Mathematics of Avian Influenza: Theory, Computation, and Data
Les mathématiques de la grippe aviaire : théorie, calculs et données
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SAYEDA IRIN AKTER, York University
Modelling the effect of social distancing on spreading and controlling infectious disease with Point Pattern Process

This work explores the spatial dynamics of disease transmission using Point Pattern Processes (PPPs) and distance-dependent infection rate within a Susceptible-Infectious-Removed-Susceptible (SIRS) framework. By modeling individuals as points in a continuous space, we examine how social distancing and spatial separation influence the spread of the virus. The infection rate is not uniform but varies with the distance between individuals, simulating the real-world effects of reduced contact through interventions like social distancing. We use mathematical models and point pattern analysis to investigate different spatial configurations, from clustered (high transmission risk) to dispersed (reflecting effective social distancing). The pair correlation function g(r) is employed to capture spatial clustering, while pair approximation simplifies the modeling of spatial interactions by considering the effect of pairwise interactions. Prior to social distancing, high P_I probability of infection values are observed due to frequent close contacts, leading to clustered transmission patterns. After implementing social distancing, P_I decreases as individuals are more dispersed, reducing the likelihood of infection. This approach allows us to quantify the impact of public health measures on transmission dynamics, providing insights for optimizing interventions to control the spread of disease.

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Delay-driven oscillatory dynamics in an avian influenza model with dose-dependent environmental transmission

Avian influenza remains a major transboundary infectious disease affecting poultry and wild birds, with important consequences for food security, agricultural economies, and public health. Environmental persistence of avian influenza viruses and dose-dependent infection risk introduce transmission mechanisms that are not fully captured by classical direct-transmission models. We develop and analyse a nonlinear delay differential equation model incorporating generalized dose-dependent environmental transmission. Positivity and boundedness are established, and the disease-free and endemic equilibria are characterized. The basic reproduction number is derived, and local stability is investigated through the associated characteristic equations. Analytical stability-switch conditions and numerical continuation show that increasing the environmental delay can destabilize the endemic equilibrium through a Hopf bifurcation. DDE-BIFTOOL computations and an independent Beretta–Kuang stability-switch analysis identify the same critical delay and oscillation frequency, providing consistent verification of the bifurcation threshold. Computation of the first Lyapunov coefficient further shows that the Hopf bifurcation is subcritical, with an unstable branch of periodic solutions emerging on the stable-equilibrium side of the critical point. Numerical simulations reveal increasingly persistent oscillatory transients as the delay approaches the Hopf threshold. Near the unstable periodic branch, perturbations in environmental viral decay, shedding, and dose-response steepness substantially influence whether oscillations grow or decay. These results demonstrate how environmental transmission delays and dose-dependent exposure can generate complex oscillatory dynamics in avian influenza transmission and highlight parameter regimes in which small changes in environmental processes may strongly affect epidemic behaviour.

NATHANIEL OSGOOD, University of Saskatchewan

CONGJIE SHI, York University

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From Wild-Bird Mortality to Poultry Farm Introductions: HPAI Spillover in Ontario, Canada

Highly pathogenic avian influenza (HPAI) has caused widespread mortality in wild birds, outbreaks on poultry farms, and occasional human infections, underscoring its One Health importance. Using Ontario, Canada, as an initial case study, we develop a modelling framework to investigate potential links between HPAI dynamics in wild birds and virus introductions into poultry farms. The framework combines a wild-bird transmission model that characterizes time-varying infection pressure with a within-farm poultry model fitted to outbreak data to infer likely introduction times on affected farms. We then compare these inferred introduction times with modelled wild-bird infection pressure to assess temporal patterns consistent with spillover. Early farm introductions were temporally aligned with elevated wild-bird infection pressure, suggesting a possible contribution of wild-bird-associated exposure. Later introductions may reflect other transmission processes, including delayed exposure through environmental contamination, although temporal patterns alone cannot identify transmission pathways. This framework provides a basis for integrating wildlife and poultry outbreak data to investigate potential spillover and inform surveillance.

WOLDEGEBRIEL ASSEFA WOLDEGERIMA, York University

Integration of mechanistic epidemiological models with AI for understanding and predicting avian influenza dynamics

Avian influenza continues to pose significant challenges to animal and public health, highlighting the need for mathematical and computational frameworks that can capture complex transmission dynamics and support reliable epidemic prediction. Traditional mechanistic models, formulated using differential equations, provide valuable insights into disease transmission, persistence, and control. However, integrating these models with heterogeneous and potentially incomplete epidemiological data remains challenging. Recent advances in artificial intelligence (AI), particularly physics-informed neural networks (PINNs) and disease-informed neural networks (DINNs), offer promising approaches for combining the interpretability of mechanistic models with the flexibility of deep learning.

In this talk, we discuss AI-integrated mechanistic modelling approaches for understanding and predicting avian influenza dynamics, with particular emphasis on DINNs. Building on our recent work, we develop a disease-informed deep learning framework based on a coupled SI bird and SIR human transmission model. The framework incorporates the governing epidemiological differential equations into the neural network training process through a loss function combining observational data fitting and mechanistic constraints. Using synthetic epidemiological data, we demonstrate the ability of the DINN to reconstruct infection trajectories, estimate model parameters, and capture disease extinction and persistence under different transmission scenarios.

Our numerical investigations highlight the influence of neural network architecture and training configurations on parameter estimation accuracy and predictive performance. We conclude by discussing opportunities and challenges in extending AI-informed mechanistic models to real-world avian influenza. This work illustrates the potential of integrating mathematical epidemiology and deep learning to advance data-informed epidemic forecasting within a One Health framework.