

DETERMINISTIC MODEL OF BIRD FLU EPIDEMIC

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Abstract

In this work a deterministic model of bird flu epidemic was investigated. The model included susceptible, infected, and removed or recovered birds. This model revealed that a non-zero population with some peak and low periods had non-zero constants that made the infectious population to have a possible limit it cannot exceed, no matter the rate of infection. We observed that the disease-free steady state of our model was globally asymptotically stable. We also observed that there should be a bound at which susceptible become infected.

Keywords: *Deterministic Model, Bird Flu Epidemic, Infectious Population, Disease Free Steady State and Globally Asymptotically Stable.*

1. Introduction

Bird Flu which is formally known as Avian influenza refers to influenza caused by viruses adapted to birds. Out of the three types of influenza viruses (A, B, C), influenza A virus is a zoonotic infection with a natural reservoir almost entirely in birds. Bird Flu (or Avian influenza), for most purposes, refers to the influenza A virus. Bird Flu strains are divided based on their pathogenicity: high pathogenicity (HP) or low pathogenicity (LP). The most well-known high pathogenicity Avian influenza (HPAI) strain, H5N1, appeared in China in 1996, while low pathogenic strains were found in North America [1]. [2] gave a mathematical model of emergent and re-emergent infectious diseases to assess the effect of public health interventions on disease spread. Also, [3] gave a mathematical model of the case of early detection of Ebola Virus. In [5] and [8] respectively, cases about Avian influenza were uniquely presented. Certain applications of Differential equations were given by [4]. [6] presented an Avian model and its fit to human Avian influenza cases while [7] gave a precise model and Implication for Control Avian Flu. Also, [9] worked on the transmission of the highly pathogenic avian influenza virus H5N1 that occurred in Thailand in 2004.

2. Model Formulation

The total population at time, t , denoted by $N(t)$, is divided into the mutually exclusive compartments of susceptible individuals $S(t)$, infectious individuals $I(t)$, and recovered individuals $R(t)$, so that

$$N(t) = S(t) + I(t) + R(t) \tag{2.1}$$

We formulate our model with the following assumptions:

- (i) Human population is constant for a short period of time
- (ii) There is no natural birth and death rate for infectious and recovered class.

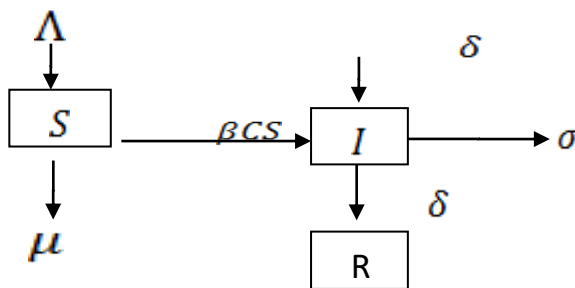


Figure 1: Schematic representation of the model

Table 1: Description of variables

Variable	Description
$S(t)$	Susceptible birds
$I(t)$	Infectious birds
$R(t)$	Recovered birds

Parameter	Description
Λ	Natural birth rate of the susceptible birds
C	Total number of birds carrying the disease at time t
δ	Recovery rate
σ	Death rate of Infectious birds
β	Rate at which susceptible birds get infectious
μ	Natural death rate of recovered birds

The model equations are therefore given by

$$\frac{dS}{dt} = \Lambda - \beta CS - \mu S \tag{2.2a}$$

$$\frac{dI}{dt} = -\delta I - \sigma I + \beta CS \quad (2.2b)$$

$$\frac{dR}{dt} = \delta I - \mu R \quad (2.2c)$$

2.1 Basic Properties of the model

Theorem 1

Let the initial data for the model equations at $t=0$ be $S(0) > 0, I(0) > 0, R(0) > 0$. Then, the solutions

$(S(t), I(t), R(t))$ of the model equations with positive initial data, will remain positive for all time $t > 0$.

Proof. Let

$$t_1 = \sup \{t > 0 : S(t) > 0, I(t) > 0, R(t) > 0\} > 0$$

It follows from Equation (2.2a) which can be re-written as

$$\frac{d}{dt} \left\{ S(t) \exp\left[\mu t + \int_0^t \beta C(\tau) d\tau\right] \right\} = \Lambda \left\{ \exp\left[\mu t + \int_0^t \beta C(\tau) d\tau\right] \right\} \quad (2.3)$$

Thus,

$$S(t_1) \left\{ \exp\left[\mu t_1 + \int_0^{t_1} \beta C(\tau) d\tau\right] \right\} - S(0) = \int_0^{t_1} \Lambda \left\{ \exp\left[\mu y + \int_0^y \beta C(\tau) d\tau\right] \right\} dy$$

\Rightarrow

$$S(t) = S(0) \exp\left[-\mu t_1 - \int_0^{t_1} \beta C(\tau) d\tau\right] + \left\{ \exp\left[-\mu t_1 - \int_0^{t_1} \beta C(\tau) d\tau\right] \right\} \times \int_0^{t_1} \Lambda \exp\left\{-\mu y - \int_0^y \beta C(\tau) d\tau\right\} dy > 0 \quad (2.4)$$

Similarly, it can be shown that $I > 0, R > 0$ for all time $t > 0$

2.2 ENDEMIC STEADY STATE

At the endemic state equilibrium, the differential equation of the model is set to zero for $I \neq 0$.

$$\frac{dS}{dt} = \Lambda - \beta CS - \mu S = 0 \quad (2.5a)$$

$$\frac{dI}{dt} = -(\delta + \sigma)I + \beta CS = 0 \quad (2.5b)$$

$$\frac{dR}{dt} = \delta I - \mu R = 0 \quad (2.5c)$$

Solving the resulting differential equation with respect to the variables S, I and R , we obtain

$$\Lambda - \beta CS - \mu S = 0 \Rightarrow \bar{A} = i + 2j - k, \bar{B} = -2i + 3k, \bar{C} = 2i + j + 3k, \bar{D} = 3j - 2k, \quad (2.6)$$

$$I = \frac{\beta CS}{\delta + \sigma} \quad (2.7)$$

$$R = \frac{\delta I}{\mu} \quad (2.8)$$

Next, we obtain the endemic steady state at $U_1 = (S^1, I^1, R^1)$.

Evaluating J at U_1

$$J_1 = \begin{pmatrix} -(\beta + \mu) & 0 & 0 \\ \beta C & -(\delta + \sigma) & 0 \\ 0 & \delta & -\mu \end{pmatrix}$$

Computing the eigenvalues, λ , we solve: $|\lambda I - J_1| = 0$

$$\Rightarrow \begin{vmatrix} \lambda + (\beta + \mu) & 0 & 0 \\ -\beta C & \lambda + (\delta + \sigma) & 0 \\ 0 & -\delta & \lambda + \mu \end{vmatrix} = 0 \Rightarrow \lambda_1 = -(\beta + \mu), \lambda_2 = -(\delta + \sigma), \lambda_3 = -\mu$$

This shows that the endemic state is locally asymptotically stable.

3. Numerical Simulation

The initial populations were assumed to be $S(0) = 8, I(0) = 5, R(0) = 3$

Assumptions of some parameter values include:

$\Lambda = 0.1/day$, $\beta = 0.91/day$, $\delta = 0.6/day$, $\mu = 0.000498/day$, $\sigma = 0.8/day$

3.1 Deterministic Model Analysis

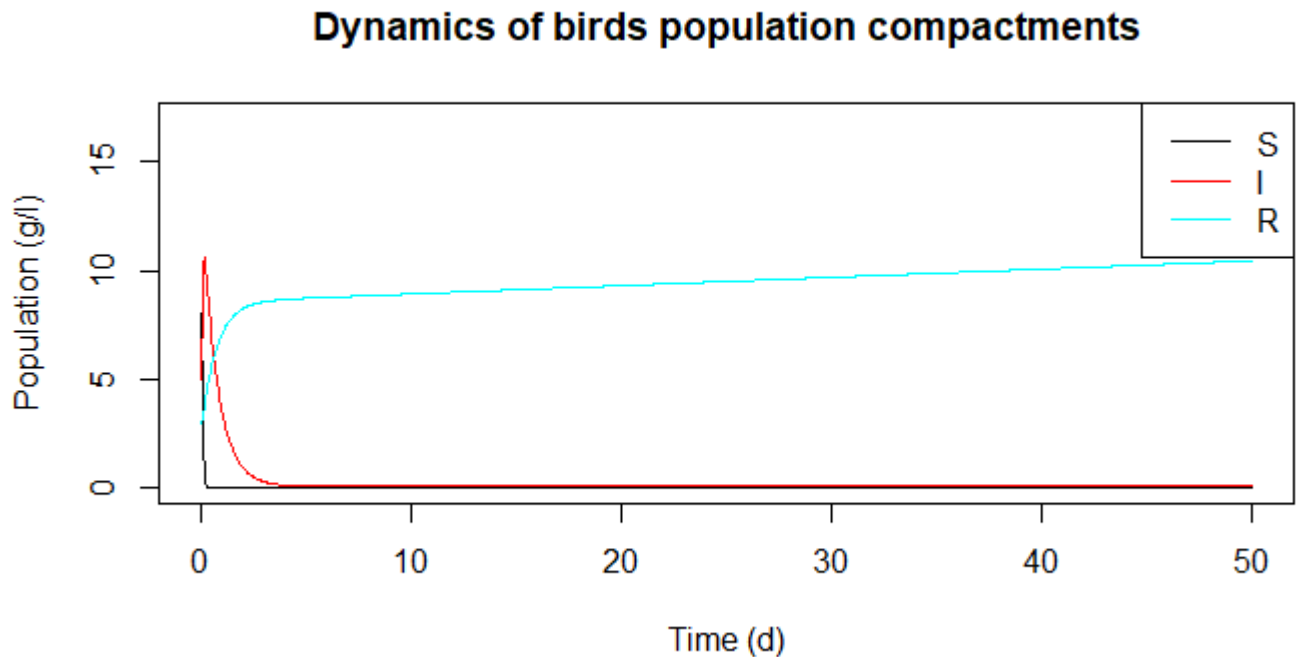


Figure 1: Graph of Susceptible, Infectious and Recovered Population against time

4. Results and Conclusion

Observe the spontaneous growth and decline of the infectious bird's population shows that the infection does not last long in the investigated model before its eradication from the entire bird population, also the recovered bird population attained its equilibrium at a very short time due to a complete eradication of infectious bird population. The eradication of Infectious bird population is due to bird's natural death (both susceptible and recovered) and death due to infection.

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