Modelling Avian Influenza using Filippov Systems to Determine Culling of Infected Birds and Quarantine

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Introduction

The spread of highly pathogenic avian influenza (HPAI) A viruses has not only triggered a major threat to avian and humains, but it has also cost a significant amount of money to treat the infected and invest in prevention to control the disease. Immediate actions have to be taken whenever the number of infecteds has gotten beyond a certain tolerable threshold to avoid a deadly outbreak.

Hence, a well-defined threshold policy is crucial to combat the outbreak efficiently.

Filippov Models

(i) The avian-only model with culling of infected domestic birds

\[ S'(t) = \lambda - \beta (1 - qu) SI - \mu S, \]
\[ I'(t) = \beta (1 - qu) SI - (\mu + d + \gamma + \epsilon) I, \]
\[ E'(t) = \beta (1 - qu) SI - \epsilon I, \]
\[ R'(t) = \gamma I + \epsilon I - \mu R, \]

with \( u = \begin{cases} 0 & \text{for } I < I_c \text{ or } I > I_c, \\ 1 & \text{for } I_c < I < I_2. \end{cases} \)

where \( S, I \) and \( I_c > 0 \) are the susceptible domestic birds, infected domestic birds and the tolerance threshold level, respectively. The descriptions of the associated parameters and their sample values that are used in the numerical simulations are as shown in the following tables.

<table>
<thead>
<tr>
<th>Parameter Description</th>
<th>Sample Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \lambda )</td>
<td>Bird inflow</td>
</tr>
<tr>
<td>( \mu )</td>
<td>Natural death of birds</td>
</tr>
<tr>
<td>( \beta )</td>
<td>Rate at which birds contract avian influenza</td>
</tr>
<tr>
<td>( d )</td>
<td>Disease death rate due to avian influenza in birds</td>
</tr>
<tr>
<td>( \epsilon )</td>
<td>Culling rate of infected birds</td>
</tr>
</tbody>
</table>

(ii) The SIIR model with quarantine

\[ S'(t) = \lambda - \beta (1 - qu) SI - \beta_0 (1 - qu) SI + \mu S, \]
\[ I'(t) = \beta (1 - qu) SI - (\mu + d + \gamma + \epsilon) I, \]
\[ E'(t) = \beta (1 - qu) SI - \epsilon I, \]
\[ R'(t) = \gamma I + \epsilon I - \mu R, \]

with \( u = \begin{cases} 0 & \text{for } I < I_c \text{ or } I > I_c, \\ 1 & \text{for } I_c < I < I_2. \end{cases} \)

where the tolerance threshold is \( I_c > 0 \). \( S, I, I_c, I_2 \) and \( E \) are the susceptible, humans infected with avian strain, humans infected with mutant strain and humans who have recovered from either strain, respectively.

<table>
<thead>
<tr>
<th>Parameter Description</th>
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</tr>
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<tbody>
<tr>
<td>( \lambda )</td>
<td>Human recruitment rate</td>
</tr>
<tr>
<td>( \mu )</td>
<td>Natural mortality rate of humans</td>
</tr>
<tr>
<td>( \beta_0 )</td>
<td>Human-to-human transmission rate for the avian strain</td>
</tr>
<tr>
<td>( d )</td>
<td>Additional disease death rate of humans due to avian influenza</td>
</tr>
<tr>
<td>( \gamma )</td>
<td>Recovery rate of humans</td>
</tr>
<tr>
<td>( q )</td>
<td>Quarantine rate</td>
</tr>
</tbody>
</table>

Types of equilibrium points

Suppose a differential equation, \( x = f(x,t) \), is discontinuous on surface \( M \) that is defined by equation \( r(x) = 0 \) where \( x \in R^n \). \( M \) separates \( x \) into domains \( G' \) and \( G'' \), and its dynamics are governed by \( f(x,t) \) in \( G' \) and \( f(x,t) \) in \( G'' \), respectively. Further, the sliding mode equation \( \chi(t) = \dot{r}(x(t)) \) describes the motion in the sliding region \( S \subset M \).

Suppose there exists an equilibrium point in such region \( G' \) or \( G'' \), denoted by \( E_1 \) and \( E_2 \), respectively. There are four types of equilibrium points that might exist in a Filippov model: real, virtual, pseudo-equilibrium and boundary equilibrium. The definition of each type of equilibrium is given as follows:

Definition:

(a) \( E \) is a real equilibrium if \( f(E) = 0 \) and \( r(E) = 0 \),
(b) \( E \) is a virtual equilibrium if \( f(E) = 0 \) or \( r(E) = 0 \) or \( \dot{r}(E) = 0 \),
(c) \( E \) is a boundary equilibrium if \( f(E) = 0 \) and \( r(E) = 0 \) or \( \dot{r}(E) = 0 \),
(d) \( E \) is a pseudo-equilibrium if \( E \) is an equilibrium point on the sliding mode, i.e., \( f(E) = 0 \) and \( r(E) = 0 \).

Results

(i) The avian-only model with culling of infected domestic birds

Let

\( G_{ID} := \{(S, I, I_c) \in R^3; I < I_c I \}\),
\( G_{ID} := \{(S, I, I_c) \in R^3; I > I_c I \}\),
\( M := \{(S, I, I_c) \in R^3; I = I_c I \}\) and
\( \Omega := \{(S, I, I_c) \in M; h_1 < S < h_2 (I_c I) \} \).

In regions \( G_{ID} \) and \( G_{ID} \), we have endemic equilibria \( E_{ID} := (h_1, h_2, h_3) \) and \( E_{ID} := (h_1, h_2, h_3) \), respectively. Further, \( E_{ID} \) is a pseudo-equilibrium if it exists on the sliding domain \( \Omega \).

- **Case 1:** \( E_{ID} \) is a virtual equilibrium if \( h_2 < I < h_3 \).
- **Case 2:** \( E_{ID} \) is a real equilibrium, whereas \( E_{ID} \) is a virtual equilibrium if \( I > h_3 \).
- **Case 3:** \( E_{ID} \) is a real equilibrium, whereas \( E_{ID} \) is a virtual equilibrium if \( I < h_2 \).

(ii) The SIIR model with quarantine

Let

\( G_{RI} := \{(S, I, I_c) \in R^3; I < I_c I \}\),
\( G_{RI} := \{(S, I, I_c) \in R^3; I > I_c I \}\),
\( M := \{(S, I, I_c) \in R^3; I = I_c I \}\) and
\( \Omega := \{(S, I, I_c) \in M; h_1 < S < h_2 (I_c I) \} \).

Endemic equilibrium \( E_{RI} := (E_1 S, E_1 I, E_1 I_c) \) and \( E_{RI} := (E_2 S, E_2 I, E_2 I_c) \) are located in regions \( G_{RI} \) and \( G_{RI} \) respectively. Moreover, \( E_{RI} := (E_1 S, E_1 I, E_1 I_c) \) is a pseudo-equilibrium if it exists on the sliding domain \( \Omega \).

- **Case 1:** \( E_{RI} \) and \( E_{RI} \) are virtual equilibria if \( E_{RI} = E_{RI} > I \) and \( E_{RI} = E_{RI} > I \) are satisfied.

References