Herbert, 1992).

The contribution of variable rate of migration (immigration and emigration) as well as density dependent rate of contact for the spread of infectious diseases are equally important but have not been studied so far.

In this paper, therefore, it is proposed to model and analyze the effect of density dependent migration as well as the non-emigrating population on the spread of infectious diseases by considering the density (immigration and emigration) dependent contact rate. The migration function $f(N)$ of human population density N with constant immigration rate A is assumed as follows.

$$f(N) = A + \mu_1(K - N) - \mu_0(N - N_0);\ A > 0, K \geq N, N \geq N_0 \geq 0. \quad (1.1)$$

In (1.1), K is the carrying capacity of the habitat, N_0 is the population density of non-emigrating population, μ_1 is the rate coefficient of immigration and μ_0 is the rate coefficient of emigration. It is noted from (1.1) that when K increases, immigration increases(i.e.when $K \to \infty$, immigration is allowed forever) .When $N = N_0$, the variable emigration is zero i.e. $f(N) = A + \mu_1(K - N)$(i.e. people are not allowed to leave the habitat).

In this paper, we also assume that the rate of contact between susceptibles and infectives is immigration and emigration dependent. Thus the variable rate of contact $\beta_c(N)$ is assumed non-negative function of N as follows:

$$\beta_c(N) = \beta + \beta_1(K - N) - \beta_0(N - N_0). \quad (1.2)$$

Where β is a constant rate of contact, β_1 is the coefficient of rate of immigration and β_0 is the coefficient of rate of emigration. It is noted that as K increases $\beta_c(N)$ increases.

1. SIS Model

In classical epidemiological models postulate that a population is divided into two class of epidemiological significance and homogeneously mixed. The spread of infectious diseases traditionally follows the principle of mass action and associated with incidence (Korobeinikiv & Maini, 2005).We consider that in the region under consideration, the total population density N which divided into two classes, the susceptibles with density X and infectives with density$Y$. If $\beta_c(N)$ is variable (density dependent) contact rate then there are $\beta_c(N)Y$ infective contacts. Then by using Equations (1.1) and (1.2), an SIS model is proposed as follows:

$$\frac{dX}{dt} = A + \mu_1(K-N) - \mu_0(N-N_0) - \big(\beta + \beta_1(K-N) - \beta_0(N-N_0)\big)XY - dX + \mu Y$$

$$\frac{dY}{dt} = \big(\beta + \beta_1(K-N) - \beta_0(N-N_0)\big)XY - (\mu + \alpha + d)Y \qquad (\mathbf{2.1})$$

$X(0) > 0, Y(0) \geq 0 \; and \; N(0) > 0$

In the model system (2.1), d is natural death rate of human population, α is death rate coefficient of infective human population due to disease related factors, $\mu$is the rate of recovery of infective human population density.

2. Equilibrium analysis

In the following, we analyze the model system (2.1). For this we consider the reduced form of model system (2.1) by using $N = X + Y, A_2 = A + \mu_1.K + \mu_0.N_0,\ d_2 = d + \mu_1 + \mu_0$

$$\frac{dY}{dt} = \Big(\big(\beta + \beta_1(K-N) - \beta_0(N-N_0)\big)\Big)(N-Y)Y - (\mu + \alpha + d)Y$$

$$\frac{dN}{dt} = A_2 - d_2N - \alpha Y \quad (3.1)$$

$$Y(0) \geq 0 \; and \; N(0) > 0$$

We need the following lemma for further analysis.

Lemma 3.1. The region of attraction of model system (3.1) is given by the set

$$\Omega = \{(Y,N) \in R^2 \; ; \; 0 \leq Y \leq N_{max} \; and \; N_{min} = \frac{A_2}{\alpha + d_2} \leq N \leq \frac{A_2}{d_2} = N_{max}\}$$

Which attracts all the solution of model system (3.1)initiating in the interior of the positive quadrant of the region**Ω.**

Theorem 3.2. The model system(3.1) has following two non-negative equilibria in **Ω**.

(i) $E_0(0, \quad \frac{A_2}{d_2})$, Thedisease free equilibrium.

(ii) $E_1 = E_1(Y^*, N^*)$is the endemic equilibrium state whichexists if$R_0 = \frac{(\beta+\beta_1 K+\beta_0.N_0)A_2}{((\alpha+\mu+d).d_2)+(\beta_1+\beta_0)\frac{{A_2}^2}{d_2}} > 1$.Here R_0 is the basic reproduction number.

Proof: The existence of the equilibrium point $E_0(0, \quad \frac{A_2}{d_2})$ is obvious. Now In the following we prove the existence of $E_1(Y^*, N^*)$.From model system (3.1),let $Y \neq 0$ then Y^* and N^* are given from the following equations.

$$\big(\beta + \beta_1(K-N) - \beta_0(N-N_0)\big)(N-Y) - (\mu + \alpha + d) = 0 (3.2)$$

$$A_2 - \; d_2 N - \alpha Y = 0 (3.3)$$

By using Equations (3.2) and (3.3) we define the following function,

$$F(Y) = \left\{\left(\beta + \beta_1 K + \beta_0.N_0 - (\beta_1+\beta_0).\frac{A_2}{d_2}\right)\frac{A_2}{d_2} - \; (\mu + \alpha + d)\right\}$$

$$+\left\{(\beta_1+\beta_0).\frac{\alpha A_2}{{d_2}^2} - \frac{(\alpha+d_2)}{d_2}\left(\beta + \beta_1 K + \beta_0.N_0 - (\beta_1+\beta_0).\frac{A_2}{d_2}\right)\right\}Y$$

$$-\left\{\frac{\alpha(\alpha+d_2)}{{d_2}^2}.(\beta_1+\beta_0)\right\}Y^2 = 0 (3.4)$$

From Equation (3.4) we note the following

(i) $F(0) = \left\{\left(\beta + \beta_1 K + \beta_0 . N_0 - (\beta_1 + \beta_0).\frac{A_2}{d_2}\right)\frac{A_2}{d_2} - (\mu + \alpha + d)\right\}$

which is positive provided $R_0 = \frac{(\beta+\beta_1 K+\beta_0 . N_0)A_2}{((\alpha+\mu+d).d_2)+(\beta_1+\beta_0)\frac{{A_2}^2}{d_2}} > 1$.

(ii) $F\left(\frac{A_2}{\alpha+d_2}\right) = -(\mu + \alpha + d) < 0$

Hence by intermediate value theorem at least one root of $F(Y) = 0$ lies in the interval

$$0 < Y < \frac{A_2}{\alpha + d_2}$$

To show the root is unique, we have to prove $F'(Y)$ is negative. To see this, by differentiating equation(3.4) with respect to Y, we get

$$F'(Y) = \left\{(\beta_1 + \beta_0).\frac{\alpha A_2}{{d_2}^2} - \frac{(\alpha + d_2)}{d_2}\left(\beta + \beta_1 K + \beta_0 . N_0 - (\beta_1 + \beta_0).\frac{A_2}{d_2}\right)\right\}$$

$$-\left\{\frac{\alpha(\alpha+d_2)}{{d_2}^2}.(\beta_1 + \beta_0)\right\}2Y. \qquad (3.5)$$

Then by using Equation (3.4) again, we have

$$YF'(Y) = -\left\{\left(\beta + \beta_1 K + \beta_0 . N_0 - (\beta_1 + \beta_0).\frac{A_2}{d_2}\right)\frac{A_2}{d_2} - (\mu + \alpha + d)\right\}$$

$$-\left\{\frac{\alpha(\alpha+d_2)}{{d_2}^2}.(\beta_1 + \beta_0)\right\}Y^2 \quad (3.6)$$

Which is negative for $R_0 > 1$. Since $Y > 0$ and $YF'(Y) < 0$ then $F'(Y) < 0$. Thus $F(Y) = 0$ has unique root in the interval $0 < Y < \frac{A_2}{\alpha+d_2}$.

Now by knowing the value of Y^*, the value of N^* can be uniquely determined from equation (3.3).

Hence $E_1(Y^*, N^*)$ exists if $R_0 > 1$.

Remark: From equations. (3.2) and (3.3), it is easy to note that $dY/d\mu_0 < 0$ and $dY/d\beta_0 < 0$. This implies that, as the μ_0 and β_0 increases, infected population density decreases.

3. Stability analysis

The mathematical model (3.1) is nonlinear in Y and N thus it may not possible to find the exact analytical solution of system of differential equaiton. Thus we have to examine the long term behavior of the system by using the stability theory of differential equation. The local stability behavior of the equilibria are stated in the following theorem.

Theorem4.1. The equilibrium$E_0(0, \frac{A_2}{d_2})$ is unstable if $R_0 > 1$ and the equilibrium$E_1(Y^*, N^*)$islocally asymptotically stable provided the following condition is satisfied.

$$\alpha\left(\{\beta_1 + \beta_0\}(N^* - Y^*)\right)^2 \langle 4d_2\left(\beta_c(N^*)\right)^2 \textbf{(4.1)}$$

Proof: The local stability behavior of each two equilibrium points E_0 and E_1 is studied by computing Jacobian Matrix at point.

Let $f_1 = \left(\beta + \beta_1(K - N) - \beta_0(N - N_0)\right)(N - Y)Y - (d + \alpha + \mu)Y$

$f_2 = A_2 - d_2N - \alpha Y$

Thus Jacobian matrix at E_0 as

$$J(E_0) = \begin{bmatrix} \left\{\left(\beta + \beta_1 K + \beta_0 . N_0 - (\beta_1 + \beta_0).\frac{A_2}{d_2}\right)\frac{A_2}{d_2} - (\mu + \alpha + d)\right\} & 0 \\ -\alpha & -d_2 \end{bmatrix}$$

Since R_0›1, one of Eigen value

$$\lambda_1 = \left\{\left(\beta + \beta_1 K + \beta_0 . N_0 - (\beta_1 + \beta_0).\frac{A_2}{d_2}\right)\frac{A_2}{d_2} - (\mu + \alpha + d)\right\} > 0$$

Hence E_0 is Unstable

Now we check the **local stability** of $E_1(Y^*, N^*)$by using the Lyapunov's method, for this the following positive definite function is used.

$$V(y,n) = \frac{1}{2}y^2 + \frac{k_1}{2}n^2 \quad (4.2)$$

By differentiating equation (4.2), we get

$$\dot{V}(y,n) = y\dot{y} + k_1 n\dot{n} \quad (4.3)$$

Now using linearization of the model system (3.1) about $E_1(Y^*, N^*)$by taking $y = Y - Y^*$, $n = N - N^*$, we get

$$\dot{V}(y,n) = -Y^*\big(\beta + \beta_1(K - N^*) - \beta_0(N^* - N_0)\big)y^2$$

$$-\big(\{\beta_1 + \beta_0\}(N^* - Y^*)Y^* + \big(\beta + \beta_1(K - N^*) - \beta_0(N^* - N_0)\big)Y^* - \alpha k_1\big)ny - k_1 d_2 n^2 \quad (4.4)$$

By choosing K_1such that $\Longrightarrow k_1 = \frac{Y^*\big(\beta+\beta_1(K-N^*)-\beta_0(N^*-N_0)\big)}{\alpha}$ then

$$\dot{V}(y,n) = -Y^*\big(\beta + \beta_1(K - N^*) - \beta_0(N^* - N_0)\big)y^2 - (\{\beta_1 + \beta_0\}(N^* - Y^*)Y^*)ny - k_1 d_2 n^2 \quad (4.5)$$

Now $\dot{V}(y,n) < 0$, provided ,

$$(\{\beta_1 + \beta_0\}(N^* - Y^*)Y^*)^2 < 4k_1 d_2 Y^*\big(\beta + \beta_1(K - N^*) - \beta_0(N^* - N_0)\big)$$

$$i.e \quad \alpha\big(\{\beta_1 + \beta_0\}(N^* - Y^*)\big)^2 < 4d_2\big(\beta_c(N^*)\big)^2 \quad (4.6)$$

$E_1(Y^*, N^*)$is locally stable providing equation (4.6) is satisfied.

Remark: It is pointed out here the inequality (4.6) is automatically satisfied if $\beta_1 = 0$and $\beta_0 = 0$. It also shows that the local stability of system increases if immigration increases but it decreases with emigration.

Theorem 4.2. The equilibrium $E_1(Y^*, N^*)$is globally asymptotically stable in Ω provided the following inequality is satisfied.

$$\alpha\left(\left\{\frac{\beta_1}{(p+K)} + \frac{\beta_0}{(q+N_0)}\right\}\frac{A_2}{d_2}\right)^2 < 4d_2\big(\beta_c(N^*)\big)^2 \quad (4.7)$$

Proof. To prove this theorem, we consider the following positive definite function

$$U = (Y - Y^* - Y^* ln\frac{Y}{Y^*}) + \frac{k_2(N-N^*)^2}{2} \quad (4.8)$$

By differentiating equation (4.8), we get,

$$\dot{U} = \left(\frac{Y-Y^*}{Y}\right)\dot{Y} + k_2(N-N^*)\dot{N} \qquad (4.9)$$

Now after using model (3.1) and equation (3.2) and (3.3) we get

$$\dot{U} = \left(\beta + \beta_1(K-N^*) - \beta_0(N^*-N_0) - \alpha k_2 - \frac{\beta_1}{p+K}(N-Y)\right)(N-N^*)(Y-Y^*)$$

$$-k_2 d_2(N-N^*)^2 - \left(\beta + \beta_1(K-N^*) - \beta_0(N^*-N_0)\right)(Y-Y^*)^2 \qquad (4.10)$$

By choosing $k_2 \quad s.t \quad k_2 = \frac{\left(\beta+\beta_1(K-N^*)-\beta_0(N^*-N_0)\right)}{\alpha}$ then

$$\dot{U} = -\left(\beta + \beta_1(K-N^*) - \beta_0(N^*-N_0)\right)(Y-Y^*)^2$$

$$- \{\beta_1 + \beta_0\}(N-Y)(N-N^*)(Y-Y^*) - k_2 d_2(N-N^*)^2 \qquad (4.11)$$

$\dot{U} < 0$, provided $(\{\beta_1 + \beta_0\}N_{max})^2 < 4k_2 d_2\left(\beta + \beta_1(K-N^*) - \beta_0(N^*-N_0)\right)$

$$i.e. \quad \alpha\left(\{\beta_1 + \beta_0\}\frac{A_2}{d_2}\right)^2 < 4d_2\left(\beta_c(N^*)\right)^2 \qquad (4.12)$$

$E_1(Y^*, N^*)$ is globally asymptotically stable Providing equation **(4.12)** satisfied.

4. Numerical simulation and discussion

Here we discuss the existence and stability of the nontrivial equilibrium point E^* by taking the following set of parameter values from table1 and using the software MAPLE.

$$A \sim 500,\ K \sim 25000,\ N_0 \sim 10000,\ d \sim 0.03,\ \alpha \sim 0.060,\ \beta \sim 0.000012,$$

$$\mu \sim 0.030,\ \mu_0 \sim 200,\ \mu_1 \sim 50,\ \beta_0 \sim 0.000002,\ \beta_1 \sim 0.0000001,$$
$$q \sim 200,\ p \sim 100$$

For these values of parameters the nontrivial equilibrium point E^* corresponding to equations. (3.2) and (3.3) is obtained as.

$$\boldsymbol{N^* = 12237.7 \cong 12238,\quad Y^* = 1899.65 \cong 1900.}$$

Further, It should be noted that for these parameter values as defined above, $R_0 > 1$, and local and global stability condition are satisfied.

The Jacobian Matrix of the model system (3.1) for above values of parameters at (1900,12238) is

$$M^* = \begin{bmatrix} -0.02205 & 0.01808 \\ -0.06 & -0.05179 \end{bmatrix}$$

The Eigen values of the Jacobian Matrix corresponding to the equilibrium point E^* for the model system(3.1) are:

$$-0.0369 + 0.02939i\,, \quad -0.0369 - 0.02939i$$

We note that both the Eigenvalues having negative real part. Hence the endemic equilibrium point E^* is asymptotically stable.

The numerical simulation of model system (3.1) are also conducted and the results are shown in figures [1-9]

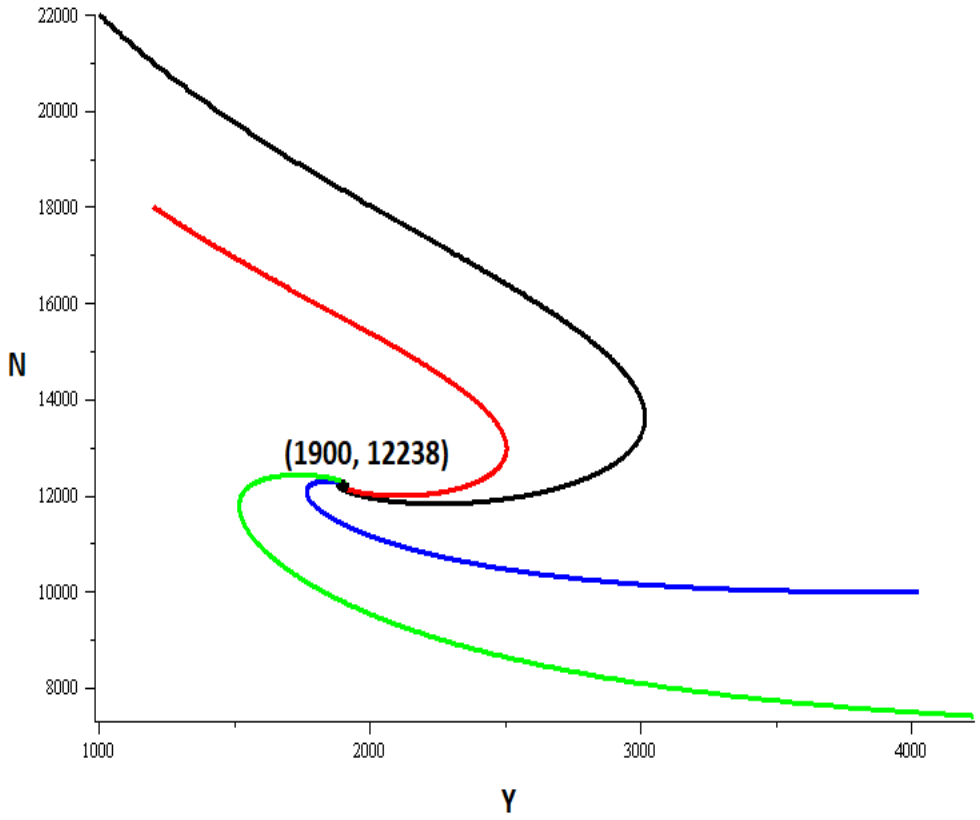

Figure1. Stability diagram for *Y* and *N*

From Fig.1 it can be seen that all trajectories goes tow ardsa single point (1900,12238) i.e. this point become locally stable point.

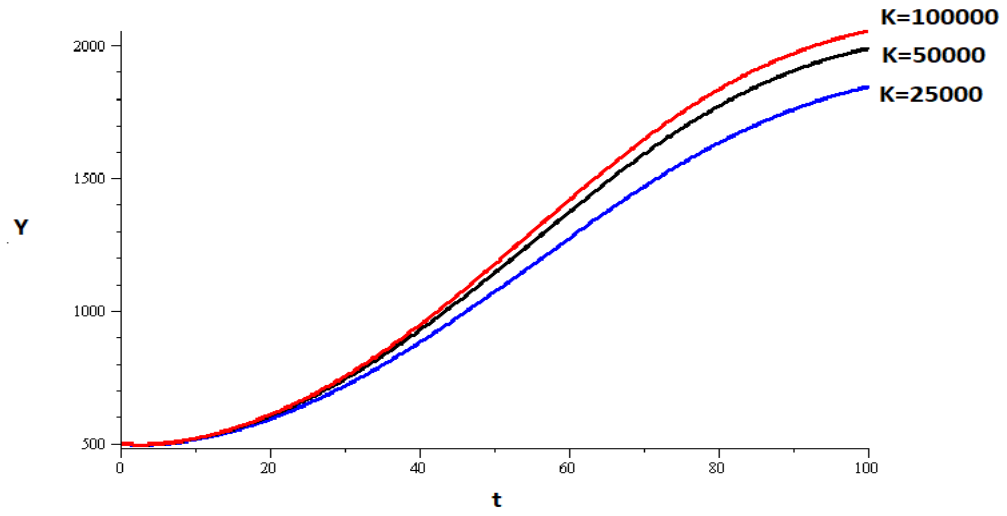

Figure2: Variation of infective population with time for different value of$K$.

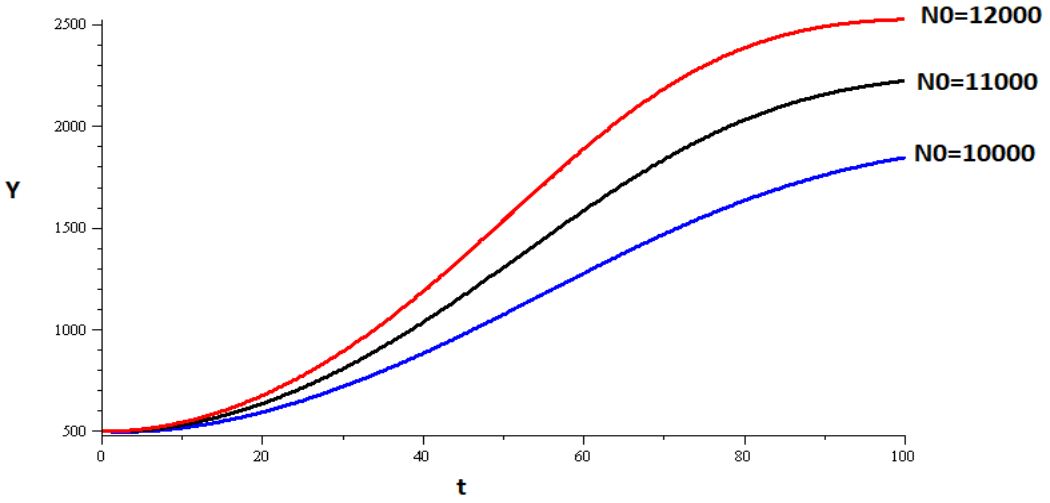

Figure3: Variation of infective population with time for different value ofN_0.

From Fig.2, it can be seen that as carrying capacity K of habitat increases (more people are allowed to immigrate in habitat) then the number of contact between

susceptible and infective increases, the infective population density (spread of disease) increases. From Fig.3, the non-emigrating population density N_0 increases i.e. population of habitat increases, the spread of disease increases.

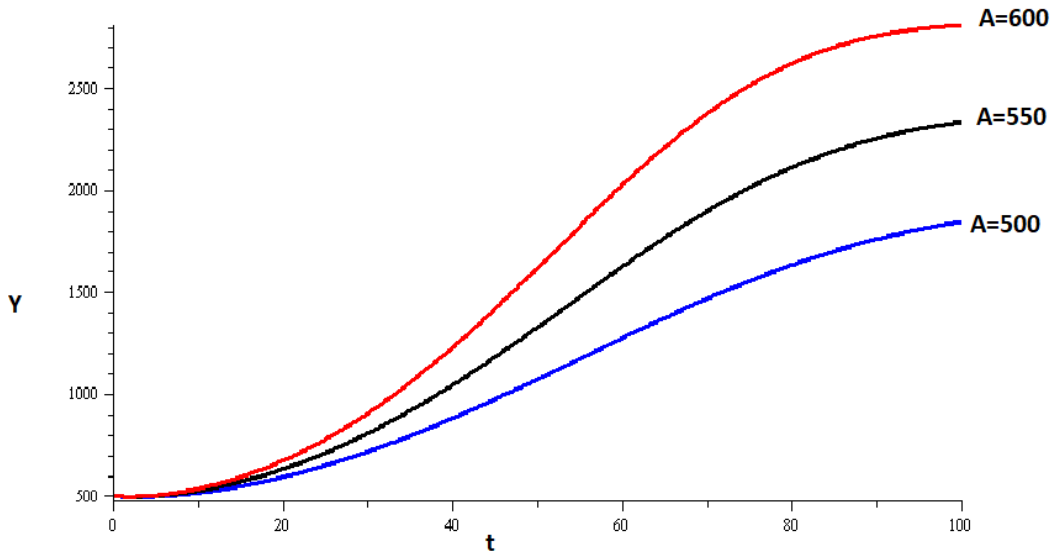

Figure4: Variation of infective population with time for different value of A.

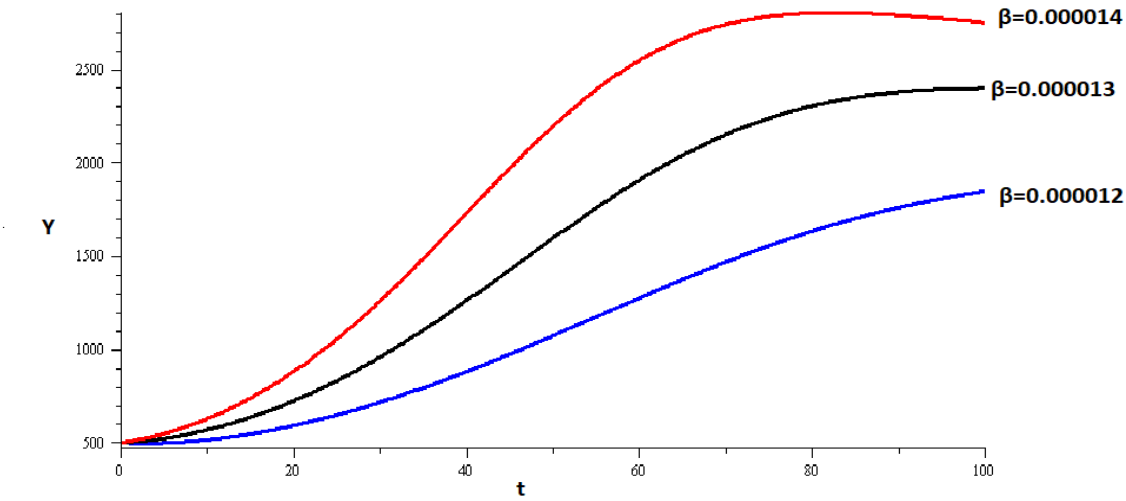

Figure 5: Variation of infective population with time for different value of β

From Fig.4, it can be seen that as the constant immigration rate A increases i.e. total population density N of habitat will increases, the infective population density Y increases. From Fig.5, as the constant contact rate β increases, the infective population density Y increases.

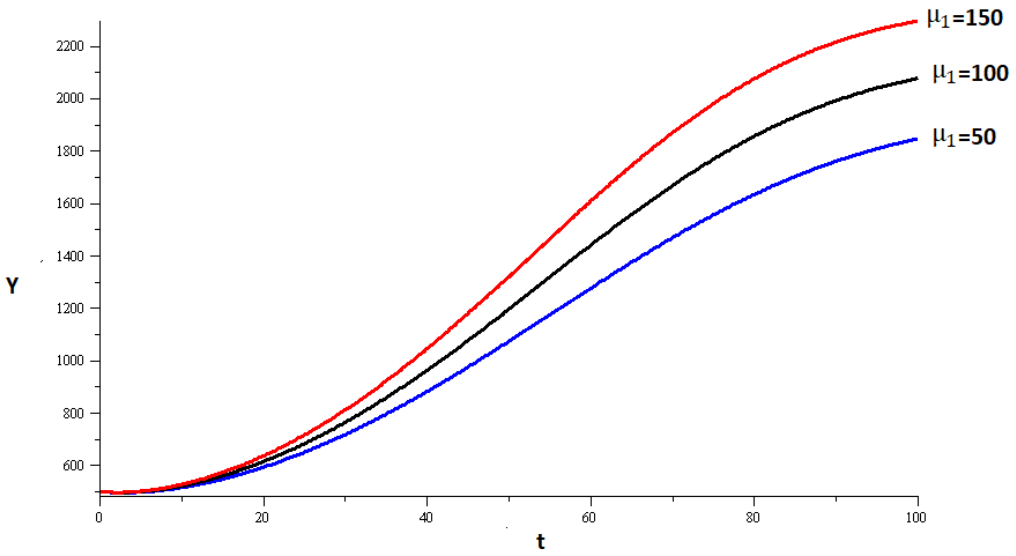

Figure 6: Variation of infective population with time for different value of μ_1.

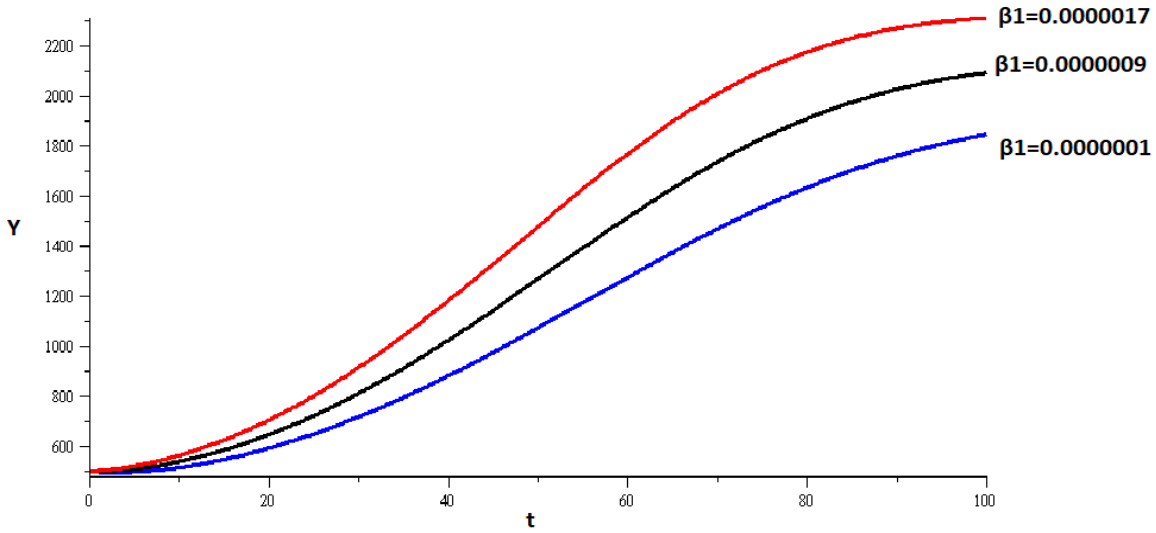

Figure 7: Variation of infective population with time for different value of β_1.

From Fig.6, as the variable immigration rate μ_1 increases i.e. total population density of habitat will increases, the infective population density Y increases. From Fig.7, as the variable contact rate β_1 increases, the infective population density Y increases

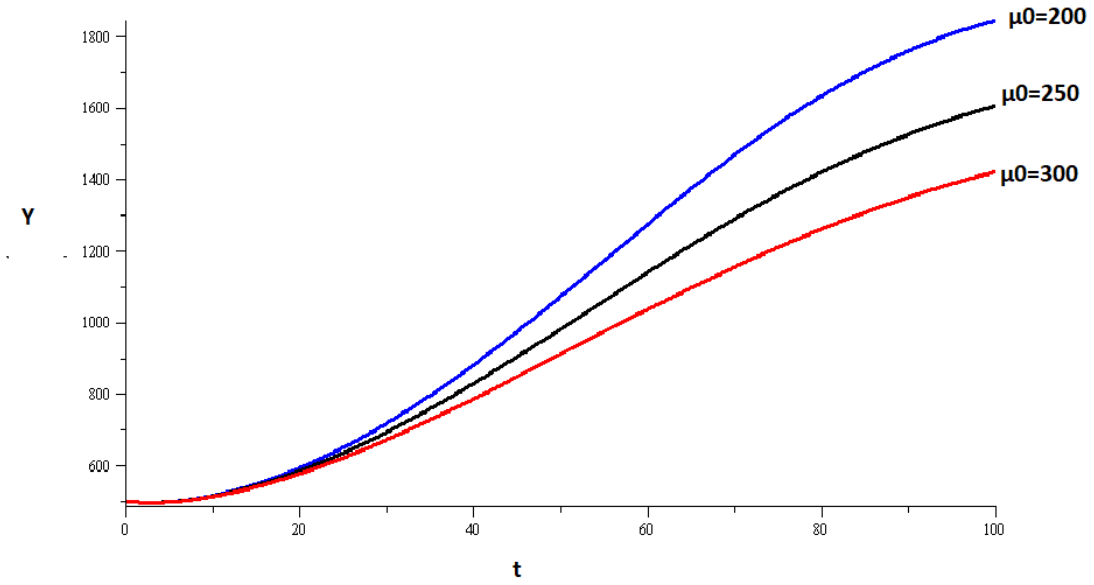

Figure 8: Variation of infective population with time for different value of μ_0.

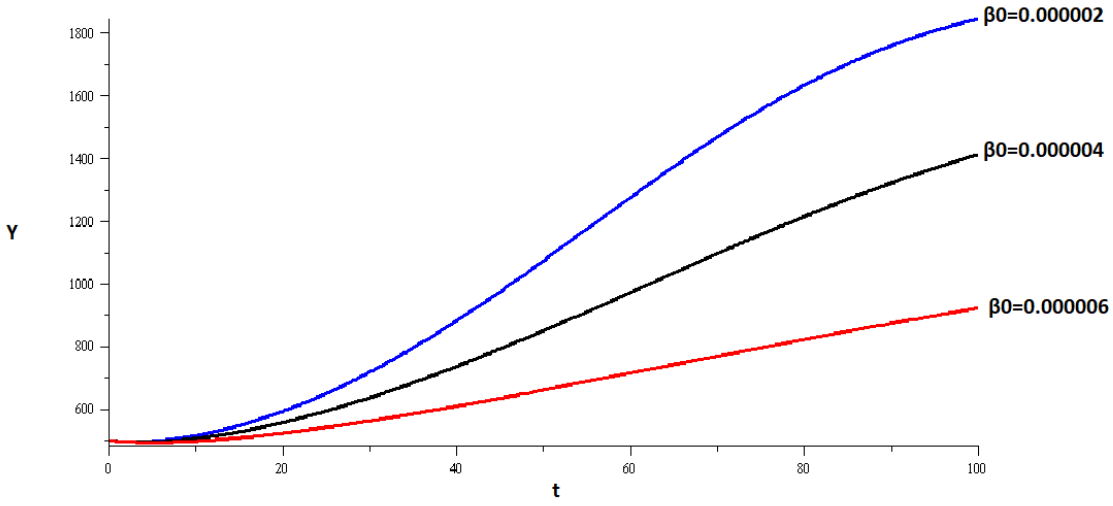

Figure 9: Variation of infective population with time for different value of β_0.

From Fig.8, it can be seen that as the variable emigration rate μ_0 increases i.e. total population density of habitat decreases, the number of infective contacts decreases in habitat i.e. infective population density Y decreases. From Fig.9, it can be seen that as the variable contact rate β_0 increases, the infective population density Y decreases.

Conclusions

In this paper, an SIS epidemic non-linear model have been proposed and analyzed to study the effects of density dependent migration as well asnon-emigrating population of the habitaton spread of infectious diseases. In the modeling process, the two variables have been considered namely, the susceptible population density and the infective population density. The rate of contact between susceptibles and infectives have been assumed to be density (immigration and emigration) dependent. The model has been analyzed by using the stability theory of differential equation and computer simulations. The model analysis has shown that if the variable carrying capacity of habitat or constant immigration rate increases, the infective population density increases. It has also been found that as the population density of non-emigrating population increases, the infective population density increases. Further, as variable immigration increases, not only the contact rate increases but the spread of infectious disease increases. But as variable emigration increases, not only the contact rate decreases but infected population density decreases. These results have been confirmed by numerical simulation of the model.

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