A deterministic model for the transmission dynamics of avian influenza in birds (wild and domestic) and humans is developed. The model, which allows for the transmission of an avian strain and its mutant (assumed to be transmissible between humans), as well as the isolation of individuals with symptoms of any of the two strains, has a globally asymptotically stable disease-free equilibrium whenever a certain epidemiological threshold, known as the reproduction number, is less than unity. Further, the model has a unique endemic equilibrium whenever this threshold quantity exceeds unity. It is shown, using a non-linear Lyapunov function and LaSalle invariance principle, that this endemic equilibrium is globally asymptotically stable for a special case of the avian-only system. Numerical simulations show that, on average, the isolation of individuals with the avian strain is more beneficial than isolating those with the mutant strain. Furthermore, disease burden increases with increasing mutation rate of the avian strain.

**Keywords:** avian influenza; equilibria; stability; reproduction number; Lyapunov function

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1. Introduction

The 1918 pandemic has been one of the deadliest public health menaces of recorded human history, claiming over 20 million lives [23,26]. Although subsequent pandemics in 1957 ('Asian Flu') and 1968 ('Hong Kong Flu') resulted in milder outbreaks, the recent emergence of the highly pathogenic avian H5N1 influenza A viruses in wild bird populations in several regions of the world, together with recurrent flu cases of H5N1 viruses in humans (arising primarily from direct contact with poultry), have triggered a major scare for a pending pandemic influenza. The current projections of the potential impact of a prospective pandemic are alarming [2,5,22].

As noted by Ferguson et al. [7], the aforementioned highly pathogenic H5N1 influenza A viruses are now endemic in avian populations in Southeast Asia, and human cases continue to rise. However, although it is currently incapable of sustained human-to-human transmission, H5N1 represents a serious pandemic threat owing to the risk of a mutation or reassortment generating a virus with increased transmissibility. This clearly calls for a coordinated global effort to help combat a possible pandemic. In line with this need, a number of countries have formulated...
their public health preparedness plans to curtail the burden of a potential influenza pandemic [4].
These plans are primarily based on the use of non-pharmaceutical interventions (such as increased
hygiene, use of protective devices (e.g. face masks), isolation in hospital wards, and quarantine
of suspected cases) and pharmaceutical interventions (e.g. the use of antivirals and vaccine).
A number of mathematical modelling studies have been carried out to quantify the poten-
tial burden of an influenza pandemic and to assess various control strategies (see, for instance,
[7,9–11,20,21,24,28]). Although many of these studies tend to emphasize the use of pharmaceu-
tical interventions, it is generally believed that such interventions (antivirals and vaccine) would
not be readily and widely available at the onset of the pandemic. Thus, it is instructive to carry
out modelling studies that focus on non-pharmaceutical intervention such as isolation of those
with symptoms. Iwami et al. [15] presented a deterministic model, which allows the possibility
of transmission of an avian influenza mutant within humans. The current study extends the Iwami
et al. study by incorporating the dynamics of both wild and domestic birds (only wild birds were
considered in [15]) and the isolation of individuals with symptoms of both the avian and mutant
strains. Further, the current model allows for the recovery of individuals infected with the avian
strain as well as disease-induced mortality in people infected with the mutant strain.
The paper is organized as follows. The model is designed in Section 2. The global asymptotic
stability property of the avian-only sub-model is investigated in Section 3. The full model is
analysed in Section 4.

2. Model formulation

The model sub-divides the total avian population at time $t$, denoted by $N_A(t)$, into susceptible wild
birds ($S_W(t)$), susceptible domestic birds ($S_D(t)$), infected wild birds ($I_W(t)$) and infected domestic
birds ($I_D(t)$), so that $N_A(t) = S_W(t) + S_D(t) + I_W(t) + I_D(t)$. Similarly, the total human pop-
ulation at time $t$, denoted by $N_H(t)$, is sub-divided into susceptible humans ($S_H(t)$), humans
infected with the avian strain ($H_A(t)$), humans infected with the mutant strain ($H_M(t)$), isolated
humans with avian ($J_A(t)$) and mutant ($J_M(t)$) strains and recovered humans ($R_H(t)$). Thus,$N_H(t) = S_H(t) + H_A(t) + H_M(t) + J_A(t) + J_M(t) + R_H(t)$.
The population of susceptible wild birds is generated by birth (recruitment) of wild birds (at a
per capita rate $\Pi_W$). It is reduced by infection, following contact with infected birds (at a rate $\lambda_W$)
and by natural death (at a rate $\mu_A$). The rate $\lambda_W$ (the force of infection in the birds population at
time $t$) is given by

$$\lambda_W = \beta_W(I_W + I_D),$$

where $\beta_W$ is the effective contact rate (contact sufficient for infection) of wild birds (the aggregate
parameter $\beta_W$ is the product of number of contacts made by susceptible birds per unit time and
the probability of infection per contact). Thus,

$$\frac{dS_W}{dt} = \Pi_W - \lambda_W S_W - \mu_A S_W.$$

Similarly, the rate of change of the population of susceptible domestic birds is given by

$$\frac{dS_D}{dt} = \Pi_D - \lambda_D S_D - \mu_A S_D,$$

where $\Pi_D$ is the per capita birth rate of domestic birds and

$$\lambda_D = \beta_D(I_W + I_D)$$

is the force of infection for domestic birds. It should be mentioned that although the number
of contacts for susceptible wild or domestic birds are assumed to be the same, the respective
probabilities of transmission per contact are assumed to differ (so that, $\beta_W \neq \beta_D$). The above simple functional forms of $\lambda_W$ and $\lambda_D$ are chosen for mathematical convenience (more elaborate forms, that take into account various mixing heterogeneities, can be derived; but these may make the qualitative analysis of the resulting model less tractable).

It is assumed that domestic and wild birds have the same natural death rate ($\mu_A$). The population of infected wild birds is increased by infection of the susceptible wild birds (at the rate $\lambda_W$) and decreased by natural death (at the rate $\mu_A$) and disease-induced mortality (at a rate $\delta_W$). Hence,

$$\frac{dI_W}{dt} = \lambda_W S_W - \mu_A I_W - \delta_W I_W.$$  

The population of infected domestic birds is generated following infection of susceptible domestic birds (at the rate $\lambda_D$), and reduced by natural death (at the rate $\mu_A$) and disease-induced mortality (at a rate $\delta_D$), so that

$$\frac{dI_D}{dt} = \lambda_D S_D - \mu_A I_D - \delta_D I_D.$$  

Susceptible humans are generated at a constant rate $\Pi_H$, and reduced by acquiring infection with the avian strain (at the rate $\lambda_A$) and the mutant strain (at a rate $\lambda_M$). The rate $\lambda_M$ is given by,

$$\lambda_M = \beta_M \eta_M (H_M + \theta J_M),$$

where, $\beta_M$ is the effective contact rate for the transmission of the mutant strain, $0 < \eta_M < 1$ accounts for the assumed reduced transmissibility of the mutant strain in relation to the avian strain, and $0 < \theta J < 1$ models the assumed reduction in the probability of transmission during isolation (in other words, the parameter $\theta J$ measures the efficacy of isolation in minimizing the risk of transmission of the mutant strain during isolation). In line with Iwami et al. [15], it is assumed that humans infected with the avian strain do not infect other humans. The use of intervention strategies, such as taking precautions against handling poultry products or using prophylaxis, is modelled using a correction term $\tau$ (with $0 < \tau \leq 1$) in $\lambda_W$, $\lambda_D$ and $\lambda_M$ (that is, $\tau$ is an infection-reduction parameter in humans). The susceptible human population is further reduced by natural death (at a rate $\mu_H$). Putting all these assumptions and definitions together leads to the following expression for the rate of change of the susceptible human population.

$$\frac{dS_H}{dt} = \Pi_H - \tau (\lambda_W + \lambda_D + \lambda_M) S_H - \mu_H S_H.$$  

The population of humans infected with the avian strain is generated following infection (at the rates $\lambda_W$ and $\lambda_D$). It is diminished by mutation of the wild strain to the mutant strain (at a rate $\xi_A$), natural death (at the rate $\mu_H$), isolation (at a rate $\psi_A$) and disease-induced death (at a rate $\delta_H$), so that

$$\frac{dH_A}{dt} = \tau (\lambda_W + \lambda_D) S_H - \xi_A H_A - \psi_A H_A - \mu_H H_A - \delta_H H_A.$$  

Similarly, the rate of change of the population of infectious individuals with the mutant strain is given by

$$\frac{dH_M}{dt} = \tau \lambda_M S_H + \xi_A H_A - \psi_M H_M - \mu_H H_M - \theta_M \delta_H H_M,$$

where the parameter $\theta_M$ accounts for the variability in mortality between the mutant and the avian strain.

The population of isolated individuals with the avian strain is generated at the rate $\psi_A$. It is diminished by recovery (at a rate $\gamma_A$), natural death (at the rate $\mu_H$) and disease-induced
death (at the reduced rate $\theta_D\delta_H$, where $0 < \theta_D < 1$; it is assumed that isolated individuals are given some treatment such as Tamiflu). This gives

$$\frac{dJ_A}{dt} = \psi_A H_A - \gamma_A J_A - \mu_H J_A - \theta_D\delta_H J_A.$$  

It is assumed that individuals in the $J_A$ class do not develop the mutant strain (since they are presumably effectively treated during isolation). Similarly, the population of isolated individuals infected with the mutant strain changes according to the following equation

$$\frac{dJ_M}{dt} = \psi_M H_M - \gamma_M J_M - \mu_H J_M - \theta_D\theta_M\delta_H J_M.$$  

Finally, the population of the recovered individuals is generated by recovery of infectious individuals (both with the avian and the mutant strains). It is decreased by natural death (at the rate $\mu_H$). Thus,

$$\frac{dR_H}{dt} = \gamma_A J_A + \gamma_M J_M - \mu_H R_H.$$  

In summary, the model for the transmission dynamics of influenza in the avian and human populations is given by the following system of differential equations (a schematic flow diagram of the model is depicted in Figure 1; and the associated model variables and parameters are described in Tables 1 and 2 respectively).

$$\frac{dS_W}{dt} = \Pi_W - \lambda_W S_W - \mu_A S_W,$$

$$\frac{dS_D}{dt} = \Pi_D - \lambda_D S_D - \mu_A S_D,$$

$$\frac{dI_W}{dt} = \lambda_W S_W - \mu_A I_W - \delta_W I_W,$$

$$\frac{dI_D}{dt} = \lambda_D S_D - \mu_A I_D - \delta_D I_D,$$

$$\frac{dS_H}{dt} = \Pi_H - \tau (\lambda_W + \lambda_D + \lambda_M) S_H - \mu_H S_H,$$

$$\frac{dH_A}{dt} = \tau (\lambda_W + \lambda_D) S_H - \xi_A H_A - \psi_A H_A - \mu_H H_A - \delta_H H_A,$$

$$\frac{dH_M}{dt} = \tau \lambda_M S_H + \xi_A H_A - \psi_M H_M - \mu_H H_M - \theta_M\delta_H H_M,$$

$$\frac{dJ_A}{dt} = \psi_A H_A - \gamma_A J_A - \mu_H J_A - \theta_D\delta_H J_A,$$

$$\frac{dJ_M}{dt} = \psi_M H_M - \gamma_M J_M - \mu_H J_M - \theta_D\theta_M\delta_H J_M,$$

$$\frac{dR_H}{dt} = \gamma_A J_A + \gamma_M J_M - \mu_H R_H.$$  

### 2.1. Basic properties

Since the model (1) monitors human populations, all the associated parameters and state variables are non-negative for $t \geq 0$ (it is easy to show that the state variables of the model
remain non-negative for all non-negative initial conditions). Consider the biologically feasible region

\[ D = \left\{ (S_W, S_D, I_W, I_D, S_H, H_A, H_M, J_A, J_M, R_H) \in \mathbb{R}^{10}_+ : N_A \leq \frac{\Pi_W + \Pi_D}{\mu_A}, N_H \leq \frac{\Pi_H}{\mu_H} \right\}. \]

**Lemma 1**  The closed set \( D \) is positively invariant and attracting.

**Proof**  Adding the first four equations in the model (1) gives the rate of change of the total avian population:

\[ \frac{dN_A}{dt} = \Pi_A - \mu_A N_A - \delta_W I_W - \delta_D I_D, \tag{2} \]

where \( \Pi_A = \Pi_W + \Pi_D \). Similarly, adding the fifth to the tenth equations of Equation (1) gives the rate of change of the total human population:

\[ \frac{dN_H}{dt} = \Pi_H - \mu_H N_H - \delta_H (H_A + \theta_M H_M + \theta_D J_A + \theta_M J_M). \tag{3} \]

It is clear from Equation (2) that

\[ \frac{dN_A}{dt} \leq \Pi_A - \mu_A N_A. \]
Thus, the total avian population \( N_A \) is bounded above by \( \frac{\Pi_A}{\mu_A} \), so that \( dN_A(t)/dt < 0 \) whenever \( N(t) > \frac{\Pi_A}{\mu_A} \). Thus, a standard comparison theorem [18, p. 31] can be used to show that \( N_A(t) \leq N_A(0)e^{-\mu_A t} + \frac{\Pi_A}{\mu_A}(1 - e^{-\mu_A t}) \). In particular, \( N_A(t) \leq \frac{\Pi_A}{\mu_A} \) if \( N_A(0) \leq \frac{\Pi_A}{\mu_A} \).

Similarly, it follows from Equation (3) that

\[
\frac{dN_H}{dt} \leq \frac{\Pi_H}{\mu_H} - \frac{\Pi_H}{\mu_H}. 
\]

Thus, \( N_H(t) \) is bounded above by \( \frac{\Pi_H}{\mu_H} \), and \( dN_H(t)/dt < 0 \) if \( N_H(t) > \frac{\Pi_H}{\mu_H} \). Here, too, a comparison theorem can be used to show that \( N_H(t) \leq N_H(0)e^{-\mu_H t} + \frac{\Pi_H}{\mu_H}(1 - e^{-\mu_H t}) \). Hence, \( N_H(t) \leq \frac{\Pi_H}{\mu_H} \) if \( N_H(0) \leq \frac{\Pi_H}{\mu_H} \). Thus, \( D \) is positively invariant. Further, if \( N_A(0) > \frac{\Pi_A}{\mu_A} \), then either the solution enters \( D \) in finite time, or \( N_A(t) \) approaches \( \frac{\Pi_A}{\mu_A} \) asymptotically (similar argument holds for the human component if \( N_H(0) > \frac{\Pi_H}{\mu_H} \)). Hence, the region \( D \) attracts all solutions in \( \mathbb{R}_+^4 \).

Since the region \( D \) is positively invariant and attracting (Lemma 1), it is sufficient to consider the dynamics of the flow generated by the model (1) in \( D \), where the usual existence, uniqueness, continuation results hold for the system (that is, the system (1) is mathematically and epidemiologically well-posed in \( D \)).

Before analysing the full model, it is instructive to study the dynamics of the avian-only model as below.

### 3. Analysis of the avian-only model

Consider the avian-only model, given by the first four equations of Equation (1), as below

\[
\begin{align*}
\frac{dS_W}{dt} &= \Pi_W - \lambda_W S_W - \mu_A S_W, \\
\frac{dS_D}{dt} &= \Pi_D - \lambda_D S_D - \mu_A S_D, \\
\frac{dI_W}{dt} &= \lambda_W S_W - \mu_A I_W - \delta_W I_W, \\
\frac{dI_D}{dt} &= \lambda_D S_D - \mu_A I_D - \delta_D I_D.
\end{align*}
\]

(4)

It should be noted that the avian system above is independent of the human system. Define the region

\[
D_A = \left\{ (S_W, S_D, I_W, I_D) \in \mathbb{R}_+^4 : S_W + S_D + I_W + I_D \leq \frac{\Pi_A}{\mu_A} \right\}.
\]

It can be shown, using a similar approach as in the proof of Lemma 1, that all solutions of the avian-only system (4) starting in \( D_A \) remain in \( D_A \) for all \( t > 0 \), and that \( D_A \) attracts all solutions in \( \mathbb{R}_+^4 \) (that is, \( D_A \) is positively invariant and attracting). Hence, it is sufficient to consider the dynamics of the avian-only system (4) in \( D_A \).
3.1. Stability of the disease-free equilibrium (DFE)

The avian-only model (4) has a DFE given by

$$E_0 = (S^*_W, S^*_D, I^*_W, I^*_D) = \left( \frac{\Pi_W}{\mu_A}, \frac{\Pi_D}{\mu_A}, 0, 0 \right).$$

The local stability of $E_0$ will be explored using the next generation operator method [6,27]. Using the notation in [27], the non-negative matrix, $F$, of new infection terms and the $M$-matrix, $V$, of transition terms associated with the model (4) are given, respectively, by

$$F = \begin{pmatrix} \beta_W S^*_W & \beta_W S^*_W \\ \beta_D S^*_D & \beta_D S^*_D \end{pmatrix},$$

and

$$V = \begin{pmatrix} \mu_A + \delta_W & 0 \\ 0 & \mu_A + \delta_D \end{pmatrix}.$$

It follows that the basic reproduction number of the avian-only system (4), denoted by $R_A$, is given by (where $\rho$ denotes the spectral radius)

$$R_A = \rho(FV^{-1}) = \frac{\Pi_D \beta_D}{\mu_A (\mu_A + \delta_D)} + \frac{\Pi_W \beta_W}{\mu_A (\mu_A + \delta_W)}.$$

(5)

Further, using Theorem 2 in [27], the following result is established.

Lemma 2 The DFE of the avian-only model (4), given by $E_0$, is locally asymptotically stable (LAS) if $R_A < 1$, and unstable if $R_A > 1$.

The basic reproduction number ($R_A$) measures the average number of new infections generated by a single infected bird in a completely susceptible avian population [1]. Thus, Lemma 2 implies that avian flu can be eliminated from the avian population (when $R_A < 1$) if the initial sizes of the sub-populations of the avian-only model are in the basin of attraction of the DFE, $E_0$. To ensure that elimination of avian flu is independent of the initial sizes of the sub-populations, it is necessary to show that the DFE ($E_0$) is globally asymptotically stable (GAS). This is done below.

3.2. Global stability of the DFE of the avian-only model

Define, first of all, the region

$$D_w = \{(S_w, S_D, I_w, I_D) \in D_A : S_w \leq S^*_w, S_D \leq S^*_D\}$$

Lemma 3 The region $D_w$ is positively invariant and attracting.

Proof It should be noted that the region $D_A$ is shown to be positively invariant and attracting (Lemma 1). Using the approach in [25], the first equation of the avian-only system (4) can be simplified to

$$\frac{dS_w}{dt} = \Pi_W - \beta_W (I_w + I_D) S_w - \mu_A S_w,$$

$$\leq \Pi_W - \mu_A S_w$$

$$= \mu_A \left(S^*_w - S_w\right).$$

Hence, $S_w(t) \leq S^*_w - (S^*_w - S_w(0))e^{-(\mu_A t)}$ (note that $dS_w/dt < 0$ if $S_w(t) > S^*_w$). Thus, it follows that either $S_w(t)$ approaches $S^*_w$ asymptotically, or there is some finite time after which
\[ S_W(t) \leq S_W^* \]. Similarly, the equation for \( dS_D/dt \) in Equation (4) can be simplified to

\[
\frac{dS_D}{dt} = \Pi_D - \beta_D(I_W + I_D)S_D - \mu_AS_D, \\
\leq \Pi_D - \mu_AS_D = \mu_A(S_W^* - S_D).
\]

Hence, \( S_D(t) \leq S_D^* - [S_D^* - S_D(0)]e^{-\mu t} \), and, either \( S_D(t) \) approaches \( S_D^* \) asymptotically, or \( S_D(t) \) becomes, and remains, less than \( S_D^* \) in finite time (note that \( dS_D/dt < 0 \) if \( S_D(t) > S_D^* \)). Thus, the set \( D_s \) is attracting and positively invariant.

We claim the following result.

**Theorem 1** The DFE of the avian-only model (4), given by \( \mathcal{E}_0 \), is GAS in \( D_s \) whenever \( R_A \leq 1 \).

**Proof** Consider the Lyapunov function

\[ \mathcal{F} = (\mu_A + \delta_D)I_W + (\mu_A + \delta_W)I_D, \]

with Lyapunov derivative (where a prime represents differentiation with respect to \( t \))

\[
\mathcal{F}' = (\mu_A + \delta_D)\left[ \beta_W(I_W + I_D)S_W - (\mu_A + \delta_W)I_W \right] \\
+ (\mu_A + \delta_W)\left[ \beta_D(I_W + I_D)S_D - (\mu_A + \delta_D)I_D \right] \\
= \left[ \beta_W(\mu_A + \delta_D)S_W + \beta_D(\mu_A + \delta_W)S_D - (\mu_A + \delta_D)(\mu_A + \delta_W) \right]I_W \\
+ \left[ \beta_W(\mu_A + \delta_D)S_W + \beta_D(\mu_A + \delta_W)S_D - (\mu_A + \delta_D)(\mu_A + \delta_W) \right]I_D \\
= \left[ \beta_W(\mu_A + \delta_D) + \beta_D(\mu_A + \delta_W) \right]I_W \\
+ \left[ \beta_W(\mu_A + \delta_D) + \beta_D(\mu_A + \delta_W) \right]I_D \\
\leq 0 \quad \text{for} \quad R_A \leq 1.
\]

Note that the inequalities \( S_W(t) \leq S_W^* \) and \( S_D(t) \leq S_D^* \) (in \( D_s \)) have been used in the computation of the Lyapunov derivative above. Further, since \( S_W^* + S_D^* = \Pi_A/\mu_A \), equality in the above inequality for \( \mathcal{F}' \) implies \( I_W = I_D = 0 \). Thus, \( \mathcal{F}' \leq 0 \) if \( R_A \leq 1 \) with \( \mathcal{F}' = 0 \) if and only if \( I_W = I_D = 0 \). Further, the cone \( D_s \) is an invariant and attracting subset of \( \mathbb{R}_+^4 \) (Lemma 3), and the largest compact invariant set in \{ \( (S_W, S_D, I_W, I_D) \in D_s : \mathcal{F}' = 0 \) \} is the singleton \{ \( \mathcal{E}_0 \) \}. Thus, it follows from the LaSalle invariance principle [13,17], that every solution to the equations in Equation (4), with initial conditions in \( \mathbb{R}_+^4 \), approaches \( \mathcal{E}_0 \) as \( t \rightarrow \infty \) whenever \( R_A \leq 1 \). Thus, the DFE, \( \mathcal{E}_0 \), is GAS in \( D_s \) for \( R_A \leq 1 \).

3.3. **Existence of endemic equilibrium**

To find condition(s) for the existence of an equilibrium \( \mathcal{E}_1 = (S_W^*, S_D^*, I_W^*, I_D^*) \) of the avian-only system (4) for which the disease is endemic in the avian population (i.e. at least one of \( I_W^* \) and \( I_D^* \) is non-zero), the equations in Equation (4) are solved at steady-state (in terms of \( \lambda_W \) and \( \lambda_D \) at
steady-state) giving
\[
S^*_W = \frac{\Pi_W}{\lambda^*_W + \mu_A}, \quad S^*_D = \frac{\Pi_D}{\lambda^*_D + \mu_A}, \quad I^*_W = \frac{\lambda^*_W S^*_W}{\mu_A + \delta_W}, \quad I^*_D = \frac{\lambda^*_D S^*_D}{\mu_A + \delta_D}.
\]

Substituting the expressions in Equation (7) into \( \lambda^*_W = \beta_W (I^*_W + I^*_D) \) and simplifying (noting that \( \lambda^*_D = \beta_D \lambda^*_W / \beta_W \)) gives the following polynomial in \( \lambda^*_W \)
\[
a_0 (\lambda^*_W)^2 + a_1 \lambda^*_W + a_2 = 0 \tag{8}
\]
where
\[
a_0 = \beta_D (\mu_A + \delta_W) (\mu_A + \delta_D), \quad a_1 = \mu_A^2 (\mu_A + \delta_D) (\mu_A + \delta_W) (1 - R_A), \quad a_2 = \beta_W \mu_A^2 (\mu_A + \delta_D) (\mu_A + \delta_W) (1 - R_A).
\]

The endemic equilibria of the avian-only model (4) are obtained by substituting the positive roots of Equation (8) into Equation (7). Since the coefficient \( a_0 > 0 \) and \( a_2 < 0 \) whenever \( R_A > 1 \), it follows that the avian-only model has a unique positive (endemic) equilibrium if \( R_A > 1 \). Further, if \( R_A \leq 1 \), then \( a_1 \geq 0 \) and \( a_2 \geq 0 \), so that the model has no positive root. This result is summarized below.

**Lemma 4** The avian-only model (4) has a unique endemic (positive) equilibrium, given by \( E_1 \), whenever \( R_A > 1 \), and no positive endemic equilibrium otherwise.

### 3.4. Stability of endemic equilibrium: special case

Establishing the stability of the unique endemic equilibrium, \( E_1 \), of the avian-only system (4) is rather daunting (the process requires the application of the Routh–Hurwitz conditions on a characteristic polynomial of order four). Consequently, for mathematical convenience, the stability analysis of the equilibrium \( E_1 \) will be carried out for a special case, as follows. Let \( S_A = S_W + S_D, I_A = I_W + I_D, \Pi_A = \Pi_W + \Pi_D \). Further, let \( \beta_W = \beta_D = \beta_A \) and \( \delta_W = \delta_D = \delta_A \). Thus, the avian-only model (4) reduces to the following system (reduced avian system)
\[
\begin{align*}
\frac{dS_A}{dt} &= \Pi_A - \beta_A I_A S_A - \mu_A S_A, \\
\frac{dI_A}{dt} &= \beta_A I_A S_A - \mu_A I_A - \delta_A I_A.
\end{align*}
\]

For the reduced system (10), the following results are well known in the literature (see, for instance, Hethcote [14]).

**Lemma 5** Consider the avian-only system (4) with \( \beta_W = \beta_D = \beta_A \) and \( \delta_W = \delta_D = \delta_A \), given by Equation (10).

(a) the DFE, \( e_0 = (S^*_A, I^*_A) = (\Pi/\mu_A, 0) \), of the reduced system (10), is GAS whenever
\[
r_0 = \frac{\beta_A \Pi_A}{\mu_A (\mu_A + \delta_A)} \leq 1;
\]
(b) the unique endemic equilibrium of the reduced avian system (10), given by
\[ e_1 = (S_A^{**}, I_A^{**}) = \left[ \frac{\mu_A + \delta_A}{\beta_A}, \frac{\mu_A}{\beta_A} (r_0 - 1) \right]. \]
is GAS whenever \( r_0 > 1 \).

It should be noted that \( R_A \) reduces to \( r_0 \) if \( \Pi_A = \Pi_W + \Pi_D, \beta_W = \beta_D = \beta_A \) and \( \delta_W = \delta_D = \delta_A \).

In summary, the avian-only system (4) has a globally asymptotically stable disease-free equilibrium whenever \( R_A \leq 1 \) (Theorem 1) and has a unique endemic equilibrium whenever \( R_A > 1 \) (Lemma 4), which is globally asymptotically stable for the special case of the avian system (10) (Lemma 5). Thus, the disease will die out within the avian population if \( R_A \leq 1 \) and would persist otherwise.

4. Analysis of the full model

4.1. Local stability of the DFE

The full avian-human model (1) has a DFE given by,
\[ E_{0f} = \left( S_W^*, S_D^*, I_W^*, I_D^*, H_A^*, H_M^*, J_A^*, J_M^*, R_H^* \right) = \left( \frac{\Pi_W}{\mu_A}, \frac{\Pi_D}{\mu_A}, 0, 0, \frac{\Pi_H}{\mu_H}, 0, 0, 0, 0 \right). \] (11)

Here, the associated next generation matrices are given by
\[ F = \begin{pmatrix}
\beta_W S_w^* & \beta_W S_w^* & 0 & 0 & 0 & 0 \\
\beta_D S_D^* & \beta_D S_D^* & 0 & 0 & 0 & 0 \\
(\beta_W + \beta_D) \tau S_H^* & (\beta_W + \beta_D) \tau S_H^* & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \tau \beta_M \eta_M S_H^* & \tau \beta_M \eta_M \theta_J S_H^* \\
0 & 0 & 0 & 0 & 0 & 0
\end{pmatrix}, \]
\[ V = \begin{pmatrix}
k_1 & 0 & 0 & 0 & 0 & 0 \\
0 & k_2 & 0 & 0 & 0 & 0 \\
0 & 0 & k_3 & 0 & 0 & 0 \\
0 & 0 & -\xi_A & k_4 & 0 & 0 \\
0 & 0 & -\psi_A & 0 & k_5 & 0 \\
0 & 0 & 0 & -\psi_M & 0 & k_6
\end{pmatrix}, \]
where \( k_1 = \mu_A + \delta_W, k_2 = \mu_A + \delta_D, k_3 = \xi_A + \psi_A + \mu_H + \delta_H, k_4 = \gamma_M + \mu_H + \theta_M \delta_H, k_5 = \gamma_A + \mu_H + \theta_D \delta_H, k_6 = \gamma_M + \mu_H + \theta_D \theta_M \delta_H. \)

Let \( R_{AH} = \rho(FV^{-1}) \). It follows then that
\[ R_{AH} = \max \{ R_A, R_H \}. \] (12)

where \( R_A \) is as defined in Section 3.1 and \( R_H = \frac{\beta_M \eta_M \Pi_H \tau (\gamma_M + \mu_H + \theta_D \theta_M \delta_H + \psi_M \theta_J)}{\mu_H (\psi_M + \mu_H + \theta_M \delta_H) (\gamma_M + \mu_H + \theta_D \theta_M \delta_H)} \) is the reproduction number associated with the transmission of avian influenza in the human population. It follows from Theorem 2 of [27] that

**Theorem 2**  The DFE of the avian-human model (1), given by \( E_{0f} \), is LAS if \( R_{AH} < 1 \), and unstable if \( R_{AH} > 1 \).
4.2. Global stability of the DFE

We claim the following:

**Theorem 3** The DFE of the avian-human model (1) is GAS in $\mathcal{D}$ whenever $\mathcal{R}_{AH} \leq 1$.

**Proof** Let $\mathcal{R}_{AH} \leq 1$. It should be recalled that for $\mathcal{R}_{AH} \leq 1$ (that is, $\mathcal{R}_A \leq 1$), the DFE of the avian-only model is globally asymptotically stable (Theorem 1). So, the task is to show that the DFE of the human-only component of the model (1) is also globally asymptotically stable whenever $\mathcal{R}_{AH} \leq 1$. Substituting $I_W = I_D = 0$ in the model system (1) gives the human-only model below:

$$
\begin{align*}
\frac{dS_H}{dt} &= \Pi_H - \tau \lambda_M S_H - \mu_H S_H, \\
\frac{dH_A}{dt} &= -\xi_A H_A - \psi_A H_A - \mu_H H_A - \delta_H H_A, \\
\frac{dH_M}{dt} &= \lambda_M \tau S_H - \xi_A H_A - \psi_M H_M - \mu_H H_M - \theta_M \delta_H H_M, \\
\frac{dJ_A}{dt} &= \psi_A H_A - \gamma_A J_A - \mu_H J_A - \theta_D \delta_H J_A, \\
\frac{dJ_M}{dt} &= \psi_M H_M - \gamma_M J_M - \mu_H J_M - \theta_D \theta_M \delta_H J_M, \\
\frac{dR_H}{dt} &= \gamma_A J_A + \gamma_M J_M - \mu_H R_H.
\end{align*}
$$

(13)

It is clear from Equation (13) that $H_A \to 0$ as $t \to \infty$. Further, $J_A \to 0$ as $t \to \infty$ (since $H_A \to 0$ asymptotically). Setting $H_A = J_A = 0$ in Equation (13) gives the following limiting (human-only) system:

$$
\begin{align*}
\frac{dS_H}{dt} &= \Pi_H - \tau \lambda_M S_H - \mu_H S_H, \\
\frac{dH_M}{dt} &= \lambda_M \tau S_H - \psi_M H_M - \mu_H H_M - \theta_M \delta_H H_M, \\
\frac{dJ_M}{dt} &= \psi_M H_M - \gamma_M J_M - \mu_H J_M - \theta_D \theta_M \delta_H J_M, \\
\frac{dR_H}{dt} &= \gamma_M J_M - \mu_H R_H.
\end{align*}
$$

(14)

The system (14) has a DFE given by $E_{0m} = (S_{H_M}^*, H_M^*, J_M^*, R_H^*) = (\Pi_H/\mu_H, 0, 0, 0)$, which can easily be shown to be LAS whenever $\mathcal{R}_H < 1$. For simplicity, the threshold quantity $\mathcal{R}_H$ is re-written as

$$
\mathcal{R}_H = \frac{\beta_M \eta_M \Pi_H \tau (k_6 + \psi_M \theta_J)}{\mu_H k_4 k_6},
$$

where $k_4$ and $k_6$ are as defined in Section 4.1.
Consider the following Lyapunov function for the system (14)
\[ F = (k_6 + \theta_j \psi_M)H_M + \theta_j k_4 J_M, \]
with Lyapunov derivative,
\[ F' = (k_6 + \theta_j \psi_M) [\beta_M \eta_M \tau (H_M + \theta_j J_M) S_H - k_4 H_M] + \theta_j k_4 (\psi_M H_M - k_6 J_M), \]
so that (noting that \( S_H \leq \Pi_H / \mu_H \) in \( D \))
\[ F' \leq (k_6 + \theta_j \psi_M) \left[ \beta_M \eta_M \tau \left( \frac{\Pi_H}{\mu_H} - k_4 H_M \right) + \theta_j k_4 (\psi_M H_M - k_6 J_M) \right], \]
\[ = \left[ \beta_M \eta_M \tau (k_6 + \theta_j \psi_M) \frac{\Pi_H}{\mu_H} + \theta_j k_4 \psi_M - k_4 (k_6 + \theta_j \psi_M) \right] H_M \]
\[ + \theta_j \left[ \beta_M \eta_M \tau (k_6 + \theta_j \psi_M) \frac{\Pi_H}{\mu_H} - k_4 k_6 \right] J_M, \]
\[ = \frac{1}{\mu_H} \left[ \beta_M \eta_M \Pi_H \tau (k_6 + \theta_j \psi_M) - \mu_H k_4 k_6 \right] H_M \]
\[ + \frac{\theta_j}{\mu_H} \left[ \beta_M \eta_M \Pi_H \tau (k_6 + \theta_j \psi_M) - \mu_H k_4 k_6 \right] J_M, \]
\[ = k_4 k_6 (R_H - 1) H_M + \theta_j k_4 k_6 (R_H - 1) J_M \]
\[ \leq 0 \quad \text{for} \quad R_H \leq 1. \]

Thus, by the same logic as outlined in the proof of Theorem 1, \( F' \leq 0 \) if \( R_H \leq 1 \), with \( F' = 0 \) if and only if \( H_M = J_M = 0 \) (note that setting \( H_M = J_M = 0 \) in the last equation of (14) shows that \( R_H \to 0 \) as \( t \to \infty \)). Hence, the DFE of Equation (14) is GAS if \( R_{AH} \leq 1 \); and so is the DFE of Equation (13). Since the DFE of both the avian-only system (4) and the human-only system (13) are GAS when \( R_{AH} \leq 1 \), it follows that the DFE of the full avian-human model (1) is GAS whenever \( R_{AH} \leq 1 \). ■

4.3. Existence and stability of endemic equilibria

Here, too, the reduced avian system (10) will be used. Let \( E = (S_A^{**}, I_A^{**}, S_H^{**}, H_A^{**}, H_M^{**}, J_A^{**}, J_M^{**}, R_H^{**}) \) represent any arbitrary equilibrium of the model (1), with its first four equations replaced by the reduced system (10). The objective is to determine the number of possible endemic equilibria the model (1) (with the first four equations replaced by Equation (10)) can have when \( R_{AH} > 1 \). Solving the model (1), with the first four equations replaced by Equation (10), at steady-state gives
\[ S_A^{**} = \frac{\Pi_A}{\lambda_A^{**} + \mu_A}, \quad I_A^{**} = \frac{\lambda_A^{**} \Pi_A}{(\mu_A + \delta_A)(\lambda_A^{**} + \mu_A)}, \quad S_H^{**} = \frac{\Pi_H}{(\lambda_A^{**} \tau + \lambda_M^{**} + \mu_H)}, \]
\[ H_A^{**} = \frac{\lambda_A^{**} \tau \Pi_H}{(\mu_H + \xi_A + \delta_H + \psi_A)(\lambda_A^{**} \tau + \lambda_M^{**} + \mu_H)}, \]
\[ H_M^{**} = \frac{\tau \Pi_H (\mu_H \lambda_A^{**} + \delta_H \lambda_A^{**} + \xi_A \lambda_M^{**} + \psi_A \lambda_A^{**} + \lambda_A^{**} \tau + \mu_H)}{(\theta_M \delta_H + \psi_M + \mu_H)(\mu_H + \xi_A + \delta_H + \psi_A)(\lambda_A^{**} \tau + \lambda_M^{**} + \mu_H)}. \]
We claim the following.

**THEOREM 4**

Thus, the quadratic Equation (16) reduces to

\[ \lambda^{**} = \frac{\psi A \lambda^{**} \tau \Pi H}{(q_1 + \gamma A)(\mu H + \xi A + \delta H + \psi A)(\lambda^{**} \tau + \lambda^{**} \tau + \mu H)}, \]

\[ J_{**}^M = \frac{\lambda^{**} \psi A M^**}{(\theta M \delta H + \psi M + \mu H)(\mu H + \xi A + \delta H + \psi A)(q_1 + \gamma A)(\gamma M + q_1)(\lambda^{**} \tau + \lambda^{**} \tau + \mu H)}, \]

where

\[ q_1 = \mu H + \theta_3 \delta H \]

\[ A^** = \lambda^{**} \psi M (q_1 + \gamma A)(\psi A + \xi A + \mu A + \delta H) + \lambda^{**} \psi A M^**(q_1 + \gamma M)(\psi M + \delta H \mu M + \mu H) \]

\[ + \lambda^{**} \psi A \xi A (q_1 + \gamma A). \]

It is evident from Equation (15) that all the components of \( \mathcal{E} \) are non-negative since \( \lambda^{**} \) and \( \lambda^{**} \) are non-negative for \( \mathcal{R}_{AH} > 1 \) (and all parameters of the model are also non-negative). Substituting \( \lambda^{**} = \beta A J^{**} \) in Equation (15), and using the relation \( \lambda^{**} = \beta M (H_{**}^M + \theta J^{**}) \), it can be shown that the the non-zero equilibria of the model (1) (with the avian component replaced by Equation (10)) satisfy the quadratic:

\[ b_1 \lambda M^{**} + b_2 \lambda M^{**} + b_3 = 0, \]  

(16)

where

\[ b_1 = \tau (\gamma M + q_1)(\theta M \delta H + \psi M + \mu H)(\mu H + \xi A + \delta H + \psi A), \]

\[ b_2 = \frac{(\mu H + \xi A + \delta H + \psi A)(-\tau \Pi H \beta M (q_1 + \gamma M + \theta J \psi M)(\mu A + \delta A))B}{\mu A + \delta A}, \]

\[ b_3 = -\frac{\beta M \tau \Pi H \xi A \mu A (q_1 + \gamma M + q_1 + \theta J \psi M)(\mathcal{R}_A - 1)}{\mu A + \delta A}, \]

with

\[ B = (\mu H + \psi M + \theta M \delta H)(q_1 + \gamma M)[\mu A(\mu H - \tau \delta A - \tau \mu A + \mu H \delta A + \tau \Pi H \beta A)]. \]

Since the coefficient \( b_1 > 0 \) and \( b_3 < 1 \) for \( \mathcal{R}_A > 1 \), it follows that the model has a unique endemic equilibrium whenever \( \mathcal{R}_A > 1 \) (this equilibrium is obtained by solving for \( \lambda^{**} \) in Equation (16) and substituting the result in Equation (15)). The case when \( \mathcal{R}_A < 1 \) makes \( b_3 > 0 \), so that the quadratic in Equation (16) has two negative roots. Further, when \( \mathcal{R}_A = 1 \), the coefficient \( b_3 = 0 \). Thus, the quadratic Equation (16) reduces to \( \lambda^{**}(b_1 \lambda^{**} + b_2) = 0 \), with solutions \( \lambda^{**} \) (which corresponds to the DFE (\( \mathcal{E}_{0f} \)) and \( \lambda^{**} = -b_2/b_1 < 0 \) (which is biologically meaningless). There, the model has no positive endemic equilibrium when \( \mathcal{R}_A \leq 1 \). This result is summarized below.

**THEOREM 4** The model (1), with the avian component represented by (10), has a unique endemic equilibrium whenever \( \mathcal{R}_A > 1 \), and no endemic equilibrium otherwise.

### 4.4. Global stability of endemic equilibrium

The global stability of the special case of the unique endemic equilibrium (\( \mathcal{E} \)) is now explored. We claim the following.
THEOREM 5  The unique endemic equilibrium, $E$, of the model (1), with the avian component represented by the reduced avian system (10), is GAS in $\mathcal{D} \setminus E_0$ whenever $R_A > 1$.

Proof  Since the equilibrium, $e_1$, of the avian-only model (4) (where the avian component is replaced by Equation (10)) is globally asymptotically stable if $R_A > 1$ (Lemma 5), it follows that the associated force of infection at time $t$, given by $\lambda_A(t)$, equals $\lambda_A^{**}$ (its value at an endemic equilibrium) when $R_A > 1$. Thus, the term $\tau \lambda_A$ in (1) becomes $\tau \lambda_A^{**}$, a constant. To prove the global stability of $E$, we only need to consider the system (1) with the avian component already at an endemic steady state, given by

\[
\begin{align*}
\frac{dS_H}{dt} &= \Pi_H - \tau \left( \lambda_A^{**} + \lambda_M \right) S_H - \mu_H S_H, \\
\frac{dH_M}{dt} &= \tau \lambda_M S_H + \xi_A H_A - \psi_M H_M - \mu_H H_M - \theta_M \delta_H H_M, \\
\frac{dJ_M}{dt} &= \psi_M H_M - \gamma_M J_M - \mu_H J_M - \theta_D \delta_H J_M, \\
\frac{dH_A}{dt} &= \tau \lambda_A^{**} S_H - \xi_A H_A - \psi_A H_A - \mu_H H_A - \delta_H H_A, \\
\frac{dJ_A}{dt} &= \psi_A H_A - \gamma_A J_A - \mu_H J_A - \theta_D \delta_H J_A, \\
\frac{dR_H}{dt} &= \gamma_A J_A + \gamma_M J_M - \mu_H R_H.
\end{align*}
\]

Let, for mathematical convenience, $\phi_1 = \tau \beta_M \eta_M$ and $\phi_2 = \tau \beta_M \eta_M \theta_J$, so that $\tau \lambda_M = \tau \beta_M \eta_M \left( H_M + \theta_J J_M \right) = \phi_1 H_M + \phi_2 J_M$. Further, let $q = \tau \lambda_A^{**}$. Since the variables $J_A$ and $R_H$ do not feature in any of the other equations in Equation (17), the equations for $dJ_A/dt$ and $dR_H/dt$ can be removed from the analysis. Thus, the global stability of the endemic equilibrium of the model (1), with the avian component at endemic equilibrium, will be based on the following equations:

\[
\begin{align*}
\frac{dS_H}{dt} &= \Pi_H - q S_H - (\phi_1 H_M + \phi_2 J_M) S_H - \mu_H S_H, \\
\frac{dH_M}{dt} &= (\phi_1 H_M + \phi_2 J_M) S_H + \xi_A H_A - \psi_M H_M - k_1 H_M, \\
\frac{dJ_M}{dt} &= \psi_M H_M - k_2 J_M, \\
\frac{dH_A}{dt} &= q S_H - \xi_A H_A - k_3 H_A,
\end{align*}
\]

where $k_1 = \mu_H + \theta_M \delta_H$, $k_2 = \gamma_M + \mu_H + \theta_D \delta_H$ and $k_3 = \psi_A + \mu_H + \delta_H$.

Consider the non-linear Lyapunov function (non-linear functions of this type have been used in [8,12,16]) for system (18)

\[
F = S_H^{**} \left( \frac{S_H}{S_H^{**}} - \ln \frac{S_H}{S_H^{**}} \right) + H_M^{**} \left( \frac{H_M}{H_M^{**}} - \ln \frac{H_M}{H_M^{**}} \right) + \frac{\phi_2 S_H^{**}}{k_2} J_M^{**} \left( \frac{J_M}{J_M^{**}} - \ln \frac{J_M}{J_M^{**}} \right) + \frac{\xi_A}{\xi_A + k_3} H_A^{**} \left( \frac{H_A}{H_A^{**}} - \ln \frac{H_A}{H_A^{**}} \right),
\]

where $\cdot^{**}$ denotes the value at an endemic equilibrium.
with Lyapunov derivative

$$
\mathcal{F}' = \left(1 - \frac{S_{H}^{**}}{S_H} \right) S_H' + \left(1 - \frac{H_{M}^{**}}{H_M} \right) H_M' + \frac{\phi_2 S_{H}^{**}}{k_2} \left(1 - \frac{J_{M}^{**}}{J_M} \right) J_M' + \frac{\xi_A}{\xi_A + k_3} \left(1 - \frac{H_{A}^{**}}{H_A} \right) H_A'.
$$

(19)

It follows from Equation (18) that

$$
\left(1 - \frac{S_{H}^{**}}{S_H} \right) S_H' = \Pi_H - q S_H - (\phi_1 H_M + \phi_2 J_M) S_H - \mu_H S_H
$$

$$
- \frac{S_{H}^{**}}{S_H} [\Pi_H - q S_H - (\phi_1 H_M + \phi_2 J_M) S_H - \mu_H S_H]
$$

$$
= q S_H + (\phi_1 H_M + \phi_2 J_M) S_H + \mu_H S_H - q S_H - (\phi_1 H_M + \phi_2 J_M) S_H - \mu_H S_H
$$

$$
- \frac{S_{H}^{**}}{S_H} \left[ q S_H + (\phi_1 H_M + \phi_2 J_M) S_H + \mu_H S_H - q S_H
$$

$$
- (\phi_1 H_M + \phi_2 J_M) S_H - \mu_H S_H \right]
$$

$$
= q S_H \left(2 - \frac{S_{H}^{**}}{S_H} - \frac{S_H^{**}}{S_{H}^{**}}\right) + \mu_H S_H \left(2 - \frac{S_{H}^{**}}{S_H} - \frac{S_H^{**}}{S_{H}^{**}}\right) - (\phi_1 H_M + \phi_2 J_M) S_H
$$

$$
+ (\phi_1 H_M + \phi_2 J_M) S_H^{**} - (\phi_1 H_M + \phi_2 J_M) \frac{S_{H}^{**}}{S_H} + (\phi_1 H_M + \phi_2 J_M) S_H^{**}
$$

(20)

In the above, we used $\Pi_H = q S_H + (\phi_1 H_M + \phi_2 J_M) S_H + \mu_H S_H$ (at endemic state). Similarly,

$$
\left(1 - \frac{H_{M}^{**}}{H_M} \right) H_M' = (\phi_1 H_M + \phi_2 J_M) S_H + \xi_A H_A - \psi M H_M - k_1 H_M
$$

$$
- \frac{H_{M}^{**}}{H_M} [(\phi_1 H_M + \phi_2 J_M) S_H + \xi_A H_A - \psi M H_M - k_1 H_M]
$$

$$
= (\phi_1 H_M + \phi_2 J_M) S_H + \xi_A H_A - (\psi M + k_1) H_M - (\phi_1 H_M + \phi_2 J_M) \frac{S_H H_M^{**}}{H_M}
$$

$$
- \xi_A H_A \frac{H_M^{**}}{H_M} + (\psi M + k_1) H_M^{**}.
$$

(21)

Furthermore,

$$
\frac{\phi_2 S_{H}^{**}}{k_2} \left(1 - \frac{J_{M}^{**}}{J_M} \right) J_M' = \frac{\phi_2 S_{H}^{**}}{k_2} \left[\psi M H_M - k_2 J_M - \frac{J_{M}^{**}}{J_M} (\psi M H_M - k_2 J_M) \right]
$$

$$
= \psi M H_M \frac{\phi_2 S_{H}^{**}}{k_2} - \phi_2 S_{H}^{**} J_M - \frac{\phi_2 S_{H}^{**}}{k_2 J_M} J_M^{**} \frac{\psi M H_M + \phi_2 S_{H}^{**} J_M^{**}}{H_M + \phi_2 S_{H}^{**} J_M^{**}}.
$$

(22)

Finally,

$$
\frac{\xi_A}{\xi_A + k_3} \left(1 - \frac{H_{A}^{**}}{H_A} \right) H_A' = \frac{\xi_A}{\xi_A + k_3} \left[q S_H - (\xi_A + k_3) H_A - \frac{H_{A}^{**}}{H_A} [q S_H - (\xi_A + k_3) H_A] \right]
$$

$$
= \frac{q \xi_A S_H}{\xi_A + k_3} - \frac{\xi_A H_A}{\xi_A + k_3} - \frac{q \xi_A H_A^{**}}{(\xi_A + k_3) H_A} + \frac{\xi_A H_A^{**}}{\xi_A + k_3}.
$$

(23)
Adding Equations (20), (21), (22) and (23), and simplifying, gives

$$\mathcal{F}' = qS^*_H (2 - \frac{S^*_H}{S_H}) + \mu_H S^*_H (2 - \frac{S^*_H}{S_H}) + (\phi_1 H^*_M + \phi_2 J^*_M) S^*_H$$

$$- (\phi_1 H^*_M + \phi_2 J^*_M) \left(\frac{S^*_H}{S_H}\right)^2 + (\phi_1 H_M + \phi_2 J_M) S^*_H - (\psi_M + k_1) H_M$$

$$- (\phi_1 H_M + \phi_2 J_M) S_H \frac{H^*_M}{H_M} - \xi_A H_A \frac{H^*_M}{H_M} + (\psi_M + k_1) H_M^*$$

$$+ \frac{\phi_2 S^*_H}{k_2} \psi_M H_M - \phi_2 S^*_H J_M - \frac{\phi_2 S^*_H}{k_2} J_M \psi_M H_M + \phi_2 S^*_H J_M$$

$$+ \frac{\xi_A}{\xi_A + k_3} qS_H - \frac{\xi_A}{(\xi_A + k_3) H_A} q H^*_A S_H + \xi_A H^*_A. \quad (24)$$

Using the relations (at endemic state)

$$(\psi_M + k_1) H^*_M = (\phi_1 H^*_M + \phi_2 J^*_M) S^*_H + \xi_A H^*_A,$$

$$\psi_M H^*_M = k_2 J^*_M \quad \text{and} \quad q S^*_H = (\xi_A + k_3) H^*_A, \quad (25)$$

it is easy to show that the following equation holds:

$$(\phi_1 H_M + \phi_2 J_M) S^*_H - (\psi_M + k_1) H_M + \frac{\phi_2 S^*_H}{k_2} \psi_M H_M - \phi_2 S^*_H J_M = -\xi_A H^*_A \frac{H_M}{H_M^*}. \quad (26)$$

Using Equations (25) and (26) in Equation (24), and simplifying, gives

$$\mathcal{F}' = qS^*_H (2 - \frac{S^*_H}{S_H}) + \mu_H S^*_H (2 - \frac{S^*_H}{S_H}) + (\phi_1 H^*_M + \phi_2 J^*_M) S^*_H$$

$$- (\phi_1 H^*_M + \phi_2 J^*_M) \left(\frac{S^*_H}{S_H}\right)^2 - (\phi_1 H_M + \phi_2 J_M) S_H \frac{H^*_M}{H_M} + (\phi_1 H_M + \phi_2 J_M) S^*_H$$

$$+ \xi_A H^*_A - \frac{\phi_2 S^*_H}{J_M H^*_M} (J_M^*)^2 H_M + \phi_2 S^*_H J_M - \xi_A H_A \frac{H^*_M}{H_M}$$

$$+ \frac{\xi_A}{\xi_A + k_3} qS_H - \frac{\xi_A}{(\xi_A + k_3) H_A} q H^*_A S_H + \xi_A H^*_A - \xi_A H^*_A \frac{H_M}{H_M^*}. \quad (27)$$

which can be further simplified to

$$\mathcal{F}' = qS^*_H \left(2 - \frac{S^*_H}{S_H} - \frac{S_H}{S^*_H}\right) + \mu_H S^*_H \left(2 - \frac{S_H}{S^*_H} - \frac{S^*_H}{S_H}\right) + \phi_1 H_M^* S^*_H \left(2 - \frac{S^*_H}{S_H} - \frac{S_H}{S^*_H}\right)$$

$$+ \phi_2 J_M^* S^*_H \left(3 - \frac{S^*_H}{S_H} - \frac{S_H}{S^*_H}\right) + \xi_A H_A \left(2 + \frac{S_H}{S^*_H} - \frac{H_A H^*_M}{H_M^*} - \frac{H^*_A H_M}{H^*_M} - \frac{H_M S^*_H}{H^*_H} \right) \quad (28)$$
Finally, using \( q S_{H}^{**} = \xi_A H_{A}^{**} + k_3 H_{A}^{**} \) in Equation (28) gives

\[
F' = \mu_H S_{H}^{**} \left( 2 - \frac{S_{H}^{**}}{S_{H}} - \frac{S_{H}}{S_{H}^{**}} \right) + k_3 H_{A}^{**} \left( 2 - \frac{S_{H}^{**}}{S_{H}} - \frac{S_{H}}{S_{H}^{**}} \right) + \phi_1 H_{M}^{**} S_{H}^{**} \left( 2 - \frac{S_{H}^{**}}{S_{H}} - \frac{S_{H}}{S_{H}^{**}} \right)
+ \phi_2 J_{M}^{**} S_{H}^{**} \left( 3 - \frac{S_{H}^{**}}{S_{H}} - \frac{J_{M}^{**} H_{M}}{J_{M} H_{M}^{**}} - \frac{J_{M} H_{M}^{**} S_{H}}{J_{M} H_{M}^{**} S_{H}} \right)
+ \xi_A H_{A}^{**} \left( 4 - \frac{S_{H}^{**}}{S_{H}} - \frac{H_{A}^{**} H_{M}}{H_{A}^{**} H_{M}} - \frac{H_{A}^{**} S_{H}}{H_{A}^{**} S_{H}} - \frac{H_{M}}{H_{M}} \right).
\] (29)

Clearly, since the arithmetic mean exceeds the geometric mean (that is, \( a_1 + a_2 + \cdots + a_n \geq n \sqrt[n]{a_1 a_2 \cdots a_n} \) for \( a_i \geq 0, i = 1, \ldots, n \), then

\[
2 - \frac{S_{H}^{**}}{S_{H}} - \frac{S_{H}}{S_{H}^{**}} \leq 0,
3 - \frac{S_{H}^{**}}{S_{H}} - \frac{J_{M}^{**} H_{M}}{J_{M} H_{M}^{**}} - \frac{J_{M} H_{M}^{**} S_{H}}{J_{M} H_{M}^{**} S_{H}} \leq 0,
4 - \frac{S_{H}^{**}}{S_{H}} - \frac{H_{A}^{**} H_{M}}{H_{A}^{**} H_{M}} - \frac{H_{A}^{**} S_{H}}{H_{A}^{**} S_{H}} - \frac{H_{M}}{H_{M}} \leq 0,
\] (30)

so that \( F' \leq 0 \), with equality if and only if equality holds in each of the inequalities in Equation (30). Thus, \( (S_{H}, H_{M}, J_{M}, H_{A}) \rightarrow (S_{H}^{**}, H_{M}^{**}, J_{M}^{**}, H_{A}^{**}) \). Using \( H_{A}^{**}, J_{M}^{**} \) and \( J_{M}^{**} \), it is easy to show that \( (J_A, R_H) \rightarrow (J_{A}^{**}, R_{H}^{**}) \). Thus, it follows, by the Lyapunov function \( F \) and the Lasalle Invariance Principle, that the largest compact invariant set in \( D \setminus E_{0f} \) for which \( F' = 0 \) is the singleton \( \{ E \} \). Hence, all solutions with initial conditions in \( D \setminus E_{0f} \) will converge to \( E \) if \( R_A > 1 \).

It should be noted that for the case \( R_A < 1 \) (that is, the avian component is at its DFE) and \( R_H > 1 \), the above non-linear Lyapunov function with \( \xi_A = 0 \) (since, for \( R_A < 1, H_A \rightarrow 0 \) so that \( \xi_A = 0 \)) can still be used to establish the global dynamics of the resulting endemic equilibrium of the human-only system.

Thus, in summary, the full model (1) has a globally asymptotically stable disease-free equilibrium whenever the reproduction number \( (R_{AH}) \) is less than unity, and has a unique endemic equilibrium whenever \( R_{AH} > 1 \). It is further shown that this endemic equilibrium is globally asymptotically stable for a special case, where the avian-only system is replaced by the reduced avian system (10). Iwami et al. [15] used the compound matrix geometric approach of Li-Muldowney [19] to establish the global stability of the endemic equilibrium in their paper.

5. Numerical simulations

Numerical simulations are carried out, to illustrate some of the theoretical results in the paper, using the parameters in Tables 1 and 2, unless otherwise stated. With this set of parameter values, \( R_A = 6.67 \) and \( R_H = 0.45 \), so that \( R_{AH} = R_A = 6.67 \). Figure 2A shows convergence of the solution profile to the endemic equilibrium as expected (it should be noted from Lemma 5 that the endemic equilibrium of the reduced avian-only model (10) is globally asymptotically stable whenever \( R_A > 1 \)). However, when the parameters are changed so that \( R_A = 0.83 \) and \( R_H = 0.06 \) (so that \( R_{AH} = 0.83 < 1 \)), the solution profiles converged to the DFE (Figure 2B). This is consistent with Theorem 4. Further, when the reproduction numbers are increased such that both
Table 1. Description of model variables.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_W(t)$</td>
<td>Susceptible wild birds</td>
</tr>
<tr>
<td>$S_D(t)$</td>
<td>Susceptible domestic birds</td>
</tr>
<tr>
<td>$S_H(t)$</td>
<td>Susceptible humans</td>
</tr>
<tr>
<td>$I_W(t)$</td>
<td>Infected wild birds</td>
</tr>
<tr>
<td>$I_D(t)$</td>
<td>Infected domestic birds</td>
</tr>
<tr>
<td>$H_A(t)$</td>
<td>Humans with avian strain</td>
</tr>
<tr>
<td>$H_M(t)$</td>
<td>Humans with mutant strain</td>
</tr>
<tr>
<td>$J_A(t)$</td>
<td>Isolated humans with avian strain</td>
</tr>
<tr>
<td>$J_M(t)$</td>
<td>Isolated humans with mutant strain</td>
</tr>
<tr>
<td>$R_H(t)$</td>
<td>Recovered humans</td>
</tr>
</tbody>
</table>

Table 2. Description of model parameters.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
<th>Baseline value</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\Pi_W$</td>
<td>Birth rate of wild birds</td>
<td>1000 per day</td>
<td>[3]</td>
</tr>
<tr>
<td>$\Pi_D$</td>
<td>Birth rate of domestic birds</td>
<td>1000 per day</td>
<td>[3]</td>
</tr>
<tr>
<td>$\Pi_H$</td>
<td>Recruitment rate of humans</td>
<td>30 per day</td>
<td>[3]</td>
</tr>
<tr>
<td>$\beta_A, \beta_W, \beta_D$</td>
<td>Effective contact rate for avian strain</td>
<td>0.4/200000 per day</td>
<td>assumed</td>
</tr>
<tr>
<td>$\beta_M$</td>
<td>Effective contact rate for mutant strain</td>
<td>0.3 $\beta_A$ per day</td>
<td>assumed</td>
</tr>
<tr>
<td>$\mu_A$</td>
<td>Natural mortality rate of avian</td>
<td>1/100 per day</td>
<td>[3]</td>
</tr>
<tr>
<td>$\mu_H$</td>
<td>Natural mortality rate of mutants</td>
<td>$1/70 \times 365$ per day</td>
<td>[3]</td>
</tr>
<tr>
<td>$\delta_W, \delta_D$</td>
<td>Avian mortality rate</td>
<td>assumed</td>
<td></td>
</tr>
<tr>
<td>$\eta_M$</td>
<td>Modification parameter</td>
<td>1</td>
<td>assumed</td>
</tr>
<tr>
<td>$\delta_H$</td>
<td>Human mortality rate</td>
<td>0.06 per day</td>
<td>[15]</td>
</tr>
<tr>
<td>$\tau$</td>
<td>Infection-reduction parameter in humans</td>
<td>0.1</td>
<td>assumed</td>
</tr>
<tr>
<td>$\theta_I$</td>
<td>Reduction of transmission of mutant strain due to isolation</td>
<td>0.6</td>
<td>assumed</td>
</tr>
<tr>
<td>$\theta_M$</td>
<td>Relative variability of mortality of mutant strain</td>
<td>1.5</td>
<td>assumed</td>
</tr>
<tr>
<td>$\theta_D$</td>
<td>Relative reduction in mortality due to isolation</td>
<td>0.6</td>
<td>assumed</td>
</tr>
<tr>
<td>$\xi_A$</td>
<td>Mutation rate</td>
<td>0.01</td>
<td>[15]</td>
</tr>
<tr>
<td>$\psi_A$</td>
<td>Isolation rate for humans with avian strain</td>
<td>0.2 per day</td>
<td>assumed</td>
</tr>
<tr>
<td>$\psi_M$</td>
<td>Isolation rate for humans with mutant strain</td>
<td>0.2 per day</td>
<td>assumed</td>
</tr>
<tr>
<td>$\gamma_A$</td>
<td>Recovery rate of humans with avian strain</td>
<td>0.05 per day</td>
<td>assumed</td>
</tr>
<tr>
<td>$\gamma_M$</td>
<td>Recovery rate of humans with mutant strain</td>
<td>0.01 per day</td>
<td>assumed</td>
</tr>
</tbody>
</table>

are greater than unity ($R_A = 8.33$ and $R_H = 3.8$), the solutions converged to the unique endemic equilibrium.

The effect of the mutation of the avian to the mutant strain (governed by $\xi_A$) is also monitored. It is shown that the total number of infected humans increases with increasing mutation rate (Figure 3). Furthermore, it is shown that isolation of infected individuals can lead to significant reduction of the total infection in humans (Figure 4). The impact of isolating individuals with one strain (whilst those with the other strain are not isolated) is also assessed. The simulations show that, on average, the isolation of individuals with the avian strain only is more beneficial than isolating those with the mutant strain alone (Figure 5A and B).

Further simulations were carried out to determine whether or not the model exhibits competitive exclusion. It is shown (Figure 6) that for the case where the reproduction numbers of each strain exceeds unity, the strain with higher reproduction number is more dominant (accounts for more cases) than the other; but does not drive the other to extinction. For example, when $R_A = 3.33$ and $R_H = 4.56$, Figure 6A and B show that the number of human cases with the mutant strain exceeds that with the avian strain. Similarly, when $R_A = 6.667$ and $R_H = 3.04$, more avian cases were recorded in comparison to the number of mutant cases (Figure 7A and B). In other words,
Figure 2. Total number of infected humans ($H_A + H_M + J_A + J_M$) as a function of time. (A) $R_A = 6.67$, $R_H = 0.58$, $\beta_A = 0.4/200000$, $\beta_H = 0.3\beta_A$. (B) $R_A = 0.83$, $R_H = 0.07$, $\beta_A = 0.05/200000$, $\beta_H = 0.3\beta_A$, and (C) $R_A = 8.33$, $R_H = 1.19$, $\beta_A = 0.5/200000$, $\beta_H = 2\beta_A$. All other parameters are as given in Table 2.
Figure 3. Effect of $\xi_A$. Parameters values used are as given in Table 2.

Figure 4. Effect of isolation of individuals with both strains. Parameter values used are as given in Table 2.
both strains co-exist when the associated reproduction numbers exceed unity (hence, the system does not exhibit competitive exclusion).

6. Conclusions

A deterministic model for the transmission dynamics of an avian and a mutant strain (which is transmissible in humans) of influenza is designed and rigorously analysed. The study, which allows for the assessment of an intervention strategy based on isolating symptomatic
Figure 6. Infected humans with (A) mutant and (B) avian strain as a function of time. Parameter values used are as given in Table 2.

individuals, shows the following:

(1) The avian-human model has a globally stable disease-free equilibrium whenever the reproduction numbers of the avian and human strains are less than unity simultaneously.

(2) The avian-human model has a unique endemic equilibrium whenever the reproduction number for the avian strain exceeds unity. This equilibrium is shown to be globally asymptotically stable, when it exists, for a special case of the avian-only system.

(3) On average, isolating individuals infected with the avian strain is more beneficial than isolating those with the mutant strain.
Figure 7. Infected humans with (A) mutant and (B) avian strain as a function of time. Parameter values used are as given in Table 2.

(4) Influenza-related burden in humans increases with increasing mutation rate.

(5) For the case when the reproduction numbers of the two strains exceeds unity, it is shown that although the strain with the higher reproduction number dominates (generates more infection), the one with the lower reproduction number still survives. In other words, both strains co-exist when their respective reproduction numbers exceed unity (system does not undergo competitive exclusion).

Although the simulation results above are based on a set of parameter values, for which uncertainties in parameter estimates may exist, the study suggests that a potential influenza
A. B. Gumel

pandemic can be effectively controlled using basic public health control measures such as isolation of symptomatic individuals and infection-reduction measures (such as taking precautions against handling poultry products, wearing face-masks, minimizing contacts etc.).

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References