Journal of Biological Engineering Research and Review, 2018; 5(2): 01-13
ISSN: 2349-3232 Online
DOI: 10.5281/zenodo.15351983

Research Article

Global Stability Analysis of Avian Influenza Model

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ARTICLE INFO:

Article History:
Received: 26/06/2018
Revised: 01/08/2018
Accepted: 16/08/2018
Available Online: 20/08/2018

Keywords:
Mathematical model, human population, Avian Influenza, Stability, Numerical simulation

Abstract: A mathematical model of Avian Influenza for both human and bird population is formulated. The basic reproduction number R_0^h and R_0^b for both human and bird population respectively is calculated and we prove that the dynamical system is both locally and globally asymptotically stable for disease-free equilibrium point when $R_0^h < 1$ and $R_0^b < 1$. We also prove that the unique endemic equilibrium point is globally asymptotically stable in bird population when $R_0^b > 1$. Extensive numerical simulations and sensitivity analysis for various parameters of the model are carried out. The effect of Vaccination and Quarantined on Recovered class is critically analyzed.

Citation: Mahato B, Mishra BK, Jayswal A. Global Stability Analysis of Avian Influenza Model. Journal of Biological Engineering Research and Review. 2018, 5(2), 01-13

INTRODUCTION

The biggest pandemic of influenza had happened in 1918, and it had killed over 20 million humans. A pandemic of influenza had happened again in 1957 and 1968 [1]. Nowadays the transmission of avian influenza A (H5N1) virus to humans has increased due to the geographical spread of extremely pathogenic in poultry and wild waterfowl in various countries such as Cambodia, China, India, Thailand, Turkey and Vietnam. In Southeast Asia, the extremely pathogenic H5N1 influenza A viruses are endemic in bird population, and cases in human population continue to increase. It shows a stern pandemic due to the menace of mutation, which causes the rise in the transmission of the virus. The first case of H5N1 avian influenza virus infection in human population from birds was reported in Hong Kong. In December 2003, the outbreak of human cases of H5N1 avian influenza virus have been reported more than 200 cases from nine countries in Asia including India, Europe, northern Africa, and the middle-east Africa [2]. The bird flu viruses are usually transmitted among wild birds. These wild birds travel to various places and get contact with domestic birds like chickens, ducks, turkey etc., due to this the bird flu virus transmit to domestic birds by its saliva, nasal swabs, feces, infected water, infected feed, dust etc. [20]. The Schematic representation of bird flu virus infection route is shown in figure 1. Avian influenza virus H5N1 has similar symptoms as other types of influenza in humans. High fever, generally more than 38°C temperature, cough, sore throat, muscle aches, vomiting, chest pain, diarrhea, bleeding from nose and gums are the initial symptoms of avian influenza. The incubation period for H5N1 in human population is approximately two to eight days, which is more than the incubation period for seasonal influenza. Research shows that the direct contact with infected or dead poultry or wild birds, or going to an infected poultry market are the biggest significant risk factors of H5N1 infection for humans. Thus, awareness of the pandemic H5N1 flu has get a high priority public health problem in most of the country. The effects of different intervention strategies, such as quarantine and vaccination, need to be investigated for the pandemic awareness plans that maximize practicality, simplification and correctness. Avian influenza, being a rising infectious disease in humans, is now getting significant awareness from the mathematical models. Since its appearance, several mathematical models have been developed. To reduce the spread of H5N1 to susceptible human class, we can isolate humans infected with mutant avian influenza and vaccine can be developed for it. Mathematical models are important tools to understand the mechanism of the transmission of H5N1 and it plays an important role in the pandemic awareness plans to forecast and compare the effects of various intervention strategies such as quarantine and vaccination [3, 4].

In past two and half decades, many epidemic models have been formulated for predicting the transmission of H5N1 in human population based on either

the classical susceptible-infected-recovered (SIR) model [3, 4, 5] developed by Kermack and McKendrick [6] or the classical susceptible-exposed-infected-recovered (SEIR) model [7, 8, 9, 10] developed by Rvachev and Longini [11]. A number of mathematical models [12,13,14] has been developed to examine the burden of highly pandemic H5N1 virus and to compute various interventions such as control measures, antiviral drugs and vaccines. A mathematical model by Gumel [15,16] has been formulated to understand the dynamics of a two-strain influenza model and concluded that the influenza-related burden in humans improved as the mutation rate improved. Chong and Smith [17] has developed a mathematical model of avian influenza with half-saturated incidence. Kaddar [18,19] has formulated a mathematical model on the dynamics of a delayed SIR epidemic model with half saturated incidence rate and with a modified saturated incidence rate. Upadhyay and Nitu has developed a model for transmission of bird flu and predicting outbreak diversity [20]. S. Gao and F. Zhang has developed a competitive model between migratory bird population & economical bird population and has shown the effects of migratory bird population in a non-autonomous eco-epidemiological model [21]. Y. Jiang, L. Mei and X. Song has formulated a SVEIRS epidemic model and shown that the global analysis of a delayed epidemic dynamical system with pulse vaccination and nonlinear incidence rate [26].

In this paper, we develop a mathematical model of avian influenza for both human and bird population. We have considered the susceptible class, exposed class, infected class, quarantine class, recovered class and the vaccination class for human population. This is the only model, which has considered all above classes in a single epidemic model for avian influenza virus with real value of parameters. In bird population, we have considered three classes (susceptible, exposed and infected) for avian influenza virus. The paper is organized as follows: Introduction is given in Section 1, the basic assumptions and parameters of the model is discussed and the epidemic model is developed in Section 2, Section 3 establishes the stability of the system developed, numerical simulations is given in Section 4, and finally conclusion in Section 5.

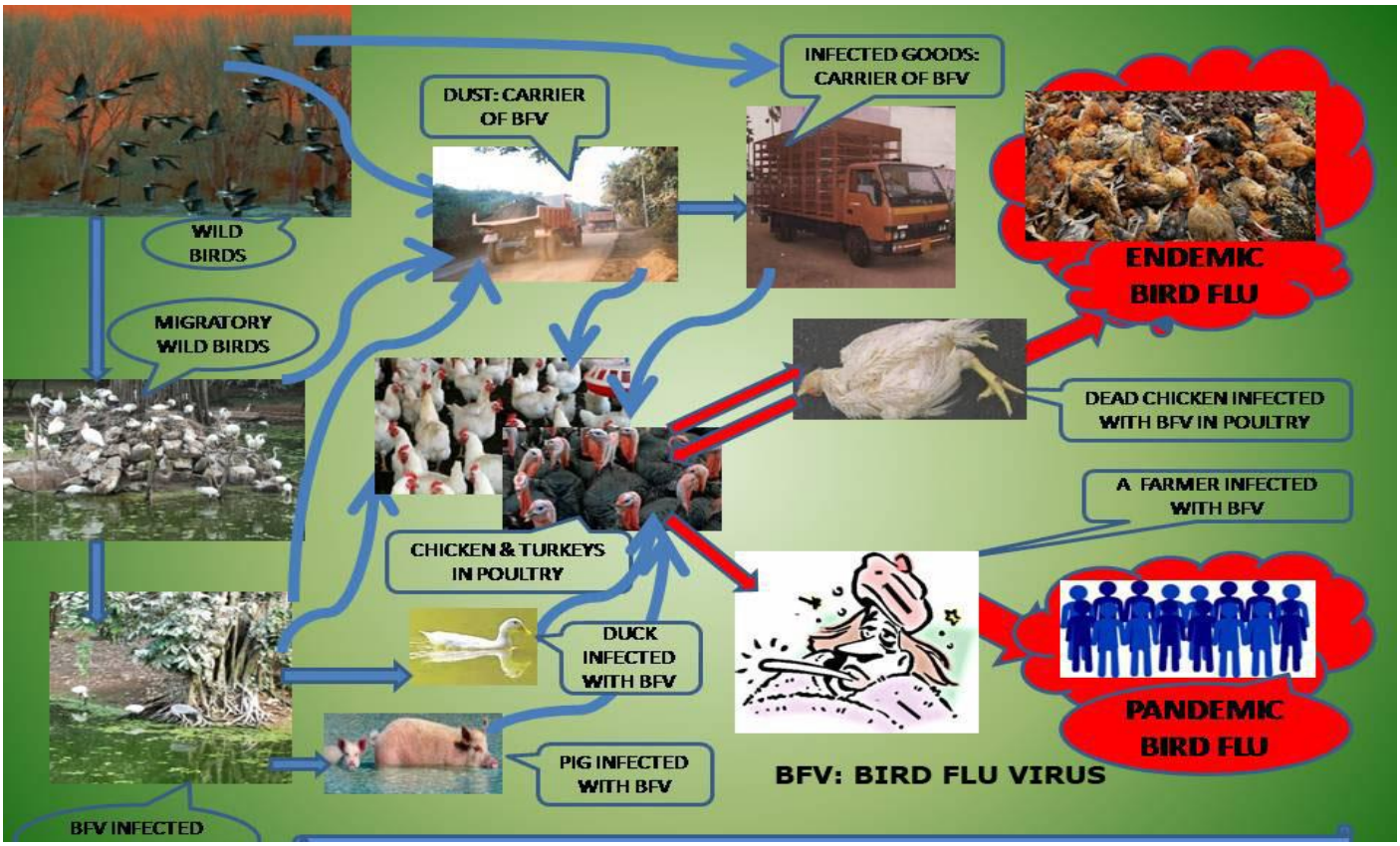

Fig. 1: Schematic representation of bird flu virus infection route.

MODEL PARAMETERS AND ITS FORMULATION

We divided the human population into six classes $SEIQRV$ (Susceptible-Exposed-Infected-Quarantined-Recovered-Vaccinated) and the bird population into three classes $S_bE_bI_b$ (Susceptible-Exposed-Infected). Schematic flow of this model is shown in figure 2 and the state variables and associated parameters of this model are given in Table 1.

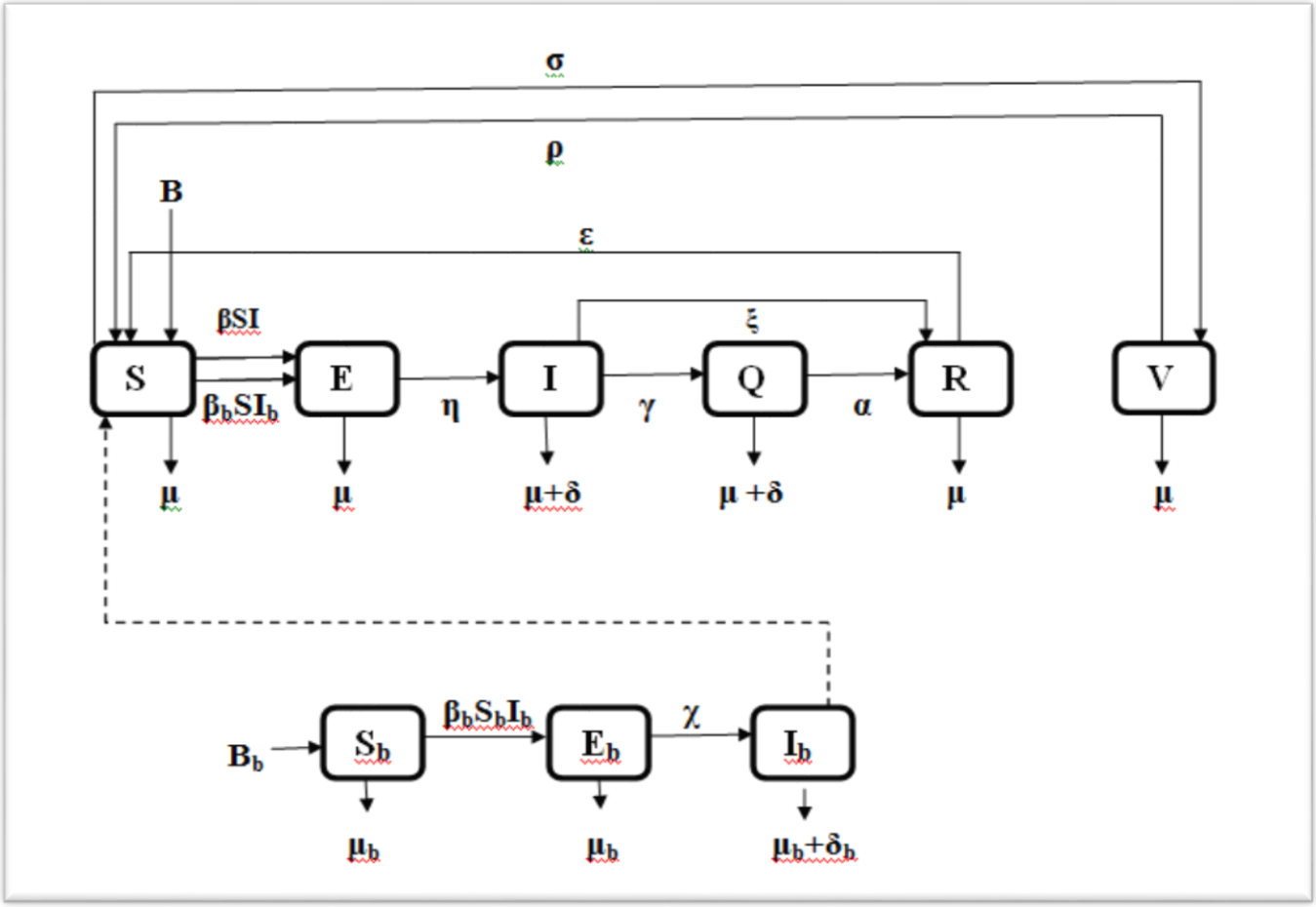

Fig. 2: Schematic flow of avian influenza.

Table 1 : The state variables and associated parameters

$S(t)$:	Susceptible humans in time t
$E(t)$:	Exposed humans in time t
$I(t)$:	Infectious humans in time t
$Q(t)$:	Quarantined humans in time t
$R(t)$:	Recovered humans in time t
$V(t)$:	Vaccinated humans in time t
$S_b(t)$:	Susceptible birds in time t
$E_b(t)$:	Exposed birds in time t
$I_b(t)$:	Infectious birds in time t
$N_h(t)$:	Total human population in time t
$N_b(t)$:	Total bird population in time t
B:	Birth rate of humans
B_b:	Birth rate of birds
β:	Transmission probability of avian and mutant influenza from human-to-human
β_b:	Transmission probability of avian influenza from bird-to-bird
β_{bh}:	Transmission probability of avian influenza from bird-to-human
η:	Rate of transmission from exposed to infected humans
γ:	Rate of transmission from infected to quarantined humans
α:	Rate of transmission from quarantined to recovered humans
σ:	Rate of transmission from susceptible to vaccinated humans
ρ:	Rate of transmission from vaccinated to susceptible humans
ξ:	Rate of transmission from infected to recovered humans
ε:	Rate of transmission from recovered to susceptible humans
χ:	Rate of transmission from exposed to infected birds
μ:	Natural death rate of humans
δ:	Death rate of humans due to avian influenza
μ_b:	Natural death rate of birds
δ_b:	Death rate of birds due to avian influenza.

Model Equations for human's population:

Based on the flow of transmission of avian influenza in human population as depicted in figure 2, we have the following system of equations:

$$\begin{aligned}
\frac{dS}{dt} &= BN_h - \beta SI - \beta_{bh} SI_b + \rho V - \sigma S - \mu S + \varepsilon R \\
\frac{dE}{dt} &= \beta SI + \beta_{bh} SI_b - (\mu + \eta)E \\
\frac{dI}{dt} &= \eta E - (\mu + \delta + \xi + \gamma)I \\
\frac{dQ}{dt} &= \gamma I - (\mu + \delta + \alpha) \\
\frac{dR}{dt} &= \alpha Q + \xi I - (\mu + \varepsilon)R \\
\frac{dV}{dt} &= \sigma S - (\mu + \rho)V
\end{aligned} \tag{1}$$

Similarly, for the flow of transmission of avian influenza in bird's population, we have the system of equations as:

$$\begin{aligned}
\frac{dS_b}{dt} &= B_b N_b - \beta_b S_b I_b - \mu_b S_b \\
\frac{dE_b}{dt} &= \beta_b S_b I_b - \mu_b E_b - \chi E_b \\
\frac{dI_b}{dt} &= \chi E_b - (\mu_b + \delta_b) I_b.
\end{aligned} \tag{2}$$

and

$$\begin{aligned}
N_h(t) &= S(t) + E(t) + I(t) + Q(t) + R(t) + V(t) \\
N_b(t) &= S_b(t) + E_b(t) + I_b(t).
\end{aligned} \tag{3}$$

STABILITY OF THE MODEL

In this section, we find the basic reproduction number and stability of the model. We prove that our model is locally and globally asymptotic stable for both disease-free-equilibrium and endemic equilibrium points.

Since all our model parameters are positive or non-negative, it is important to show that all state variables remain positive or non-negative for all positive initial conditions at $t \geq 0$. From our model equation, we have

$\frac{dN_h}{dt} = B - \mu N_h - \delta(I + Q) \leq B - \mu N_h$
and, $\frac{dN_b}{dt} = B_b - \mu_b N_b - \delta_b I_b \leq B_b - \mu_b N_b$.
The closed set

$$D = \left\{(S, E, I, Q, V, S_b, E_b, I_b) \in \mathbb{R}_+^8 : N_h \leq \frac{B}{\mu}, N_b \leq \frac{B_b}{\mu_b}\right\} \tag{4}$$

is a feasible region of the model.

Theorem 1 *The closed set D is bounded and positive invariant.*

Proof Since $\frac{dN_b}{dt} \leq B_b - \mu_b N_b$,

So N_b is bounded above by $\frac{B_b}{\mu_b}$.
Hence $\frac{dN_b}{dt} < 0$ whenever $N_b(t) > \frac{B_b}{\mu_b}$.
On simplification, we have
$N_b(t) \leq N_b(0)e^{-\mu_b t} + \frac{B_b}{\mu_b}(1 - e^{-\mu_b t})$.
As $t \to \infty$, $e^{-\mu_b t} \to 0$ and so $\lim_{t\to\infty} N_b(t) \leq \frac{B_b}{\mu_b}$.
The other case is similar. Thus D is bounded and positively invariant in $\mathbb{R}_+^8$.

Basic reproduction number*:*

For any epidemic model, the basic reproduction number is the average number of secondary infectious cases produced by a single infection in total susceptible population. The basic reproduction number is calculated by $R_0 = \rho(FV^{-1})$, where ρ is spectral radius of the matrix FV^{-1} and F & V are the matrices of new infection terms and the remaining transmission terms respectively [22].

For the systems (1) & (2), the matrices F and V are as follows:

$$F = \begin{bmatrix} 0 & \beta & 0 & 0 & \beta_{bh} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \beta_b \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \text{ and}$$

$$V = \begin{bmatrix} (\mu+\eta) & 0 & 0 & 0 & 0 \\ -\eta & (\mu+\delta+\xi+\gamma) & 0 & 0 & 0 \\ 0 & -\gamma & (\mu+\delta+\alpha) & 0 & 0 \\ 0 & 0 & 0 & (\mu_b+\chi) & 0 \\ 0 & 0 & 0 & -\chi & (\mu_b+\delta_b) \end{bmatrix}.$$

$$FV^{-1} = \begin{bmatrix} \frac{\beta\eta}{(\mu+\eta)(\mu+\delta+\xi+\gamma)} & \frac{\beta}{(\mu+\delta+\xi+\gamma)} & 0 & \frac{\beta_{bh}\chi}{(\mu_b+\chi)(\mu_b+\delta_b)} & \frac{\beta_{bh}}{\mu_b+\delta_b} \\ 0 & 0 & 0 & 0 & 0 \\ 0 & \gamma & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_b\chi}{(\mu_b+\chi)(\mu_b+\delta_b)} & \frac{\beta_b}{\mu_b+\delta_b} \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix},$$

$$R_0 = \rho(FV^{-1}) = max\left\{\frac{\beta\eta}{(\mu+\eta)(\mu+\delta+\xi+\gamma)}, \frac{\beta_b\chi}{(\mu_b+\chi)(\mu_b+\delta_b)}\right\}.$$

The basic reproduction number for human population R_0^h and bird population R_0^b are given by

$R_0^h = \frac{\beta\eta}{(\mu+\eta)(\mu+\delta+\xi+\gamma)}$ and $R_0^b = \frac{\beta_b\chi}{(\mu_b+\chi)(\mu_b+\delta_b)}$ respectively.

Theorem 2 *The systems (1) and (2) are locally asymptotically stable for disease-free equilibrium, when $R_0^h < 1$ and $R_0^b < 1$.*

Proof: Jacobian matrix of the system (1) and (2) is as follows:

$$J = \begin{bmatrix} -(\sigma+\mu) & 0 & -\beta & 0 & \varepsilon & \rho & 0 & 0 & -\beta_{bh} \\ 0 & -(\mu+\eta) & \beta & 0 & 0 & 0 & 0 & 0 & \beta_{bh} \\ 0 & \eta & A & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma & -(\mu+\delta+\alpha) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \xi & \alpha & -\mu & 0 & 0 & 0 & 0 \\ \sigma & 0 & 0 & 0 & 0 & -(\rho+\mu) & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\mu_b & 0 & -\beta_b \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\mu_b-\chi & \beta_b \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \chi & -\mu_b-\delta_b \end{bmatrix},$$

where $A = -(\mu+\delta+\xi+\gamma)$.

The eigenvalues of Jacobian matrix J are as follows:

$\lambda_1 = -(\mu+\delta+\alpha), \lambda_2 = -\frac{(\mu+\delta+\xi+\gamma)}{2} - \frac{\mu+\eta}{2} + \frac{\sqrt{(\delta+\xi+\gamma-\eta)^2+4\beta\eta}}{2}$, $\lambda_3 = -\frac{(\mu+\delta+\xi+\gamma)}{2} - \frac{\mu+\eta}{2} - \frac{\sqrt{(\delta+\xi+\gamma-\eta)^2+4\beta\eta}}{2}$, $\lambda_4 = -\mu$, $\lambda_5 = -\frac{\rho+\mu}{2} - \frac{\sigma+\mu}{2} + \frac{\sqrt{(\rho-\sigma)^2+4\rho\sigma}}{2}$, $\lambda_6 = -\frac{\rho+\mu}{2} - \frac{\sigma+\mu}{2} - \frac{\sqrt{(\rho-\sigma)^2+4\rho\sigma}}{2}$, $\lambda_7 = -\mu_b$, $\lambda_8 = -\frac{\mu_b+\chi}{2} - \frac{\mu_b+\delta_b}{2} + \frac{\sqrt{(\chi-\delta_b)^2+4\beta_b\chi}}{2}$ and $\lambda_9 = -\frac{\mu_b+\chi}{2} - \frac{\mu_b+\delta_b}{2} - \frac{\sqrt{(\chi-\delta_b)^2+4\beta_b\chi}}{2}$.

Eigenvalues $\lambda_1, \lambda_3, \lambda_4, \lambda_6, \lambda_7, \lambda_9$ have negative real value and on simplifying λ_5, we get $\lambda_5 = -\mu$. We can easily verify that the eigenvalue $\lambda_2 < 0$, when $R_0^h < 1$ and $\lambda_8 < 0$, when $R_0^b < 1$. Hence all eigenvalues of Jacobian matrix J are negative when $R_0^h < 1$ and $R_0^b < 1$. This proves that our the system (8.2.1) for human population and the system (8.2.2) for bird population are locally asymptotically stable when $R_0^h < 1$ and $R_0^b < 1$.

Global stability of disease-free equilibrium:

We show the global stability of the model using the method given by Kamgang and Sallet [23]. In this method, to show global stability, the model has to satisfy the five hypotheses, which has been summarized briefly as follows:

Consider the system

$$\dot{Y}_1 = M_1(Y)(Y_1 - Y_1^*) + M_{12}(Y)Y_2$$

$$\dot{Y}_2 = M_2(Y)Y_2$$

on the positively invariant set $\Omega \subset \mathbb{R}_+^{n_1+n_2}$, and under following assumptions:

A_1: The system is defined and dissipative on a positively invariant set Ω.

A_2: The sub-system $\dot{Y}_1 = M_1(Y_1, 0)(Y_1 - Y_1^*)$ is globally asymptotically stable at the equilibrium Y_1^* on the canonical projection of Ω on $\mathbb{R}_+^{n_1}$.

A_3: The matrix $M_2(Y)$ is Metzler and irreducible for any given $Y \in \Omega$.

A_4: There exists an upper-bound matrix $\bar{M}_2$ for $\Re = \{M_2(Y)/Y \in \Omega\}$ such that $\bar{M}_2 = max_\Omega \Re$.

A_5: $\alpha(\bar{M}_2) \leq 0$, where $\alpha(\bar{M}_2)$ is maximum real part of eigenvalues of $\bar{M}_2$.

If above assumptions A_1-A_5 are satisfied, the DFE is globally asymptotically stable for above system in $\bar{\Omega}$.

Theorem 3 *The system (1) and (2) are globally stable for disease-free equilibrium when $R_0^h \leq 1$ and $R_0^b \leq 1$.*

Proof: We have shown above that $D = \left\{(S, E, I, Q, V, S_b, E_b, I_b) \in \mathbb{R}_+^8 : N_h \leq \frac{B}{\mu}, N_b \leq \frac{B_b}{\mu_b}\right\}$ is bounded and positively invariant in $\mathbb{R}_+^8$, where the hypotheses A_1 and A_2 are satisfied.

In our model, $X_1 = (S, V, Q, R, S_b)$ and $X_2 = (E, I, E_b, I_b)$.
The matrix $A_2(x)$ is given by

$$\begin{bmatrix} -(\mu+\eta) & \beta S & 0 & \beta_b S \\ \eta & -(\mu+\delta+\xi+\gamma) & 0 & 0 \\ 0 & 0 & -(\mu_b+\chi) & \beta_b S_b \\ 0 & 0 & \chi & -(\mu_b+\delta_b) \end{bmatrix}.$$

As required by hypothesis A_3, for any $x \in \mathbb{R}_+^8$ the matrix is irreducible.
Now, for hypothesis A_4 , there is a maximum and uniquely realized in $\mathbb{R}_+^8$ if $S = 1$ and $S_b = 1$ at Disease-free equilibrium state. This maximum matrix is J_2, the block of the Jacobian at DFE, corresponding to the matrix $A_2(x)$ is given by

$$J_2 = \begin{bmatrix} -(\mu+\eta) & \beta S & 0 & \beta_b S \\ \eta & -(\mu+\delta+\xi+\gamma) & 0 & 0 \\ 0 & 0 & -(\mu_b+\chi) & \beta_b S_b \\ 0 & 0 & \chi & -(\mu_b+\delta_b) \end{bmatrix}.$$

For the hypothesis A_4 the diagonal block matrix A_{11}^2 and A_{22}^2 are bounded by the matrices
$\bar{A}_{11}^2 = \begin{bmatrix} -(\mu+\eta) & \beta \\ \eta & -(\mu+\delta+\xi+\gamma) \end{bmatrix}$ and
$\bar{A}_{22}^2 = \begin{bmatrix} -(\mu_b+\chi) & \beta_b \\ \chi & -(\mu_b+\delta_b) \end{bmatrix}$, which are maximum. This maximum is realized at each point of manifolds $\mathcal{M}_1$ (E $= 0$, I $= 0$) and $\mathcal{M}_2$ ($E_b = 0, I_b = 0$). This implies that these points belong to the manifold with equations E $=$ I $= E_b = I_b = 0$. Thus the hypothesis A_4 is satisfied.
Now for the hypothesis A_5 , the condition $\alpha(\bar{A}_{11}^2) \leq 0$ and $\alpha(\bar{A}_{22}^2) \leq 0$ can be expressed as:
$\frac{\beta\eta}{(\mu+\eta)(\mu+\delta+\xi+\gamma)} \leq 1$ and $\frac{\beta_b\chi}{(\mu_b+\chi)(\mu_b+\delta_b)} \leq 1$. Thus the hypothesis A_5 is equivalent to $R_0^h \leq 1$ and $R_0^b \leq 1$.
This proves that the model is globally stable for disease-free equilibrium when $R_0^h \leq 1$ and $R_0^b \leq 1$.

Endemic Equilibrium:

We assume the endemic equilibrium points of system (2) are $E^* = (S_b^*, E_b^*, I_b^*)$.

Using equation (3), we have for endemic equilibrium point,
$\frac{dN_b}{dt} = \frac{dS_b}{dt} + \frac{dE_b}{dt} + \frac{dI_b}{dt} = 0$.
On simplification, we get
$I_b^* = \frac{(B_b-\mu_b)N_b}{\delta_b}$.
Now, applying $\frac{dS_b}{dt} = 0$ and putting the above value of I_b^*, we get
$S_b^* = \frac{B_b N_b \delta_b}{\beta_b N_b (B_b-\mu_b) - \mu_b \delta_b}$.
Similarly, applying $\frac{dI_b}{dt} = 0$ and putting the above value of I_b^*, we get
$E_b^* = \frac{(\mu_b+\delta_b)(B_b-\mu_b)N_b}{\chi\delta_b}$.

So, the endemic equilibrium points of system (2) are as follows:

$E^* = (\frac{B_b N_b \delta_b}{\beta_b N_b (B_b - \mu_b) - \mu_b \delta_b}, \frac{(\mu_b + \delta_b)(B_b - \mu_b) N_b}{\chi \delta_b}, \frac{(B_b - \mu_b) N_b}{\delta_b})$.

Theorem 4 *The unique endemic equilibrium point E^* is globally asymptotically stable if $R_0^b > 1$.*

Proof: We will prove the global stability of endemic equilibrium E^* using geometric approach [24, 25]. We discuss in brief the geometric approach to global stability problems, developed by Li and Muldowney [24].

Consider an autonomous dynamical system $\dot{Y} = f(Y)$, where $f(Y) \in \mathbb{R}^n$is C^1 function of Y in open subset Ω of $\mathbb{R}^n$.

Assumptions of two hypotheses:

H_1: There exists a compact absorbing set K in Ω.

H_2: Above dynamical system has unique equilibrium $\bar{Y}$ in Ω.

Define $\bar{q}_2 = lim_{t\to\infty}^{sup} \max_{y_0 \in \Omega} \frac{1}{t} \int_0^t \mu \left(B\left(y(s, y_0)\right)\right) ds$, where the Lozinskii measure of matrix B is defined as $\mu(B) = \lim_{h\to 0} \frac{|I + hB| - 1}{h}$.

If the system satisfies the above hypothesis H_1-H_2 and $\bar{q}_2 < 0$, then the unique equilibrium $\bar{Y}$ is globally stable in Ω.

The sufficient conditions for the global stability are shown in the hypothesis (H1) and (H2) with the Bendixson criteria given in Theorem (Appendix 2).

For the general solution $\left(S_b(t), E_b(t), I_b(t)\right)$ of system (2), the Jacobian matrix is

$$J = \begin{bmatrix} -\beta_b I_b - \mu_b & 0 & -\beta_b S_b \\ \beta_b I_b & -\mu_b - \chi & \beta_b S_b \\ 0 & \chi & -\mu_b - \delta_b \end{bmatrix}.$$

The matrix $J^{[2]}$, the second additive compound matrix of the jacobian for n=3, is defined as

$$J^{[2]} = \begin{bmatrix} j_{11} + j_{22} & j_{23} & -j_{13} \\ j_{32} & j_{11} + j_{33} & j_{12} \\ -j_{31} & j_{21} & j_{22} + j_{33} \end{bmatrix}.$$

So, its second additive compound matrix $J^{[2]}$ is

$$J^{[2]} = \begin{bmatrix} -\beta_b I_b - 2\mu_b - \chi & \beta_b S_b & \beta_b S_b \\ \chi & -\beta_b I_b - 2\mu_b - \delta_b & 0 \\ 0 & \beta_b I_b & -2\mu_b - \chi - \delta_b \end{bmatrix}$$

Let the function $P = P(S_b, E_b, I_b)$ be defined as

$$P = P(S_b, E_b, I_b) = \begin{bmatrix} 1 & 0 & 0 \\ 0 & \frac{E_b}{I_b} & 0 \\ 0 & 0 & \frac{E_b}{I_b} \end{bmatrix} = diag\left\{1, \frac{E_b}{I_b}, \frac{E_b}{I_b}\right\}$$

Then, $P_f P^{-1} = \begin{bmatrix} 0 & 0 & 0 \\ 0 & \frac{E_b'}{E_b} - \frac{I_b'}{I_b} & 0 \\ 0 & 0 & \frac{E_b'}{E_b} - \frac{I_b'}{I_b} \end{bmatrix}$, where P_f is the matrix obtained by replacing each elements of P by its derivative in the direction of f.

$$B = P_f P^{-1} + P_f J^{[2]} P^{-1} = \begin{bmatrix} -\beta_b I_b - 2\mu_b - \chi & \beta_b S_b \frac{E_b}{I_b} & \beta_b S_b \frac{I_b}{E_b} \\ \chi \frac{E_b}{I_b} & -\beta_b I_b - 2\mu_b - \delta_b + \frac{E_b'}{E_b} - \frac{I_b'}{I_b} & 0 \\ 0 & \beta_b I_b & \frac{E_b'}{E_b} - \frac{I_b'}{I_b} \end{bmatrix} = \begin{bmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{bmatrix},$$

where $B_{11} = [-\beta_b I_b - 2\mu_b - \chi]$, $B_{12} = \begin{bmatrix} \beta_b S_b \frac{E_b}{I_b} & \beta_b S_b \frac{I_b}{E_b} \end{bmatrix}$, $B_{21} = \begin{bmatrix} \chi \frac{E_b}{I_b} \\ 0 \end{bmatrix}$ and

$$B_{22} = \begin{bmatrix} -\beta_b I_b - 2\mu_b - \delta_b + \frac{E_b'}{E_b} - \frac{I_b'}{I_b} & 0 \\ \beta_b I_b & \frac{E_b'}{E_b} - \frac{I_b'}{I_b} \end{bmatrix}.$$

Now, for a vector (u, v, w) in $\boldsymbol{R}^3$, we select a norm as $|(u, v, w)| = max\{|u|,\ |v + w|\}$ and denote $\mathcal{L}$ the Lozinskii measure for this norm. So, $\mathcal{L}(B) \leq \sup\{k_1, k_2\}$, where k_1 and k_2 are defined as follows:

$k_1 = \mathcal{L}_1(B_{11}) + |B_{12}|$ and $k_2 = \mathcal{L}_1(B_{22}) + |B_{21}|$, where $|B_{12}|$ and $|B_{21}|$ are matrix norms with respect to the vector norm L^1 and $\mathcal{L}_1$ denotes the Lozinskii measure with respect to the vector norm L^1. So, we have $k_1 = \mathcal{L}_1(B_{11}) + |B_{12}| = -\beta_b I_b - 2\mu_b - \chi + Sup\left\{\beta_b S_b \frac{E_b}{I_b},\ \beta_b S_b \frac{I_b}{E_b}\right\} = -\beta_b I_b - 2\mu_b - \chi + \beta_b S_b \frac{I_b}{E_b} = -\beta_b I_b - \mu_b + \frac{E_b'}{E_b}$, (by putting $\frac{E_b'}{E_b} = \frac{\beta_b S_b I_b}{E_b} - \mu_b - \chi$ from model equation of exposed class in bird population (2)).

This implies that $k_1 \leq \frac{E_b'}{E_b} - \mu_b$.

Similarly, $k_2 = \mathcal{L}_1(B_{22}) + |B_{21}| \leq \frac{E_b'}{E_b} - \frac{I_b'}{I_b} - 2\mu_b - \delta_b + \chi \frac{E_b}{I_b}$.

Putting $\frac{I_b'}{I_b} = \frac{\chi I_b}{E_b} - \mu_b - \delta_b$ from model equation of infected class in bird population (2), we have, $k_2 \leq \frac{E_b'}{E_b} - \mu_b$.

Hence, $\mathcal{L}(B) \leq \sup\{k_1, k_2\} \leq \frac{E_b'}{E_b} - \mu_b$ and so, $\frac{1}{t}\int_0^t \mathcal{L}(B)ds \leq \frac{1}{t}\log_e \frac{E_b'}{E_b} - \mu_b$.

So, $\bar{q}_2 < 0$, and hence the Bendixson criteria is also satisfied, which thus proves the global stability of the endemic equilibrium.

NUMERICAL SIMULATIONS AND EFFECT OF PARAMETRIC VALUES:

In this section, using Runge-kutta-Fehlberg method of order 4 and 5, we numerically simulate our system (1) and (2) with real parametric values as given in Table 2 **[10, 15, 16, 17]** and also establish the stability of models by taking different examples. MATLAB is used to simulate the systems.

Table 2: Parametric values for systems (1) & (2)

Parameter	Value	Parameter	Value
β_{bh}	0.2	γ	0.05
β_b	0.4	α	0.6
β	0.12	ξ	0.08
B	1000	μ	1/(25550)
B_b	30	σ	0.1
β_{bh}	0.2	δ	1.06
η	0.5	ε	0.05
ρ	0.02	χ	0.6
μ_b	0.01	δ_b	0.5

Example 1: Consider the human population with different values of η from η=0.01 to η=0.9 and parametric values given in Table 2. We have the basic reproduction number $R_0^h = 0.0023$ and $R_0^h = 0.0542$ when η=0.01 and η=0.9 respectively. To show the global stability of disease-free equilibrium point, when $R_0^h < 1$, in infected-recovered phase plane, we consider the global dynamics of the infected-recovered plane and try to understand the nature of the trajectory towards the disease-free equilibrium point. From figure 3, we observe that the nature of trajectory tends to disease-free equilibrium point from any initial point, which shows the global stability of disease-free equilibrium point, when $R_0^h < 1$.

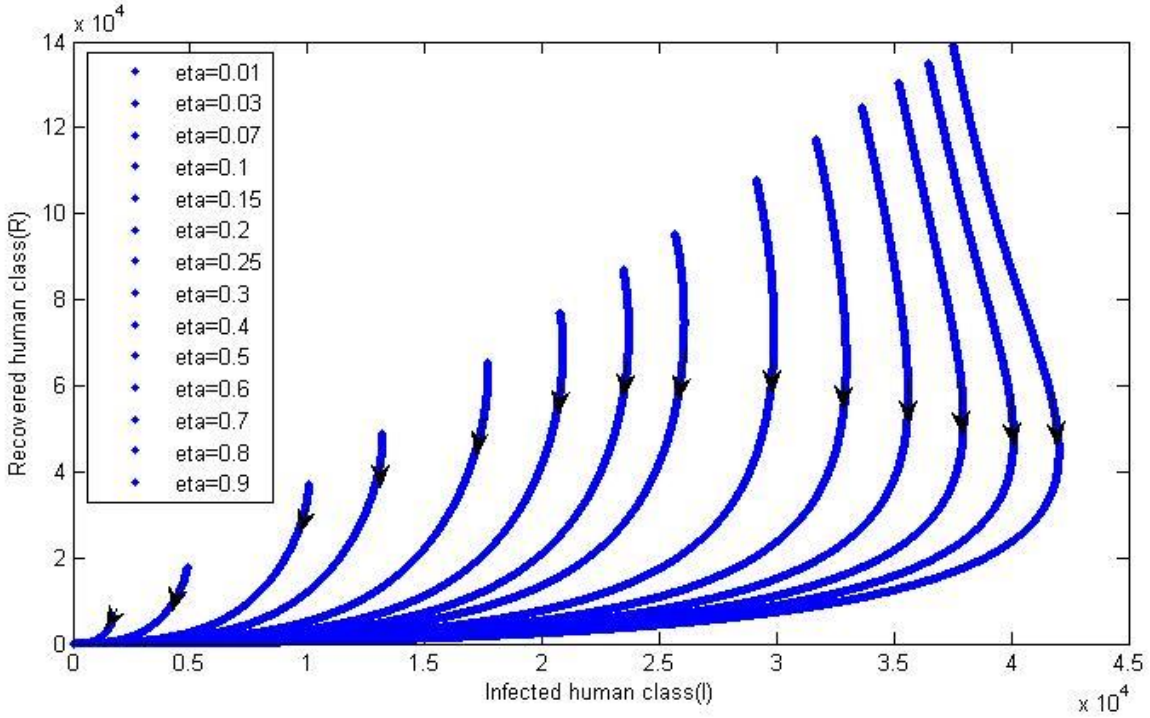

Fig. 3: Global stability of human population when $R_0^h < 1$.

Example 2: Consider the bird population with different values of χ from χ=0.3 to χ=0.95, and the parametric values given in Table 2. We get the basic reproduction number $R_0^b = 0.151$ and $R_0^b = 0.2479$ when χ=0.3 and χ=0.95 respectively. To show the global stability of disease-free equilibrium point, when $R_0^b < 1$ in exposed-infected phase plane, we consider the global dynamics of the exposed-infected plane and try to understand the nature of the trajectory towards the disease-free equilibrium point. From figure 4, we observe that the nature of trajectory tends to disease-free equilibrium point from any initial point, which shows that the global stability of disease-free equilibrium point when $R_0^b < 1$.

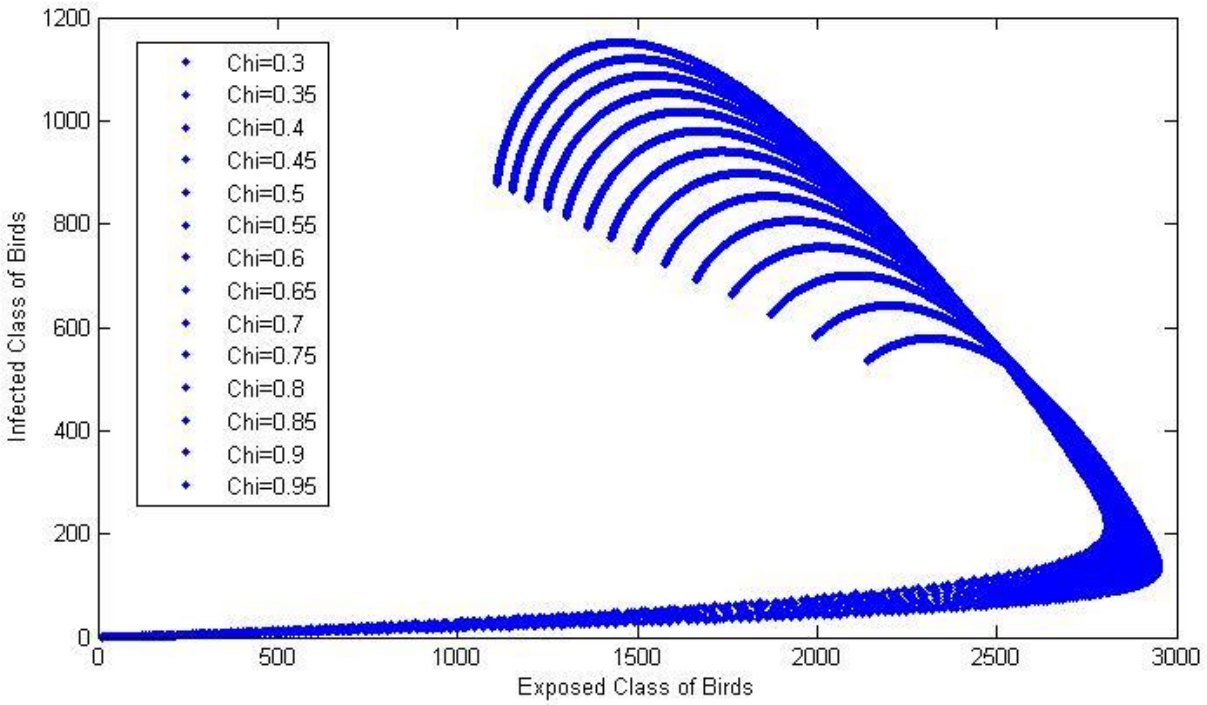

Fig. 4: Global stability of bird population when $R_0^b < 1$.

Example 3: Consider the infected-quarantined phase plane of human population to compare the both classes when $R_0^h < 1$ and $R_0^h > 1$. In figure 4, we have plotted the infected and quarantined class for different values of γ, from γ=0.3 to γ=0.95. In this case, the basic reproduction number $R_0^h = 0.575$ and $R_0^h = 0.0398$ for γ=0.3 and γ=0.95 respectively. In figure 5, we have plotted the infected and quarantined class for different parameter values of α, from α=0.25 to α=0.9. In this case, the basic reproduction number is $R_0^h = 1.0720$ for all the above values of α. it is clear that we need to increase the quarantined human population to control the disease when, $R_0^h > 1$.

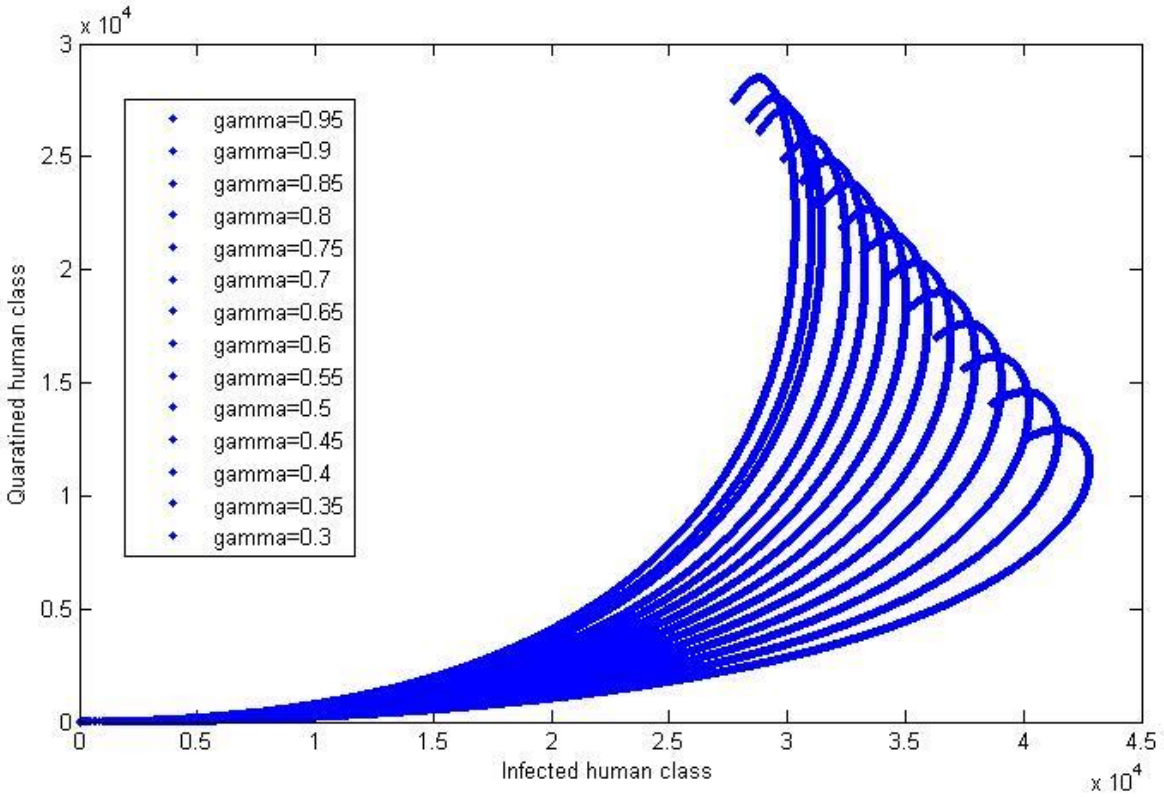

Fig. 5: Comparison of Infected and quarantined human when $R_0^h < 1$.

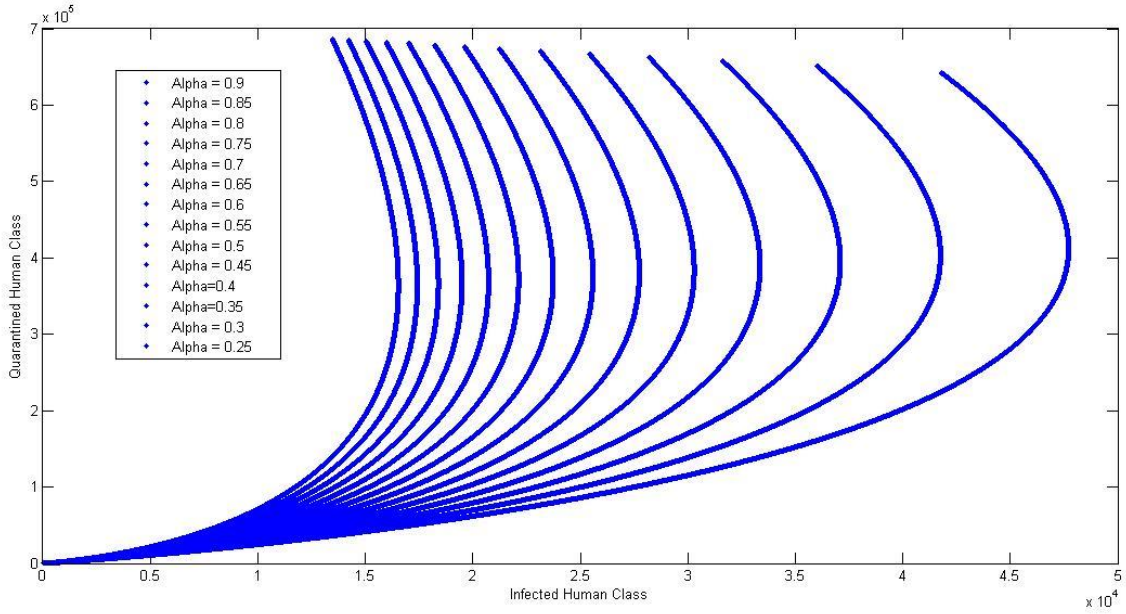

Fig. 6: Comparison of Infected and quarantined human when $R_0^h > 1$.

Example 4: Consider the bird population with different values of χ from χ=0.61 to χ=0.99 and using parametric values given in Table 2. We have the basic reproduction number $R_0^b = 1.0023$ and $R_0^b = 1.0596$ when χ=0.61 and χ=0.99 respectively. In this case, we have considered different initial points and $R_0^b > 1$ for each point. We simulate the system (2) and the graph is shown in figure 7, which indicates that all trajectories for different initial point tend to the endemic equilibrium point, which clearly establishes the global stability of endemic equilibrium, when $R_0^b > 1$.

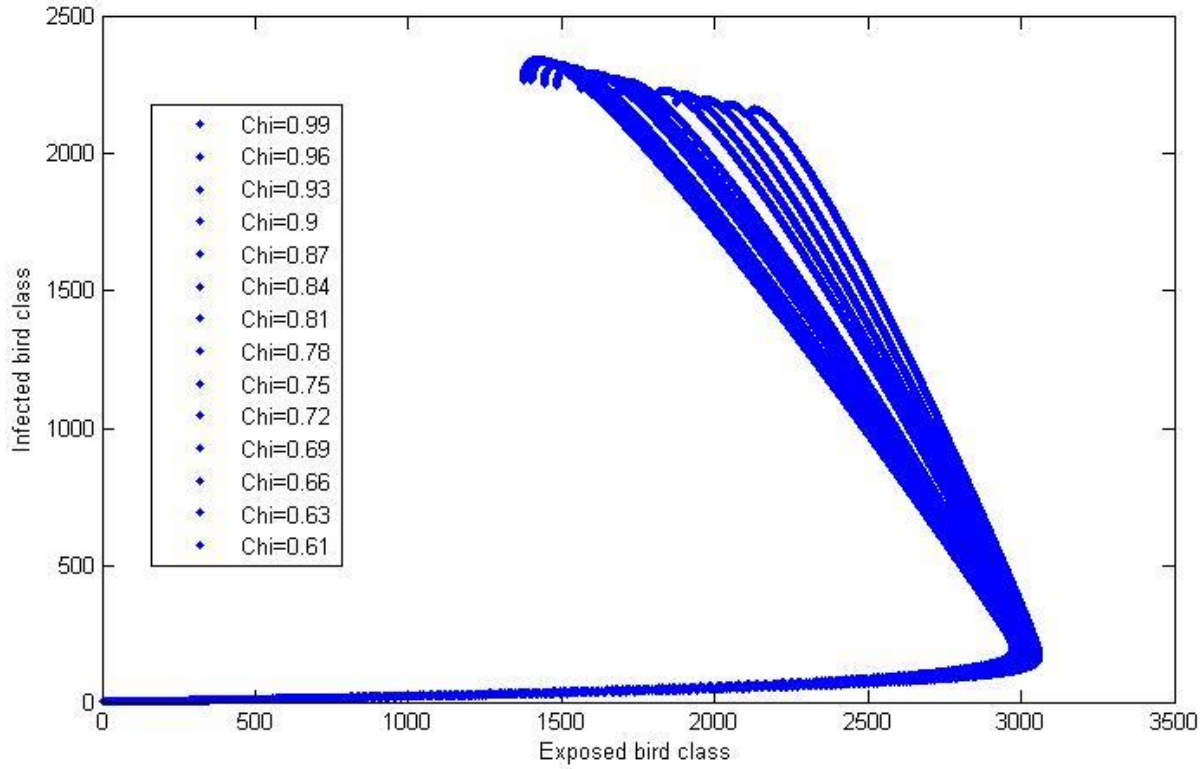

Fig. 7: Global stability of bird population when $R_0^b > 1$.

Example 5: We consider the human population to show the sensitivity analysis of vaccination class and the comparison between recovered and quarantined class. Figure 8, shows the sensitivity analysis between infected and vaccination class. It indicates that as we increase the vaccination parameter σ, the infection rate decreases, which is very true. From Figure 9, it is very clear that as we increase the population of quarantined humans, the recovered population of human also increases. It clearly indicates that quarantining the infectious population is a strong remedial action. Figure 10 shows that time duration of vaccination class, which is around 4-5 days.

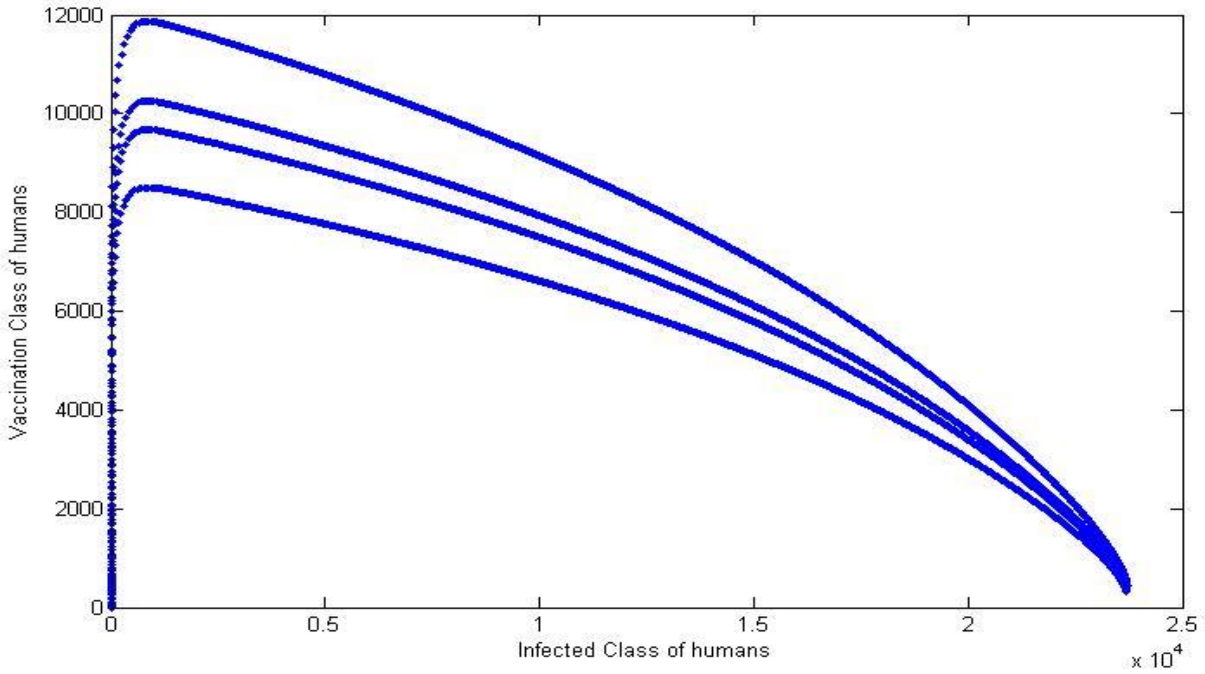

Fig. 8: Sensitivity analysis of infected human with vaccination

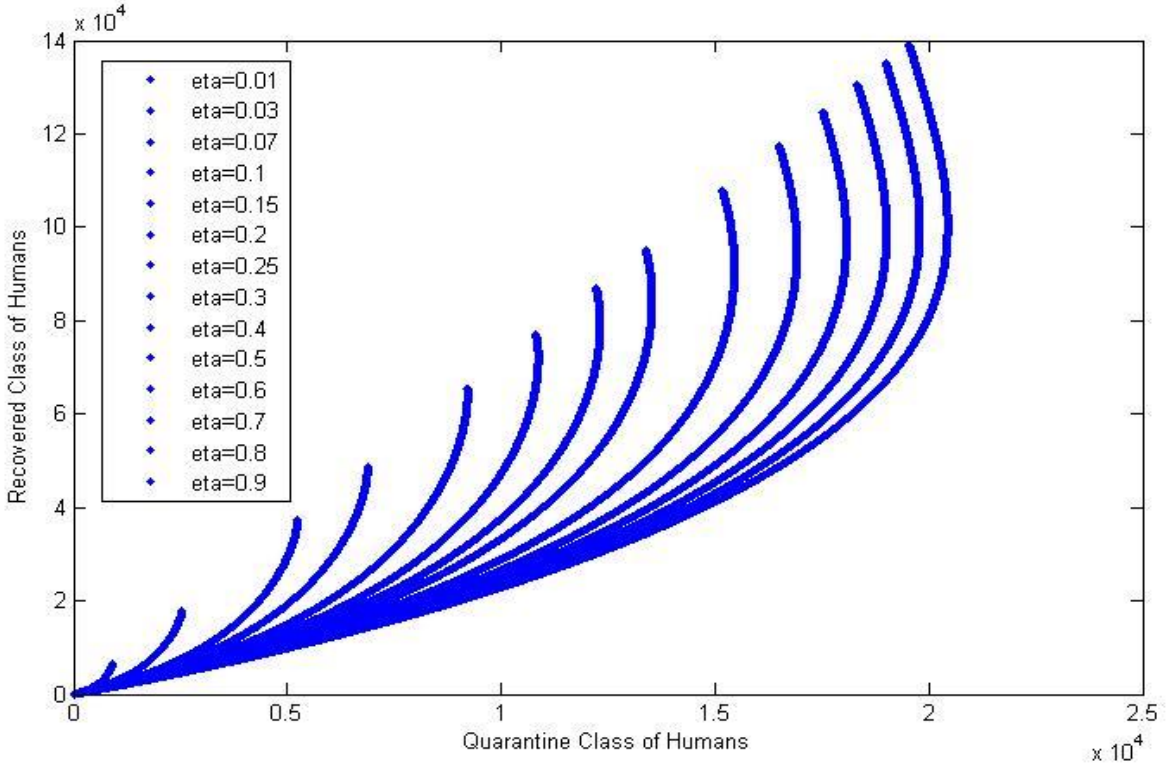

Fig. 9: Sensitivity analysis of recovered human with quarantined human.

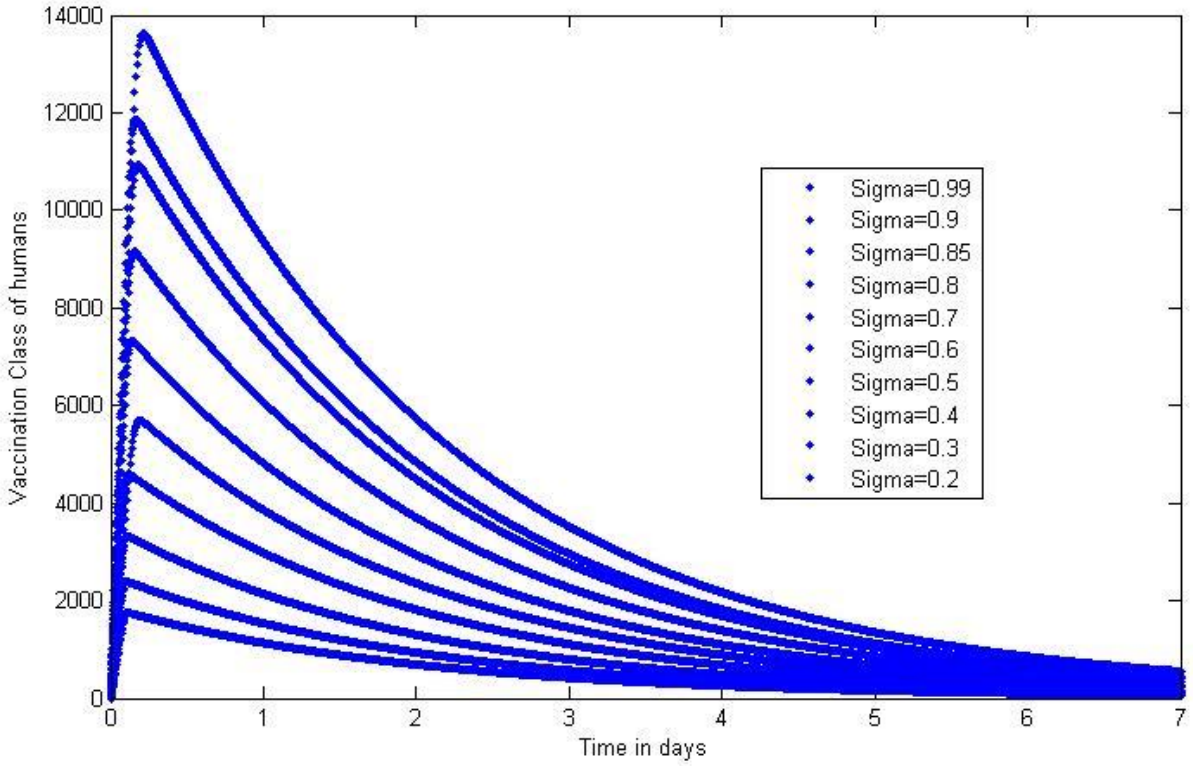

Fig. 10: Sensitivity analysis of vaccination class of humans.

CONCLUSION

We have formulated a mathematical model of avian influenza for both human and bird population. Susceptible-Exposed-Infected-Quarantined-Recovered-Vaccination (SEIQRV) epidemic model is developed for human population and Susceptible-Exposed-Infected ($S_bE_bI_b$) epidemic model is developed for bird population. The basic reproduction number for both epidemic models are computed, which are $\boldsymbol{R_0^h} = \frac{\beta\eta}{(\mu+\eta)(\mu+\delta+\xi+\gamma)}$ and $\boldsymbol{R_0^b} = \frac{\beta_b\chi}{(\mu_b+\chi)(\mu_b+\delta_b)}$ for human and bird population respectively. We proved that the model is locally and globally asymptotically stable for disease-free equilibrium point when $R_0^h < 1$ and $R_0^b < 1$. We also prove that the unique endemic equilibrium point is globally asymptotically stable in bird population, when $R_0^b > 1$. Analytically and numerically, by taking appropriate examples, stabilities of

the results are established. The effect of quarantine & vaccination is discussed. From the results, it is evident that quarantine & vaccination play a vital role for early recovery of the disease. The more we quarantine the infectious population, more is the recovery. Suitable vaccine should be developed & appropriate interval of vaccination should be chosen for recovery of the disease.

ACKNOWLEDGEMENT: None

CONFLICT OF INTEREST: None

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