ANALYTICAL STUDY AND NUMERICAL SIMULATION OF ONE DIMENSIONAL BIRD FLU PROPAGATION WITHIN A POULTRY FARM

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Abstract

Bird flu viruses do not spread easily among humans. However, if those viruses were given a chance to infect simultaneously with human influenza viruses, then a highly contagious disease for humans would emerge and start spreading from human to human. This is a starting point of a pandemic. A poultry farm is one of contact point between hosts of bird flu virus and human. Once the bird flu virus intrudes into a poultry farm, it transmits rapidly to entire farm and causes domestic birds serious symptoms that eventually lead to death. Although culling and vaccination are effective measures that are usually used, but they are not entirely effective. Now, another measure to control outbreak of bird flu in a poultry farm is needed. In this respect, mathematical model is a tool for analysis the transmission of bird flu and to evaluation of control measures.

In this study, bird flu transmission process within a poultry farm was investigated mathematically. A mathematical model that is a nonlinear system of ordinary differential equations was analyzed. Stability of stationary points of the model was investigated. Furthermore, a spatial effect of virus concentration in a medium was considered, and the model was reformulated with spatial diffusion. That model is a nonlinear parabolic system of partial differential equations. Stability of constant solutions of this model was discussed. Those stabilities depend on values of parameters that correspond to the infection rate, the local capacity of the farm, and the removal rate of infected birds.

This study shows that a transmission process is expressible in terms of a traveling wave solutions. Existence of those solutions in a singular limit was established by a center manifold reduction for certain ranges of parameters. Analytical results show that there is a unique heteroclinic orbit that corresponds to a traveling wave solution for a small value of removal rate of infected birds. Finally, the analytical results were confirmed by numerical results. Solutions of nonlinear parabolic system of partial differential equations with some boundary conditions and initial conditions were numerically investigated. Numerical results confirm that a nonlinear parabolic of partial differential equations admits a traveling wave solution for small removal rate of infected birds.
Alhamdulillahirabbil’alamin

To my lovely husband and my son, you are my inspiration.
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Chapter 1
INTRODUCTION

1.1 Background

Bird flu, known as avian influenza (AI), is a highly infectious and fatal disease for domestic birds. The disease is caused by virus such as H5N1 strain carried by wild birds. Those viruses usually attack poultry, and bird to human infection has also been reported. A poultry farm is one of contacts points between carriers of bird flu viruses and human. Once bird flu intrudes in a poultry farm, it transmits rapidly over the entire farm and causes domestic birds serious symptoms that eventually lead to death with no exception.

In current practice, if infection is detected from only one bird, the entire population in the farm (susceptible and infected birds) are culled, which has been causing a catastrophic damage to the poultry industry [13]. Moreover, culling is often locally targeted in the sense that this severe action is limited regions. Other than culling, vaccination is another effective measure against bird flu infection because vaccinated chickens produce up to 100 thousand times less viruses when infected. Vaccination is generally applied reduce the number of susceptible birds. Although vaccination offers a very powerful method of disease control, vaccines are not entirely effective. Moreover, there are also difficulties associated with vaccination. One of the difficulties is that it affects export trade. Some countries set no policies concerning vaccination of domestic of domestic birds [14].

Bird flu infection was feared by poultry industries in many countries because of the direct consequence of loss due to infection, but also because there are secondary effects that can harm poultry industries. Those secondary effects include decrease in demand due to view that the bird flu is a zoonosis that is infectious to human by consuming infected birds. Although bird flu cases in poultry farm tend to decrease (Fig. 1.1), and there has been no report yet on human to human infection of bird flu, frequent outbreaks of bird flu in poultry farms increase chances for human to human infection virus to appear. Before that happens, mechanism of bird flu transmission within a poultry farm must be investigated, and measures against outbreaks of bird flu must be developed.

A number of mathematical models concerning bird flu have been proposed. Mathematical models were proposed and analyzed for simulation of avian influenza infection process from the bird world to human world [6,16,17,18]. A mathematical model which involves human influenza was analyzed [15]. The transmission dynamics and spatial spread rate by size of susceptible birds population were analyzed [7]. A disease transmission model with spatial diffusion was analyzed for spatial spread of avian influenza among flock and human [8,9]. Those studies did not deal with any aspect of bird flu transmission
within a closed system such as a poultry farm, and techniques to control outbreaks in such a closed system must be developed. In this study, transmission processes of bird flu within a poultry farm was analyzed mathematically. A natural way to model the transmission process of bird flu is formulation of nonlinear system of ordinary differential equations (ode’s) and nonlinear system of partial differential equations (pde’s).

Figure 1.1: Bird flu cases on poultry in Indonesia.
Source: Poultry Indonesia 77, July 2016.

1.2 Statement of the Problem

Bird flu transmission processes within a poultry farm involves three essential factors: virus as source of disease, domestic birds as host, and the environment as medium, such as feed, dirt, and air. Wild birds carry the bird flu virus as they migrate from one place to another place. They can infect domestic birds as host through dirt on the poultry farm ground. Once bird flu intrudes into a poultry farm, some infected birds die at an early stage, and some others live longer. During the infection process, infected birds become hosts of virus, except that they are completely removed from the population. Mathematical model based on those factors was proposed [10]. The model is a nonlinear system of ordinary differential equations for susceptible birds (X) and infected birds (Y). The model was reformulated for incorporation of bird flu virus concentration (Z) in a medium [11].

In this study, mathematical analysis of bird flu transmission process within a poultry farm is continued. A model proposed in a previous study was reformulated with assumption that vacancies are instantaneously replaced with new birds, so that the total population always balances with the capacity of the farm. This assumption is important
in order for the population of domestic birds in a poultry farm be maintained at the manageable capacity for efficient production with supply of new healthy birds for vacancies. The assumption led from the previous model [11] to a nonlinear system of ordinary differential equations whose unknown variables correspond to the number of susceptible birds ($X$) and the virus concentration ($Z$). The model was analyzed to investigate effects of vaccination and removal rate of infected birds on security of the poultry farm system.

Any spatial effects of virus concentration were considered for formulation of those models. In order to propose effective measure against of bird flu infection within a poultry farm, spatial effect of virus concentration should be incorporated into formulation for virus concentration in a medium. The previous model was reformulated with incorporation of spatial diffusion. This model is a nonlinear parabolic system of partial differential equations. It was analyzed to investigate bird flu diffusive process in a poultry farm.

1.3 Mathematical Approach to Bird Flu Transmission Processes

In a typical chicken house of a poultry farm in Indonesia, bird cages are lined up in one direction (Fig. 1.2). There are ten chicken houses each of which contains few thousands chickens. Each chicken in a house is approximate placed in 25x50 [cm] wire net cages. Four lines of cages are lined up in one direction on each side of chicken house. So, viruses are assumed to be transmittable through one dimensional medium. Let $x$ be the one dimensional coordinate variable.

Spatial diffusion was introduced into for modeling of transmission process of bird flu infection in a poultry farm. When a diffusive term is included in the rate of the change of the virus concentration, a bird flu transmission process within a poultry farm was reformulated to a nonlinear parabolic system of partial differential equations. The unknown variables $X$ and $Z$ are now functions of one dimensional coordinate $x$ and time $t$, and denoted by $X(x, t)$ and $Z(x, t)$, respectively. Traveling wave solutions of the model represent bird flu transmission processes. Those solutions are investigated by converting a nonlinear parabolic system of partial differential equations to a nonlinear system of ordinary differential equations. Stability of stationary points for the three dimensional system was determined by Routh-Hurwitz criterion. The three dimensional system was reduced to a two dimensional system by a center manifold reduction. Phase plane analysis of the two dimensional system leads to existence traveling wave solutions for nonlinear parabolic system of partial differential equations. The original nonlinear parabolic system was solved numerically for confirmation of analytical results. Solutions were generated with mixed boundary conditions and homogeneous Neumann boundary conditions, and some initial conditions. Numerical results were obtained by MATLAB program.

1.4 Outline

This thesis is organized into five main chapters. Chapter 1 is an introductory chapter, which consists of the background, statement of the problem, mathematical approach to bird flu transmission processes, and outline of the thesis. Chapter 2 contains results from literature review, which focuses on briefly work done by other researcher on
the topic. This chapter consists of introductory theory of bird flu and its transmission processes that include results from previous studies on mathematical model related to bird flu infection, in particular mathematical models of bird flu outbreak within a poultry farm, nonlinear diffusion equations, and its traveling wave solutions. Chapter 3 focuses on analysis of bird flu transmission process within a poultry farm. This chapter consists of: 1) nonlinear system of ordinary differential equations, local and global stability of stationary points, 2) nonlinear system of partial differential equations, that are formulated as mathematical model with spatial virus diffusion. Results of this section include stability of constant solutions, traveling wave solutions of host virus model, and solutions in a singular limit. Chapter 4 introduces numerical results. Finally, conclusions and prospect for future research are presented in Chapter 5.

![Figure 1.2](image_url)

**Figure 1.2:** Typical of poultry farm in Indonesia.
The photo was taken at Gunung Nago Group Farm, Padang City, West Sumatra, July 2016.
Chapter 2

LITERATURE RIVIEW

This chapter consists of results from literature review, which focuses on works done by other researcher in the field. Mathematical models related to bird flu infection, in particular mathematical models of bird flu outbreak within a poultry farm, nonlinear diffusion equations, and their traveling wave solutions are described.

2.1 Theory of Bird Flu

Infectious disease such as influenza can be passed between individuals, whereas non-infectious diseases such as rheumatics develop over an individual’s lifespan [13]. Avian influenza is a infectious disease which is caused by influenza viruses. Those viruses are categorized into two types based on symptoms that appear in domestic birds: High Pathogenic (HP) and Low Pathogenic (LP). LP avian influenza is a natural infection of waterfowl, and it causes minimal damage to domestic birds and wild birds. It is not a serious threat to wild birds. HP avian influenza is rarely found in waterfowl, but causes severe disease in domestic poultry with a high fatality rate. Influenza viruses are classified into subtypes based on the two proteins: haemaglutinin (H) with 16 H types and neuraminidase (N) with 9 N types. One of combinations of those types forms H5N1 which is included into HP [26].

Bird flu is a highly infectious disease caused by virus such as H5N1 strain. This virus is carried by wild birds such as waterfowl. Bird flu infections occur most often direct contact between infected birds and healthy birds or indirectly through contact with equipments, materials, and surfaces that have been contaminated with the viruses [3,12]. The infection with HP avian influenza transmitted rapidly over a poultry farm, and it causes domestic birds serious symptoms that eventually lead to death. On the other hand, the infection with LP avian influenza causes symptoms such as ruffled feathers and decrease in egg production and it may be undetected. However, the symptoms caused by LP avian influenza may be exacerbated by other diseases or environmental conditions to more serious symptoms.

Bird flu has been documented since the latter half of the 19th century when E. Perrocinto reported on outbreaks of a severe and highly contagious new poultry disease in Northern Italy and other European countries in 1878, which caused extremely high mortality of chickens [2]. The most well known HP avian influenza, H5N1 strains, is appeared in China in 1996, while LP avian influenza strain was found in North America. Low level HP avian influenza H5N1 viruses spread in East Asia from 1996 to 2003. Those
viruses had spread all over Asia since 2003, before it reached Europe in 2005 and Middle East, as well as Africa in 2006. The disease is now endemic in poultry populations in several countries in Asia and in Africa including Indonesia, China, and Malaysia. It has not been found in North or South America, including the Caribbean. Cases of infected poultry farms were reported from several provinces of Indonesia including Bali, East Java, West Java, and West Borneo in 2004. Bird flu infection of poultry farms are now endemic to some regions (Table 2.1) [1,2,5].

H5N1 virus has also shown potential for cross-species infection, it can be transmitted from birds to humans although it is highly unlikely. Several cases of bird flu to human infection have also been reported since 1997. Those include cases found in 12 provinces in Indonesia.

<table>
<thead>
<tr>
<th>Year</th>
<th>Infected (per case)</th>
<th>Susceptible (per case)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2011</td>
<td>31,508</td>
<td>841</td>
</tr>
<tr>
<td>2012</td>
<td>1,164</td>
<td>1,073</td>
</tr>
<tr>
<td>2013</td>
<td>11,038</td>
<td>-</td>
</tr>
<tr>
<td>2014</td>
<td>2,170</td>
<td>338</td>
</tr>
<tr>
<td>2015</td>
<td>3</td>
<td>7</td>
</tr>
</tbody>
</table>

Source: Department of Animal Husbandry, West Sumatra, Indonesia.

### 2.2 Previous Studies

Application of mathematics for study of infectious disease was initiated by Daniel Bernoulli in 1760. A mathematical model was used to evaluate the effectiveness of the techniques of vaccinating against smallpox, with the aim of influencing public health policy [13,20]. This model called S-I-R model categorizes hosts within a population as Susceptible (if previously unexposed to the pathogen, who can catch the disease), Infected (if currently colonized by the pathogen, who have the disease and can transmit it), and Recovered (if they have successfully cleared the infection, they are either recovered, immune, or isolated until clear or dead). The progress of individuals is described by

\[ S \rightarrow I \rightarrow R. \]

The model was initially studied in depth [4]. This model leads to the following equations

\[
\begin{align*}
\frac{dS}{dt} &= -\beta IS, \\
\frac{dI}{dt} &= \beta IS - \gamma I, \\
\frac{dR}{dt} &= \gamma I,
\end{align*}
\]

(2.1)

where \( S \) is the number of susceptible, \( I \) is the number of infected, and \( R \) is the number of recovered individuals, \( \beta IS \) is the rate at which new infection occur and \( \gamma I \) is the rate of infective individuals who enter the recovered class. \( \beta \) is the transmission rate and \( \gamma \) is...
the recovery rate, where \( \gamma \) and \( \beta \) are positive constant. Fig. 2.1 shows graphs of solutions of the system (2.1) for initial values \( S_0 = 0.9, I_0 = 0.1, \) and \( R_0 = 0. \)

\[ \frac{dS}{dt} = -\beta IS, \]
\[ \frac{dI}{dt} = \beta IS - \gamma I. \]  

(2.2)

Figure 2.1: Solutions of the system (2.1) for \( \beta = 2 \) and \( \gamma = 1. \)

The first two equation of the system (2.1) is

\[ \frac{dS}{dt} = -\beta IS, \]
\[ \frac{dI}{dt} = \beta IS - \gamma I. \]  

The \( S \)-nullclines are

\( S = 0, \quad I = 0, \)  

(2.3)

and the \( I \)-nullclines are

\[ S = \frac{\gamma}{\beta}, \quad I = 0. \]  

(2.4)

If \( S(0) = S_0 < \frac{\gamma}{\beta} \), then both \( S(t) \) and \( I(t) \) decrease and converges to a point on the S-axis. It means that there is no outbreak. If \( S(0) = S_0 > \frac{\gamma}{\beta} \), \( I(t) \) first increases in the region \( \left( \frac{\gamma}{\beta}, 1 \right) \) and then decrease to 0. It means that an outbreak occurs. Here, \( \frac{\gamma}{\beta} \) is a threshold number, which indicates whether an outbreak occurs or it does not occur. Fig. 2.2 shows the vector field and some trajectories of the system (2.2).
A first mathematical model is proposed to interpret the spread of bird flu in a bird world system with autonomous ordinary differential equations [6]

\[
\begin{align*}
\frac{dX}{dt} & = c - bX - \omega XY, \\
\frac{dY}{dt} & = \omega XY - (b + m)Y.
\end{align*}
\] (2.5)

The system (2.5) called the Susceptible Infected (SI) model which formulates the interaction among birds. The population is divided into two classes: susceptible birds \((X)\) and infected birds \((Y)\). The parameter \(c\) is the rate at which new birds are born, \(b\) and \(b + m\) are the death rate for susceptible birds and infected birds, respectively, where \(m\) is the additional death rate for infected birds. The term \(\omega XY\) is the number of susceptible birds infected per unit time, where \(\omega\) is the rate at susceptible individuals is infected from infected individuals per unit time, unit susceptible individuals, and unit infected individual. The system (2.5) has two stationary points

\[
(X, Y) = \left( \frac{c}{b}, 0 \right),
\] (2.6)

\[
(X, Y) = \left( \frac{b + m}{\omega}, \frac{c}{b + m} - \frac{b}{\omega} \right).
\] (2.7)

The stationary point (2.6) is the disease free stationary point, which represents the state in which the infected birds are absent. The stationary point (2.7) is bird endemic stationary point, which represents the state in which a portion the entire population is infected.
The system (2.5) is inappropriate for closed systems such as poultry farms, where the entire population is maintained. In the production process of a poultry farm, the entire population is maintained at the capacity of the farm with supply of new healthy birds for vacancies, even though some of susceptible birds are infected as time elapses, while some of infected birds are removed from the population. Supply of new birds per unit time is proportional to the difference between the capacity of the farm $c$ and the entire population $X + Y$. So, the first two terms on the right hand side of the first equation of the system (2.5) are replaced with $a\{c - (X + Y)\}$, where $a$ is the rate of supply of new healthy birds for vacancies. Some infected birds die at early stages, and others stay alive longer, but the infected birds do not recover from the infection and eventually die. Regardless of being alive or dead, infected birds are hosts for viruses unless they are removed from the population. The removal of infected birds per unit time is proportional to their population, and the second term in the right hand side of the second equation of the system (2.5) is replaced with $-mY$, where $m$ is the removal rate of infected birds. A mathematical model was proposed for interpretation of infection process the spread of bird flu within a poultry farm by the following system of differential equations [10]

$$
\frac{dX}{dt} = a(c - (X + Y)) - \omega XY, \quad (2.8)
$$

$$
\frac{dY}{dt} = \omega XY - mY.
$$

There are two stationary points of the system (2.8)

$$(X, Y) = (c, 0), \quad (2.9)$$

$$(X, Y) = \left( \frac{m}{\omega}, \frac{a(\omega c - m)}{\omega(a + m)} \right). \quad (2.10)$$

Stationary point (2.9) corresponds to non infected state, in which none of the birds in the farm is infected, and the other stationary point corresponds to endemic state, in which some of the birds are infected.

Fig. 2.3 and Fig. 2.4 show the graph of the solutions of the system (2.8) for initial values $X_0 = 0.9$ and $Y_0 = 0.1$. The figure shows that those solutions converge to the stationary points. The solution converges to the stationary point (2.9) for $\omega c - m < 0$ as illustrated in Fig. 2.3, which confirms that the stationary point (2.9) is asymptotically stable and the stationary point (2.10) is unstable. The Fig 2.3 also shows that there is no change of the entire population. On the other hand, solution converges to the stationary point (2.10) for $\omega c - m > 0$ as illustrated in Fig. 2.4, which confirms that the stationary point (2.10) is asymptotically stable and the stationary point (2.9) is unstable. The Fig. 2.4 also shows that some birds in the population are infected.
Figure 2.3: Solution of the system (2.8) for $a = 1$, $c = 1$, and $\omega = 2$, and $m = 3$ ($\omega c < m$).

Figure 2.4: Solution of the system (2.8) for $a = 1$, $c = 1$, and $\omega = 2$, and $m = 1$ ($\omega c > m$).
Nullclines of the system (2.8) are curves in the \(XY\) plane obtained by setting the right-hand sides equal to zero. In particular, \(X\)-nullcline is the curve expressed by
\[
Y = \frac{a(c-X)}{a + \omega X},
\]
and \(Y\)-nullclines are the curve expressed by
\[
Y = 0 \text{ and } X = \frac{m}{\omega}.
\]
Denote by \(X(t)\) and \(Y(t)\) the \(X\) component and the \(Y\) component of the solution of the system (2.8), respectively. Function \(X(t)\) is an increasing function of \(t\) when it lies below the curve (2.11), and it is decreasing function of \(t\) when it lies above the curve (2.11). Function \(Y(t)\) is an increasing function if it lies in the region expressed by \(X < m/\omega\) and \(Y < 0\), or \(X > m/\omega\) and \(Y > 0\). It is a decreasing function if it lies in the region defined by \(X > m/\omega\) and \(Y < 0\), or \(X < m/\omega\) and \(Y > 0\). The nullclines (2.11) and (2.12) divide the \(XY\) plane into seven subregions:

Region I: \(dX/dt < 0, \ dY/dt > 0\).
Region II: \(dX/dt > 0, \ dY/dt > 0\).
Region III: \(dX/dt < 0, \ dY/dt < 0\).
Region IV: \(dX/dt > 0, \ dY/dt < 0\).
Region V: \(dX/dt < 0, \ dY/dt < 0\).
Region VI: \(dX/dt > 0, \ dY/dt < 0\).
Region VII: \(dX/dt > 0, \ dY/dt > 0\).

Fig. 2.5 and Fig. 2.6 show the dynamic of the system (2.8) under the conditions \(\omega c - m < 0\) and \(\omega c - m > 0\), respectively. Vector field defined by the right hand sides of the system (2.8) are also plotted. The figures also show the nullclines, the stationary points, and some trajectories generated numerically.
Figure 2.5: Trajectories of the system (2.8) for $a = 1$, $c = 1$, and $\omega = 2$, and $m = 3$ ($\omega c < m$). Green curve: $X$-nullclines, red curves: $Y$-nullclines, blue curves: trajectories, black points: stationary points.

Figure 2.6: Trajectories of the system (2.8) for $a = 1$, $c = 1$, and $\omega = 2$, and $m = 1$ ($\omega c > m$). Green curve: $X$-nullclines, red curves: $Y$-nullclines, blue curves: trajectories, black points: stationary points.
The system (2.8) did not provide information about the virus concentration of bird flu. The virus concentration diffuses through a medium. It was incorporated into the model, and led to the following system of equations [11]

\[
\begin{align*}
\frac{dX}{dt} &= a\{c - (X + Y)\} - \omega r XZ, \\
\frac{dY}{dt} &= \omega r XZ - mY, \\
\frac{dZ}{dt} &= p(Y - rZ).
\end{align*}
\]

Here \( Z \) denotes the virus concentration. The time rate of change in the number of susceptible birds is the difference between supply of new healthy birds per unit time \( a\{c - (X + Y)\} \) and the decreasing rate of susceptible birds due to infection \( \omega r XZ \), where \( \omega r \) is the infected rate, and \( r \) is positive constant. The time rate of change in the number of infected birds is the difference between the decreasing rate of susceptible birds due to infection and the infected birds removed from the population in the poultry farm. The time rate of change in the of virus concentration in a medium is proportional to the difference between the number of infected birds and the constant multiple of the virus concentration itself.

There are two stationary points of the system (2.13)

\[
(X, Y, Z) = (c, 0, 0),
\]

\[
(X, Y, Z) = \left( \frac{m}{\omega}, \frac{a(\omega c - m)}{\omega(a + m)}, \frac{a(\omega c - m)}{r\omega(a + m)} \right).
\]

The stationary point (2.14) corresponds to an infection free state stationary and the other one (2.15) corresponds to an endemic state. Fig. 2.7 and Fig. 2.8 show components of a solution of the system (2.13) for initial values \( X_0 = 0.9, Y_0 = 0.1, \) and \( Z_0 = 0.5 \). Fig. 2.7 shows that the solution converges to the stationary point (2.14) for \( \omega c - m < 0 \), which confirms that the stationary point (2.14) is asymptotically stable and stationary point (2.15) is unstable. Fig. 2.8 shows that the solution converges to the stationary point (2.15) for \( \omega c - m > 0 \), which confirms that the stationary point (2.14) is unstable and stationary point (2.15) is asymptotically stable.

Previous studies [10,11] show that proper vaccination and proper removal of infected birds secured a population of domestic birds against an outbreak of bird flu. Those studies also show that the population was not made secure by vaccination alone without removal of infected birds.
Figure 2.7: Components of solution of the system (2.13) for $a = 1$, $c = 1$, $\omega = 2$, $p = 1$, and $r = 1$, and $m = 3$ ($\omega c < m$).

Figure 2.8: Components of solution of the system (2.13) for $a = 1$, $c = 1$, $\omega = 2$, $p = 1$, and $r = 1$, and $m = 1$ ($\omega c > m$).
2.3 Nonlinear Diffusion Equations

Partial differential equation is one of natural ways for description the dynamics of populations that depends on spatial coordinates. A system of partial differential equations was derived under the assumption that infected birds transmit viruses only to susceptible birds at their location. This process is called diffusion [22]. The diffusion equation is a partial differential equation. The use of diffusion is one of the simplest techniques used for modeling the spread of the viruses. If a system of ordinary differential equations is coupled with diffusion, then it leads to a system of partial differential equations.

Second order quasilinear of partial differential equations classified into: a) parabolic, b) hyperbolic, and c) elliptic. Those types of equation are models for diffusive phenomena, wave phenomena, and steady state phenomena, respectively. The three most important types of boundary conditions are: a) Dirichlet boundary condition, b) Neumann boundary conditions, and c) Mixed boundary conditions. If the specified functions in a set of condition are all equal to zero, then they are homogeneous [23].

A diffusive model derived from SIR model of the system (2.1) in the previous section was studied [21]. Suppose that the population consists of only two classes: susceptible \( S(x,t) \) and infective \( I(x,t) \) which are now functions of a spatial variable \( x \) as well as time \( t \). Both classes have the diffusion coefficient \( d_1 \) and \( d_2 \), respectively. Consideration of the spatial spread as a diffusive process led to the following system

\[
\begin{align*}
\frac{\partial S}{\partial t} &= -\beta IS + d_1 \frac{\partial^2 S}{\partial x^2}, \\
\frac{\partial I}{\partial t} &= \beta IS - \gamma I + d_2 \frac{\partial^2 I}{\partial x^2}, \\
\text{for } 0 < x < L, t > 0, \text{ where } \beta, \gamma, d_1, d_2, \text{ and } L \text{ are positive constant.}
\end{align*}
\] (2.16)

for \( 0 < x < L, t > 0 \), where \( \beta, \gamma, d_1, d_2, \text{ and } L \) are positive constant. The system (2.16) was supplemented with Neumann (no flux) boundary conditions at both end point, \( x = 0, L \)

\[
\begin{align*}
S_x(0,t) &= 0, \quad S_x(L,t) = 0, \\
I_x(0,t) &= 0, \quad I_x(L,t) = 0,
\end{align*}
\] (2.17)

and with initial conditions

\[
\begin{align*}
S(x,0) &= S_0(x), \\
I(x,0) &= I_0(x).
\end{align*}
\] (2.18)

Traveling wave solutions of the system (2.16) will be discussed in the following section.

2.4 Traveling Wave Solutions

A traveling wave is a solution to the evolution equation

\[ U_t = f(U, U_x, U_{xx}, ...), \]

takes the form \( U(x,t) = u(x - kt) \), where \( k \) is the speed of the traveling wave. Transformation according to traveling wave coordinate \( \xi = x - kt \) converts the system of partial
differential equations into system of ordinary differential equations by combining two independent variables to one independent variable which is called traveling wave variable. Traveling waves are fundamental solutions that represent the transportation of information in a single direction [22]. Traveling wave solutions of the system (2.16) were obtained by setting

\[ S(x, t) = s(\xi), \quad I(x, t) = i(\xi), \quad \xi = x - kt, \]  

(2.19)

where \( k \) is the wave speed. Substituting expressions (2.19) to the system (2.16) leads to

\[
\begin{align*}
  d_1 s'' + cs' + \beta is &= 0, \\
  d_2 i'' + ci' + i(\beta s - \gamma) &= 0,
\end{align*}
\]

(2.20)

where ('') is differentiation with respect to \( \xi \). The system (2.20) now reduces to system of ordinary differential equations

\[
\begin{align*}
  s' &= u, \\
  u' &= -\frac{c}{d_1} u - \frac{\beta}{d_1} is, \\
  i' &= v, \\
  v' &= -\frac{c}{d_2} u - \frac{i}{d_2} (\beta s - \gamma),
\end{align*}
\]

(2.21)

Note that a traveling wave solution of the system of partial differential equations (2.16) corresponds to a trajectory in the four dimensional phase space of the system (2.21). There are different kinds of traveling wave solutions associated with the phase portraits of dynamical system. A traveling front corresponds to a heteroclinic orbit, that is, a trajectory that connects two different stationary points, for example a saddle and a node. A traveling pulse corresponds to a homoclinic orbit, that is, a trajectory in space that connects a stationary point to itself. It connects a saddle stationary point to itself.
This chapter focuses on analysis of bird flu transmission process within a poultry farm. A nonlinear system of ordinary differential equations was analyzed for local and global stability of stationary points. A nonlinear parabolic system of partial differential equations was proposed as a model for a bird flu transmission process within a poultry farm and analyzed. Stability of constant solutions, traveling wave solutions of host virus model, and solutions in a singular limit were also investigated.

3.1 Nonlinear System of Ordinary Differential Equations

3.1.1 Mathematical Model

The assumption that vacancies due to infection are instantly replaced with new birds, so that the total population always balances with the capacity of the farm

\[ X + Y = c, \]
\[ \frac{dX}{dt} = \frac{dY}{dt} = -\omega r X Z + m (c - X) \]  \hspace{1cm} (3.1)

led from the previous model proposed [11] to a nonlinear system of differential equations whose unknown variables correspond to the number of susceptible birds \( X \) and the virus concentration \( Z \) [27]

\[ \frac{dX}{dt} = m (c - X) - \omega r X Z, \]
\[ \frac{dZ}{dt} = p (c - X - r Z). \]  \hspace{1cm} (3.2)

The first equation of the system (3.2) represents the fact that the rate of change in the number of susceptible birds is the difference between the removal rate of infected birds and
the loss due to infection per unit time. The second equation of the system (3.2) represents
the fact that the rate of change in the virus concentration is the difference between increase
proportional to the number of infected birds and the loss due to inviability. Local and
global stability of stationary points of the system (3.2) will be discussed in the following
section.

3.1.2 Local Stability of Stationary Points

There are two stationary points of the system (3.2)

\[(X, Z) = (c, 0), \quad (3.3)\]

\[(X, Z) = \left( \frac{m}{\omega}, \frac{\omega c - m}{\omega r} \right), \quad (3.4)\]

and there are two states that corresponds to the steady state solutions, infection free state
and endemic state. The stationary point (3.3) corresponds to the infection free state, in
which no birds in the population is infected, and the stationary point (3.4) corresponds to
the endemic state, in which some birds are infected. The latter is practically significant
provided its \(Z\) component is positive \((\omega c - m > 0)\), while it is practically insignificant
\((\omega c - m < 0)\). Note that the stationary points (3.3) and (3.4) are identical for

\[\omega c - m = 0.\]

Let \((X^*, Z^*)\) be a stationary point of the system (3.2). The stability of the sta-
tionary point is characterized in terms of the eigenvalues of the matrix

\[A = \begin{bmatrix} -(m + \omega r Z^*) & -\omega r X^* \\ p & -pr \end{bmatrix}. \quad (3.5)\]

The stationary point \((X^*, Z^*)\) is asymptotically stable when the real parts of the eigen-
values of \(A\) are all negative, and it is unstable when at least one of the eigenvalues has a
positive real part \([19]\). The eigenvalues \(\lambda_1, \lambda_2\) of \(A\) are

\[\lambda_1 = \frac{\text{tr}A - \sqrt{(\text{tr}A)^2 - 4\det A}}{2}, \quad \lambda_2 = \frac{\text{tr}A + \sqrt{(\text{tr}A)^2 - 4\det A}}{2},\]

where

\[\text{tr}A = -(m + \omega r X^* + pr), \quad \det A = pr(m + \omega r Z^*) - pr\omega X^*.\]

Since \((\text{tr}A)^2 - 4\det A = (pr - m - \omega r Z^*)^2 + pr\omega X^*, \lambda_1\) and \(\lambda_2\) are always real values.

For the stationary point (3.3), \(\text{tr}A = -(m + pr)\) and \(\det A = pr(m - \omega c)\). It follows
that the stationary point (3.3) is asymptotically stable for \(\omega c - m < 0\), and it is unstable
for \(\omega c - m > 0\). For the stationary point (3.4), \(\text{tr}A = -(\omega c + pr)\) and \(\det A = pr(\omega c - m)\).
It follows that the stationary point (3.4) is asymptotically stable for \(\omega c - m > 0\), and it
is unstable for \(\omega c - m < 0\). Fig. 3.1 and Fig. 3.2 show solution of the system (3.2) with
initial values \(X_0 = 1.0\) and \(Z_0 = 0.5\). Fig. 3.1 shows that the solution converges to the
stationary point (3.4) for \(\omega c - m > 0\) and Fig. 3.2 shows that the solution converges to
the stationary point (3.3) for \(\omega c - m < 0\).
Figure 3.1: Solution of the system (3.2) for $c = 1$, $p = 1$, $r = 1$, and $\omega = 1$, and $m = 0.5$ ($\omega c - m > 0$).

Figure 3.2: Solution of the system (6) for $c = 1$, $p = 1$, $r = 1$, and $\omega = 1$, and $m = 1.5$ ($\omega c - m < 0$).
3.1.3 Global Stability of Stationary Points

Given a pair of initial values \(X_0\) and \(Z_0\), the system (3.2) and the initial condition
\[
X(0) = X_0, \quad Z(0) = Z_0, \quad (3.6)
\]
form an initial value problem. The initial value problem (3.2), (3.6) is formulated for a point \((X_0, Z_0)\) lying in the region \(\Gamma = \{(X_0, Z_0)|0 \leq X_0 \leq c, Z_0 > 0\}\). The region \(\Gamma\) is invariant region of the dynamical system defined by the initial value problem (3.2), (3.6) in the sense that \((X(t), Z(t))\) lies in \(\Gamma\) for all non-negative \(t\) if \((X_0, Z_0)\) is a point of \(\Gamma\). To see that \(\Gamma\) is an invariant region, let
\[
f(X, Z) = m(c - X) - \omega r X Z \quad \text{and} \quad g(X, Z) = p(c - X - r Z).
\]
Note that \(f(X, Z)\) and \(g(X, Z)\) are the right hand sides of the system (3.2), respectively. Moreover,
\[
f(0, Z) = mc > 0, \quad g(X, 0) = p(c - X) > 0, \quad \text{for } 0 \leq X \leq c,
\]
and
\[
f(c, Z) = -\omega r c Z < 0.
\]
Those inequalities (3.7), (3.8) show that the vector fields points inward to \(\Gamma\) at points on the boundary, and that \(\Gamma\) is an invariant region of the dynamical system defined by the initial value problem (3.2), (3.6).

The stationary solution (3.3) is globally asymptotically stable for \(\omega c - m < 0\) in the sense that for any initial value \((X_0, Z_0)\) in \(\Gamma\), the solution converges to the stationary solution (3.3). On the other hand, the stationary solution (3.4) is globally asymptotically stable for \(\omega c - m > 0\). To show this global stability of the stationary solutions, let
\[
v(X) = \frac{m}{\omega r} \left(\frac{c}{X} - 1\right), \quad w(X) = \frac{c - X}{r}.
\]
The curves \(Z = v(X)\) and \(Z = w(X)\) are the \(X\)-nullcline and \(Z\)-nullcline, respectively, that is, \(f(X, v(X)) = 0, g(X, w(X)) = 0\). Note that \(f(X, Z) < 0\) for \(Z > v(X)\), and that \(f(X, Z) > 0\) for \(Z < v(X)\). In particular, the \(X\) component of solution of the system (3.2) is a decreasing function for \(Z > v(X)\) and an increasing function for \(Z < v(X)\). Note also that \(g(X, Z) > 0\) for \(Z < w(X)\), and that \(g(X, Z) > 0\) for \(Z < w(X)\). In particular, the \(Z\) component of solutions of the system (3.2) is a decreasing function for \(Z > w(X)\) and an increasing function for \(Z < w(X)\).

The region \(\Gamma\) is divided into three parts for \(\omega c - m < 0\),
\[
I : \{(X, Z)|0 < X < c, Z < w(X)\}.
\]
\[
II : \{(X, Z)|0 < X < c, w(X) < Z < v(X)\}.
\]
\[
III : \{(X, Z)|0 < X < c, Z > v(X)\}.
\]
Both the \(X\) component and the \(Z\) component of a solution are increasing function in region \(I\). Similarly, both the \(X\) component and the \(Z\) component of a solution are decreasing function in region \(III\). So, any solution that starts from a point \((X_0, Z_0)\) in region \(I\) or region \(III\) eventually enters region \(II\). In region \(II\), the \(X\) component of a solution is an increasing function while the \(Z\) component is a decreasing function, and so it converges to the stationary solution (3.3).
The region $\Gamma$ is divided into four parts for $\omega c - m > 0$,

$I$ : \[\{(X, Z)|0 < X < c, Z < \min\{v(X), w(X)\}\}\].

$II$ : \[\{(X, Z)|0 < X < \frac{\omega c - m}{\omega r}, w(X) < Z < v(X)\}\].

$III$ : \[\{(X, Z)|0 < X < c, Z < \max\{v(X), w(X)\}\}\].

$IV$ : \[\{(X, Z)|\frac{\omega c - m}{\omega r} < X < c, v(X) < Z < w(X)\}\].

Both the $X$ component and the $Z$ component of a solution are increasing function in region $I$. Similarly, both the $X$ component and the $Z$ component of a solution are decreasing function in region $III$. So, any solution that starts from a point $(X_0, Z_0)$ in region $I$ or region $III$ eventually enters region $II$ or region $IV$. In region $II$, the $X$ component of a solution is an increasing function while the $Z$ component is a decreasing function, and so it converges to the stationary solution (3.4). In region $IV$, the $X$ component of a solution is a decreasing function while the $Z$ component is an increasing function, and so it converges to the stationary solution (3.4). The dynamics generated by the initial value problem is depicted in Fig. 3.3 and 3.4. Fig. 3.3 shows that the steady state (3.3) is unstable and that the steady state (3.4) is asymptotically stable for $\omega c - m > 0$. Fig. 3.4 shows that the steady state (3.4) is unstable and that the steady state (3.3) is asymptotically stable for $\omega c - m < 0$.

The stability analysis of stationary points of the system (3.2) has shown that the stationary point corresponding to the infection free state infection is asymptotically stable for $\omega c - m < 0$ while the other stationary point is unstable, and that the stationary point corresponding to the infection free state is unstable for $\omega c - m > 0$ while the other the stationary point is asymptotically stable.
Figure 3.3: Vector fields, nullclines, and trajectories in the variant region \( \Gamma \) of the system (3.2) for \( c = 1, p = 1, r = 1, \) and \( \omega = 1, \) and \( m = 0.5 \) (\( \omega c - m > 0 \)). Green curve: \( X \)-nullcline, red curve: \( Z \)-nullcline, blue curves: trajectories, green points: stationary points.

Figure 3.4: Vector fields, nullclines, and trajectories in the variant region \( \Gamma \) of the system (3.2) for \( c = 1, p = 1, r = 1, \) and \( \omega = 1, \) and \( m = 1.5 \) (\( \omega c - m < 0 \)). Green curve: \( X \)-nullcline, red curve: \( Z \)-nullcline, blue curves: trajectories, green points: stationary points.
3.2 Nonlinear System of Partial Differential Equations

3.2.1 Mathematical Model with Spatial Virus Diffusion

The model (3.2) does not incorporate any spatial effects of virus concentration. In order to create effective measures against outbreaks of bird flu within a poultry farm, it is important to take spatial effect of virus concentration into formulation. The susceptible virus model (3.2) was reformulated with incorporation of a spatial effect. The basic assumption is that viruses diffuse through one dimensional medium, because bird cages are usually lined up in one direction in a chicken house of a typical poultry. Let \( x \) be the one dimensional coordinate variable. When a diffusive term was added to the rate of the change of the virus concentration, system of ordinary differential equations (3.2) was reformulated to a nonlinear system of partial differential equations [28]

\[
\frac{\partial X}{\partial t} = m(c - X) - \omega r X Z, \\
\frac{\partial Z}{\partial t} = p(c - X - rZ) + \frac{d}{\partial x^2} Z,
\]

(3.7)

where \( d \) is the diffusion constant. Here parameter \( c \) represents the capacity per unit length. The unknown variables \( X \) and \( Z \) of the system (3.2) are now functions of the one dimensional coordinate variable \( x \) and time \( t \), \( X(x,t) \) and \( Z(x,t) \). They represent the number of susceptible birds and the number of virus concentration at coordinate \( x \) and time \( t \), respectively. Solutions \( X(x,t) \) and \( Z(x,t) \) are defined in the region in the \( xt \) plane \( \{(x,t)|0 \leq x \leq L, t \geq 0\} \). System (3.7) is associated with boundary conditions at points \( x = 0 \) and \( x = L \)

\[
\frac{\partial X}{\partial x}(0,t) = \frac{\partial Z}{\partial x}(0,t) = \frac{\partial X}{\partial x}(L,t) = \frac{\partial Z}{\partial x}(L,t) = 0, \quad (t \geq 0),
\]

(3.8)

The system is also associated with the initial conditions

\[
X(x,0) = X_0(x) \quad \text{and} \quad Z(x,0) = Z_0(x), \quad (0 \leq x \leq L).
\]

(3.9)

The system (3.7), the boundary conditions (3.8), and the initial conditions (3.9) form an initial boundary-value problem. Note that steady state solutions of the system (3.2) are constant solutions of the initial boundary-value problem. Solutions of the initial boundary-problem will be solved numerically for some parameter values in the Chapter 4.

3.2.2 Constant Solutions

The system (3.7) has the infection free state constant solution

\[
E_0 = (X, Z) = (c, 0),
\]

(3.10)

which represents that no infected birds exist. The system (3.7) also has the endemic state constant solution

\[
E_+ = (X, Z) = \left( \frac{m}{\omega}, \frac{\omega c - m}{\omega r} \right).
\]

(3.11)
which represents that a part of the birds in the capacity per unit length is infected. If the condition
\[ R_0 = \frac{\omega c}{m} > 1 \]  
(3.12)
is satisfied, the endemic state is realistic in the sense that it lies in the first quadrant. Here, \( R_0 \) gives a measure of infectious intensity. The stability of those constant solutions depend on parameter values. The stability of those constant solutions should depend on the capacity per unit length \( c \), the infection rate of susceptible birds \( \omega r \), and the removal rate of infected birds \( m \).

Other authors reported stability criteria of constant solutions of nonlinear system such as the system (3.7) [9]. Denoted by \( \Delta \) the operator \( \frac{\partial^2}{\partial x^2} \). Let \( \mu_i \) be the eigenvalue of \( -\Delta \) with homogeneous boundary conditions on the interval \([0, L]\), that is,
\[ Z'' + \mu Z = 0, \quad Z'(0) = Z'(L) = 0. \]

Solution of this equation is
\[ Z(x) = acos(\sqrt{\mu} x) + bsin(\sqrt{\mu} x). \]

Since
\[ Z'(x) = -\sqrt{\mu}asin(\sqrt{\mu} x) + \sqrt{\mu}bcos(\sqrt{\mu} x), \]
and
\[ Z'(0) = Z'(L) = 0, \]
then those eigenvalues are \( \mu_i = \left( \frac{i\pi}{L} \right)^2, \quad i = 0, 1, 2, \ldots \)

Jacobian matrix of the system (3.7) for constant solutions \((X, Z)\) is
\[ J = \begin{bmatrix} 0 & 0 \\ 0 & -d\Delta \end{bmatrix} + \begin{bmatrix} -m - \omega r Z & -\omega r X \\ -p & -pr \end{bmatrix}. \]  
(3.13)

Let \( \lambda \) be an eigenvalue of \( J \) if and only if it is an eigenvalue of the matrix
\[ \phi = \begin{bmatrix} -m - \omega r Z & -\omega r X \\ -p & -d\mu_i - pr \end{bmatrix}. \]  
(3.14)
The characteristic equation of \( \phi \) is
\[ \phi_i(\lambda) = [\lambda + (m + \omega r Z)][\lambda + (d\mu_i + pr)] - \omega pr X. \]  
(3.15)
For the infection free state (3.10), the characteristic equation is
\[ \lambda^2 + (d\mu_i + pr + m)\lambda + [md\mu_i + pr(m - \omega c)] = 0. \]  
(3.16)
If \( R_0 < 1 \), then \( pr(m - \omega c) > 0 \), eigenvalues are all negative for any non-negative value of \( \mu_i \) and \( E_0 \) is asymptotically stable. On the other hand, if \( R_0 > 1 \), then \( pr(m - \omega c) < 0 \),
there is a possibility that eigenvalue is positive for some non-negative value of \( \mu_i \) and \( E_0 \) is unstable. For the endemic state, the characteristic equation is

\[
\lambda^2 + (d\mu_i + pr + \omega c)\lambda + [\omega c d\mu_i + pr(\omega c - m)] = 0.
\] (3.17)

If \( R_0 > 1 \), then \( pr(\omega c - m) > 0 \), eigenvalues are all negative for any non-negative value of \( \mu_i \) and \( E_++ \) is asymptotically stable. It means that the endemic state is significant, and that a part of the population is always infected. Otherwise, if \( R_0 < 1 \), then \( pr(\omega c - m) < 0 \), there is a possibility that eigenvalue is positive for some non-negative value of \( \mu_i \) and \( E_+ \) is unstable.

### 3.2.3 Traveling Wave Solutions of Host Virus Model

Traveling wave solutions of the system (3.7) are solutions that expressed in terms of function \( U \) and \( V \) one variable \( \xi \) such that

\[
X(x,t) = U(\xi), \quad Z(x,t) = V(\xi), \quad \xi = x - kt,
\] (3.18)

Those solutions represent waves traveling to the right. Parameter \( k \) is a positive constant called the wave speed. Substituting the expressions (3.18) for \( X(x,t) \) and \( Z(x,t) \), system (3.7) is transformed to

\[
-kU' - m(c - U) + \omega r U V = 0,
\]

\[
-dV'' + kV' + p(c - U - rV) = 0.
\] (3.19)

Let \( W = V' \). System (3.19) lead to the third order system of ordinary differential equations

\[
U' = -\frac{1}{k} \{m(c - U) - \omega r U V\},
\]

\[
V' = W,
\]

\[
W' = -kW - \frac{p}{d}(c - U - rV).
\] (3.20)

There are two stationary points of the system (3.20)

\[
A = (U,V,W) = (c,0,0),
\] (3.21)

\[
B = (U,V,W) = \left(\frac{m}{\omega}, \frac{\omega c - m}{\omega r}, 0\right).
\] (3.22)

Jacobian matrices \( J_A \) and \( J_B \) associated with the stationary points \( A \) and \( B \) are

\[
J_A = \begin{bmatrix}
\frac{m}{k} & \frac{\omega r c}{k} & 0 \\
0 & 0 & 1 \\
\frac{p}{d} & \frac{pr}{d} & -\frac{k}{d}
\end{bmatrix},
\]

\[
J_B = \begin{bmatrix}
\frac{\omega c}{k} & \frac{mr}{k} & 0 \\
0 & 0 & 1 \\
\frac{p}{d} & \frac{pr}{d} & -\frac{k}{d}
\end{bmatrix}.
\]
respectively, and characteristic equations associated with the Jacobian matrices $J_A$ and $J_B$ are

$$\lambda^3 + \left( \frac{k^2 - md}{kd} \right) \lambda^2 - \left( \frac{m + pr}{d} \right) \lambda + \frac{pr}{kd} (m - \omega c) = 0,$$

$$\lambda^3 + \left( \frac{k^2 - \omega cd}{kd} \right) \lambda^2 - \left( \frac{\omega c + pr}{d} \right) \lambda + \frac{pr}{kd} (\omega c - m) = 0,$$

respectively.

Stability of the stationary points $A$ and $B$ was determined by the Routh-Hurwitz criterion. Consider an $n^{th}$ degree polynomial

$$P(\lambda) = \lambda^n + a_1 \lambda^{n-1} + \ldots + a_{n-1} \lambda + a_n,$$

where coefficients $a_i$ are real constant, $i = 0, 1, \ldots, n$, $a_n > 0$, and $a_0 \neq 0$. The Hurwitz matrices using the coefficient $a_i$ of the characteristic polynomial are

$$H_1 = [a_1], \ H_2 = \begin{bmatrix} a_1 & 1 \\ a_3 & a_2 \end{bmatrix}, \ H_3 = \begin{bmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \end{bmatrix}, \ldots, \ H_n = \begin{bmatrix} a_1 & 1 & 0 & 0 & \ldots & 0 \\ a_3 & a_2 & a_1 & 1 & \ldots & 0 \\ a_5 & a_4 & a_3 & a_2 & \ldots & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}.$$

All of the roots of the polynomial $P(\lambda)$ are negative or have negative real parts if and only if the determinants of all Hurwitz matrices are all positive [24]

$$\det H_j > 0, \ j = 1, 2, \ldots, n.$$

The Hurwitz matrices for the stationary point $A$ are

$$H_{A1} = \begin{bmatrix} \frac{k^2 - md}{kd} \end{bmatrix},$$

$$H_{A2} = \begin{bmatrix} \frac{k^2 - md}{kd} & 1 \\ \frac{pr}{kd} (m - \omega c) - \left( \frac{m + pr}{d} \right) \end{bmatrix},$$

$$H_{A3} = \begin{bmatrix} \frac{k^2 - md}{kd} & 1 & 0 \\ \frac{pr}{kd} (m - \omega c) - \left( \frac{m + pr}{d} \right) & \frac{k^2 - md}{kd} \\ 0 & 0 & \frac{pr}{kd} (m - \omega c) \end{bmatrix}.$$

According to the Routh-Hurwitz criterion, stationary point $A$ is asymptotically stable if and only if

1. $\frac{k^2 - md}{kd} > 0,$
2. $\frac{pr}{kd} (\omega c - m) - \left( \frac{k^2 - md}{kd} \right) \left( \frac{m + pr}{d} \right) > 0,$
3. $\left( \frac{k^2 - md}{kd} \right) \left( \frac{m + pr}{d} \right) - \frac{pr}{kd} (\omega c - m) > 0$ and $\frac{pr}{kd} (\omega c - m) > 0.$

The Hurwitz matrices for the stationary point $B$ are
According to the Routh-Hurwitz criterion, the stationary point $B$ is asymptotically stable if and only if

i. \( k^2 - \omega cd > 0, \)

ii. \( \frac{pr}{kd} (m - \omega c) - \left( \frac{k^2 - \omega cd}{kd} \right) \left( \frac{\omega c + pr}{d} \right) > 0, \)

iii. \( \left( \frac{k^2 - \omega cd}{kd} \right) \left( \frac{\omega c + pr}{d} \right) - \frac{pr}{kd} (m - \omega c) > 0 \) and \( \frac{pr}{kd} (m - \omega c) > 0. \)

Conditions (ii) and (iii) are not satisfied for the stationary point $A$ and the stationary point $B$. It means that the stability criteria are unfulfilled, and so, neither of the stationary points $A$ nor $B$ are unstable. This criterion is verified by computing eigenvalues under condition \( d \) and \( \omega c - m > 0 \). There are some eigenvalues with positive real parts (Table 3.1). Condition of real and imaginary part of eigenvalues of Jacobian matrices $J_A$ and $J_B$ for parameter of values $c = 1$, $k = 1$, $\omega = 1$, $p = 1$, $r = 1$, $m = 0.5$, and $d = (0, 4)$ are shown in Fig. 3.5, Fig. 3.6 and Fig. 3.7.

### Table 3.1: Eigenvalues of Jacobian Matrices $J_A$ and $J_B$ for $\omega c - m > 0$.

<table>
<thead>
<tr>
<th>Jacobian</th>
<th>$0 &lt; d &lt; 2$</th>
<th>$d \geq 2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$J_A$</td>
<td>real: one (+) and two (-)</td>
<td>one real (+) and two complex number with (-) real part</td>
</tr>
<tr>
<td>$J_B$</td>
<td>real: two (+) and one (-)</td>
<td>real: two (+) and one (-)</td>
</tr>
</tbody>
</table>
Figure 3.5: Real and imaginary part of eigenvalues of Jacobian matrices $J_A$ for $0 < d < 2$.

Figure 3.6: Real and imaginary part of eigenvalues of Jacobian matrices $J_A$ for $d \geq 2$. 

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3.2.4 Solutions In Singular Limit

In order to identify traveling wave solutions of the system (3.7), existence of heteroclinic orbit of the system (3.20) connecting two stationary points was established. Proof for existence of heteroclinic orbits is difficult for three dimensional system such as the system (3.20). The three dimensional system was reduced to a two dimensional system on a center manifold, and one of method is center manifold reduction. A nonlinear system reduced on a center manifold was investigated in other studies including [25].

Solution in the limit $k \to 0$

In the limit $k \to 0$, the system (3.20) is reduced to a two dimensional on center manifold. Let

$$S = U - \frac{mc}{m + \omega r V}.$$  \hfill (3.23)

Equation (3.23) leads to

$$U' = S' - \frac{mc\omega r V'}{(m + \omega r V)^2}.$$  \hfill (3.24)

Substituting expression (3.24) into system (3.20) leads to

$$kS' = -\delta S + k\tilde{Z},$$

where

$$\tilde{Z} = \frac{mc\omega r W}{\delta^2} \quad \text{and} \quad \delta = (m + \omega r)$$
According to this transformation, the system (3.20) becomes

\[ kS' = \delta S + k\tilde{Z}, \]
\[ V' = W, \]
\[ W' = -\frac{k}{d} W - \frac{p}{d} \left( c - S - \frac{mc}{m + \omega r V} - rV \right). \]

A center manifold of the form

\[ S = f (V, W, \delta, k), \]
exists for all sufficiently small \(|\delta|\) and \(|k|\). Moreover, the center manifold satisfies

\[ S = O(k). \]

In the limit \(k \to 0\), the system (3.25) is reduced to

\[ V' = W, \]
\[ W' = -\frac{k}{d} W - \frac{p}{d} \left( c - S - \frac{mc}{m + \omega r V} - rV \right). \]

The system (3.26) has two stationary points

\[ (V, W) = (0, 0), \]
\[ (V, W) = \left( \frac{\omega c - m}{\omega r}, 0 \right). \]

The Jacobian matrices \(J_1\) and \(J_2\) associated with the stationary points (3.27) and (3.28) are

\[ J_1 = \begin{bmatrix} 0 & 1 \\ -\frac{\omega c r}{m d} + \frac{p r}{d} - \frac{k}{d} & -\frac{k}{d} \end{bmatrix}, \quad J_2 = \begin{bmatrix} 0 & 1 \\ -\frac{m p r}{\omega c d} + \frac{p r}{d} - \frac{k}{d} & -\frac{k}{d} \end{bmatrix}, \]

respectively. The eigenvalues of \(J_1\) and \(J_1\) are

\[ \lambda_\pm = \frac{1}{2} \left( -\frac{k}{d} \pm \sqrt{\left( \frac{k}{d} \right)^2 - \frac{4 p r}{d m} (\omega c - m)} \right), \]
\[ \mu_\pm = \frac{1}{2} \left( -\frac{k}{d} \pm \sqrt{\left( \frac{k}{d} \right)^2 - \frac{4 p r}{d c \omega} (m - \omega c)} \right), \]

respectively. For \(\omega c - m > 0\), \(\lambda_\pm\) are both negative, on the other hand \(\mu_-\) is negative and \(\mu_+\) is positive. Under this condition, the stationary point (3.27) is asymptotically stable and the stationary point (3.28) is unstable. Fig. 3.8 shows solutions of the system (3.26) for \(\omega c - m > 0\). Those solutions are shown for initial values \(V_0 = 0\) and \(W_0 = 0.5\).
It shows that solutions converge to the stationary point (3.27), which confirms that the stationary point (3.27) is asymptotically stable for $\omega c - m > 0$.

Figure 3.8: Solution of the system (3.26) for $m = 0.5$, $c = 1$, $p = 1$, $r = 1$, $\omega = 1$, and $d = 1$.

The $V$-nullclines and $W$-nullclines of the system (3.26) are expressed by $W = f(V)$ and $W = g(V)$, respectively, where

$$f(V) = 0 \quad \text{and} \quad g(V) = -\frac{p}{k} \left( c - \frac{mc}{m + \omega r V} - r V \right).$$
Those nullclines divide the plane of the system (3.33) into two regions:

\[
I_1 \cdot \{(V, W) | W > f(V), W < g(V)\}
\]
\[
I_2 \cdot \{(V, W) | W < f(V), W > g(V)\}
\]

Both the $V$ component and the $W$ component are increasing function in region $I_1$. Similarly, both the $V$ component and the $W$ component are decreasing function in region $I_2$.

Fig. 3.9 shows dynamic of the system (3.26) for $\omega_c - m > 0$. It shows that the system (3.26) has a heteroclinic orbit for $\omega_c - m > 0$, which leads to a conclusion that the system (3.20) admits a traveling wave solution.

Figure 3.9: Dynamics of the system (3.26): Vector fields, nullclines, and some trajectories are shown for $m = 0.5$, $c = 1$, $p = 1$, $r = 1$, $\omega = 1$, and $d = 1$. Red curve: $W$-nullcline, blue curves: trajectories.
Solution in the limit \( d \to 0 \)

In the limit \( d \to 0 \), the system (3.20) is reduced to a two dimensional system on a center manifold. Let

\[
S = W + \frac{p}{k}(c - U - rV).
\]  

(3.29)

Equation (2.23) leads to

\[
W' = S' - \frac{p}{k}(c - U' - rV').
\]  

(3.30)

Substituting expression (3.30) into the system (3.20) leads to

\[
dS' = -kS + d\tilde{Z},
\]

where

\[
\tilde{Z} = \frac{p}{k} \left[ c + \frac{1}{k} (m(c - U) - \omega rV) - r \left( S - \frac{p}{k}(c - U - rV) \right) \right].
\]

Differentiation of the right side of this equation with respect to \( S \) leads to

\[
\frac{\partial \tilde{Z}}{\partial S} = -\frac{pr}{k} = -\delta,
\]

where \( \delta = pr/k \). According to this transformation, the system (3.20) becomes

\[
\begin{align*}
U' & = -\frac{1}{k} (m(c - U) - \omega rUV), \\
V' & = S - \frac{p}{k}(c - U - rV), \\
dS' & = -kS + d\tilde{Z}.
\end{align*}
\]

(3.32)

Under condition (3.31), a center manifold of the form

\[
S = f(U, V, \delta, d),
\]

exists for all sufficiently small \(|\delta|\) and \(|d|\). Moreover, the center manifold satisfies

\[
S = O(d).
\]

In the limit \( d \to 0 \), the system (3.32) is reduced to

\[
\begin{align*}
U' & = -\frac{1}{k} (m(c - U) - \omega rUV), \\
V' & = -\frac{p}{k}(c - U - rV).
\end{align*}
\]

(3.33)

The system (3.33) has two stationary points

\[
C = (U, V) = (c, 0),
\]

(3.34)
\[ D = (U, V) = \left( \frac{m}{\omega}, \frac{\omega c - m}{\omega r} \right). \] (3.35)

The Jacobian matrices associated with the stationary points (3.34) and (3.35) are

\[ J_C = \begin{bmatrix} m & \omega r c \\ \frac{k}{p} & \frac{k}{p} \end{bmatrix}, \quad J_D = \begin{bmatrix} \omega c & m \\ \frac{k}{p} & \frac{k}{p} \end{bmatrix}, \]

respectively. The eigenvalues of \( J_C \) and \( J_D \) are

\[ \lambda_{1,2} = \frac{1}{2} \left( \frac{m + pr}{k} \pm \sqrt{\left( \frac{m + pr}{k} \right)^2 - \frac{4pr}{k^2} (m - \omega c)} \right), \]

\[ \mu_{1,2} = \frac{1}{2} \left( \frac{\omega c + pr}{k} \pm \sqrt{\left( \frac{\omega c + pr}{k} \right)^2 - \frac{4pr}{k^2} (\omega c - m)} \right), \]

respectively. The Jacobian matrix \( J_C \) associated with stationary point \( C \) has one real negative eigenvalue and one real positive eigenvalue for \( \omega c - m > 0 \), and it is unstable saddle point. This stationary point has a stable manifold, and there is a unique solution which converges to the stationary point \( C \) in the tangent direction of the eigenvector associated with the negative eigenvalue. On the other hand, Jacobian matrix \( J_D \) associated with stationary point \( D \) has two positive eigenvalues, and it is unstable node.

The change variables from \( \xi = -\xi \) leads to the system of ordinary differential equations

\[ U' = \frac{1}{k} (m(c - U) - \omega rUV), \]
\[ V' = \frac{p}{k} (c - U - rV). \] (3.36)

The stationary points (3.34) and (3.35) of the system (3.33) are stationary points of the system (3.36). The eigenvalues associated with the stationary points (3.34) and (3.35) of the reversed-time system are

\[ \lambda_{1,2} = \frac{1}{2} \left( -\frac{m + pr}{k} \pm \sqrt{\left( \frac{m + pr}{k} \right)^2 - \frac{4pr}{k^2} (m - \omega c)} \right), \]

\[ \mu_{1,2} = \frac{1}{2} \left( -\frac{\omega c + pr}{k} \pm \sqrt{\left( \frac{\omega c + pr}{k} \right)^2 - \frac{4pr}{k^2} (\omega c - m)} \right), \]

respectively. The Jacobian matrix \( J_C \) associated with stationary point \( C \) has one real negative eigenvalue and one real positive eigenvalue for \( \omega c - m > 0 \), and it is an unstable saddle point. On the other hand, Jacobian matrix \( J_D \) associates with stationary point \( D \) has two negative eigenvalues for \( \omega c - m > 0 \), and it is asymptotically stable. Fig. 3.10
shows graphs on some solutions of the system (3.36) for $\omega c - m > 0$. Initial values those solutions are $U_0 = 0$ and $V_0 = 0.5$.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{solution.png}
\caption{Solution of the system (3.36) for $c = 1$, $p = 1$, $r = 1$, $\omega = 1$, $k = 1$, and $m = 0.5$ ($\omega c - m > 0$).}
\end{figure}

The $U$-nullclines and $V$-nullclines of the system (3.33) and the system (3.36) are expressed by $V = f(U)$ and $V = g(U)$, respectively, where

$$f(U) = \frac{m(c - U)}{\omega r U} \quad \text{and} \quad g(U) = \frac{1}{r}(c - U).$$

Those nullclines divide the plane of the system (3.33) into four regions:

- **I** : $\{(U, V) | 0 < U < c, V < \max\{f(U), g(U)\}\}$
- **II** : $\{(U, V) | 0 < U < \frac{\omega c - m}{\omega r}, g(U) < V < f(U)\}$
- **III** : $\{(U, V) | 0 < U < c, V < \min\{f(U), g(U)\}\}$
- **IV** : $\{(U, V) | \frac{\omega c - m}{\omega r} < U < 0, f(U) < V < g(U)\}$

The $U$ component and the $V$ component of solutions of the system (3.33) are both increasing functions in region I, and decreasing functions in region III. In region II, $U$ component is an increasing function while the $V$ component is decreasing function. In region IV, $U$ component is a decreasing function while the $V$ component is an increasing function. Fig. 3.11 shows the vector field, some trajectories, and the nullclines of the system (3.33). It shows that trajectories are attracting along one direction and repulsing along another direction from the stationary point $C$, and that trajectories are moving away from the stationary point $D$. 

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Figure 3.11: Vector fields, nullclines, and some trajectories of the system (3.33) are shown for $c = 1$, $p = 1$, $r = 1$, $\omega = 1$, and $k = 1$, and $m = 0.5$ ($\omega c - m > 0$). Green curve: $U$-nullcline, red curve: $V$-nullcline, blue curves: trajectories.

The nullclines also divide plane the reversed-time system (3.36) into four regions:

1. $\{(U, V)| 0 < U < c, V < \max\{f(U), g(U)\}\}$
2. $\{(U, V)| 0 < U < \frac{\omega c - m}{\omega r}, g(U) < V < f(U)\}$
3. $\{(U, V)| 0 < U < c, V < \min\{f(U), g(U)\}\}$
4. $\{(U, V)| \frac{\omega c - m}{\omega r} < U < 0, f(U) < V < g(U)\}$

The $U$ component and the $V$ component of solutions of the system (3.36) are both decreasing functions in region I, and increasing functions in region III. In region II, $U$ component is an decreasing function while the $V$ component while the $V$ component is a increasing function. In region IV, $U$ component is a increasing function while the $V$ component is a decreasing function. Fig. 3.12 shows the vector field, some trajectories, and the nullclines of the reversed-time system (3.36). It shows that region bounded by two nullclines (region II) is an invariant region and that it is a globally attracting region in the sense that any solution with initial point in the first quadrant eventually enters the region and converges to the stationary point $D$. All trajectories are converging to stationary point $D$. In particular, unstable manifold of stationary point $C$ is connected to the stationary point $D$. This is a heteroclinic orbit connecting $C$ and $D$. Since a heteroclinic orbit of reversed-time system (3.36) is also a heteroclinic orbit of system (3.33), it is a unique heteroclinic orbit of system (3.33).
Figure 3.12: Vector fields, nullclines, and some trajectories of the system (3.36) are shown for $c = 1$, $p = 1$, $r = 1$, $\omega = 1$, $k = 1$, and $m = 0.5$ ($\omega c - m > 0$). Green curve: $U$-nullcline, red curve: $V$-nullcline, blue curves: trajectories.
Chapter 4

NUMERICAL RESULTS

In this chapter, numerically solutions of nonlinear system of partial differential equations (3.7) are introduced. Solutions were obtained with MATLAB pdepe which is a software module for initial boundary-value problem of time dependent partial differential equations with one spatial dimension. Solutions were generated for mixed boundary conditions, homogeneous Neumann boundary conditions, and some initial conditions. Results were investigated for comparison with analytical results obtained in the previous chapter.

4.1 Description of Numerical Procedure

The MATLAB pdepe is a solver for parabolic partial differential equations in one space dimension $x$ and time $t$

$$h \left(x, t, u, \frac{\partial u}{\partial x}\right) \frac{\partial u}{\partial t} = x^{-M} \frac{\partial}{\partial x} \left(x^M f \left(x, t, u, \frac{\partial u}{\partial x}\right)\right) + s \left(x, t, u, \frac{\partial u}{\partial x}\right). \quad (4.1)$$

The partial differential equations must hold for $t_0 \leq t \leq t_f$ and $x_1 \leq x \leq x_2$ and the interval $[x_1, x_2]$ must be finite. $M$ can be 0, 1 or 2 corresponding to slab, cylindrical, or spherical symmetry, respectively. In equation (4.1), $f \left(x, t, u, \frac{\partial u}{\partial x}\right)$ is a flux term and $s \left(x, t, u, \frac{\partial u}{\partial x}\right)$ is a source term. The coupling of the partial derivatives with respect to time is restricted to multiplication by a diagonal matrix $h \left(x, t, u, \frac{\partial u}{\partial x}\right)$. The diagonal elements of this matrix are either identically zero or positive. For $t = t_0$ and all $x$, the solution components satisfy initial conditions of the form

$$u \left(x, t_0\right) = u_0 \left(x\right). \quad (4.2)$$

For all $t$ and either $x = x_1$ or $x = x_2$, the solution components satisfy a boundary condition of the form

$$p \left(x, t, u\right) + q \left(x, t\right) f \left(x, t, u, \frac{\partial u}{\partial x}\right) = 0. \quad (4.3)$$

Elements of $q$ are either identically zero or never zero [28].
Part of pdepe’s argument list is the vector \( xmesh \) which is a set of points in the interval \( x_1 \leq x \leq x_2 \) such that \( xmesh(1) = x_1 \) and \( xmesh(\text{end}) = x_2 \) and where \( xmesh(i) < xmesh(i + 1) \). This specifies the values for \( x \) at which the numerical solution is computed. The vector \( tspan \) defines the points in time within the interval \( t_0 \leq t \leq t_f \) where the solution is to be presented, with \( tspan(1) = t_0 \), \( tspan(\text{end}) = t_f \), and \( tspan(i) < tspan(i + 1) \). In this study, \( x_1 = 0 \) and \( x_2 = 100 \) with the interval \( 0 \leq x \leq 100 \) was divided into one hundred equally spaced subinterval. \( t_0 = 0 \) and \( t_f = 100 \) with one hundred time steps for all values between \( 0 \leq t \leq 100 \). Functions in MATLAB for the initial conditions and boundary conditions were created. All the functions were provided to main program called \( sol \). The output argument \( sol \) is a 3-D array, which is the approximation to the \( ith \) component of \( u \) at point \( t = tspan(j) \) and \( x = xmesh(k) \). Putting all those together, numerical solutions of the system (3.7) were generated.

4.2 Numerical Simulations

In order to investigate the transmission process of bird flu within a poultry farm, nonlinear system of partial differential equations (3.7) was analyzed numerically under the following boundary conditions (4.4) and (4.5), and initial conditions (4.6).

**Mixed boundary conditions**

\[
\begin{align*}
\frac{\partial X}{\partial x} (0, t) &= 0, \\
Z(0, t) &= 0.5, \\
\frac{\partial X}{\partial x} (L, t) &= 0, \\
Z(L, t) &= 0,
\end{align*}
\]

(4.4)

**Homogeneous Neumann boundary conditions**

\[
\frac{\partial X}{\partial x} (0, t) = \frac{\partial Z}{\partial x} (0, t) = \frac{\partial X}{\partial x} (L, t) = \frac{\partial Z}{\partial x} (L, t) = 0.
\]

(4.5)

**Initial conditions**

\[
X(x, 0) = X_0(x) \quad \text{and} \quad Z(x, 0) = Z_0(x).
\]

(4.6)

The initial boundary-value problems (3.7), (4.4 or 4.5), and (4.6) were solved for fixed values of the parameters, \( c = 1 \), \( \omega = 1 \), \( r = 1 \), and \( p = 1 \).

System (3.7) is expressed in the following form

\[
\begin{bmatrix}
1 & 0 \\
0 & 1
\end{bmatrix}
\times \frac{\partial}{\partial t}
\begin{pmatrix}
X \\
Z
\end{pmatrix}
= \frac{\partial}{\partial x}
\begin{pmatrix}
0 \\
\frac{\partial Z}{\partial x}
\end{pmatrix}
+ \begin{pmatrix}
m(c - X) - \omega r X Z \\
p(c - X - r Z)
\end{pmatrix}.
\]

(4.7)
The following values for $M, h, f$ and $s$ were set:

\[
M = 0
\]

\[
h \left( x, t, u, \frac{\partial u}{\partial x} \right) = \begin{pmatrix} 1 \\ 1 \end{pmatrix}
\]

\[
f \left( x, t, u, \frac{\partial u}{\partial x} \right) = \begin{pmatrix} 0 \\ \frac{\partial Z}{\partial x} \end{pmatrix}
\]

\[
s \left( x, t, u, \frac{\partial u}{\partial x} \right) = \begin{pmatrix} m(c - X) - \omega r X Z \\ p(c - X - rZ) \end{pmatrix}
\]

The boundary conditions for the system (3.7) with $L = 100$ were set up in \textit{pdepe} with the following expressions.

Mixed boundary conditions

\[
p(0, t, u) = \begin{pmatrix} 0 \\ u^2 - 0.5 \end{pmatrix},
\]

\[
q(0, t) = \begin{pmatrix} 1 \\ 0 \end{pmatrix},
\]

\[
p(L, t, u) = \begin{pmatrix} 0 \\ u^2 \end{pmatrix},
\]

\[
q(L, t) = \begin{pmatrix} 1 \\ 0 \end{pmatrix}.
\]

Homogeneous Neumann boundary conditions

\[
p(0, t, u) = \begin{pmatrix} 0 \\ 0 \end{pmatrix},
\]

\[
q(0, t) = \begin{pmatrix} 1 \\ 1 \end{pmatrix},
\]

\[
p(L, t, u) = \begin{pmatrix} 0 \\ 0 \end{pmatrix},
\]

\[
q(L, t) = \begin{pmatrix} 1 \\ 1 \end{pmatrix}.
\]

4.2.1 Numerical Solutions For Different Value of $d$ and $m$

The initial boundary-value problem (3.7), (4.4), and (4.6) with the following initial conditions

\[
X_0 = \begin{cases} 1/2(1 - x) & ; 0 \leq x < 1 \\ 1 & ; 1 \leq x \leq L \end{cases} \quad Z_0 = \begin{cases} 1/2(1 - x) & ; 0 \leq x < 1 \\ 0 & ; 1 \leq x \leq L \end{cases}
\]

was solved numerically. Figures 4.1, 4.2, 4.3, and 4.4 show some numerical results for different values of the parameter $m$ and $d$.

Let $m = 1.5$, then $R_0 = 0.667 < 1$, so that, the infection free state $E_0$ of the system (3.7) is asymptotically stable, as shown in Fig. 4.1. The figure depicts the persistence of the infection free state, in which the number of the susceptible bird remains equal to
capacity per unit length and the virus concentration decrease as time elapses. On the other hand, let \( m = 0.5 \), then \( R_0 = 2 > 1 \), so that, the endemic state \( E_+ \) of the system (3.7) is asymptotically stable, as shown in Fig. 4.2. It shows the asymptotic stability of the endemic state in which a part of the population is always infected. Numerical results show that traveling wave solutions appear when \( E_+ \) is asymptotically stable, and they do not exist when \( E_0 \) is asymptotically stable. Profiles of traveling wave solutions were shown in Fig. 4.3 for \( m = 1.5 \) and in Fig. 4.4 for \( m = 0.5 \). Progressive waves of bird flu infection were profiled for diffusivity \( d = 0.1, 1, 10 \). The Fig. 4.4 shows that the diffusivity is more or less proportional to the wave speed, that is, the smaller the diffusivity is, the slower the propagation of the virus transmission.

![Figure 4.1: Solution of the system (3.7) for \( d = 1 \) and \( m = 1.5 \) \((\omega c - m < 0)\). The state is free of infection. A solution approaches the infection free equilibrium \( E_0 \) [30].](image)

a) \( X \) component  
b) \( Z \) component
Figure 4.2: Solution of the system (3.7) for $d = 1$ and $m = 0.5$ ($\omega c - m > 0$). The state is endemic. A solution approaches the endemic equilibrium $E_+$ [30].

Figure 4.3: Profile of the virus concentration for $m = 1.5$ ($\omega c - m < 0$) [30].
4.2.2 Numerical Solutions For Fixed Value of $d$ and $m$

The initial boundary-value problem (3.7), (4.5), and (4.6) with some initial conditions was solved numerically. Numerical solutions of the system of equations (3.7) were generated for fixed values of the parameter $d = 1$ and $m = 0.5$ ($\omega_c - m > 0$).

**Example 1.** The following initial conditions were set as shown in Fig. 4.5.

\[
X_0 = \begin{cases} 
0.1(x + 5); & 0 \leq x < 5 \\
1; & 5 \leq x \leq L 
\end{cases}, \quad Z_0 = \begin{cases} 
0.1(5 - x); & 0 \leq x < 5 \\
0; & 5 \leq x \leq L 
\end{cases}, \quad (4.12)
\]

![Figure 4.5: Initial conditions of example 1.](image-url)
Fig. 4.6 shows the graph of $X$ component and $Z$ component of the solutions for the initial boundary-value problem (3.7), (4.5), (4.12). It shows the transition of virus concentration distribution. Note that the wave front progresses into the positive $x$ direction. Fig. 4.7 shows profile of virus concentration. Note that the traveling wave moves from the left to the right as time elapses.

![Graph of $X$ component and $Z$ component](image)

(a) $X$ component  
(b) $Z$ component

Figure 4.6: Solution of the initial boundary-value problem of example 1 [31].

![Profile of $Z(x,t)$](image)

Figure 4.7: Profile of $Z(x,t)$ in the example 1. Curves $(x, Z(x,t))(t = 0, 50, 60, 70, 80, 90, 100)$ are shown. The traveling wave of transmission process in the positive $x$ direction [31].
Example 2. The following initial conditions were set as shown in Fig. 4.8.

\[
X_0 = \begin{cases}
1 & ; 0 \leq x < 95 \\
0.1(105 - x) & ; 95 \leq x \leq L,
\end{cases} \quad Z_0 = \begin{cases}
0 & ; 0 \leq x < 95 \\
0.1(x - 95) & ; 95 \leq x \leq L
\end{cases}
\]  

(4.13)

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure4.8}
\caption{Initial conditions of example 2.}
\end{figure}

In this example, traveling wave solutions of system (3.7) are expressed in terms

\[
X(x, t) = U(\xi), \quad Z(x, t) = V(\xi), \quad \xi = x + kt,
\]

that represents a wave traveling to the left with speed with positive \(k\). Fig. 4.9 shows the graph of \(X\) component and \(Z\) component of the solutions for the initial boundary-value problem (3.7), (4.5), (4.13). It shows the transition of virus concentration distribution. Note that the wave front progresses into the negative \(x\) direction. Fig. 4.10 shows profile of virus concentration. Note that the traveling wave moves from the right to the left as time elapses.
Figure 4.9: Solution of the initial boundary-value problem of example 2 [31].

Figure 4.10: Profile $Z(x, t)$ in the example 2. Curves $(x, Z(x, t))(t = 0, 50, 60, 70, 80, 90, 100)$ are shown. The traveling wave of transmission process in the negative $x$ direction [31].

Example 3. The following initial conditions were set as shown in Fig. 4.11.

$$X_0 = \begin{cases} 
1 & ; 0 \leq x < 45 \\
0.1(55 - x) & ; 45 \leq x < 50 \\
0.1(x - 45) & ; 50 \leq x < 55 \\
1 & ; 55 \leq x \leq L
\end{cases} \quad Z_0 = \begin{cases} 
0 & ; 0 \leq x < 45 \\
0.1(x - 45) & ; 45 \leq x < 50 \\
0.1(55 - x) & ; 50 \leq x < 55 \\
0 & ; 55 \leq x \leq L
\end{cases}$$

(4.14)
Example 3 is combination of example 1 and 2. Traveling wave solutions of system (3.7) are expressed in terms

\[ X(x, t) = U(\xi), \quad Z(x, t) = V(\xi), \quad \xi = x \pm kt, \]

Fig. 4.12 shows the graph of \( X \) component and \( Z \) component of the solutions of the initial boundary-value problem (3.7), (4.5), (4.14). It shows the transition of virus concentration distribution. Note that the wave front progresses into the positive \( x \) direction and the negative \( x \) direction at simultaneously. Fig. 4.13 shows profile of virus concentration. Note that the traveling wave moves from the left to the right and the right to the left as time elapses at simultaneously.
Figure 4.13: Profile $Z(x, t)$ in the example 3. Curves $(x, Z(x, t))(t = 10, 20, 30, 40, 50)$ are shown. The traveling wave of transmission process in the positive and negative $x$ direction [31].

**Example 4.** The following initial conditions were set

$$Z_0 = \begin{cases} 
0.1(x + 5) & ; 0 \leq x < 5 \\
1 & ; 5 \leq x \leq L 
\end{cases}, \quad X_0 = \begin{cases} 
0.1(5 - x) & ; 0 \leq x < 5 \\
0 & ; 5 \leq x \leq L 
\end{cases} \quad (4.15)$$

The infection rate of susceptible birds $\omega_r$ was set as a step function

$$\omega_r = \begin{cases} 
1 & ; x \leq 30 \\
0.1 & ; 30 \leq x \leq 40 \\
1 & ; x > 40 
\end{cases}, \quad (4.16)$$

as shown in Fig. 4.14.
Fig. 4.14: Step function of $\omega r$.

Fig. 4.15 shows the graph of $X$ component and $Z$ component of the solutions for the initial boundary-value problem (3.7), (4.5), (4.15). It shows the transition of virus concentration distribution. Fig. 4.16 shows some profiles of virus concentration. Note that the traveling wave moves from the left to the right as time elapses. The infection seems to stop at the interval where the infection free zone $30 \leq x \leq 40$. However, infection eventually spreads the remaining zone $30 \leq x \leq 40$.

Figure 4.15: Solution of the initial boundary-value problem of example 4 [31].
The numerical results have shown that bird flu transmission process is expressive of in terms of traveling wave solutions of the nonlinear parabolic system (3.7). Numerical results chapter 4 suggest that traveling wave solutions are asymptotically stable solutions as solutions of the initial boundary-value problem in this study.
Chapter 5

CONCLUSIONS AND FUTURE RESEARCH

In this chapter, conclusions and prospect of future study on bird flu infection process within a poultry farm are summarized.

5.1 Conclusions

Bird flu transmission process within a poultry farm was analyzed mathematically. Nonlinear systems of ordinary differential equations were formulated as models of bird flu transmission process. Those models were analyzed for investigation effects of vaccination and removal of infected birds for prevention of bird flu outbreak in a poultry farm. Stability analysis of stationary points of the model has shown that the infection free state is asymptotically stable when the endemic state is unstable. On the other hand, the infection free state is unstable when the endemic state is asymptotically stable.

Furthermore, a spatial effect of virus concentration in a medium was considered. A model proposed in a previous study was reformulated with spatial diffusion of virus concentration in a medium taken into consideration. The nonlinear system of partial differential equations was analyzed for investigation of bird flu diffusive process in a poultry farm. As solutions of system of partial differential equations, stabilities of constant solutions that correspond to the infection free state and the endemic state were analyzed. An infection process is interpreted as a traveling wave solution, that is the virus infection propagates in one direction with finite speed. The change of variables led to a system of ordinary differential equations. Existence of traveling wave solutions in a singular limit was established by a center manifold reduction. There is a unique heteroclinic orbit that corresponds to a traveling wave solution. The structure of dynamics in the singular limit persist for some ranges of parameters, which means that the traveling wave solutions exist for some ranges of parameters. The stability of constant solutions of the diffusive model and existence of traveling wave solutions depend on the local capacity of the farm, the removal rate of infected birds, and the infection rate. Those analytical results should be taken into consideration of strategies for prevention against bird flu outbreak within a poultry farm.

The analytical results were confirmed by numerical results. The numerical results were obtained by MATLAB program. Solutions of nonlinear system of partial differential
equations with some boundary conditions and some initial conditions were investigated. Numerical results have shown that transmission process is expressive in terms of a progressive wave. Those traveling wave solutions exist for a small removal rate.

5.2 Future Research

This study will be continued for future study, which includes the study of the availability of data and the ability to accurately estimate parameters for practical application of mathematical techniques to prevention of bird flu outbreaks in poultry farms, models will be developed for understanding of the complex problems that associated with bird flu outbreaks within a poultry farm.
Bibliography


[29] MATLAB 7.10.0 (R2010a) help.

Appendix

% The following is MATLAB program to generate solutions and phase plane
% for nonlinear system of ordinary differential equations,
% and solutions for nonlinear system of partial differential equations.

%% This function codes the equations for the model of nonlinear system
%% of ordinary differential equation (3.2)

function xdot=ode1(t,x)
X=x(1); Z=x(2);
Xdot=0.5*(1-X)-X*Z;
Zdot=(1-X-Z);
xdot=[Xdot; Zdot];

% Main program
[t,x] = ode23('ode1',[0 100],[1;0.5]);

figure(1)
hold on
f = @(t,Y) [0.5*(1-Y(1))-(Y(1)*Y(2)); 1-Y(1)-Y(2)];
y1 = linspace(0,1,20);
y2 = linspace(0,1,20);
[x,y] = meshgrid(y1,y2);
size(x)
size(y)
u = zeros(size(x));
v = zeros(size(x));

% we can use a single loop over each element to compute the derivatives at % each point (y1, y2)
t=0; % we want the derivatives at each point at t=0, i.e. the starting time
for i = 1:numel(x)
    Yprime = f(t,[x(i); y(i)]);
    u(i) = Yprime(1);
    v(i) = Yprime(2);
end

quiver(x,y,u,v,'r'); figure(gcf)

tspan=[0 20];
for i=0:0.1:1
  x0=[0; i]; % defines initial conditions
  [t, x]=ode23('ode1', tspan, x0);
  plot(x(:,1), x(:,2))
  drawnow
  [t, x]=ode23('ode1', tspan, [i; 0]);
  plot(x(:,1), x(:,2), '-b')
  drawnow
end

for i=0:0.1:1
  x0=[1; i]; % defines initial conditions
  [t, x]=ode23('ode1', tspan, x0);
  plot(x(:,1), x(:,2))
  drawnow
  [t, x]=ode23('ode1', tspan, [i; 1]);
  plot(x(:,1), x(:,2), '-b')
  drawnow
end

% Next, plot the nullclines
axis([0 1.0 0 1.0])
x1=0:0.05:10;
y1=1-x1; % Z-nullcline
plot(x1, y1, '-r', 'linewidth', 2) % plots Z-nullcline
plot(0.5./(0.5+x1), x1, '-g', 'linewidth', 2)% plots X-nullcline;
% Note dot
x = [1 0.5];
y = [0 0.5]
plot(x,y,'go')
% Finally, add the axis labels and the title
grid on
xlabel('X')
ylabel('Z')

% Plot solutions
tspan=[0 100];
x0=[1; 0.5]; % Initial values
[t,x]=ode23('ode1', tspan, x0);
X=x(:,1);
Z=x(:,2);
figure(2)
plot(t,X,'blue','linewidth',2)
hold on
plot(t,Z,'red','linewidth',2)
axis([0 100.0 0 1.0])
xlabel('Time (t)')
ylabel('X and Z')
Legend('Susceptible (X)','Virus concentration (Z)')

%% This function codes the equations for the model of nonlinear system
%% of ordinary differential equation (3.26)

function xdot=ode2(t,x)
V=x(1); W=x(2);
Bdot=W;
Adot=-2*W-1*(1-(0.5./((0.5)+V))-V);
xdot=[Vdot; Wdot];

% Main program
[t,x] = ode23('ode2',[0 100],[0;0.5]);

figure(1)
hold on
f = @(t,Y) [Y(2); -2*Y(2)-1*(1-(0.5./(0.5+Y(1)))-Y(1))];

y1 = linspace(0,1.0,20);
y2 = linspace(-0.4,0.4,20);
[x,y] = meshgrid(y1,y2);
size(x)
size(y)
u = zeros(size(x));
v = zeros(size(x));

% we can use a single loop over each element to compute the derivatives at
% each point (y1, y2)
t=0; % we want the derivatives at each point at t=0, i.e. the starting time
for i = 1:numel(x)
    Yprime = f(t,[x(i); y(i)]);
    u(i) = Yprime(1);
    v(i) = Yprime(2);
end

quiver(x,y,u,v,'r'); figure(gcf)
tspan=[1 20];
for i=0:0.1:0.4
    x0=[0; i]; % defines initial conditions
    [t, x]=ode23('ode2', tspan, x0);
    plot(x(:,1), x(:,2))
    drawnow
end

tspan=[1 20];
for i=0:0.1:1
    x0=[0; i]; % defines initial conditions
    [t, x]=ode23('ode2', tspan, [i,0.4]);
    plot(x(:,1), x(:,2))
    drawnow
end

tspan=[1 20];
for i=0:0.1:1
    x0=[0; i]; % defines initial conditions
    [t, x]=ode23('ode2', tspan, [i,-0.4]);
    plot(x(:,1), x(:,2))
    drawnow
end

tspan=[1 20];
for i=-0.4:0.1:0
    x0=[1; i]; % defines initial conditions
    [t, x]=ode23('ode2', tspan, x0);
    plot(x(:,1), x(:,2))
    drawnow
end

% Next, plot the nullclines
axis([0 1.0 -0.4 0.4])
x1=0:0.05:10;
y1= -(1/2)*(1-((0.5)./(0.5+x1))-x1); % W-nullcline
plot( x1, y1, '-r', 'linewidth', 2) % plots W-nullcline
plot(0, x1, '-g', 'linewidth', 2) % plots V-nullcline;
% Note dot
x = [0 0.5];
y = [0 0];
plot(x,y,'go','linewidth', 2)
% Finally, add the axis labels and the title
grid on
xlabel('V')
ylabel('W')

% Plot solutions
tspan=[0 100];
x0=[0; 0.5]; % Initial values
[t,x]=ode23('ode2', tspan, x0);
V=x(:,1);
W=x(:,2);
figure(2)
plot(t,V,'blue','linewidth',2)
hold on
plot(t,W,'green','linewidth',2)
axis([0 100.0 -0.1 1.0])
xlabel('Time (t)')
ylabel('V and W')
Legend('V', 'W')

%% This function codes the equations for the model of nonlinear system
%% of partial differential equation (3.7)

% Main program

function pde1
clear; close all;

% Parameters
L = 100;
maxt = 100;

m = 0;
t = linspace(0,maxt,101) %tspan
x = linspace(0,L,101) %xmesh

% PDEPE
sol = pdepe(m,@pde1PDEfun,@pde1ICfun,@pde1BCfun,x,t,[],P);

u1 = sol(:,:,1);
u2 = sol(:,:,2);

% Plotting
figure(1)
surf(x,t,u1,'edgecolor','none');
xlabel('Spatial (x)');
ylabel('Time (t)');
zlabel('X');
axis([0 L 0 maxt 0 max(max(u1))])
set(gcf(), 'Renderer', 'painters');
set(gca,'FontSize',12,'fontweight','b','fontname','arial');
figure(2)
surf(x,t,u2,'edgecolor','none');
xlabel('Spatial (x)');
ylabel('Time (t)');
zlabel('Z');
axis([0 L 0 maxt 0 max(max(u2))]);
set(gcf(), 'Renderer', 'painters');
set(gca,'FontSize',12,'fontweight','b','fontname','arial');

% A solution profile can also be illuminating
figure(3)
hold all
xaxis([0 100 0 0.6])
plot(x,u2(1,:),'LineWidth',1)
plot(x,u2(51,:),'LineWidth',1)
plot(x,u2(61,:),'LineWidth',1)
plot(x,u2(71,:),'LineWidth',1)
plot(x,u2(81,:),'LineWidth',1)
plot(x,u2(91,:),'LineWidth',1)
plot(x,u2(end,:),'LineWidth',1)

% Homogeneous Neumann Boundary Conditions
function [pl,ql,pr,qr] = pde1BCfun(xl,ul,xr,ur,t,P)
pl = [0; 0];
ql = [1; 1];
pr = [0; 0];
qr = [1; 1];

% Initial Conditions
function u0 = pde1ICfun(x,P)
u0 = [0.1*(x+5).*(0<=x && x<5) + 1.*(5<=x && x<=100);
     0.1*(5-x).*(0<=x && x<5) + 0.*(5<=x && x<=100)];

% PDEs
function [c,f,s] = pde1PDEfun(x,t,u,dudx,P)
c = [1];
f = [0;1].*dudx;
s = [0.5*(1-u(1))-1*u(1)*u(2); (1-u(1)-u(2))];