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# Stability and Bifurcation Analysis of a Bird Flu Model with Vaccination in Poultry Farm

## Analisis Kestablian dan Bifurkasi Model Flu Burung dengan Vaksinasi di Peternakan Unggas

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**Abstract**

We analyze a nonlinear compartmental model describing bird flu transmission dynamics within a poultry farm, incorporating susceptible, infectious, and removed compartments with vaccination. The basic reproduction number $R_0$ is derived, and the local stability of the disease-free and endemic equilibrium is investigated using linearization techniques. Bifurcation analysis based on standard bifurcation theory is conducted to identify parameter leading to qualitative changes in disease dynamics, revealing the occurrence of a forward transcritical bifurcation. Numerical simulations are used to illustrate threshold behavior and assess the impact of vaccination as a mitigation strategy on outbreak persistence. The results provide insights into control thresholds and the design of effective on-farm intervention strategies.
**Keywords:** Bird flu, Population dynamics, Stability analysis, Bifurcation

**Abstrak**

Dalam penelitian ini dianalisis suatu model kompartemen nonlinier yang menggambarkan dinamika peyebaran flu burung pada peternakan unggas, dengan memasukkan kompartemen rentan, terinfeksi, dan pulih, serta mempertimbangkan vaksinasi. Bilangan reproduksi dasar $R_0$ ditentukan, dan kestabilan lokal dari titik kesetimbangan bebas penyakit dan endemik dikaji menggunakan teknik linearisasi. Analisis bifurkasi berdasarkan teori bifurkasi dilakukan untuk mengidentifikasi parameter yang menyebabkan terjadinya perubahan kualitatif pada dinamika penyakit, yang menunjukkan terjadinya bifurkasi transkritikal maju. Simulasi numerik digunakan untuk menggambarkan perilaku ambang serta menilai dampak vaksinasi sebagai strategi mitigasi terhadap keberlanjutan wabah. Hasil penelitian ini memberikan wawasan mengenai ambang pengendalian dan perancangan strategi intervensi yang efektif di tingkat peternakan.
**Kata kunci:** Flu burung, Dinamika populasi, Analisis kestabilan, Bifurkasi

# 1. INTRODUCTION

Avian influenza (AI), popularly known as bird flu, is a contagious viral disease that affects domestic and wild birds which can leads to a severe economic and public health consequences for poultry industries. Bird flu disease caused by virus types H5N1 has continued to be a highly infectious and fatal disease for domestic birds [18]. However, the persistence and high transmission rate of bird flu, particularly in heavily concentrated poultry farms has pointed out a substantial concern among researchers, veterinarians, and policymakers. Understanding the transmission dynamics of the disease is the most important factor in effective intervention and control measures.

Bird A virus strains is classified into two types, low pathogenic (LPAI) or highly pathogenic (HPAI) [24]. One of which causes a serious disease in domestic birds with a high death rate while the other one is not a serious threat to domestic birds [19]. In contrast, the most highly pathogenic strain (H5N1) has been spreading across regions, including Asia, since 2003, before reaching Europe in 2005 and the Middle East, as well as Africa, in 2006 [18]. Bird flu viruses circulate among birds worldwide [24]. Meanwhile, bird flu not only infects poultry, but it also infects human [3]. Moreover, the cases of transmission of bird flu from bird to human have been occurred since 1997 when this virus infected 18 people in Hong Kong, causing 6 deaths during poultry outbreak [3], [15]. The transmission process of bird flu involves three factors: the existence of avian influenza virus as the source of the disease, poultry as the host, and the environment as the medium [12].

The disease is transmitted chiefly by close contact with infected birds, faeces, secretions, and droppings of infected poultry, and contaminated water, feed, and equipment. Transmission of virus occurs by airborne droplets also occurs within closed settings such as commercial poultry housing. After it infects, it spreads rapidly within flocks, and timely control and diagnosis become imperative. Due to its elusive state at early phases, it becomes difficult to control and still persists and mutates within poultry farm. The bird's health status changes from susceptible to infected when they have contact with contaminated nasal, respiratory, or fecal material from infected birds [24].

Various studies have explored the impact of Mathematical modeling as a strong tool for studying the spread and control of infectious disease by utilizing appropriate systems of differential equations. For instance, mathematical models to study the bird flu transmission from the bird to bird, and bird world to human world were analyzed [6], [20], [2], [9]. Nonetheless, vaccination within the poultry farm, burning infected poultry, quarantining and giving treatment to infected humans was studied [23], [8]. Similarly, modeling and analysis of bird flu outbreak within a poultry farm was carried out by [13]. The findings reveal the effective measure to prevent the outbreak of avian influenza within a poultry farm by constant removal of infected birds. Notably, mathematical model of bird flu infection process with age structured model was studied [12]. Additionally, mathematical model of bird flu transmission with diffusive terms to investigate spatial transmission of bird flu among poultry and human was studied [1], [16], [14]. Interestingly, [18], [19], [15], [3] studied the traveling wave solutions associated with bird flu transmission in a poultry farm. Particularly, the work [4] studied bifurcation analysis of epidemic model waning immunity. Furthermore, a SEIAVR compartmental model for avian influenza was developed and showed that the basic reproduction number determines local stability at the disease-free equilibrium and global stability at the endemic equilibrium [10]. Modeling the effects of contaminated environments shows significant influence on avian influenza transmission and equilibrium stability through the basic reproduction number [21]. In essence, the basic reproduction number governs avian influenza transmission dynamics and determines the overall disease outcome [22]. It is proved that the bird flu transmission can be controlled when the basic reproduction number is reduced below unity through effective vaccination and antiviral treatment strategies [11]. Despite extensive evidence of the severe economic, social, and public health impacts of Highly Pathogenic Avian Influenza (H5N1), particularly through environmental and zoonotic transmission, there remains a need for

rigorous quantitative frameworks to better understand and predict its transmission dynamics [7], [5].

This study focuses on the mathematical modeling and analysis of avian influenza transmission within a poultry farm. The proposed model captures the interaction between susceptible, infected, and removed birds by incorporating essential biological processes such as recruitment, natural mortality, disease-induced mortality, removal, and transmission. While numerous avian influenza models exist, most studies primarily emphasize equilibrium existence and local stability, with limited attention to how control measures fundamentally alter the qualitative dynamics of disease transmission. In particular, a rigorous comparative bifurcation analysis of models with and without vaccination at the farm level remains insufficiently explored. To address this gap, we employ a nonlinear system of ordinary differential equations to derive the basic reproduction number, analyze equilibrium stability, and investigate bifurcation behavior. Numerical simulations are conducted to validate the analytical findings, illustrating time trajectories and phase portraits, and providing quantitative insights into vaccination-based control strategies for poultry farm management.

## 2. A BIRD FLU MODEL

In order to analyze bird flu (H5N1) spreading in a poultry farm, we extent the model in [19]. A model that separates the birds into three health status, the susceptible X(t) infected Y(t) and recovered Z(t) populations respectively. The model was reformulated based on the following assumptions:

a. The poultry farm is considered to be a closed environment (closed system).
b. Birds are removed from the population only through natural death, disease-induced mortality or removed (fixed population).
c. Birds may exit the susceptible group either by acquiring infection through contact with infected birds or by natural death.
d. The population is homogeneously mixed.
e. Vaccination is given to all newborn birds.

Let $X(t)$denote the number of susceptible birds at time $t$, $Y(t)$the number of infected birds, and $Z(t)$the number of removed birds. New birds are recruited into the population at a constant rate $c$and enter the susceptible class, while all birds experience natural mortality at a rate $b$, regardless of their disease status. In addition, infected birds are subject to disease-induced mortality at a rate $m$. Transmission occurs when susceptible birds come into contact with infected birds, at a rate governed by the transmission coefficient $\omega$. Once infected, birds remain in that state until they are removed, either through natural death or disease-induced death, at a removal rate $\gamma$. Vaccination is administered at the point of recruitment, with a vaccination rate $\rho$, where $\rho \in [0,1)$. This implies that a fraction $\rho$ of newly recruited birds is effectively immunized before entering the susceptible compartment. The flow diagram of the model is illustrated in Figure 2.1.

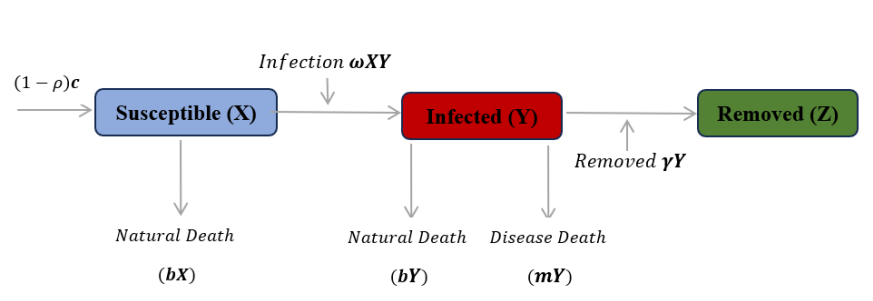


**Figure 2.1.** Flow chart of the SIR compartment model

Hence, based on those assumptions, the system of equations for bird flu model without vaccination can be written as:

$$\begin{aligned} \frac{dX}{dt} &= c - bX - \omega XY, \\ \frac{dY}{dt} &= \omega XY - (b + m + \gamma)Y, \\ \frac{dZ}{dt} &= \gamma Y, \end{aligned} \qquad 2.1$$

with initial conditions $X \geq 0, Y \geq 0, Z \geq 0$, the system will serve as a basis of further analysis, including finding equilibrium points, stability analysis, and bifurcation analysis. From the three basic notations of the model, the total bird population, $N(t) = X(t) + Y(t) + Z(t)$. Therefore, we assume that the total population $N(t) = X(t) + Y(t) + Z(t)$ is governed by the net inflow and death rates. From the original system:

$$\frac{dN}{dt} = \frac{dX}{dt} + \frac{dY}{dt} + \frac{dZ}{dt} = (c - bX - \omega XY) + (\omega XY - (b + m + \gamma)Y) + \gamma Y$$
$$\frac{dN}{dt} = c - bX - bY - mY = c - b(X + Y) - mY$$

Equivalently, since $X + Y = N - Z$. Therefore,

$$\frac{dN}{dt} = c - b(N - Z) - mY.$$

However, the total living population at time t can be denoted as L, such that:

$$L(t) = X(t) + Y(t)$$

Then

$$\frac{dL}{dt} = c - bL - mY$$

This shows that birds exist the living population only through by natural deaths (bL) and by disease-induced mortality (mY). Let, the proportion of susceptible birds be $x(t) = \frac{X(t)}{N(t)}$, the proportion of infected birds be $y(t) = \frac{Y(t)}{N(t)}$, and the proportion of the removed birds be $z(t) = \frac{Z(t)}{N(t)}$. With $x(t) + y(t) + z(t) = 1$. Since the recovered class $Z(t)$ does not directly influence the dynamics of the susceptible and infectious populations. Therefore, it is enough to consider Equation 2.2.

$$\begin{aligned} \frac{dX}{dt} &= c - bX - \omega XY \\ \frac{dY}{dt} &= \omega XY - (b + m + \gamma)Y \end{aligned} \qquad 2.2$$

Similarly, the system of equations for bird flu model with vaccination is presented in Equation 2.3.

$$\begin{aligned} \frac{dX}{dt} &= (1 - \rho)c - bX - \omega XY \\ \frac{dY}{dt} &= \omega XY - (b + m + \gamma)Y \end{aligned}$$

Where the parameter $\rho$ is the vaccination rate. Furthermore, the Stability of the system (2.2) and (2.3) will be discussed in the next following subsection.

# 3. STABILITY ANALYSIS

***Model without vaccination***

There are two equilibrium points of the system equations 2.2. The first one is disease-free equilibrium, $E_0 = \left(\frac{c}{b}, 0\right)$, and the other one is endemic equilibrium, $E_1 = \left(\frac{b+m+\gamma}{\omega}, \frac{\omega c - b(b+m+\gamma)}{\omega(b+m+\gamma)}\right)$. Let the basic reproduction number $(R_0)$ be $R_0 = \frac{\omega c}{b(b+m+\gamma)}$. By defining $f(x,y) = c - bx - \omega xy, g(x,y) = \omega xy - (b+m+\gamma)y$.

**Theorem 1**. The disease-free equilibrium $E_0$ of the system (2.2), is locally asymptotically stable if only if $R_0 < 1$, else it is unstable.
*Proof.*
The Jacobian matrix of the equations 2.2 is presented in Equation 3.1.

$$J(X,Y) = \begin{pmatrix} \frac{\partial f}{\partial x} & \frac{\partial f}{\partial y} \\ \frac{\partial g}{\partial x} & \frac{\partial g}{\partial y} \end{pmatrix} = \begin{pmatrix} -b-\omega y & -\omega x \\ \omega y & \omega x - (b+m+\gamma) \end{pmatrix} \qquad 3.1$$

Evaluating the Jacobian matrix at $E_0$:

$$J(E_0) = \begin{pmatrix} -b-\omega.0 & -\omega.\frac{c}{b} \\ \omega.0 & \omega.\frac{c}{b} - (b+m+\gamma) \end{pmatrix} = \begin{pmatrix} -b & -\frac{\omega c}{b} \\ 0 & \frac{\omega c}{b} - (b+m+\gamma) \end{pmatrix}$$

Eigenvalues of this lower triangular matrix are the diagonal entries:

$$\lambda_1 = -b, \lambda_2 = \frac{\omega c}{b} - (b+m+\gamma)$$

Let

$$R_0 = \frac{\omega c}{b(b+m+\gamma)} \Rightarrow \lambda_2 = (b+m+\gamma)(R_0 - 1)$$

Eigenvalues of the Jacobian matrix are $\lambda_1 = -b$ and $\lambda_2 = \frac{\omega c}{b} - (b+m+\gamma)$. It means that the disease-free equilibrium point is asymptotically stable for $R_0$ and it is unstable for $R_0 > 1$.

**Theorem 2.** The endemic equilibrium $E_1$ of the system (2.2) is locally asymptotically stable if only if $R_0 > 1$, else it is unstable.
*Proof.*
The Jacobian matrix evaluated at the endemic equilibrium point that is $E_1$, is:

$$J(E_1) = \begin{pmatrix} -b - \dfrac{\omega c - b(b+m+\gamma)}{b+m+\gamma} & -(b+m+\gamma) \\ \dfrac{\omega c - b(b+m+\gamma)}{b+m+\gamma} & 0 \end{pmatrix}$$

Let $K = \frac{\omega c - b(b+m+\gamma)}{b+m+\gamma}$. Thus,

$$J(E_1) = \begin{pmatrix} -(b+K) & -(b+m+\gamma) \\ K & 0 \end{pmatrix}$$

Therefore, the characteristic polynomial is:

$$\det(J - \lambda I) = 0 \Rightarrow \lambda^2 + (b+K)\lambda + K(b+m+\gamma) = 0.$$

We obtain.

$$a_1 = b + K, a_0 = K(b+m+\gamma)$$

The eigenvalues are.

$$\lambda_{1,2} = \frac{-(b+K) \pm \sqrt{(b+K)^2 - 4K(b+m+\gamma)}}{2}$$

From the Routh–Hurwitz criterion, for the quadratic $\lambda^2 + a_1\lambda + a_0 = 0$, it requires $a_1 > 0$ and $a_0 > 0$. Therefore, $a_1 = b + K > 0$. Since $b > 0$ (natural death rate) and $K > 0$ when $R_0 > 1$, it follows that $a_1 > 0$. Similarly, $a_0 = K(b+m+\gamma) > 0$. Since $b + m + \gamma > 0$ (sum of positive parameters) and $K > 0$, this implies that $a_0 > 0$. In essence, both Routh–Hurwitz conditions are satisfied whenever $R_0 > 1$ and thus, the endemic equilibrium is locally asymptotically stable for $R_0 > 1$ and unstable for $R_0 < 1$.

***Model with vaccination***

There two equilibrium point of the system (2.3), the disease-free equilibrium, $\mathrm{E_0^v} = (\mathrm{X}, \mathrm{Y}) = \left(\frac{(1-\rho)\mathrm{c}}{\mathrm{b}}, 0\right)$, and the endemic equilibrium, $\mathrm{E_1^v} = (\mathrm{X}^*, \mathrm{Y}^*) = \left(\frac{\mathrm{b+m+\gamma}}{\omega}, \frac{(1-\rho)\omega\mathrm{c} - \mathrm{b(b+m+\gamma)}}{\omega(\mathrm{b+m+\gamma})}\right)$. With the reproduction number $R_v = \frac{(1-\rho)\omega c}{b(b+m+\gamma)}$.

**Theorem 3**. The disease-free equilibrium $\mathrm{E_0^v}$ of the system (2.3), is locally asymptotically stable if only if $R_0 < 1$, else it is unstable.

*Proof.*

The Jacobian matrix of the system (2.3) is presented in Equation 3.1.

$$\mathrm{J(X,Y)} = \begin{pmatrix} -\mathrm{b} - \omega\mathrm{Y} & -\omega\mathrm{X} \\ \omega\mathrm{Y} & \omega\mathrm{X} - (\mathrm{b} + \mathrm{m} + \gamma) \end{pmatrix} \qquad 3.1$$

Evaluating at $E_0^v$,

$$\mathrm{J(E_0^v)} = \begin{pmatrix} -\mathrm{b} & -\dfrac{(1-\rho)\omega\mathrm{c}}{\mathrm{b}} \\ 0 & \dfrac{(1-\rho)\omega\mathrm{c}}{\mathrm{b}} - (\mathrm{b} + \mathrm{m} + \gamma) \end{pmatrix}$$

$$\lambda_1 = -b < 0,\ \lambda_2 = \frac{(1-\rho)\omega c}{b} - (b+m+\gamma)$$

Using the vaccinated reproduction number, we rewrite:

$$\lambda_2 = (b+m+\gamma)(R_v - 1)$$

The disease-free equilibrium is locally asymptotically stable when $R_v < 1$, which implies $\lambda_2 < 0$, and unstable when $R_v > 1$, for which $\lambda_2 > 0$. Since the effective reproduction number satisfies $R_v = (1-\rho)R_0$, the condition $R_v < 1$ holds if and only if $\rho > 1 - \frac{1}{R_0}$. Therefore, vaccinating at a rate exceeding the critical threshold $\rho_c = 1 - \frac{1}{R_0}$, guarantees elimination of the disease.

**Theorem 4.** The endemic equilibrium $E_1^v$ of the system (2.3) is locally asymptotically stable if only if $R_0 > 1$, else it is unstable.

*Proof.*

Evaluating at $E_1^v$ and using $\omega X^* = b+m+\gamma$, we obtain:

$$J(E_1^v) = \begin{pmatrix} -b - \dfrac{(1-\rho)\omega c - b(b+m+\gamma)}{b+m+\gamma} & -(b+m+\gamma) \\ \dfrac{(1-\rho)\omega c - b(b+m+\gamma)}{b+m+\gamma} & 0 \end{pmatrix}$$

Let $K_v = \frac{(1-\rho)\omega c - b(b+m+\gamma)}{b+m+\gamma}$

Then,

$$J(E_1^v) = \begin{pmatrix} -(b+K_v) & -(b+m+\gamma) \\ K_v & 0 \end{pmatrix}$$

With

$$K_v = b(R_v - 1)$$

The characteristic equation is:

$$\det(J - \lambda I) = 0 \quad \Rightarrow \quad \lambda^2 + (b+K_v)\lambda + K_v(b+m+\gamma) = 0.$$

Thus,

$$a_1 = b + K_v, a_0 = K_v(b+m+\gamma)$$

The eigenvalues are:

$$\lambda_{1,2} = \frac{-(b+K_v) \pm \sqrt{(b+K_v)^2 - 4K_v(b+m+\gamma)}}{2}$$

From Routh-Hurwitz criterion, if all eigenvalues of the Jacobian have strictly negative real parts. If $R_v > 1$, then $K_v > 0$ and hence $a_1 > 0, a_0 > 0$. Therefore, the endemic equilibrium $E_1^v$ is locally asymptotically stable whenever it exists.

## 4. BIFURCATION ANALYSIS

The bifurcation analysis of the system (2.2) and (2.3) is carried out using the theorem Castillo – Chávez and Song [1].

**Theorem 5.** Consider the system $\dot{z} = f(z, \mu), z \in \mathbb{R}^n,\ \mu \in \mathbb{R}$, with $f(0, \mu) = 0$ for all $\mu$. Suppose that the Jacobian matrix $D_z f(0,0)$ has a simple zero eigenvalue and that all remaining eigenvalues have negative real parts. Let $v$ and $w$ be the corresponding right and left eigenvectors, normalized such that $w \cdot v = 1$. Define:

$$\alpha = w \cdot D_{z\mu} f(0,0)v, \beta = \frac{1}{2} w \cdot D_{zz} f(0,0)(v, v)$$

If $\alpha > 0$ and $\beta < 0$, then the system undergoes a forward transcritical bifurcation at $\mu = 0$.

*Proof*

Let

$$x = X - X_0, \qquad y = Y, \qquad \mu = \mathrm{R}_0 - 1$$

System (2.2) and (2.3) can be rewritten as:

$$\begin{aligned} \dot{x} &= -bx - (b + m + \gamma)(1 + \mu)y - \omega xy \\ \dot{y} &= (b + m + \gamma)\mu y + \omega xy \end{aligned} \tag{4.1}$$

The equilibrium $(x, y) = (0,0)$ corresponds to the DFE. At $\mu = 0$, the Jacobian matrix of the system (4.1) at $(0,0)$ is:

$$D_{(x,y)} G(x, y, \mu) = \begin{pmatrix} -b - \omega y & -(b + m + \gamma)(1 + \mu) - \omega x \\ \omega y & (b + m + \gamma)\mu + \omega x \end{pmatrix}$$

Evaluating at $(x, y, \mu) = (0,0,0)$, we obtain the linearized matrix:

$$A = D_{(x,y)} G(0,0,0) = \begin{pmatrix} -b & -(b + m + \gamma) \\ 0 & 0 \end{pmatrix}$$

This matrix has eigenvalues $-b < 0$ and 0. A right eigenvector corresponding to the zero eigenvalue is $v = \begin{pmatrix} -\frac{b+m+\gamma}{b} \\ 1 \end{pmatrix}$, and a left eigenvector is $w = (0,\ 1)$, satisfying $w \cdot v = 1$

Let $f = (f_1, f_2)^{\mathsf{T}}$ denote the right-hand side of system (4.1). Therefore,

$$\frac{\partial^2 f_2}{\partial \mu\ \partial y} = b + m + \gamma$$

Thus,

$$\alpha = w \cdot D_{z\mu} f(0,0)v = b + m + \gamma > 0$$

Similarly,

$$\frac{\partial^2 f_1}{\partial x\ \partial y} = -\omega, \qquad \frac{\partial^2 f_2}{\partial x\ \partial y} = \omega$$

Hence,

$$D_{zz}f(0,0)(v,v) = \begin{pmatrix} -2\omega v_1 v_2 \\ 2\omega v_1 v_2 \end{pmatrix}$$

Substituting $v_1 = -(b+m+\gamma)/b$ and $v_2 = 1$, we obtain

$$\beta = -\frac{\omega(b+m+\gamma)}{b} < 0$$

Since $\alpha > 0$ and $\beta < 0$, all the hypotheses of the Castillo-Chávez and Song theorem are satisfied. Therefore, system (2.2) and (2.3) undergoes a forward transcritical bifurcation at $R_0 = 1$ and $R_v = 1$, respectively.

## 5. NUMERICAL SIMULATION

The analytical findings presented in the preceding section have been validated through comprehensive numerical simulations conducted using MATLAB software. The parameter values and initial conditions used in the numerical simulations were assumed for illustrative purposes. These simulations serve to confirm the accuracy and reliability of the theoretical results, demonstrating consistency between the analytical approach and numerical simulation. The simulation was carried out using the following parameters and initial conditions shown in Table 5.1.

Table 5.1. Model Parameters and their Interpretations

| Parameter | Description | Estimated Value |
|---|---|---|
| $N$ | Total number of birds in the location | 10000 |
| $c$ | Average birth rate in birds | 0.03 |
| $S$ | Proportion of susceptible birds | 0.95 |
| $I$ | Proportion of infected birds | 0.05 |
| $b$ | Natural death rate in birds | 0.05 |
| $\omega$ | Infection transmission rate from bird to bird | 1.0 |
| $\gamma$ | Removal rate | 0.3 |
| $m$ | Flu-induced death rate for birds | 0.1 |
| $\rho$ | Vaccination rate | 0.6 |

***Model without vaccination***

A bifurcation of a dynamical system occurs when the parameter value of a system is changed. The bifurcation figure of the system (2.2) is presented in Figure 5.1.

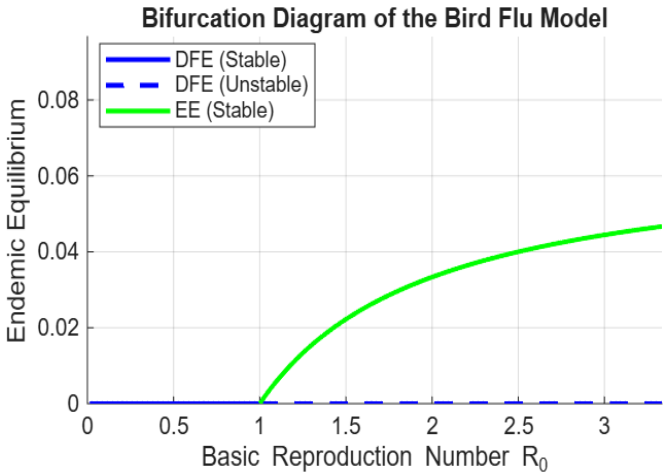


**Figure 5.1.** Bifurcation diagram of the system (2.2)

The Figure 5.1 illustrates the systems bifurcation indicating a forward transcritical bifurcation at $R_0 = 1$. Bifurcation diagram of system equations 2.2 is given in Figure 2.1. The figure illustrates forward transcritical bifurcation at the critical threshold $R_0 = 1$, where the stable disease-free equilibrium $R_0 < 1$ (blue solid line) becomes unstable when $R_0 > 1$ (blue dashed line). Thus, indicating that disease control depends upon keeping $R_0 < 1$. Similarly, the endemic critical point is asymptotically stable when $R_0 > 1$ and unstable when $R_0 < 1$ .

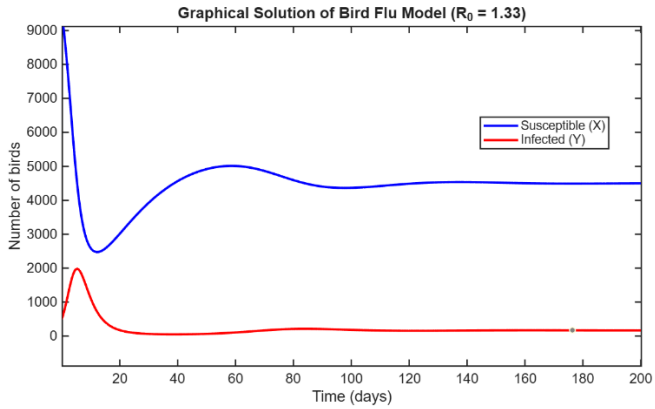


**Figure 5.2.** Graphical solution of the system (2.2)

The Figure 5.2 demonstrate the dynamics of the susceptible and infected compartments of bird population at $R_0 = 1.33$, indicating convergence to the endemic equilibrium. This confirms that the disease persists in the population rather than dying out.

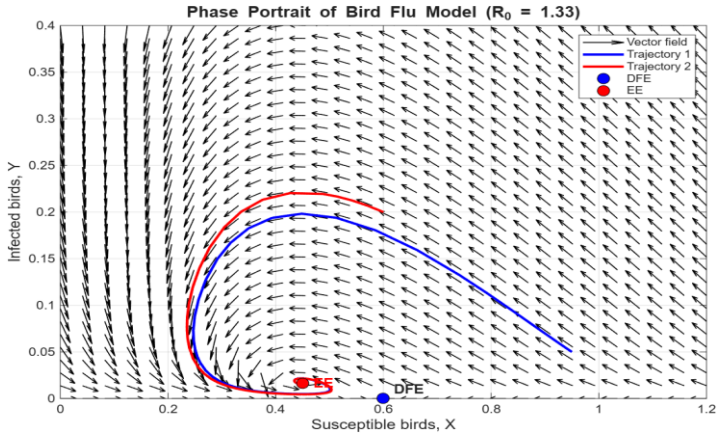


**Figure 5.3.** Phase Portrait of the system (2.2)

The Figure 5.3 shows the endemic equilibrium point $E_1 = (0.45,\ 0.0167)$, as $R_0 = 1.33$, its result in a positive endemic equilibrium, and the eigenvalues $\lambda_1 = -0.0333 + 0.0799i$, $\lambda_2 = -0.0333 - 0.0799i$, which have negative real parts. Thus, the equilibrium is locally asymptotically stable. Moreover, the existence of complex conjugates is indicative of oscillatory convergence. So, the endemic state is a stable spiral, i.e., the system converges to equilibrium through damped oscillations of the populations of the infected and of the susceptible birds.

***Model with vaccination***

The bifurcation figure of the system (2.3) is presented in Figure 5.4.

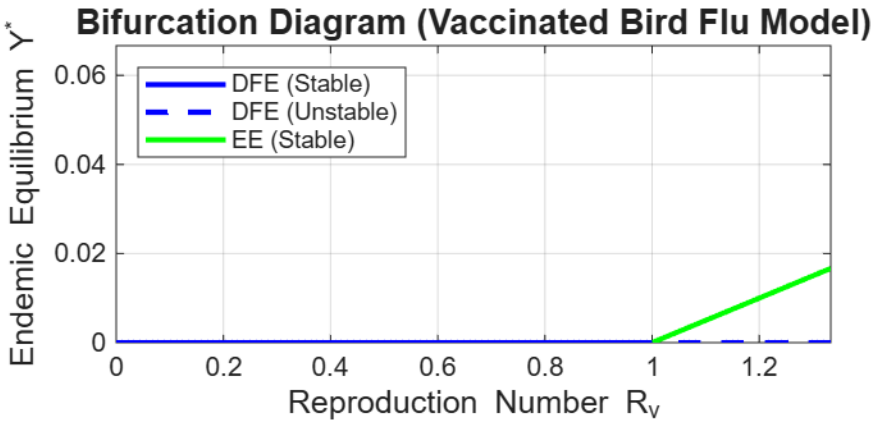


**Figure 5.4.** Bifurcation plot of the system (2.3)

The bifurcation diagram Figure 5.4 illustrates a forward (transcritical) bifurcation of the bird flu model with respect to the effective reproduction number $R_v$. When $R_v < 1$, the disease-free equilibrium is locally asymptotically stable, and no endemic equilibrium exists, indicating eventual elimination of the disease. As $R_v$increases and crosses the critical threshold $R_v = 1$, the disease-free equilibrium loses stability and a unique endemic equilibrium emerges. For $R_v > 1$, this endemic equilibrium is stable, while the disease-free equilibrium becomes unstable, leading to persistent infection within the population.

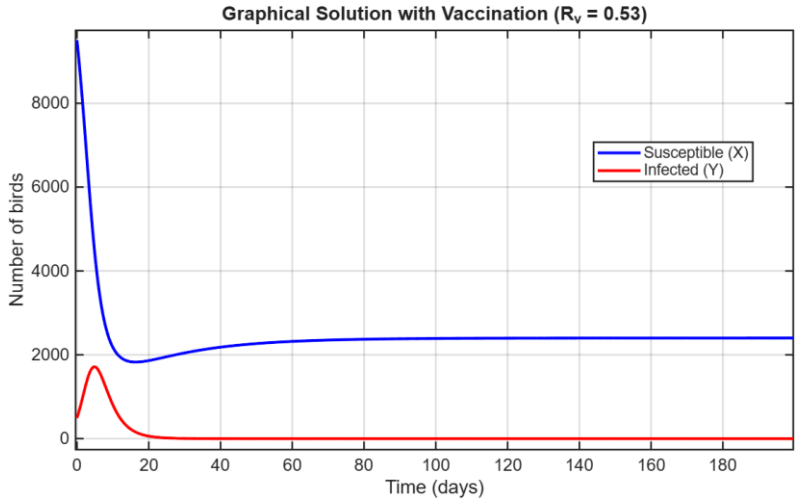


**Figure 5.5.** Graphical solution of the system (2.3)

The Figure 5.5 shows how vaccination significantly alters the disease dynamics. The number of susceptible birds decreases initially due to infection but later stabilizes as vaccination limits new infections. The infected population rises briefly and then steadily declines to zero, indicating that sustained transmission cannot be maintained.

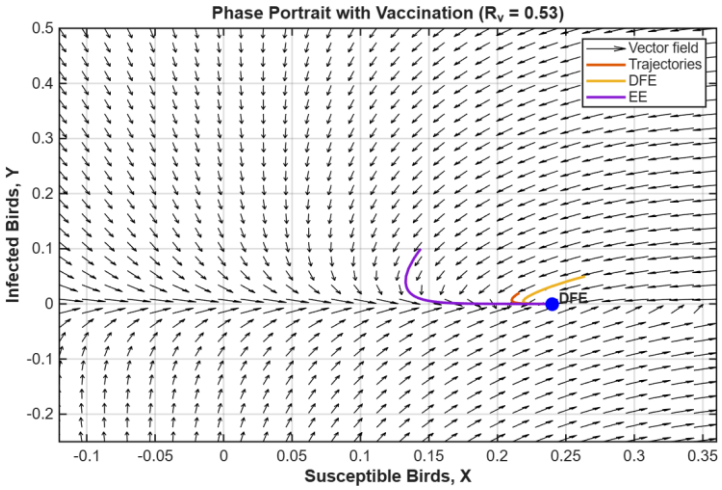


**Figure 5.6.** Phase Portrait of the system (2.3)

The phase portraite Figure 5.6 demonstrates how vaccination reduces the effective reproduction number to $R_v \approx 0.53 < 1$, ensuring that infection cannot persist. The disease-free equilibrium $E_0^v = (0.24,0)$ is locally asymptotically stable, with eigenvalues $\lambda_1 = -0.05$and $\lambda_2 = -0.21$, while the endemic equilibrium is biologically infeasible. Consequently, all trajectories in the phase portrait converge to the disease-free state, confirming vaccination as an effective control strategy.

## 6. CONCLUSION

The current research analyzes mathematical models with and without vaccination to assess bird flu dynamics in poultry farm. The findings show that the basic reproduction number determines the dynamics of the system, where the transcritical bifurcation at the value of $R_0 = 1$ and $R_v = 1$ separates the disease-free equilibrium and the endemic equilibrium. The vaccine reduces the

effective reproduction number to $R_v = (1-\rho)R_0$, meaning that the disease is not sustained when the threshold value is not attained. The findings of the study are important to poultry managers since they highlight the need to maintain vaccination rate above the critical threshold ($\rho > \rho_c = 1 - \frac{1}{R_0}$), for the disease to be eliminated. However, the study has limitations since it assumes that the mixing level of the population is homogeneous, the parameters are constant, and it does not account for environmental dynamics. Future research should incorporate environmental factors, stochastic dynamics, and case study validation for increased practical applicability.

## CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

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