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.

NICOLA LUIGI BRAGAZZI, Saarland University
Artificial Intelligence for Avian Influenza: A Comprehensive Public Health Perspective

Avian influenza demands a One Health response that connects animal surveillance, environmental information, and public health preparedness. Artificial intelligence can support this response through outbreak prediction, hotspot detection, early warning, and risk communication, while mathematical modelling provides an interpretable basis for understanding transmission and evaluating interventions. Drawing on our published research, this talk integrates contributions on data sources and early warning systems, mathematical and machine learning models, and generative artificial intelligence for avian influenza preparedness. Our review of past outbreaks and surveillance resources maps conventional and unconventional data streams to opportunities for forecasting and coordinated response. Our systematic review examines mathematical, statistical, machine learning, and hybrid approaches, assessing methodological developments, validation practices, and evidence supporting their public health use. Our empirical study of large language models evaluated factual questions and synthetic outbreak vignettes representing diverse stakeholders. Differences in factual accuracy, communication, and ethical framing highlight the importance of evaluating generative systems according to their intended users and decision contexts. Their potential contribution lies in communicating evidence and supporting contextualized guidance, subject to expert oversight and appropriate verification. The presentation will connect these publications through questions of identifiability, uncertainty, generalizability, and reproducibility. Particular attention will be given to integrating heterogeneous surveillance data, distinguishing infection dynamics from detection processes, and assessing performance across settings and epidemic periods. The resulting perspective positions artificial intelligence within a public health workflow linking surveillance, analysis, communication, and action, with priorities including timely alerts, targeted surveillance, transparent decision support, and coordinated One Health preparedness.

DAVID DICK, Public Health Agency of Canada
Barrier crossing and identifiability in an agent-based migration model for avian influenza

Although most transmission models of highly pathogenic avian influenza incorporate wild-bird migration data, few simulate the movement of birds at the individual level. A spatially explicit agent-based model was developed which combines the movement wild birds in North America to an environmental-transmission model. Each simulated bird holds a wintering and a breeding site and, on each day of migration, draws its next landing cell by taking the element-wise product of a flight kernel and that week's

eBird relative-abundance map. A calibrated parameter set reproduces the seasonal ranges and arrival timing of blue-winged teals. When the destination lies across water, the product vanishes over the kernel's support. This creates the local-minimum problem encountered in potential-field navigation, requiring an additional rule to guide movement. Four escape mechanisms were implemented, each with a counterpart in robot navigation. A 300-set parameter search and a controlled sweep show that the operating mechanism is set by the heading concentration, κ, through a threshold that follows from the kernel's numerical cut-off. Calibration on arrival within an eBird's season selects κ above that threshold: crossers and detourers both arrive, so routes are not identifiable from endpoints, and the threshold rather than the data chose the route. Consequences for specifying and calibrating movement rules at geographic barriers are discussed, with work in progress on an explicit blocked condition and route-based calibration targets.

LAHCEN LAAYOUNI, Al Akhawayn University
Tensor-Based Computational Methods for Multiscale Spatial Models of Avian Influenza

Avian influenza involves complex interactions between multiple host populations, environmental processes, and spatial transmission. These interactions can lead to high-dimensional computational models that are challenging to simulate efficiently. In this work, we investigate tensor-based computational methods for the efficient representation and numerical solution of multiscale spatial models of avian influenza. Tensor decompositions are used to reduce the computational and storage requirements associated with high-dimensional model representations while preserving the main features of the underlying dynamics. The approach is designed to support parallel computation and large-scale numerical simulations. Numerical experiments will examine accuracy, computational efficiency, scalability, and the effect of spatial and temporal scales on the resulting simulations. The proposed framework provides a computational approach for studying complex spatial transmission dynamics and may contribute to more efficient simulation and data-informed analysis of avian influenza.

MICHAEL Y. LI, University of Alberta
Pandemic Modeling: Lessons from COVID-19 and Seasonal Influenza forecasting

Avian influenza has the potential to cause a global pandemic once a mutation leads to human-to-human transmission. In such a pandemic scenario, model forecasting will be heavily relied on to inform public health interventions. Many of the models used for the COVID-19 pandemic can be expected to be heavily leveraged. The assessment of the National Science Foundation of the overall performance of COVID-19 mathematical models during the COVID-19 pandemic is "insufficient" and "far less useful than possible" in aiding the development of measures to mitigate ongoing pandemics (NSF-IHBEM). Mathematically, some fundamental questions remain: are there mathematical reasons for the collective under-performance of COVID-19 models? Are there mathematical benchmarks that can be used to evaluate model performance or quantify improvements in model performance when applied to real-world epidemics or a pandemic?

In this talk, I will demonstrate three key reasons that impact the performance of mathematical models for real-world epidemics: (1) mismatches of model outputs with data; (2) nonidentifiability of model parameters in model fitting to data; and (3) the final-size formula that dictates that models will over-project the epidemic size. Collectively, I call these three challenges the "final-size trap." To break the trap, new and improved models should be able to produce a good fitting between model output and the correct data and produce an epidemic size that can be validated by seroprevalence data. I will present some modeling experiences during COVID-19 and for seasonal influenza forecasting to show that non-autonomous models offer a dependable solution for the final-size trap.

JUNLING MA, University of Victoria
Comparative Analysis of Simplifications in Behavior-Structured SIRS Dynamics

Human behavior can substantially impact disease dynamics, but fully behavior-structured compartmental models are often high-dimensional and analytically challenging. We compare methods for simplifying a baseline behavior-stratified SIRS model and assess their reliability. We first aggregate the behavioral subclasses within the susceptible and recovered compartments while retaining infectious stratification. Then we use two different approximations, a quasi-steady-state approximation (QSSA) and a population-coverage closure, to combine the stratified infectious classes. The population-coverage closure may increase

the threshold transmission rate, while the other two simplifications always retain the disease threshold. Our analytical and numerical analyses show that both the simplification retaining infectious stratification and the QSSA closure reproduce the overall epidemic trends of the baseline model, particularly under fast behavior change. The population-coverage closure can also capture these trends, especially under weaker attenuation, but may substantially underestimate peak prevalence and exhibit large time-averaged absolute prevalence errors under higher transmission, strong attenuation, and slow behavior change. Overall, our results show that it is possible to use a QSSA closure to find a nonlinear force of infection to simplify a behavior-stratified multigroup model to an unstructured model while retaining good qualitative and quantitative fidelity.

ANDREW OMAME, York University Toronto Canada

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.

CONGJIE SHI, York University

Human Disease Burden and Key Symptoms Associated with Highly Pathogenic Avian Influenza: A Systematic Review and Meta-analysis

Highly pathogenic avian influenza (HPAI), referring to H5 and H7 subtypes of bird flu that lead to high mortality rates in poultry or wild birds, is an emerging zoonotic disease that poses a significant global public health threat because of its high disease severity and substantial mortality among infected individuals. The continued circulation among wild birds and poultry leads to the potential of causing future pandemics. Human infections with HPAI remain a major public health concern and are primarily associated with exposure to infected poultry. The risk is particularly high among individuals who have close contact with poultry on farms or in live poultry markets, or with wild birds along migratory routes.

Quantitative evidence on HPAI remains fragmented across geographical regions and viral subtypes. We conducted a systematic review and meta-analysis to assess the human disease burden, clinical severity, and key signs and symptoms associated with HPAI for the Americas and the European regions. Our systematic review and meta-analysis follow the Preferred Reporting Items for Systematic Review and Meta-Analyses (PRISMA) guidelines. Although avian influenza incidence and prevalence were low across studies (incidence, 0.93%; prevalence, 0.83%), an interesting finding was the relatively high severity among confirmed cases, with pooled hospitalization, ICU admission, and mortality rates of 3.24%, 2.79%, and 1.51%, respectively. Our results also indicate that the leading signs and symptoms for HPAI are conjunctivitis/eye symptoms (89.5%), pneumonia (86.7%), and fever (61.0%).

MANTING WANG, Université de Montréal

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.