

Spatiotemporal Patterns of Avian Influenza Spread: A Narrative of Modeling and Analysis

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Topics to be covered

- Avian influenza as a prototype of emerging vector-borne diseases (West Nile virus, Lyme diseases);
- Biological issues: spatiotemporal spread as consequences of the interaction of host ecology and disease epidemiology;
- Mathematical challenges: seasonality/periodicity; spatial movement/patch models or PDEs with nonlocal nonlinearity; physiological structure/delay;
- Relevance to surveillance (satellite tracking, GIS), to policy and intervention (culling, environmental impact).

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The Mathematics: Delay Differential Equations

A delay differential equation describes the evolution of a system for which the change rate of the state depends not only the current but also the historical state of the system: non-Newton mechanics.

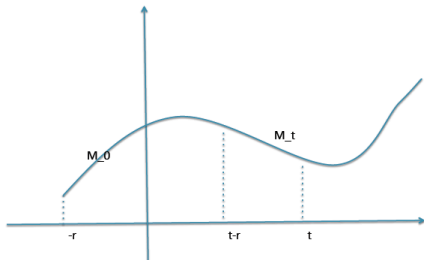
In population dynamics, time lags arise naturally from consideration of heterogeneity of individual hosts (maturation) or environment (transition time between patches).

Example: Consider a stage structured population with two stages: immature and mature populations with a fixed maturation time r .

- Birth rate $b(M(t))$ is a function of the matured/reproductive female population size $M(t)$;
- Death rate is δ for matured, and d_I for the immature.

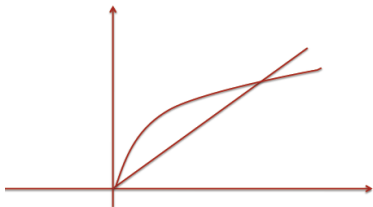
$$\frac{d}{dt}M(t) = \underbrace{b(M(t-r))}_{\text{maturation rate}} e^{-d_I r} - \delta M(t).$$

Solutions: $M'(t) = b(M(t - r))e^{-d_1 r} - \delta M(t)$



- To specify a solution for $t \geq 0$, one needs to specify the initial condition $M(\theta) = \phi(\theta)$ for $\theta \in [-r, 0]$;
- Once the initial condition $\phi \in X := C([-r, 0]; R)$ is given, one can solve the equation for all $t \geq 0$ (backward extension may not exist and may not be unique—non-Newton mechanics);
- Description of the **global dynamics** of even a scalar delay differential equation is difficult.

Global Dynamics: Simplicity due to Monotonicity



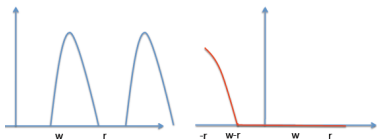
- $M'(t) = b(M(t-r))e^{-d_1 r} - \delta M(t)$ with monotone b has **threshold dynamics**: If $b'(0)e^{-d_1 r} < \delta$ then every solution converges to zero; if $b'(0)e^{-d_1 r} > \delta$, then every nontrivial solution of the model converges to the positive equilibrium.
- The semiflow is order-preserving and the modern theory of monotone dynamical systems can apply.

Interaction of Periodicity and Delay

It is important to incorporate seasonality: for example, birth occurs for migratory birds only during certain seasons:

$$b(t, M) = p(t)b(M), \quad p(t + T) = p(t)$$

$$M'(t) = b(t, M(t - r))e^{-d_1 r} - \delta M(t).$$

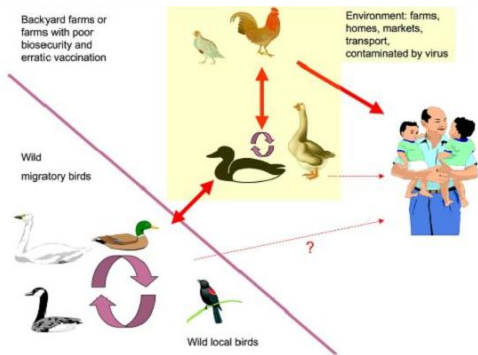


- nontrivial initial condition may give rise to a zero solution; global dynamics must be addressed in an appropriate setting determined by the seasonality; threshold dynamics (convergence to a periodic solution) holds.
- Interaction of seasonality and delay is critical for disease control (WNV, Lyme disease, bird flu).

The Ecology and Epidemiology in the context H5N1

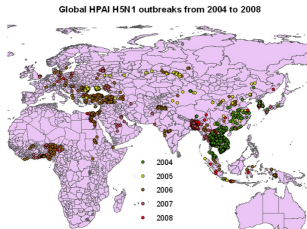
- Influenza viruses are isolated from a wide range of hosts. Types (A, B, C) are based on antigenic differences of gene products.
- Avian influenza, an infectious disease of birds, was identified first in Italy (E. Perroncito, 1878) (caused by type A strain).
- Avian influenza viruses are (based on pathogenicity) categorized into two distinct groups: Highly Pathogenic Avian Influenza (HPAI) and LPAI.
- Avian origin-H5N1 strains was primarily isolated from a poultry farm of Scotland, UK during 1959.
- Rapid assortment ability boosted the continuous evolution, leading to spread to different continents since 1996-Asian outbreak.
- The HPAI H5N1 strain poses high risk for wild and domesticated animals, and could pose a threat to humans (WHO, CIDRP 2009).

Transmission Cycle of H5N1

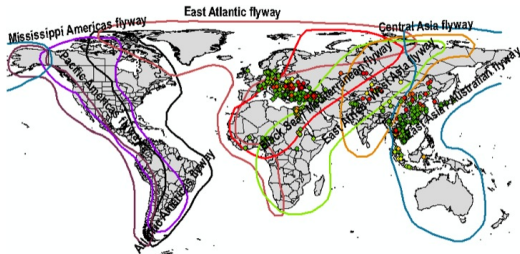


The spread of H5N1 combines interactions between local and long-range dynamics. The **local** dynamics involve interactions/cross-contamination of domesticated birds, local poultry industry, and temporary migratory birds. The **nonlocal dynamics** involve the long-range transportation of industrial material and poultry, and the long-range bird migrations.

Migratory Route and H5N1 Global Spread



(a)



(b) Migration Route

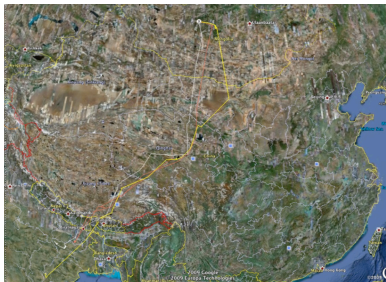
Spatiotemporal Patterns of Migratory Birds

- Bird migration: is a major biological phenomenon with billions of birds extending over distances from the Arctic to Antarctic using 8 broad overlaing corridors during annual cycles.
- A typical migration process involves different phases of biological activities and seasonality, as **wintering, spring migration, breeding, maturation and autumn migration**.
- Migration routes are "interrupted" by stopovers, which provide the resting locations between the fights for refueling and for recovering from climatic and physiologic stress.

Surveillance Data of Migratory Birds: Satellites Tracking

Using satellites tracking, the U.S. Geological Survey recorded the migration path of a dozen Bar-headed geese.

- The migratory routes follow elongated closed curved routes.
- The birds breed in the summer in the northern part of their path (e.g., Mongolia).
- In the fall, they initiate their southward migration route, until reaching their wintering grounds (e.g., India).
- In the spring, they initiate a northward migration returning to their breeding location.
- Despite variable trajectories, the major stopover locations are common to most tracked flocks.



Model for Spatiotemporal Distributions of Migratory Birds

Assume that migration occurs along a one dimensional continuum (the migration route), which could be a curve. Let $S_i(t)$ be the number of birds in patch i .

$$\left\{ \begin{array}{l} S_1'(t) = b(S_1(t), t) + \alpha_{2,1}d_{2,1}(t - \tau_1)S_2(t - \tau_1) \\ \quad - d_{1,2}(t)S_1(t) - \mu_1(t)S_1(t), \\ \quad \vdots \\ S_i'(t) = \alpha_{i-1,i}d_{i-1,i}(t - \tau_{i-1})S_{i-1}(t - \tau_{i-1}) - d_{i,i+1}(t)S_i(t) \\ \quad + \alpha_{i+1,i}d_{i+1,i}(t - \tau_i)S_{i+1}(t - \tau_i) - d_{i,i-1}(t)S_i(t) - \mu_i(t)S_i(t), \\ \quad \vdots \\ S_n'(t) = \alpha_{n-1,n}d_{n-1,n}(t - \tau_{n-1})S_{n-1}(t - \tau_{n-1}) \\ \quad - d_{n,n-1}(t)S_n(t) - \mu_n(t)S_n(t). \end{array} \right.$$

Well-posedness of the Model

Phase Space (Smith, JDE 1987)

$$Y = \prod_{i=1}^n C[I_i, R]$$

with

$$C[I_1, R] = C([- \tau_1, 0], R);$$

$$C[I_2, R] = C([- \max(\tau_1, \tau_2), 0], R);$$

$$C[I_3, R] = C([- \max(\tau_2, \tau_3), 0], R);$$

\vdots

$$C[I_{n-1}, R] = C([- \max(\tau_{n-2}, \tau_{n-1}), 0], R);$$

$$C[I_n, R] = C([- \tau_{n-1}, 0], R)$$

$$\|S\| = \max_{i=1, \dots, n} \left(\max_{s \in I_i} |S_i(s)| \right).$$

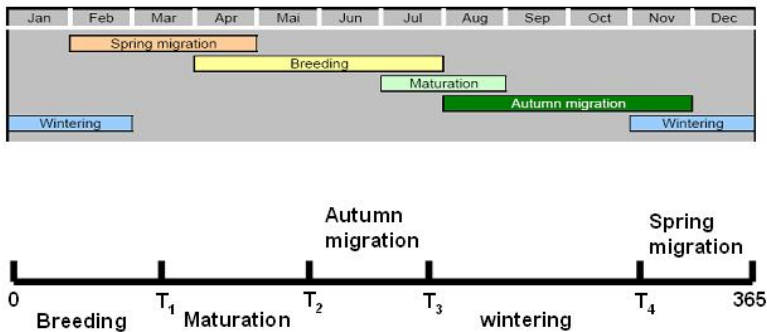
Qualitative Behaviors: Nonnegativeness, boundedness of solutions, dissipativeness and existence of global attractors (assume $b(0, t) = 0$, $b(S_1, t) \geq 0$ if $S_1 \geq 0$ and $\sup_{S_1 \geq 0, t \geq 0} b(S_1, t) < \infty$).

Challenge for Studying the Global Dynamics: Seasonality

- The model generates an order-preserving periodic process. This process however is NOT strongly order-preserving.

$$S'_i(t) = \alpha_{i-1,i}d_{i-1,i}(t - \tau_{i-1})S_{i-1}(t - \tau_{i-1}) - d_{i,i+1}(t)S_i(t) \\ + \alpha_{i+1,i}d_{i+1,i}(t - \tau_i)S_{i+1}(t - \tau_i) - d_{i,i-1}(t)S_i(t) - \mu_i(t)S_i(t)$$

Seasonal migrations



Seasonal Migration Null Space

Need to remove the subspace

$$M := \{ \phi \in Y; \phi_i(0) = 0, 1 \leq i \leq n; \\ d_{i,i+1}(\theta_i)\phi_i(\theta_i) = 0 \text{ for } 1 \leq i \leq n-1, \theta_i \in [-\tau_i, 0]; \\ d_{i,i-1}(\theta_i)\phi_i(\theta_i) = 0 \text{ for } 2 \leq i \leq n, \theta_i \in [-\tau_{i-1}, 0] \}.$$

- This, determined by the migration patterns, is a closed subspace of Y .
- Nontrivial initial data from M will give rise to a solution identically to zero for all future time.
- A natural phase space is Y/M .
- The model gives a periodic process in this quotient space.

Threshold Dynamics Theorem

Theorem: Suppose that $\lambda b(S_1, t) < b(\lambda S_1, t)$ when $\lambda \in (0, 1)$ and $S_1 > 0$. Then either

- (i) every solution tends to zero as $t \rightarrow \infty$, or
- (ii) the system has a T -periodic solution which is strictly positive (componentwise) at all times, and this solution attracts all solutions with initial data not in the subspace M ;
- (iii) conclusion (i) (resp. (ii)) holds if the spectral radius of $DF(0)$ is strictly less (resp. larger) than 1, where F is the Poincare operator which maps the initial datum to the state at time T .

Reference: S. Gourley, R. Liu, J. Wu, "Spatiotemporal distributions of migratory birds: patchy models with delay", *SIAM Journal on Applied Dynamical Systems*, 2010.

Validation (Long-term Pattern) and Initial Condition for H5N1 Outbreak

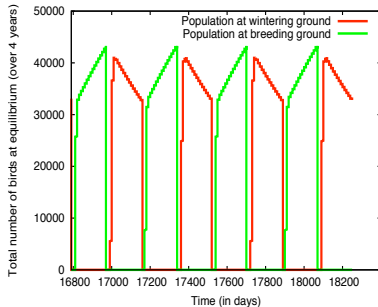
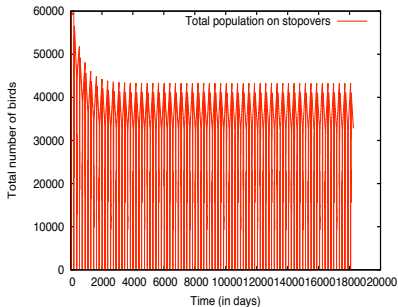
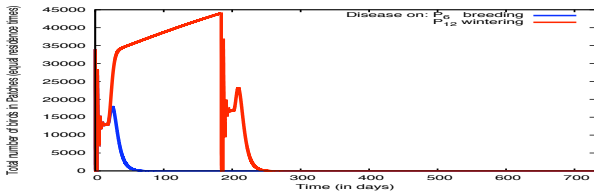
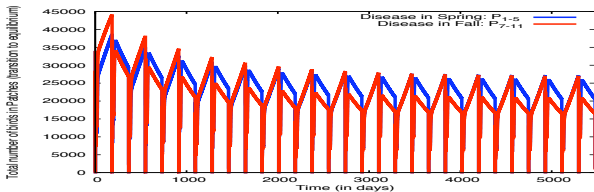
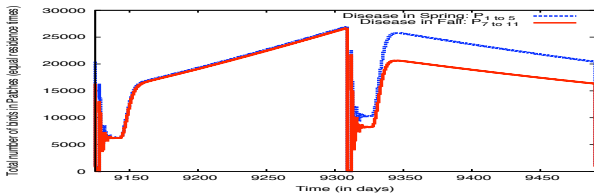


Figure: Simulation with satellite track data

Applications: How Disease Impacts on the Ecology

- H5N1 cases are not new, and H5N1 induced death among animals dates to the 1990s.
- A new strain, lethal to migratory wild birds, was found to cause massive deaths in 2005 in Central Chinas Qinghai Lake leading to a cumulative death toll of more than 6,000 wild birds of various species including 3,018 Bar-headed geese representing 5%-10% of global population.
- H5N1 virus is now endemic in poultry and local birds in several regions of the world.
- **Questions:** How the disease endemic and the disease mortality impact the bird ecology? How limited resources can be best used to mitigate the disease impact on bird species?
- L. Bourouiba, J. Wu and FAO/USGS/international avian influenza project team, Spatial dynamics of Bar-headed geese migration in the context of H5N1, J. R. Soc. Interface, published online before print May 14, 2010.

Impact of Disease Induced Mortality



Impact of Disease Induced Death: Seasonality and Transient vs Long-term Patterns

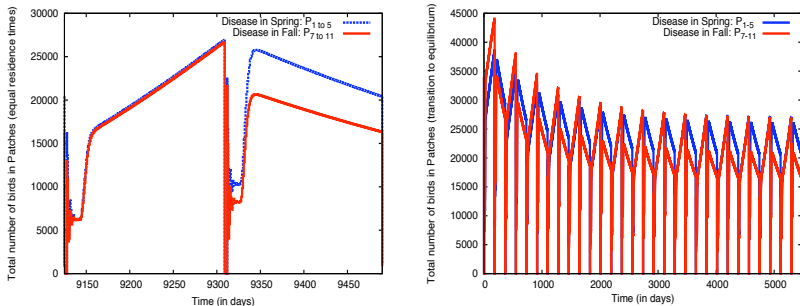


Figure: critical (top). However, for equal duration of residence, the average number of birds is higher when the disease occurs during the spring migration (P₄ and P₁₁). In the early adjustment years the opposite is observed (bottom). **This was the main hypothesis advanced in the literature.**

Disease Epidemiology: Dynamics and Spread

The interaction of migratory birds and domestic poultry must be incorporated in order to understand the role of this interaction in sustaining and spreading the avian Influenza: need to stratify the migratory birds by their disease status, and need to add domestic poultry.

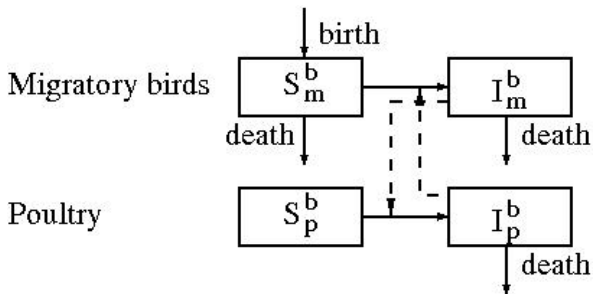
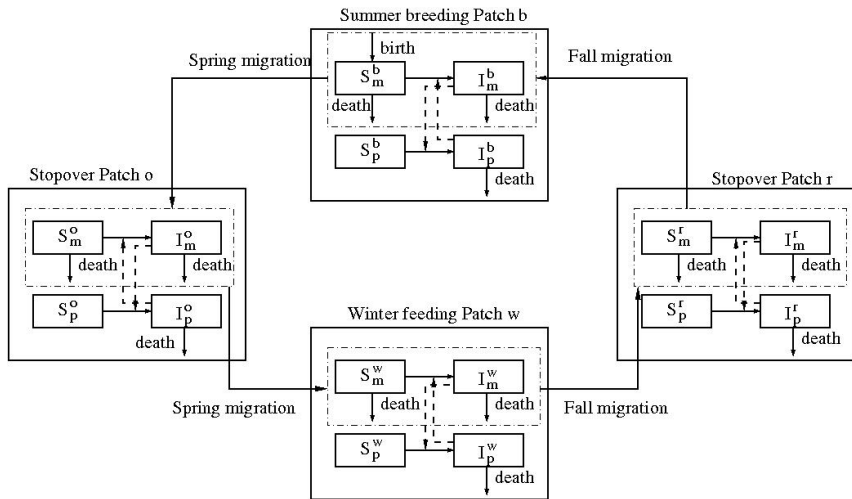


Figure: A schematic illustration of the local transmission cycle

Integration: global seasonal migration and local transmission via a meta-population



The Meta-Population Model

Migratory bird dynamics

$$\begin{aligned}
 \dot{S}_m^b &= B_m(t, S_m^b) + \alpha_{rb}^s d_{rb}^s S_m^r(t - \tau_{rb}^s) - \beta_m^b S_m^b I_m^b \\
 &\quad - \beta_{pm}^b S_m^b I_p^b - d_{bo}^s S_m^b - \mu_{ms}^b S_m^b, \\
 \dot{I}_m^b &= \alpha_{rb}^i d_{rb}^i I_m^r(t - \tau_{rb}^i) + \beta_m^b S_m^b I_m^b + \beta_{pm}^b S_m^b I_p^b - d_{bo}^i I_m^b - \mu_{mi}^b I_m^b, \\
 \dot{S}_m^o &= \alpha_{bo}^s d_{bo}^s S_m^b(t - \tau_{bo}^s) - \beta_m^o S_m^o I_m^o - \beta_{pm}^o S_m^o I_p^o - d_{ow}^s S_m^o - \mu_{ms}^o S_m^o, \\
 \dot{I}_m^o &= \alpha_{bo}^i d_{bo}^i I_m^b(t - \tau_{bo}^i) + \beta_m^o S_m^o I_m^o + \beta_{pm}^o S_m^o I_p^o - d_{ow}^i I_m^o - \mu_{mi}^o I_m^o, \\
 \dot{S}_m^w &= \alpha_{ow}^s d_{ow}^s S_m^o(t - \tau_{ow}^s) - \beta_m^w S_m^w I_m^w - \beta_{pm}^w S_m^w I_p^w - d_{wr}^s S_m^w - \mu_{ms}^w S_m^w, \\
 \dot{I}_m^w &= \alpha_{ow}^i d_{ow}^i I_m^o(t - \tau_{ow}^i) + \beta_m^w S_m^w I_m^w + \beta_{pm}^w S_m^w I_p^w - d_{wr}^i I_m^w - \mu_{mi}^w I_m^w, \\
 \dot{S}_m^r &= \alpha_{wr}^s d_{wr}^s S_m^w(t - \tau_{wr}^s) - \beta_m^r S_m^r I_m^r - \beta_{pm}^r S_m^r I_p^r - d_{rb}^s S_m^r - \mu_{ms}^r S_m^r, \\
 \dot{I}_m^r &= \alpha_{wr}^i d_{wr}^i I_m^w(t - \tau_{wr}^i) + \beta_m^r S_m^r I_m^r + \beta_{pm}^r S_m^r I_p^r - d_{rb}^i I_m^r - \mu_{mi}^r I_m^r.
 \end{aligned}$$

Poultry population dynamics:

$$\begin{aligned}
 \dot{I}_p^b &= \beta_p^b (N_p^b - I_p^b) I_p^b + \beta_{mp}^b (N_p^b - I_p^b) I_m^b - \mu_p^b I_p^b, \\
 \dot{I}_p^o &= \beta_p^o (N_p^o - I_p^o) I_p^o + \beta_{mp}^o (N_p^o - I_p^o) I_m^o - \mu_p^o I_p^o, \\
 \dot{I}_p^w &= \beta_p^w (N_p^w - I_p^w) I_p^w + \beta_{mp}^w (N_p^w - I_p^w) I_m^w - \mu_p^w I_p^w, \\
 \dot{I}_p^r &= \beta_p^r (N_p^r - I_p^r) I_p^r + \beta_{mp}^r (N_p^r - I_p^r) I_m^r - \mu_p^r I_p^r.
 \end{aligned}$$

Disease Extinction and Persistence of the Full Model

Global Threshold Theorem: A threshold, given in terms of the spectral radius $r(T_I)$ of the time T -solution operator of the linearized periodic system of delay differential equations at a disease free equilibrium, can be theoretically derived but without a close form in terms of the model parameters.

- The nontrivial disease free equilibrium is global asymptotically stable once the threshold is below 1;
- If the threshold is larger than 1, then **the disease is uniformly strongly persistent** in the sense that there exists some constant $\eta > 0$, which is independent of the initial conditions, such that, for each $c = b, o, w, r$,

$$\liminf_{t \rightarrow \infty} I_m^c(t) \geq \eta, \quad \liminf_{t \rightarrow \infty} I_p^c(t) \geq \eta.$$

Common Teals in Poyang Lake (China) as a Case Study

- The Common Teal is the smallest alive dabbling duck, which feed mainly at the surface rather than by diving.
- Common Teals were recently confirmed to migrate north after wintering in the Poyang Lake area and can be observed to travel as far as 2,700 km from their wintering ground.



In the absence of avian influenza

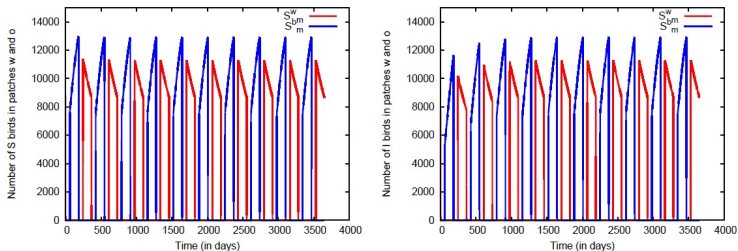


Figure: Number of susceptible migratory birds over 10 years in the absence of avian influenza.

H5N1 spread in the absence of interaction with poultry

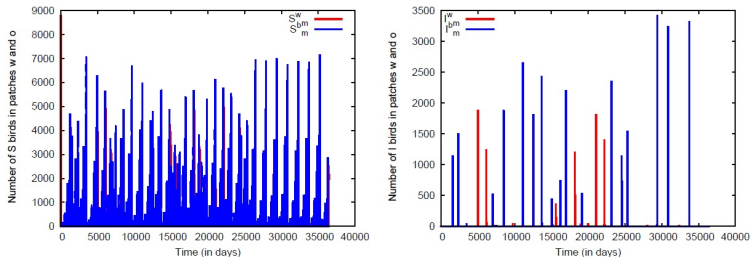


Figure: Number of (left) susceptible and (right) infected migratory birds over 100 years in the absence of poultry showing disease persistence and appearance of **non-periodic oscillation** of the number of migratory birds.

In the presence of both avian influenza and interaction of poultry

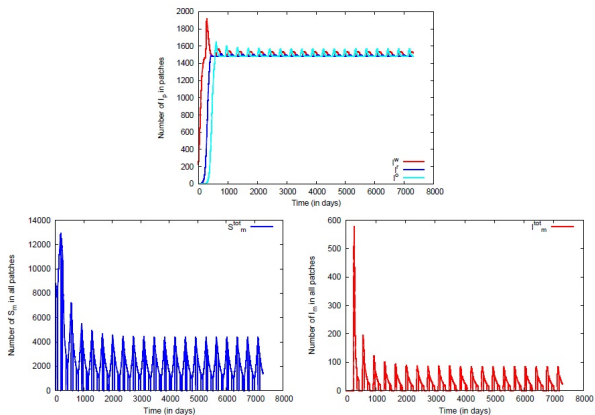
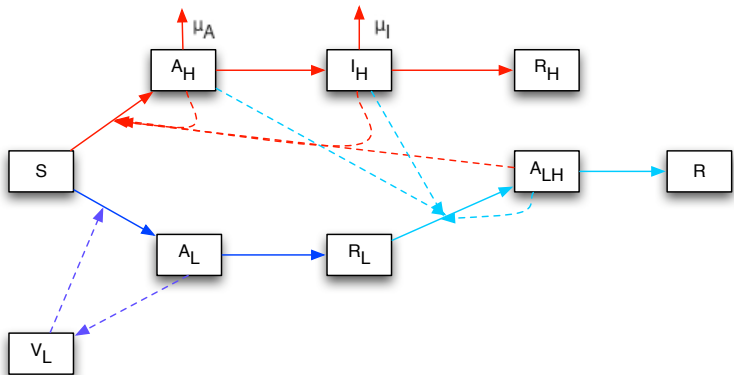


Figure: (top) Number of infected poultry on endemic farmed patches and (bottom) number of susceptible and infected migratory birds showing the persistence of the disease and convergence to periodic solutions.

HPAI outbreak mitigated by seasonal LPAI

- LPAI strains have been reported to induce partial immunity to HPAI in poultry and some wild birds inoculated with both HPAI and LPAI strains.
- What is the extent to which this partial immunity observed at the individual level can affect the outcome of the outbreaks among migratory birds at the population level during different seasons?
- We found a distinct mitigating effect of LPAI on the death toll induced by HPAI strain, particularly important for populations previously exposed to and recovered from LPAI.
- We examined the effect of the dominant mode of transmission of an HPAI strain on the outcome of the epidemic, and found that for a given infection peak of HPAI, indirect fecal-to-oral transmission of HPAI can lead to a higher death toll than that associated with direct transmission.
- The mitigating effect of LPAI can, in turn, be dependent on the route of infection of HPAI.

Two strains: flow chart



Model Equation

$$\begin{aligned}
 \dot{S} &= -\epsilon_L V_L S - (\beta_A A_H + \beta_I I_H + \beta_{LH} A_{LH}) S / N, \\
 \dot{A}_L &= \epsilon_L V_L S - \alpha_L A_L, \\
 \dot{A}_H &= (\beta_A A_H + \beta_I I_H + \beta_{LH} A_{LH}) S / N - \mu_{A_H} A_H - \gamma_H A_H, \\
 \dot{I}_H &= \gamma_H A_H - \mu_{I_H} I_H - \alpha_H I_H, \\
 \dot{R}_L &= \underbrace{\alpha_L A_L}_{\text{recovery from LP AI}} - \underbrace{(\beta_A A_H + \beta_I I_H + \beta_{LH} A_{LH}) R_L / N}_{\text{2nd infection by HPAI strain}}, \\
 \dot{R}_H &= \underbrace{\alpha_H I_H}_{\text{recovery from HPAI}}, \\
 \dot{A}_{LH} &= (\beta_A A_H + \beta_I I_H + \beta_{LH} A_{LH}) R_L / N - \alpha_{LH} A_{LH}, \\
 \dot{R} &= \underbrace{\mu_{A_H} A_H + \mu_{I_H} I_H}_{\text{disease induced death}} + \underbrace{\alpha_{LH} A_{LH}}_{\text{recovery from 2nd HPAI}}, \\
 \dot{V}_L &= \phi_{A_L} A_L - \nu_L V_L.
 \end{aligned}$$

Dynamics Analysis: Equilibria and Reproduction Numbers

Two equilibria are of significance on the time scale considered.

- A disease free equilibrium in a fully susceptible population $E_0 = (S^*, 0, 0, 0, 0, 0, 0, 0, 0)$.
- Another corresponds to a population that has been previously exposed to LPAI, but remains susceptible to HPAI: $E_1 = (S^*, 0, 0, 0, R_L^*, 0, 0, 0, 0)$.
- At E_0 , we have

$$\bar{R}_{0H1} = \frac{S^*/N\beta_I\gamma_H}{(\gamma_H + \mu_{AH})(\mu_{IH} + \alpha_H)} + \frac{\beta_AS^*/N}{\gamma_H + \mu_{AH}}, \bar{R}_{0L1} = \sqrt{\frac{\epsilon_LS^*\phi_{AL}}{\nu_L\alpha_L}},$$

as the reproduction numbers for the HPAI and LPAI strains.

- At E_1 , we have

$$\bar{R}_{0H2} = \frac{S^*/N\beta_I\gamma_H}{(\gamma_H + \mu_{AH})(\mu_{IH} + \alpha_H)} + \frac{\beta_AS^*/N}{(\gamma_H + \mu_{AH})} + \frac{R_L^*/N\beta_{LH}}{\alpha_{LH}},$$
$$\bar{R}_{0L2} = \sqrt{\frac{\epsilon_LS^*\phi_{AL}}{\nu_L\alpha_L}},$$

with similar interpretations, but for the spread of HPAI in a population of birds naive to HPAI only.

Parameters and scenarios: multi-scales, seasonality and migration

With fast virus dynamics in the environment, the subsystem for LPAI strain is a standard SIR model and the final size relation holds, so we can use the final attack rate to parametrize the transmission rates and basic reproduction numbers of particular seasons.

	ϵ_L	S_{max}	$S(\infty)$	A_L^{max}	\bar{R}_{0L1}
R1	$\epsilon_{L1} = 7.42 \times 10^{-9}$	700.92	468	5%	1.19
R2	$\epsilon_{L2} = 8.85 \times 10^{-9}$	587.54	308	10%	1.30
R3	$\epsilon_{L3} = 1.19 \times 10^{-8}$	434.46	141	20%	1.51
R4	$\epsilon_{L4} = 1.56 \times 10^{-8}$	333.72	60	30%	1.73

Table: Set of parameters for groups of simulations $R1$ to $R4$, with four values of ϵ_L , $R_{0L} = \sqrt{\epsilon_L \phi_{A_L} N / (\nu_L \alpha_L)}$, $\alpha_L = 7.14 \times 10^{-2} \text{ day}^{-1}$, $\nu_L = 8.75 \times 10^{-1} \text{ day}^{-1}$, $\phi_{A_L} = 2.397 \times 10^{3.7} \text{ day}^{-1}$, and the total population $N = 1000$.

Parameters and scenarios: HPAI strain and cross-infection

- The infection parameter β_{IH} is the product of the number of contacts c between an infectious and susceptible bird per unit time and p , the probability of successful infection upon such contact. That is, $\beta_{IH} = c \times p$.
- We take a range of values for the transmission probability p of 0.03975 to 0.80. We selected four values displayed: $p_1 = 0.03975$, $p_3 = 0.0443$, $p_5 = 0.05$, and $p_6 = 0.1$. These lead to HPAI isolated dynamics with peak infectious populations of about 7.44, 10.8, 15, and 53% , corresponding to HPAI reproduction numbers of $\bar{R}_{0H1} \approx 1.55, 1.7, 1.8$, and 3.9, respectively.

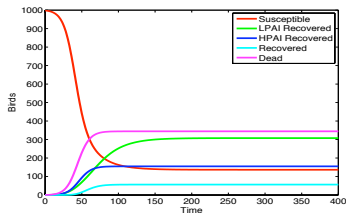
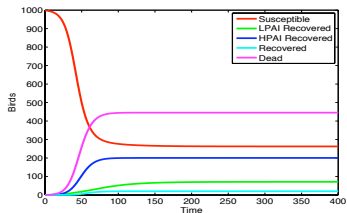
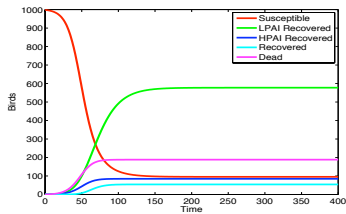
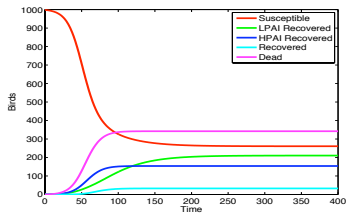
Effect of LPAI on the onset /dynamics of HPAI

- We focus on sixteen sets of parameters: Four LPAI specific sets of parameters (R1 to R4) correspond to a change of seasonality faced by the birds during their migration; and the four HPAI specific sets of parameters correspond to case scenarios of HPAI in the range of data reported.
- The relative values of LPAI and HPAI control parameters lead to roughly three types of configurations.
- The co-circulating LPAI and HPAI strains can lead to a reduction of HPAI induced death at the population level. In particular, the increase of the prevalence of LPAI with seasonality affects more significantly the final number of dead birds compared to its effect in reducing the final number of HPAI recovered groups.
- The outcome of the HPAI epidemic is highly dependent on the season in which the HPAI strain is introduced into the population, under-detection in the wild in post-LPAI peak season (usually in the Fall).

Three Regimes

- The first regime is that in which the HPAI strain dominates and the increase of prevalence of LPAI from one season to the next does not significantly influence the HPAI death toll.
- In the second regime in which \bar{R}_{0H1} and \bar{R}_{0L1} are almost equal ($O(10^{-1}) \gtrsim |\bar{R}_{0H1} - \bar{R}_{0L1}|$), the influence of LPAI is significant in reducing the number of birds infected by HPAI. The overall death toll of HPAI is reduced. We note that the main difference between cases with $\bar{R}_{0L1} \gtrsim \bar{R}_{0H1}$ and $\bar{R}_{0L1} \lesssim \bar{R}_{0H1}$ is the final number of LPAI recovered birds and as a result, the final number of birds escaping both LPAI and HPAI.
- The last regime is that in which the reproduction number of the LPAI strain is larger than that of HPAI with $\bar{R}_{0L1} - \bar{R}_{0H1} > O(10^{-1})$. In this regime, the LPAI dynamics is sufficiently rapid to hinder the initiation of the epidemic of HPAI. A considerable reduction in the number of HPAI dead and recovered birds can be observed.

Some simulations

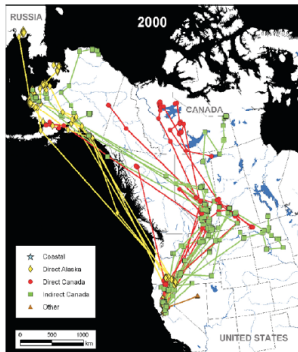


On-going Bird Flu Modeling Projects

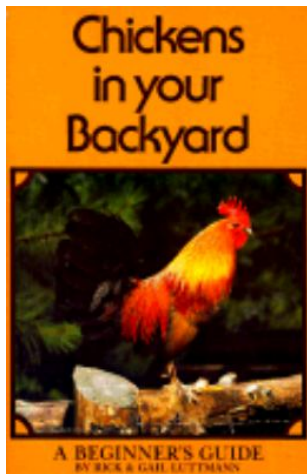
- Impact of maturation and age-structured models (Bourouiba and Wu, 2010);
- The interface of bird ecology and disease epidemiology: disease persistence (Bourouiba, Gourley, Liu and Wu, SIAM J. Appl. Math.);
- Environmental contamination: direct transmission vs indirect transmission (Bourouiba, Teslya and Wu, J. Theo. Bio.)
- The evaluation of effectiveness of intervention measures (Liu, Duvvuri and Wu, MMNP, 2008);
- The (local) spatial spread: traveling waves and PDE models (Liu, Wang and Wu, in revision);
- Interaction of LPAI and HPAI (Bourouiba, Teslya and Wu, JTB);
- Risk assessment for North American (Northern pintails migration) (Du and Wu, in progress)

Relevance to North America

Northern Pintail (*Anas acuta*)



Relevance to the Region (Ontario)



Topics covered

- Prototype diseases: **Avian influenza**, West Nile virus, Lyme diseases;
- Biological Issues: Spatiotemporal transmission dynamics from the interaction of host ecology and disease epidemiology;
- Mathematical challenges: seasonality/periodicity; spatial movement/patch models or PDEs with nonlocal nonlinearity; physiological structure/delay;
- Relevance to surveillance (satellite tracking, GIS), to policy and intervention (culling, environmental impact).

Collaborators

- Lydia Bourouiba, McGill/York/MIT
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- FAO/USGS/international avian influenza project team