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 loss of birds and humans life, but it has also cost a significant amount of money to treat the infecteds and invest in prevention to control the disease.

Immediate actions have to be taken whenever the number of infected has gone beyond a certain tolerant 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**

$$\begin{aligned} S_d'(t) &= \Lambda_d - \beta_d S_d I_d - \mu_d S_d \\ I_d'(t) &= \beta_d S_d I_d - (\mu_d + d_d) I_d - u_d c I_d \end{aligned} \qquad (1)$$

with $u_d = \begin{cases} 0 & \text{for } I_d < I_T \\ 1 & \text{for } I_d > I_T, \end{cases}$

where S_d, I_d and $I_T > 0$ are the susceptible domestic birds, infected domestic birds and the tolerance threshold level, respectively. The descriptions of the associated parameters and its sample values that are used in the numerical simulations are as shown in the following table.

Parameter	Description	Sample Value
Λ_d	Bird inflow	$\frac{2060}{365}$
μ_d	Natural death of birds	$\frac{1}{2 \times 365}$
β_d	Rate at which birds contract avian influenza	0.4
d_d	Disease death rate due to avian influenza in birds	0.1
c	Culling rate of infected birds	1.5

(ii) **The SIIR model with quarantine**

$$\begin{aligned} S'(t) &= \Lambda - \beta_a(1-qu)SI_a - \beta_m(1-qu)SI_m - \mu S \\ I_a'(t) &= \beta_a(1-qu)SI_a - (\mu + d + \gamma + \epsilon)I_a \\ I_m'(t) &= \beta_m(1-qu)SI_m + \epsilon I_a - (\mu + d + \gamma)I_m \\ R'(t) &= \gamma(I_a + I_m) - \mu R \end{aligned} \qquad (2)$$

with $u = \begin{cases} 0 & \text{for } I_a + I_m < I_c \\ 1 & \text{for } I_a + I_m > I_c, \end{cases}$

where the tolerance threshold is $I_c > 0$. S, I_a, I_m and R are the susceptible humans, humans infected with avian strain, humans infected with mutant strain and humans who have recovered from either strain, respectively.

Parameter	Description	Sample Value
Λ	Human recruitment rate	$\frac{1000}{365}$
μ	Natural mortality rate of humans	$\frac{1}{65 \times 365}$
β_a	Human-to-human transmission rate for the avian strain	0.4
β_m	Human-to-human transmission rate for the mutant strain	$0.3 \times \beta_a$
d	Additional disease death rate of humans due to avian influenza	0.15
γ	Recovery rate of humans	0.2669
ϵ	Mutation rate	0.01
q	Quarantine rate	0.6

Types of equilibrium points

Suppose a differential equation, $\dot{x} = f(x,t)$, is discontinuous on surface M that is defined by equation $\sigma(x) = 0$ where $x \in \mathbb{R}^n$.
M separates $x \in \mathbb{R}^n$ into domains G^- and G^+, and its dynamics are governed by $f^-(x,t)$ and $f^+(x,t)$, respectively.
Further, the sliding mode equation $f^0(x,t)$ describes the motion in the sliding region $\Omega \subset M$.
Suppose there exists an equilibrium point in each region G^-, G^+ and Ω, denoted by E_1, E_2 and E_s, respectively.
There are four types of equilibria that might exist in a Filippov model: real, virtual, pseudoequilibrium and boundary equilibria. The definition of each type of equilibrium is given as follows:
Definition:

(a) E^R is a **real equilibrium** if $f^-(E^R) = 0$ and $\sigma(E^R) < 0$ or $f^+(E^R) = 0$ and $\sigma(E^R) > 0$.

(b) E^V is a **virtual equilibrium** if $f^-(E^V) = 0$ and $\sigma(E^V) > 0$ or $f^+(E^V) = 0$ and $\sigma(E^V) < 0$.

(c) E^B is a **boundary equilibrium** if $f^-(E^B) = 0$ and $\sigma(E^B) = 0$ or $f^+(E^B) = 0$ and $\sigma(E^B) = 0$.

(d) E^P is a **pseudoequilibrium** if E^P is an equilibrium point on the sliding mode; i.e., $f^0(E^P) = 0$ and $\sigma(E^P) = 0$.

Results

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

$$\begin{aligned} G_{1d} &:= \left\{(S_d, I_d) \in \mathbb{R}_+^2; I_d < I_T\right\}, \\ G_{2d} &:= \left\{(S_d, I_d) \in \mathbb{R}_+^2; I_d > I_T\right\}, \\ M_d &:= \left\{(S_d, I_d) \in \mathbb{R}_+^2; I_d = I_T\right\} \text{ and} \\ \Omega_d &:= \left\{(S_d, I_d) \in M_d; h_{1d} < S_d < h_{2d}\right\}. \end{aligned}$$

In regions G_{1d} and G_{2d}, we have endemic equilibria $E_{11d} = (h_{1d}, h_{4d})$ and $E_{21d} = (h_{2d}, h_{3d})$, respectively. Further, E_d is a pseudoequilibrium if it exists on the sliding domain Ω_d.

- Case 1: E_{11d} and E_{21d} are virtual equilibria if $h_{3d} < I_T < h_{4d}$.

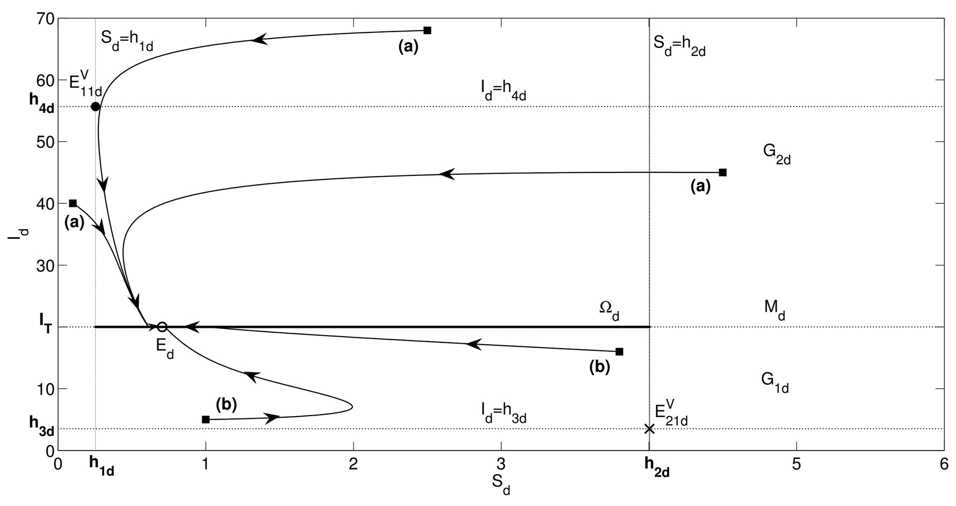

Figure 1: $E_d \in \Omega_d \subset M_d$ is globally asymptotically stable if $h_{3d} < I_T < h_{4d}$.

- Case 2: E_{11d} is a real equilibrium, whereas E_{21d} is a virtual equilibrium if $I_T > h_{4d}$.

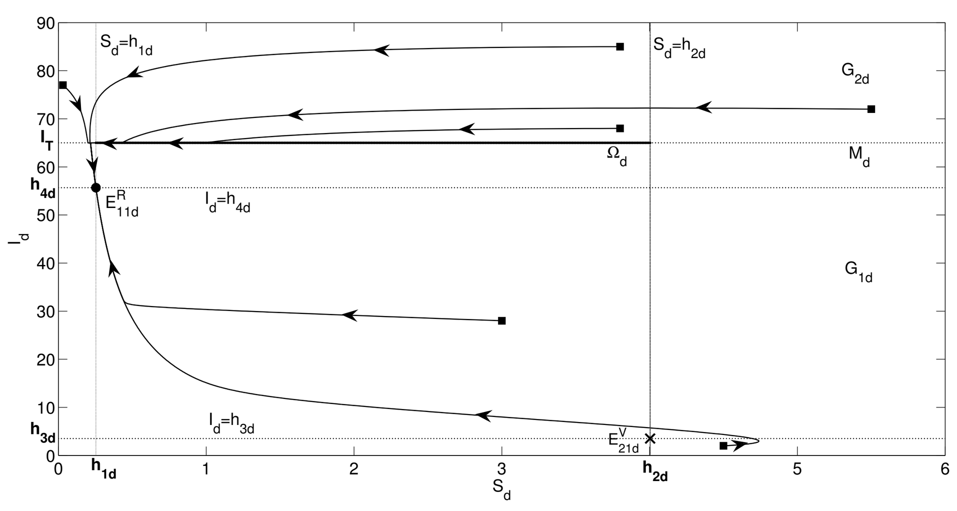

Figure 2: $E_{11d}^R \in G_{1d}$ is globally asymptotically stable if $I_T > h_{4d}$.

- Case 3: E_{21d} is a real equilibrium, whereas E_{11d} is a virtual equilibrium if $I_T < h_{3d}$.

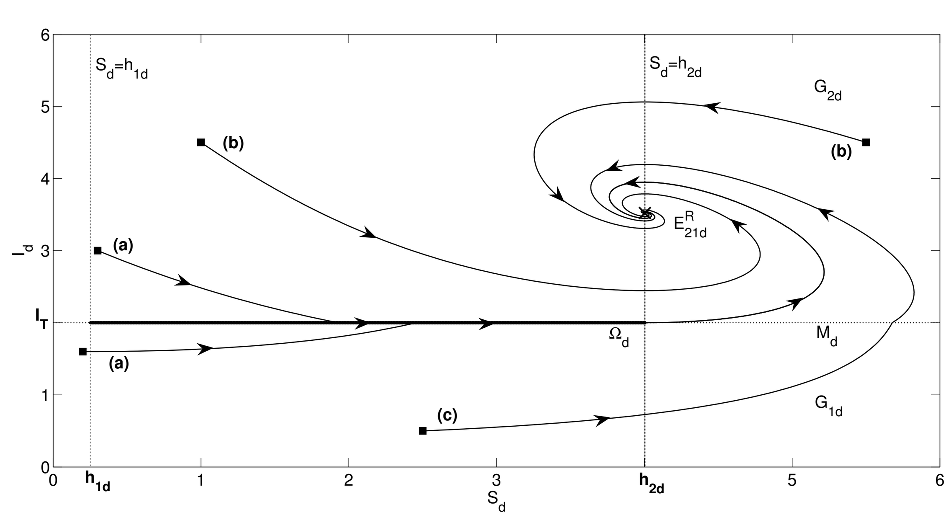

Figure 3: $E_{21d}^R \in G_{2d}$ is globally asymptotically stable if $I_T < h_{3d}$.

(ii) **The SIIR model with quarantine**
Let

$$\begin{aligned} G_1 &:= \left\{(S, I_a, I_m) \in \mathbb{R}_+^3; I_a + I_m < I_c\right\}, \\ G_2 &:= \left\{(S, I_a, I_m) \in \mathbb{R}_+^3; I_a + I_m > I_c\right\}, \\ M &:= \left\{(S, I_a, I_m) \in \mathbb{R}_+^3; I_a + I_m = I_c\right\} \text{ and} \\ \Omega &:= \left\{(S, I_a, I_m) \in M; h_1(I_a) < S < h_2(I_a)\right\}. \end{aligned}$$

Endemic equilibria $E_{11} = (E_{11}S, E_{11}I_a, E_{11}I_m)$ and $E_{21} = (E_{21}S, E_{21}I_a, E_{21}I_m)$ are located in regions G_1 and G_2, respectively. Moreover, $E_s = (E_sS, E_sI_a, E_sI_m)$ is a pseudoequilibrium if it exists on the sliding domain Ω.

- Case 4: E_{11} and E_{21} are virtual equilibria if $E_{11}I_a + E_{11}I_m > I_c$ and $E_{21}I_a + E_{21}I_m < I_c$ are satisfied.

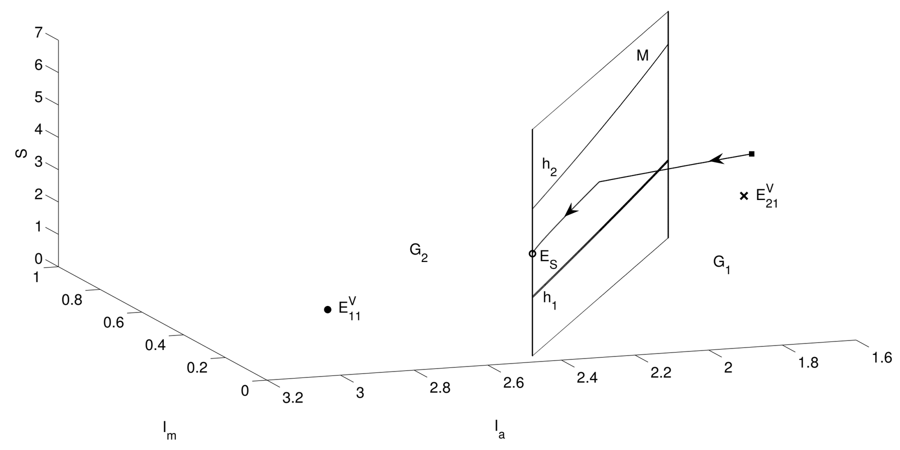

Figure 4: A trajectory with initial point in G_1 will hit and slide to the left on $\Omega \subset M$ before moving towards E_s. In this case, $E_s \in \Omega \subset M$ is locally asymptotically stable if the requirements of $E_{11}I_a + E_{11}I_m > I_c$ and $E_{21}I_a + E_{21}I_m < I_c$ are met.

- Case 5: E_{11} is a real equilibrium, whereas E_{21} is a virtual equilibrium if $E_{11}I_a + E_{11}I_m < I_c$ and $E_{21}I_a + E_{21}I_m < I_c$ are fulfilled

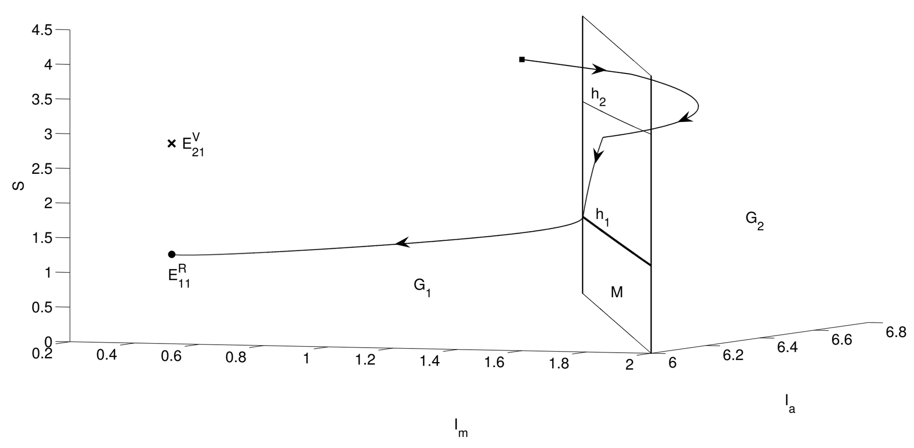

Figure 5: A trajectory will pass through M moving towards G_2 from G_1 and hit the manifold M again from the direction of G_2. Then it will slide down on $\Omega \subset M$ before converging to E_{11}^R in G_1. For Case 5, $E_{11}^R \in G_1$ achieves local asymptotic stability if $E_{11}I_a + E_{11}I_m < I_c$ and $E_{21}I_a + E_{21}I_m < I_c$ are fulfilled.

- Case 6: E_{21} is a real equilibrium, whereas E_{11} is a virtual equilibrium if $E_{11}I_a + E_{11}I_m > I_c$ and $E_{21}I_a + E_{21}I_m > I_c$ are satisfied

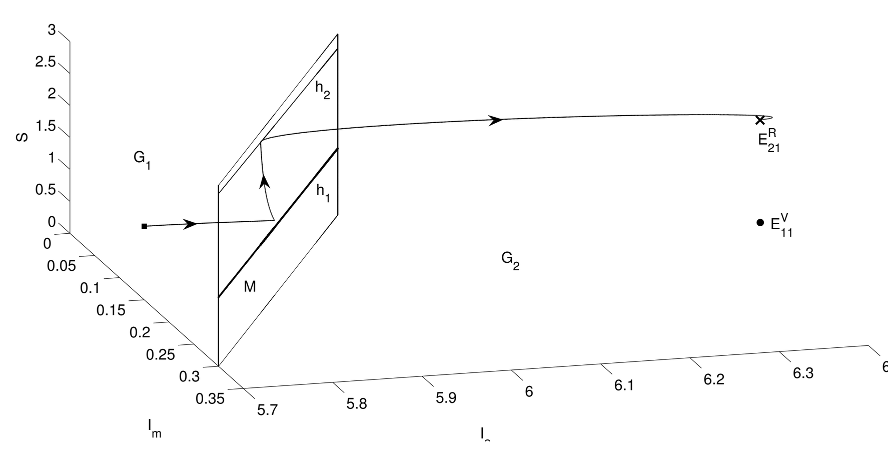

Figure 6: A trajectory hits $\Omega \subset M$ from G_1 and then moves up on Ω before converging to E_{21}^R in G_2. So in this case, we have $E_{21}^R \in G_2$ is locally asymptotically stable if the conditions of $E_{11}I_a + E_{11}I_m > I_c$ and $E_{21}I_a + E_{21}I_m > I_c$ are fulfilled.

Conclusion

- Whenever the trajectory of the avian-only Filippov model is found to be converging to $E_{11d} \in G_{1d}$ or $E_d \in \Omega_d \subset M_d$, we consider that the infection of avian influenza in the avian population is still bearable.
- However, if the solution of this model converges to $E_{21d} \in G_{2d}$, we assume that an outbreak is emerging. As a response to the outbreak, control methods have to be implemented in order to suppress the transmission and contain the disease.
- An SIIR model with quarantine is designed to assess an appropriate quarantine threshold level that will lead to disease elimination.
- The solutions of this model will converge to either one of the two endemic equilibria or the sliding equilibrium.
- In order to inhibit an outbreak or to stabilize the infection, we have to choose a suitable tolerance threshold I_c such that the trajectory of the model is approaching $E_{11} \in G_1$ or the sliding equilibrium $E_s \in \Omega \subset M$.
- Our findings show that we can either preclude the influenza outbreak or stabilize the infection at a desired level by choosing an appropriate threshold level.
- A well-defined threshold policy is essential in order to combat an outbreak effectively and efficiently.

References

[1] Xiao, Y., Xu, X. & Tang, S. 2012. Sliding mode control of outbreaks of emerging infectious diseases. *Bull Math Biol* 74: 2403–2422.

[2] Zhao, T., Xiao, Y. & Smith?, R.J. 2013. Non-smooth plant disease models with economic thresholds. *Mathematical Biosciences* 241: 34–48.

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