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About

ModAH Hub and ModAH Conf

ModAH Hub is an international initiative bringing together the scientific community working on epidemiological modelling in animal health. It aims to foster collaboration, promote the sharing of modelling practices, methods, data and tools, and encourage joint efforts to address current and emerging challenges in animal health. ModAH Conference, the international scientific conference dedicated to modelling in animal health, is a key meeting point for this community.

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Talks

A meta-population disease model for the transmission of highly pathogenic avian influenza H5N1 within and between dairy herds in Ontario, Canada to assess the potential risk of pathogen spillover to dairy workers

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Since first being identified in March 2024, the outbreak of highly pathogenic avian influenza H5N1 (HPAI-H5N1) in United States (US) dairy cattle has affected 1,093 herds across 19 states. The outbreak among cattle has subsequently led to 41 confirmed spillover cases in humans with a known exposure to infected dairy cattle. Canadian cattle remain unaffected by the HPAI-H5N1 outbreak. Preparedness and preparation during this time is critical and may help to mitigate the size and duration of such an outbreak should introduction of HPAI-H5N1occur in Canada. The objectives of this study were to construct a meta-population disease model of HPAI-H5N1 in Ontario dairy cattle, parameterized by empirical dairy cow movement networks, and to assess the potential for spillover infections to occur within Ontario dairy farm workers. The meta-population model was built using the 'SimInf' package in R. The within-herd disease model was constructed using a stochastic SIR model framework and the system of between-herd dairy cow movements was based on semi-random networks parameterized using historical Ontario dairy cow network data. Introduction of HPAI-H5N1 was assumed to occur through importation of infected cattle from the United States, the number and regional distribution of which were also based on historical data. A human spillover function was parameterized using data from the 2024 HPAI-H5N1 dairy outbreak in California, and the spillover function was applied to the results of the meta-population model simulations to estimate the number of projected dairy cow-to-human spillover events in Ontario. Ten thousand model simulations were run for one year and the number of primary herd infections (infected through importing infectious dairy cattle), secondary herd infections (infected through the domestic movements of an infectious dairy cow(s) between Ontario herds), and human spillover cases were quantified. Simulations of the meta-population model resulted in the majority of infected herds being those that imported infectious dairy cows (IQR: 12-16; range: 4-26). The number of secondary infection herds ranged from 0-5, with approximately 56% of model iterations resulting in no between-herd transmission of HPAI-H5N1 within Ontario. Spillover of HPAI-H5N1 to human farm workers was very rare, occurring in only 8/10,000 model iterations with no more than a single spillover event per iteration. Overall, the highly fragmented structure of the Ontario dairy movement networks resulted in limited sustained between-herd transmission of HPAI-H5N1 and very rare occurrences of spillover to dairy farm workers.

A multi-layer network-based modeling framework for epizootic hemorrhagic disease transmission in France

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Epizootic Hemorrhagic Disease (EHD) was first reported in France in September 2023 in the Pyrénées-Atlantiques and Hautes-Pyrénées departments and rapidly spread across large parts of the territory by the end of 2024. In response, enhanced surveillance and movement restrictions were implemented to limit disease spread, as well as voluntary vaccination, starting on 23rd September 2024, using a temporarily authorized vaccine due to exceptional circumstances. The virus type 8 (EHDV-8) is still circulating at lower levels, with only 5 official clinical outbreaks declared so far in 2025. The mechanisms driving its spatial expansion remain unclear, in particular the relative contribution of vector dispersal and host movements. We developed a stochastic compartmental model of EHDV transmission in cattle to investigate these mechanisms at the scale of French administrative units (cantons). Transmission is represented both within and between cantons. Within each canton, transmission is modeled using a Susceptible–Infected–Recovered (SIR) framework, extended to account for additional epidemiological features such as colostral immunity in newborn animals. Within-canton transmission is vector-borne and depends on demographic drivers, environmental factors such as pasture density and elevation, and temperature-dependent vector activity. Between-canton spread occurs through three contact networks capturing (i) short-range vector movements between nearby pastures, (ii) cattle movements between pastures of the same farm across cantons, and (iii) trade-related cattle movements. We compiled and processed environmental data from January 2023 to May 2025 to be used as input of our model. Regarding epidemiological data, we used antibody detection data from ELISA tests done in both milk and blood matrices, in more than 1100 dairy herds at least every two months across 15 departments (mainly in Occitanie, Normandie, and Pays de la Loire) between November 2023 and April 2025. We estimated herd-level seroprevalence from bulk tank milk data using a generalized linear model. The model will be fitted to this transformed data at the canton-level using an Approximate Bayesian Computation inference method. Once our model is able to reproduce the EHD epidemic wave observed in France between 2023 and 2025, we plan to develop constrained and optimized vaccination strategies to support decision-making during future crises.

An agent-based model of bovine tuberculosis transmission dynamics in high-risk cattle herds in Northern Ireland

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Bovine tuberculosis (bTB) remains a costly zoonotic disease affecting cattle as well as other mammals, with transmission occurring primarily via close contact and, in Northern Ireland, sustained by both in-herd processes and between-herd cattle movements and wildlife reservoirs. Existing modeling efforts focused on compartmental or highly aggregated solutions, limiting representation of varied herding and control strategies as well as emergent behaviours. This study develops a regional agent-based model (ABM) of bTB transmission for a high-risk zone in Northern Ireland, extending a previously developed single-herd solution to an interconnected network of herds and farmland. The model uses Northern Irish Department of Agriculture, Environment and Rural Affairs (DAERA) records (herd structure, land use, testing outcomes, and movements) along with data from other sources such as regional GIS data. The solution is designed to realistically reproduce the infection patterns observed in real life, driven by organic behaviours of the agents, involving between-herd cattle movement as one of the main drivers of the disease spread. Further uses of the model allow for the identification of other likely causes of transmission such as wildlife reservoirs, physical location and insufficient control measures. Parameterisation and optimisation are undertaken using sensitivity analysis and evolutionary algorithms, with candidate parameter sets evaluated against a variety of model metrics derived from routine test-and-removal protocols. Predictive validation is pursued by calibrating the ABM on an historical period and testing its ability to reproduce subsequently observed events in a later period. The resulting ABM provides a data-driven platform for exploring policy-relevant hypotheses and generating risk estimates at both herd and regional scales. The resulting model offers an ethical and cost effective in-silico method of testing bTB control measures in Northern Ireland.

Artificial intelligence and modeling for real-time monitoring of the health and welfare of captive foxes

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Monitoring and improving animal health and welfare is a pressing need. Technological advances are increasing our ability to do so in experimental settings but there are limited applications for less common model species such as wildlife. Red foxes (Vulpes vulpes) are used by the French National Agency for Food, Environmental, and Occupational Health and Safety (ANSES) for regulatory and research purposes related to its role as the European Union and French Reference Laboratory for rabies and Echinococcus spp. In 2022, four captive foxes were continuously filmed and surgically fitted with internal implants that recorded body temperature and activity levels. They were subsequently inoculated with rabies virus for European regulatory needs. We retrospectively tested the potential of these two data sets (video and implants) to provide an early warning for the onset of rabies symptoms, in order to refine protocols. For video recordings, we trained the AI neural network YOLOv4 to recognize a fox in an image and identify its posture (sitting, standing, or lying down). We obtained a global recall (sensibility) of 87% and precision (positive predictive value) of 93% considering all three postures. We then applied the trained algorithm to the full data set from one of the foxes (with the most complete set of video recordings). We created several indicators based on the proportion of time per day in each posture or not visible. Using the Shewhart anomaly detection algorithm on a time series of each indicator, we noted a significant increase in time spent lying down or hidden up to three days before the appearance of observed clinical symptoms. For the implant data, we applied two anomaly detection algorithms (Shewhart and EWMA) to both the temperature and activity data sets for each individual fox and compared how early the different models could detect significant changes compared with baseline while limiting false alarms during the calibration period. All the foxes significantly changed their activity during infection, at a much earlier date than the onset of symptoms observed by caretakers. We were best able to detect these changes using the EWMA algorithm, in some cases producing consecutive alarms up to two weeks before the death of an animal, while limiting false alarms. We found no evidence of fever in any of the infected foxes and body temperature was not a reliable indicator of foxes' health in this context. While we applied our methods to a particularly severe and rarely implemented model with a limited sample size, this proof of concept illustrates the potential of these methods to provide a powerful support tool for animal caretakers that can be applied to a wide range of situations that would benefit from similar long-term monitoring, including experimental protocols with milder clinical signs such as Echinoccocus infection, and routine monitoring for unexpected declines in health or welfare.

ASPIRE: A Domain-Specific Language for Sensitivity Analysis and Parameter Inference in Epidemiological Models

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Calibrating mechanistic epidemiological models requires connecting simulation outputs to real-world observation data through two complementary analytical steps: sensitivity analysis (SA), to identify the most influential parameters, and parameter estimation (PE), to infer values that best reproduce observed dynamics. In practice, these steps are typically implemented through ad hoc R or Python scripts tightly coupled to specific models and datasets. Such scripts are difficult to maintain, must be rewritten when methodological choices evolve, and hinder reproducibility, reuse, and accessibility ---particularly for domain experts with limited software engineering background.We present ASPIRE (\textit{Analysis of Sensitivity and Parameter Inference for Robust Epidemiology}), a domain-specific language (DSL) designed to structure SA and PE workflows for mechanistic epidemiological models in a declarative, modular, and reproducible way. From a single textual specification describing the model, the observation data, the experimental design, and the estimation method, ASPIRE automatically generates a complete and executable R workflow---without requiring manual scripting. Changes in methodological choices require updating only the relevant part of the specification, leaving the rest unchanged.The ASPIRE metamodel captures recurring concepts underlying SA and PE workflows, independently of any specific simulation framework or statistical method. It supports multiple SA methods (Sobol, Morris, ANOVA) and PE approaches (ABC, MLE), and includes dedicated constructs to bridge mismatches between simulated and observed data. It also enables the explicit integration of domain knowledge into the workflow, for instance, by flagging epidemiologically critical parameters .The approach is validated on two mechanistic models built on different simulation platforms: a stochastic individual-based SIRD model developed with EMULSION, and a deterministic SIR compartmental model implemented in Python. In both cases, the same DSL structure and code generation pipeline produced executable workflows without any manual adaptation, demonstrating the portability of the approach. Applied to the EMULSION SIRD model, the generated workflow successfully recovered nominal parameter values from synthetic observation data, confirming its correctness.ASPIRE represents a step towards model-driven calibration workflows in animal health modelling, promoting a clear separation between epidemiological knowledge and computational implementation, and lowering the barrier to adopting systematic, reproducible analytical practices.

Assessing the impact of epidemiological indicators on aquatic animal disease dispersal using a coupled hydrodynamic-particle tracking model

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Hydrodynamic models are commonly used to simulate and predict the movement of water in marine environments. They can represent the mixing of passive tracers such as temperature and salinity, and, when coupled with Lagrangian particle tracking models (PTMs), drive the transport of infectious pathogens in order to assess epidemiological connectivity at the regional level. Here, the high-resolution hydrodynamic model TELEMAC-2D and its online PTM have been adapted and successfully applied to simulate the dispersal of ostreid herpesvirus-1 microvariants (OsHV-1 µvar), a viral pathogen which causes mass mortality in the Pacific oyster (Magallana [Syn. Crassostrea] gigas), within an English coastal environment. The aim was to investigate (1) how OsHV-1 µvar spreads from infected populations to the surrounding environment, (2) how dispersal distance results impact the implementation of disease control measures, namely zoning, and (3) how changes in environmental conditions influence the pattern of disease spread. The parameterisation of the model was done through literature review and expert elicitation. The transmission and survival of OsHV-1 µvar in marine environments are shown to be temperature-sensitive and subject to high uncertainty due to a lack of robust experimental and observational data. Scenarios were thus simulated to better understand the complex interplay between temperature conditions optimal for viral survival, infectiousness and prevalence. Sensitivity analysis was conducted to evaluate the influence of environmental and epidemiological factors on the spatio-temporal dispersal of the virus. Future climate projections were considered, simulating dispersal under elevated seawater temperatures than currently observed. Addressing challenges that often arise in biophysical modelling, this coupled hydrodynamic-particle tracking model offers key indicators for assessing the risks of virus transmission between local susceptible populations under optimal conditions. Results produced by this model will be discussed, providing advice on the effectiveness of existing disease control measures over time, thereby facilitating effective aquatic animal health management.

Bayesian simulation of pig trading networks applying categorical and spatial priors

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Realistic simulation of livestock trading networks is central to modelling animal disease dynamics and evaluating surveillance and control strategies. In pig production systems, trading behavior is strongly structured by producer categories and spatial constraints. Still individual producers might exhibit stable and characteristic purchasing patterns which slightly diverse from the expected pattern based on producer category and spatial distances to potential sellers. This study presents a Bayesian framework for simulating pig trading networks in Norway that explicitly exploits this hierarchical structure. Using data from the Norwegian Livestock Register, comprising 2,867 pig producers and more than 28,000 recorded movements, trade partner selection is modelled within a multinomial–Dirichlet framework. Producer category and inter-farm distance are used to construct an informative and interpretable prior distribution over potential trading partners. Category-specific trading preferences define the baseline probability of interaction, while spatial effects are modelled using distance-dependent Weibull functions. This prior structure represents biologically and operationally plausible trading constraints and allows incorporation of expert knowledge. Observed producer-specific trading behavior is then utilized to update the prior, yielding posterior distributions that reflect individual purchasing tendencies while remaining consistent with system-level constraints. Prior sample sizes are calibrated using an empirical Bayes approach by maximizing the marginal likelihood. Temporal dynamics are modelled separately by simulating inter-purchase times using category-specific mixed Gaussian models. The proposed approach combines realism, transparency and flexibility, and generates synthetic trade networks that reproduce key structural, spatial and temporal properties of observed data. By naturally integrating categorical knowledge and spatial structure with individual-level behavior, the framework is well suited for disease spread modelling, scenario analysis and evaluation of outbreak preparedness measures. The basic principles for simulation might be applied in other countries and/ or for different species.

Connect'BRD: A sensor-informed mechanistic modelling framework for decision support in bovine respiratory disease management

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Bovine Respiratory Disease (BRD) is a major health and economic issue in young beef cattle production during the fattening period where rapid transmissions and delayed detection often lead to severe clinical outcomes and widespread antimicrobial use. Improving early detection and interventions strategies is therefore a key challenge. We present Connect'BRD, a novel decision-support tool developed within the SEPTIME and DECIDE projects, which integrates real-time sensor data with mechanistic epidemiological modelling to support proactive disease management. The system combines three key components: (i) machine-learning-based detection of early clinical signals from behavioural sensor data (activity, feeding, rumination), (ii) a stochastic, individual-based mechanistic model of BRD, accounting for pathogen dynamics, disease severity, management practices, and treatment strategies and (iii) a simulation-based ranking of intervention strategies across contrasted scenarios under uncertainty. This pipeline enables continuous updating of model projections based on observed field conditions and generates prioritised recommendations for farmers sent via SMS. The tool was evaluated in 9 commercial fattening farms in France (~550 animals) under operational conditions. Field trials compared three configurations: full Connect'BRD system, sensors alone, and no device. Machine-learning detection achieved high sensitivity (≈88%) for identifying BRD cases, but much lower specificity, highlighting the need for combining detection with model-based ranking. Preliminary results show that increased surveillance improved disease management: monitored groups exhibited lower disease severity and fewer relapse episodes compared to controls. Yet, higher detection sensitivity led to increased antimicrobial, highlighting the need for careful calibration of alert thresholds and decision rules. Beyond quantitative performance, qualitative feedback from farmers highlights the tool's value as a surveillance aid rather than an automated decision-maker, supporting informed intervention while preserving user control. Connect'BRD demonstrates the feasibility and added value of coupling real-time data streams produced by commercial devices with mechanistic epidemiological models for operational decision support. The modular and largely open-source architecture enables adaptation to other diseases, livestock systems, and sensor types. More broadly, it illustrates a generic framework for translating epidemiological modelling into actionable tools in animal health, bridging the gap between predictive modelling and field-level disease management.

Connecting the dots: estimating the amplification of H9N2 AIV along poultry production and distribution networks in Bangladesh

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H9N2 avian influenza viruses (AIVs) are endemic in Bangladesh and are consistently detected at high prevalence in live bird markets (LBMs), raising concerns over their potential for zoonotic spillover. Previous work demonstrated that LBMs are characterised by frequent viral introductions, which further undermine efforts to control AIV in LBMs. This observation appears to contrast with reports of low AIV circulation in poultry farms supplying those LBMs. In this work we seek to better characterise the amplification of H9N2 virus circulation along poultry production and distribution networks, and to identify the segments that contribute to frequent viral introductions into LBMs. Using a Bayesian data augmentation approach, we fit a hierarchical transmission model to RT-PCR results from samples collected from multiple farms along the entire duration of their production cycles (n=520). We estimated that around 15% of broiler flocks are ever infected with H9N2 AIV, but these incursions usually occur late during production, leading to limited opportunities for viral growth in this setting. Overall, only 5% of broiler chickens are actively infected when they leave farms. Second, we estimate AIV prevalence at LBM gates by fitting mechanistic models to multiple data streams, specifically RT-PCR results and genetic sequences collected during two distinct observational studies. Both analyses indicate that between 7% and 13% (depending on the considered model and dataset) of chickens enter LBMs as infected. Finally, we use these results to estimate the force of infection required to explain the observed levels of viral amplification occurring between endpoints of interests, i.e. farms and LBMs. In doing so, we account for the typical duration of transport. Our work provides a systemic assessment of H9N2 AIV viral circulation in multiple nodes alongside poultry production and distribution networks, which are often studied in isolation. Importantly, this is the first study to quantify the extent of viral amplification between farms and LBMs. These results highlight the role of the late production stage on farms and of the transport segment generally operated by middlemen, in (i) creating opportunities for AIV transmission before LBMs and (ii) shaping viral genetic diversity observed within LBMs. Ultimately, understanding where and when chickens are infected along distribution channels will enable more effective control interventions.

Cryptic invasion and evolutionary dynamics of peste des petits ruminants virus across Europe

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Since July 2024, Europe has experienced its largest recorded epizootic of peste des petits ruminants (PPR), with outbreaks reported across seven countries and the culling of hundreds of thousands of sheep and goats. Despite intensive control measures, continued spread highlights major challenges for early detection and containment. Many recent outbreaks have been associated with limited mortality and mild clinical signs, increasing the risk of silent circulation. Understanding the epidemiological drivers of this emergence is therefore critical to inform surveillance and control strategies. To reconstruct the emergence and spread of PPR virus across Europe between 2024 and early 2026, we combined whole-genome sequencing, phylodynamic analyses, official live small ruminant trade records, and field epidemiological investigations. We analysed 47 viral sequences sampled from affected holdings in Romania, Greece, Bulgaria, Hungary, Albania, Kosovo, and Croatia. Phylogenetic relationships were inferred using maximum likelihood methods, while Bayesian phylodynamic approaches were used to estimate viral migration dynamics between countries and reconstruct spatiotemporal diffusion patterns. Associations between inferred migration events and recorded live animal movements were assessed statistically. Phylogenetic analyses showed that all European viruses formed a single well-supported monophyletic cluster within lineage IV, consistent with a common introduction followed by regional dissemination. Bayesian reconstruction identified eastern Romania as the primary source of viral spread, with repeated introductions into Greece, sporadic dissemination to Bulgaria and Croatia, east-to-west spread within Romania reaching Austria, and subsequent transmission to Hungary, Albania, and Kosovo. Cross-border transmission was positively associated with official live animal trade between affected countries ($p < 0.05$), supporting a major contribution of legal trade to regional dissemination. Epidemiological investigations additionally suggested roles for illegal animal movements and indirect transmission. Long phylogenetic branches separating several country clusters further indicated substantial unsampled viral diversity and periods of undetected circulation. Our findings suggest that PPR is likely circulating undetected in parts of South-Eastern Europe, posing a continued risk of further spread across the continent. This work highlights the need for strengthened cross-border surveillance, enhanced traceability of animal movements, testing of at-risk holdings irrespective of clinical suspicion, and rapid data sharing. The emergence of PPR in Europe underscores important remaining gaps in our understanding of this globally significant transboundary disease and the need for coordinated regional preparedness.

Decision Support Modelling for ASF intervention: Dynamics and Optimization in Wild Boar Populations in West-Central Germany

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African swine fever (ASF) persists in wild boar populations through direct transmission and carcass-mediated infection, posing major challenges for surveillance and control. Decision-making is complicated by imperfect detection and the need to balance hunting and carcass removal under limited resources. We developed a modelling framework that explicitly links ASF transmission dynamics with surveillance outputs to support optimization of control strategies. We constructed a stochastic compartmental model capturing ASF transmission, carcass-mediated infection, and surveillance. The model explicitly represents four observable surveillance streams: hunted positives, hunted negatives, carcass positives, and carcass negatives. Surveillance data (~50,000 records; 2024 – 2025) from outbreak-affected municipalities in west-central Germany were aggregated and used for model calibration. Wild boar abundance was informed by a hybrid prior combining ENETWILD baseline estimates with local hunting data. Model parameters were inferred using Approximate Bayesian Computation, ensuring consistency with observed surveillance. The calibrated model was then used as a decision-support tool to evaluate intervention strategies by jointly optimizing hunting effort and carcass removal rates across a range of operational costs. The model reproduced observed surveillance dynamics across all four data streams, including timing and magnitude of carcass detections, indicating that key transmission pathways were adequately captured. Simulations showed persistent low-level transmission with peak prevalence below 1%, primarily sustained by environmental infection from undetected carcasses. Optimization identified a well-defined region of cost-efficient strategies. Increasing intervention intensity reduced outbreak duration and infections, but with diminishing marginal returns beyond moderate effort levels. Across cost scenarios, optimal strategies consistently combined intermediate hunting pressure with sustained carcass removal, outperforming strategies focusing on a single measure. In particular, scenarios with balanced interventions achieved substantial reductions in outbreak duration while avoiding higher costs associated with maximal effort. Sensitivity analyses indicated that optimal strategies were robust to uncertainty in transmission parameters but more sensitive to assumptions on carcass persistence and detection, underlining the importance of passive surveillance. This study demonstrates how integrating surveillance data into a transmission model enables robust calibration and provides a basis for decision support. The framework allows comparison of intervention strategies under realistic epidemiological and economic constraints and supports evidence-based optimization of ASF control in wild boar populations.

Dynamics of gastro-intestinal nematodes' resistance to anthelmintics at the interface between ibex and sheep populations on alpine pastures

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The high prevalence of gastro-intestinal nematodes (GIN) resistant to anthelmintics is a major issue in livestock production. Resistant GIN strains are also detected in wild mountain ungulates, and GIN transmission was demonstrated between domestic and wild populations, which raise questions on the respective epidemiological roles of these populations in the dynamics of resistance spread. Indeed, they often exhibit different movement patterns and thus encounter climatic conditions that are more or less favorable to GIN development, and their respective GIN populations are not subject to the same anthelmintic pressure, as only domestic ungulates are usually treated. In this study, we developed an individual-based, climate-driven model, integrating the GLOWORM mechanistic equations of GIN transmission, to better understand how GIN, and their resistance, may spread and persist at the interface between wild and domestic hosts populations, respectively ibex and sheep. Teladorsagia circumcincta was chosen as the GIN of interest in the model due to its high reported frequency in both host species in mountain pastures. To do so, within-host epidemiological model parameters were fitted over longitudinal fecal egg counts data from a pre-existing study on the Marmolada (Italy) ibex population, whereas model validation was carried out over fecal egg counts data that we gathered from interacting sheep and ibex populations in the Belledonne mountain range (France). We considered that the diploid GIN population underwent sexual reproduction, and resistance was modeled as a mutation of a single gene, generating homozygous resistant GIN, homozygous susceptible GIN and heterozygous GIN of intermediate sensitivity to antiparasitic drugs. In the simulations, a yearly anthelmintic treatment was only applied to sheep, in agreement with reported management strategies. We found that the presence of sheep on pasture in summer generated a spike in GIN egg deposition when conditions were most favorable for their development, increasing ibex infestation level. In turn, ibex ensured the survival of a GIN population on pasture through winter and the re-infestation of pastures in spring. At constant total host density, the speed of development of resistance in the global GIN population was negatively correlated with the proportion of ibex. A higher ibex proportion was also associated with a higher long-term GIN load in the host population. Overall, the two host populations seem to have complementary roles in the maintenance of the infestation. These results also suggest that ibex may serve as a refugia for GIN sensitivity genes by providing a favorable treatment-free environment, thus slowing down the spread of resistance, but this might come with an increase in total infestation. This potential trade-off recalls the complexity of disease dynamics at the interface between wild and domestic populations.

Epidemiological impact of Neospora caninum in Victorian Dairy Farms: Modelling Effective Control Strategies

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Background: Neospora caninum is a major cause of abortion in cattle worldwide, causing significant economic losses and reduced reproductive performance. Despite Victoria's critical role in Australian dairy production, the knowledge about the local epidemiology of N. caninum and the effectiveness of control measures is scarce. This study aimed to evaluate infection dynamics and management strategies in Victorian dairy farms. Methods: Field data were collected from five dairy farms in Gippsland, including serological testing of 1,029 cow and calf samples. Diagnostic performances of PCR and ELISA were compared, and the true prevalence was estimated. Vertical, horizontal, and colostral transmission were assessed through longitudinal monitoring and adjusted for misclassification. We developed an epidemiological model based on our collected data, age-structure and the literature, incorporating offspring, heifers and adult cows, and representing vertical, external (environmental) and within-herd transmission processes. Both deterministic and stochastic frameworks models were developed and calibrated using local data, allowing the evaluation of realistic control strategies. Scenarios included baseline management, testing of replacement animals and test-and-cull strategies, each evaluated under internal and external herd replacement and varying biosecurity conditions. Results: The true prevalence of N. caninum was 36.7% in cows, 25.7% in calves, and 32.3% overall. Vertical transmission occurred in 43% of calves from infected cows, while horizontal and colostral transmission contributed to 16% of infections in calves from uninfected cows. Longitudinal monitoring revealed 8.3% of previously negative dams seroconverted during gestation. Model projections indicated rising prevalence under baseline conditions, particularly in closed herds. The “Test and Cull” strategy consistently reduced prevalence, achieving

Evaluation of different vaccination strategies against enzootic swine influenza A in a seven-batch farrow-to-finish French farm system

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Introduction:Swine influenza A viruses (SwIAV) pose a persistent threat to pig production systems worldwide.Vaccination is used to control these viruses on farms. However, the effectiveness of vaccination depends on the timing and strategy adopted, whether focusing on a specific set of animals in the same physiological stage (batch-to-batch (BB)) or vaccinating simultaneously across the entire farm (mass vaccination(MV)).This study evaluated the impact of several vaccination strategies within a typical French farrow-to-finish farm. Materials and methods:A stochastic transmission model has been developed to integrate both demographic dynamics and epidemiological model within a farm. The model accounts for direct and indirect transmission pathways, as well as immunity dynamics (natural or vaccine-induced). The immunity duration post-vaccination or recovery followed Gaussian and gamma distributions, approximated through a novel deterministic-stochastic approach. Two populations were structured with different dynamics: breeding females (sows and gilts) and growing pigs (including piglets). Transmission parameters were derived from expert opinions and existing literature. The vaccine efficacy was set at 40% as reported in a previously published study. Five vaccination strategies were evaluated and compared to the baseline scenario (no vaccination) along seven-year simulations, to assess the reduction in cumulative incidence. Two strategies focused on breeding females using either BB or MV. Two additional strategies mirrored these approaches, including BB vaccination in growing pigs. The final strategy considered a combination of BB and MV in growing pigs. Results:All strategies reduced the cumulative incidence in both populations compared to the baseline scenario. The most common strategy used, which is vaccinating sows at the end of gestation, reduces incidence more in breeding females (ratio: 0.71 [CI95% 0.68-0.73]) than in growing pigs (0.96 [CI95% 0.94-0.99]).The most effective strategy combined batch-to-batch vaccination of gilts, mass vaccination of sows, and two-dose post-weaning vaccination of pigs, achieving ratios of 0.54 [CI95%0.50-0.56] and 0.62 [CI95% 0.58-0.64], respectively. Discussions and limitationsThis work highlights the added value of high vaccination frequency to increase immune protection along the entire production lifespan. Vaccinating sows by the end of gestation provides limited protection during suckling and leaves growing pigs fully susceptible. Reduction of the cumulative incidence increased when vaccination was applied twice in growing pigs.A limitation of this study is the need for empirical data to improve the accuracy and relevance of the predictions.

Fewer holdings, persistent connectivity: long-term structural change in the French cattle movement network and implications for pathogen spread

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Background. Over the past two decades, French cattle production has undergone a unprecedented decline in the number of holdings. Yet the consequences for cattle movement network structure and epidemic vulnerability remain unknown. We analysed cattle movements in France (2005–2024) to assess how this contraction has reshaped the movement network and its potential for sustaining pathogen transmission. Methods. Directed weighted networks were reconstructed using 28-day sliding windows, with cattle holdings as nodes, animal movements as directed edges, and the number of animals moved as edge weights, excluding terminal destinations (slaughterhouses and rendering plants). We quantified temporal changes in structural features relevant to pathogen spread, including connectivity, mixing patterns and reachability. To disentangle the effects of network structure from those of premise composition, observed metrics were compared against two configuration models: one preserving the empirical degree distribution irrespective of premise type, and a second preserving both degree distribution the number of animals moved within and between different premise types. Results. Although the number of holdings declined by 46% (~240,000 to ~130,000), network density increased by 57% and mean strength per holding nearly doubled, indicating that the smaller number of premises were increasingly connected. Despite this increase in local connectivity, the relative size of the largest subsets of connected holdings remained broadly stable over time. Local clustering increased over time, mirroring trends in both null models and reflecting changes in network density. Degree assortativity, indicating preferential connections between highly and weakly connected premises, remained stable over time; because observed values were closely reproduced by the null model preserving premise-type composition, this pattern appeared to be driven largely by mixing between farms and assembly centres rather than by additional higher-order network structure. Out-reachability declined moderately (~8,000 to ~5,000 holdings reachable within 3 movements) but remained substantial. Additional analyses assessed temporal changes in the extent of potential movement-mediated spread and in the identity and characteristics of the most central premises. Conclusion. Although the number of active holdings has almost halved over 20 years, the network still presents a high risk for epidemic spread. Trade is now concentrated among fewer holdings, which are more active and handle almost twice as many movements as in 2005. These changes represent both a structural vulnerability and a potential leverage point for targeted, movement-based surveillance and control.

From Livestock Movements to Infection Dynamics: Mechanism-Informed Learning for Synthetic Contact Networks

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Livestock pathogens spread through animal movement systems characterized by directed, weighted, and time-ordered contacts. For animal health risk assessment and infection control, epidemic models require synthetic movement networks that preserve both daily contact patterns and cross-day dependencies that allow infections to move through time. We introduce NetForge, a network generation and evaluation infrastructure designed for sensitive livestock movement data. By combining unsupervised network learning with temporal activity and contact turnover constraints, we distill Dutch pig movements into a generative representation, allowing synthetic network realizations to be sampled. In our framework, a layered stochastic block model (SBM) infers trading roles through block partitioning, and the fitted blocks are used to guide network generation. We evaluate synthetic networks using daily network structure, temporal reachability, turnover metrics, and hybrid transmission simulations. Ablation tests reveal that independent SBM sampling preserves daily network structure but fails to capture cross-day temporal dependencies. In contrast, random trade proposals with activity-path and turnover constraints improve temporal alignment but compromise mesoscale realism. The optimal configuration--combining SBM proposals, activity-path filtering, and turnover quotas--achieves the best alignment with observed temporal reachability and epidemic trajectories under various transmission scenarios. Paired with HerdLink.nl, an online tool for trade-network exploration and simulation, we offer a solution for generating privacy-preserving, uncertainty-aware, and distributable synthetic movement networks for livestock epidemiology and animal health modeling.

Heterogeneity in transmission and diagnosis of Mycobacterium bovis in Irish cattle herds

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Background Mycobacterium bovis, a globally significant multi-host pathogen, causes bovine tuberculosis (bTB) in cattle. To maintain market access for dairy and beef, and protect human and animal health, Ireland been operating a test-and-cull bTB elimination programme since the 1950s. Every bovine aged over six weeks is skin-tested annually. In addition, there is slaughterhouse, risk-based skin and gamma interferon (GIF) testing. Badger interventions include reactive culling and vaccination. Yet, despite increasing costs to the exchequer (€122 million in 2025) and farmers, bTB cases increased between 2016 and 2024. Uncertainties about transmission dynamics and diagnostic test performance impede control. To address these gaps and inform interventions, we developed a mechanistic model of within-herd M. bovis transmission dynamics, diagnosis and control. Methods The study population comprises 9325 Irish bTB breakdowns (herd-level trade restrictions and enhanced testing due to bTB detection) ending between 2015 and 2020. Models are informed with herd-specific demographic, movement and spatial bTB burden data. Introduction of infection, cattle-to-cattle transmission, demographics and movements are modelled stochastically in continuous time. Concurrently, we model skin, slaughterhouse and GIF testing with removal of test-positives and follow-up testing, based on policy and models of observed surveillance. We calibrate to a suite of bTB breakdown characteristics related to transmission, persistence and diagnosis using Approximate Bayesian Computation–Sequential Monte Carlo. Results Incorporating individual bovine heterogeneity in transmission enabled better consistency between model outputs and breakdown data. Our current framework suggests that 63% (95% CrI 31 – 89%) of infected cattle are “zero transmitters,” with the remainder of infecteds transmitting sufficiently to bring overall transmission in line with previous estimates in the literature. Incorporating herd-level diagnostic test heterogeneity also improved calibration. Results suggest that infected cattle are missed in routine herd-level skin tests in advance of the breakdown start, allowing undetected infected cattle to accumulate and disperse infection, but that effective test sensitivity increases after the initial case detection. Conclusions Our results support efforts to target high transmitters and detect infected cattle sooner in apparently clear herds, as these may have a disproportionate benefit for bTB control. Increasing dairy herd size combined with transmission heterogeneity amplifies stochastic high-transmission opportunities. This may help explain the increasing national burden of bTB in Ireland. Our framework also represents a foundation for developing more efficient calibration methods for stochastic transmission models.

Host heterogeneity matters - Comparison of multiscale and single scale frameworks applied to West Nile virus transmission dynamics

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The transmission of infectious diseases involves complex interactions across multiple biological scales, from within-host viral and immunological processes to between-host transmission dynamics. While multiscale models could better capture these interactions, a challenge lies in increased complexity and limited data availability. For vector-borne diseases, coupling between scales can be described through dose-response relationships, particularly linking host viremia to the probability of infecting vectors. Previously, we developed a mechanistic multiscale model combining within-host, within-vector, and population-level dynamics in a deterministic framework using ordinary differential equations. We showed that the form of the dose-response relationship matters, with nonlinear coupling inducing complex behaviors such as multiple endemic equilibria not captured by single-scale models. However, this implementation is not adapted to study transient dynamics and individual variability at the within-host level. Here, we present a stochastic, individual-based model of West Nile virus (WNV) transmission between birds and mosquitoes, and compare equivalent multiscale and single-scale frameworks. In the multiscale model, each infected host has its own within-host dynamics, explicitly linked via dose-response to its ability to infect vectors. These dynamics are derived from a phenomenological model fitted to experimental data from 25 avian species infected with WNV. The equivalent single-scale model uses parameters derived from the same within-host model, including mean latent period, infectious period, and transmission probability. Remaining variability arises only from stochasticity, without individual-level correlations between traits. Preliminary results suggest that the single-scale model may overestimate extinction probability under unfavorable conditions (low vector-to-host ratio), as it cannot capture rare highly infectious hosts that can initiate outbreaks. When large outbreaks occur, the multiscale model predicts higher and earlier peaks in prevalence. This work helps assess when multiscale frameworks are necessary over simpler models, contributing to a better understanding of the conditions underlying the emergence of mosquito-borne viruses in complex multi-host, multi-vector systems.

Impact of recent climate on Bluetongue and Epizootic Hemorrhagic Disease Virus emergence in France

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Biting midges of the genus Culicoides (Diptera: Ceratopogonidae) are vectors of bluetongue virus (BTV), and epizootic hemorrhagic disease virus (EHDV). Understanding the environmental drivers of vector populations is essential for anticipating the emergence of these orbiviruses, which pose significant economic and health challenges to domestic ruminant sectors. We developed a Bayesian modeling framework, based on Integrated Nested Laplace Approximations (INLA), to analyze 24 years (2001–2024) of Culicoides surveillance in France, integrating daily entomological, climatic and environmental data from different sources. Species-specific and multi-species models identified temperature as the predominant driver of vector abundance, with rainfall, soil moisture, vegetation, photoperiod, and wind showing species-dependent effects. Simulations revealed a recent increase in annual Culicoides abundances, an earlier seasonal onset of activity by up to six weeks, and the emergence of regions with near-year-round vector presence. Years of high vector abundance coincided with reported outbreaks of BTV, EHDV and Schmallenberg virus, and modeled basic reproduction numbers (R_o) indicated an increased transmission risk over the recent years. Overall, this work demonstrates the value of integrating high-resolution entomological and environmental data to anticipate fine-scale variations in vector activity and disease risk. Our framework provides a foundation for operational forecasting and targeted interventions to mitigate the impact of Culicoides-borne viruses on livestock health under climate change.

Leveraging High-Performance Computing for swift Calibration - A case study for the HPAI modelling challenge

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The HPAI Modelling Challenge, held from January to April 2026, asked participants to predict case numbers and simulate intervention scenarios for highly pathogenic avian influenza (HPAI) on the fictitious “Jolly Island”. The island comprises 9,160 poultry farms across five production types, distributed over an area of 3,667 km². Participants were provided with example mortality ledgers, trade and farm data, as well as monthly updates on observed case numbers. For our simulations, we used the “high-performance Modular EpideMIcs simuLatIOn software MEmilio” [1], marking its first application in an animal-health context. We developed a metapopulation model combining stochastic within-farm disease dynamics, stochastic trade patterns, and distance-based spatial transmission. While the model itself is implemented in C++, it can also be called from Python, allowing interoperability with established libraries for plotting, inference, and analysis. We first estimated disease-related parameters from mortality ledgers using an ODE model together with gradient-based optimization methods provided by pyPESTO [3]. The remaining 22 parameters were calibrated using simulation-based inference with the pyABC package [2]. By exploiting the available parallelization options, we ran simulations across 3,000 cores on a high-performance computing (HPC) system, enabling millions of model evaluations. We also explored several distance functions and ultimately selected a Wasserstein distance comparing simulated and observed outbreak patterns in a three-dimensional space defined by farm coordinates and outbreak dates. In this talk we show how even complex and spatially resolved infectious disease models with many parameters can be calibrated in short time frames by suitably leveraging HPC techniques and infrastructure. In particular, we have been able to generate spatially resolved disease dynamic patterns and closely reconstructed the course and terminating plateau in case numbers on Jolly Island after effective mitigation.[1] Julia Bicker et al. MEmilio – A high performance Modular EpideMIcs simuLatIOnsoftware for multi-scale and comparative simulations of infectious disease dynamics. 2026. doi: 10.48550/ARXIV.2602.11381.[2] Y. Sch¨alte et al. “pyABC: Efficient and robust easy-to-use approximate Bayesiancomputation”. In: Journal of Open Source Software 7.74 (2022), p. 4304. doi: 10.21105/joss.04304.[3] Yannik Sch¨alte et al. “pyPESTO: a modular and scalable tool for parameter esti-mation for dynamic models”. In: Bioinformatics 39.11 (Nov. 2023). Ed. by Anthony Mathelier. issn: 1367-4811. doi: 10.1093/bioinformatics/btad711.

Mitigating the Impact of OsHV-1 on Pacific Oyster Production Using a Spatial Compartmental Modelling Approach

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Over the past few years, methodological advances have driven major progress in epidemiological modelling tools, improving our ability to understand pathogen dynamics and inform disease management strategies. However, despite their strong potential, these approaches remain underused in the field of marine mollusc health, where infectious diseases continue to threaten the long-term sustainability of shellfish production. To address this gap, we developed a modelling framework to better characterize the dynamics of Ostreid herpesvirus type 1 (OsHV-1), a pathogen associated with recurrent and severe mortality events in juvenile Pacific oysters worldwide. We first adapted the classical SEIR compartmental framework to build a stochastic SWEIRD model specifically tailored to the transmission dynamics of OsHV-1 µVar in Pacific oysters. This model incorporates a waterborne viral compartment to represent environmental transmission and explicitly accounts for host phenotypic differences in survival capacity through distinct epidemiological pathways. After calibration and validation using experimental data, the model identified key parameters driving local viral transmission dynamics, including the viral shedding rate and the proportion of surviving hosts. This local modelling unit was then used as the basis for the development of a spatial model at the scale of an oyster production area, integrating environmental data relevant to pathogen spread. Model parameters were adjusted and the spatial framework was validated by comparing simulation outputs with field data on viral occurrence collected in 2025. These simulations should enable the identification of high-risk areas and periods, and the comparison of the potential effectiveness of several management measures that could be implemented by oyster farmers. More broadly, this approach provides a robust framework for exploring the transmission dynamics of mollusc pathogens and lays the foundation for the development of a national-scale model. Such a tool could ultimately support stakeholder decision-making, helping to reduce the still substantial annual impact of this pathogen on oyster production and to anticipate future risks associated with climate change or the emergence of new variants.

Modelling the within-host dynamics of immunological markers for Mycobacterium bovis infection in European badgers (Meles meles).

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European badgers (Meles meles) are recognised as a wildlife reservoir of Mycobacterium bovis, which contributes to the persistence of bovine tuberculosis (bTB) and poses challenges to controlling cattle disease in several countries. Detection of bTB is mainly bacteriological in bovine carcasses, but specific blood immunological tests are indispensable for diagnostic in live badgers. Within-host models can provide quantitative relationships between immune responses and underlying infection processes. Although mainly developed for viral infections, they are fully relevant for bacterial pathogens such as M. bovis, and, they can estimate key kinetic parameters and identify predictors of infection dynamics at the individual level. A dataset was set, comprising longitudinal immunological and bacteriological analyses generated from 119 captive badgers that were experimentally infected with M. bovis in the United Kingdom, the Republic of Ireland, and Spain between 2002 and 2020. The same animals were repeatedly tested from seven to sixteen times. Three immunological markers were quantified: antigen-specific Interferon-gamma (IFN-γ) T-cell responses (at the cell level by ELISPOT and as secreted protein in supernatant by ELISA) and antigen-specific antibody responses (by ELISA- Idexx test). These data were fitted simultaneously using a nonlinear mixed-effects model. The model included four interacting compartments representing cellular immunity (Lymphocytes TH1 and IFN-γ), humoral immunity (antibodies) and bacterial load. Seven parameters (phi, β, ξ, μ, c, λ, γ) were estimated, accounting for fixed and random effects. The error model was tailored for each response variable. Following infection, M. bovis bacteria proliferate at rate phi and induce the activation of TH1 cells at rate β. TH1 cells, in turn, produce or stimulate the production of IFN-γ at rate ξ, before decaying at rate μ. IFN-γ is cleared at a constant rate (c), and contributes to bacterial control at rate λ. Antibody production rate γ increases at the same time as bacterial load. Parameters were estimated using the SAEM (Stochastic Approximation Expectation-Maximization) algorithm implemented in Monolix 2024R1 (Simulations Plus). The model adequately captured observed dynamics across all three data types, providing a quantitative framework for investigating within-host infection dynamics, improving diagnostic strategies and integrating immunological data into bTB epidemiological models.

Optimizing sampling and diagnostic testing protocols for African swine fever detection in swine farms

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African swine fever (ASF) is a highly transmissible, highly pathogenic disease with high mortality that poses an immediate risk to the U.S. commercial swine industry. Despite progress in establishing surveillance and eradication strategies for ASF, there is a need to better understand the sample-collection and testing needs of commercial swine farms to address logistical challenges, given the large number of pigs that will need to be sampled. In this study, we designed an integrated sample-collection and disease-transmission system to optimize personnel requirements during simulated ASF outbreaks. We simulated the transmission dynamics of ASF disease in commercial swine farms using a stochastic statistical model and calculated the number of sample collectors and laboratory tests needed during 150-day ASF epidemics in North Carolina. Our model complied with the sampling priorities outlined in the USDA ASF Response Plan and evaluated two sampling techniques: blood sampling and oral fluid sampling. We optimized the allocation of sample collectors to at-risk premises using state-of-the-art machine learning techniques, including reinforcement learning. Our results showed that, in 150-day simulations, a median of 68 premises (99% range: 1-762) became infected. As a result, a median of 216 (99% range: 2-1,706) sample collectors was needed to complete sampling on time when blood samples were collected. In contrast, oral fluid sampling required a median of 112 (99% range: 1-617) sample collectors under the same conditions. Given a limited laboratory processing capacity of 1000 samples/day, the delays in testing caused a 4-day (99\% range: 0-6) delay in the detection of infection spread. Increasing the number of trained sample collectors by 100 reduced the detection delay by 1.4 days (99% range: 0 - 3.1 days), and increasing laboratory capacity by 500 reduced the detection delay by 0.4 days (99% range: 0 - 2.3 days). Delays in sample collection and testing significantly increase ASF secondary infections and have the potential to overwhelm national laboratory systems and delay ASF eradication. Our results underscore the importance of optimizing sample-collector availability and increasing testing capacity to efficiently combat the spread of ASF.

Reconstructing the silent spillover of USUV and WNV in the Netherlands: insights from a multi-species serocatalytic model

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Usutu Virus (USUV) and West Nile Virus (WNV) are emerging vector-borne flaviviruses in Europe. While transmission occurs between mosquitoes and birds, these pathogens can also spill over to horses and humans. Only a small proportion of infections in humans results in clinical disease, making it difficult to accurately assess exposure levels in humans. This limits the understanding of spillover risks in humans and the interpretation of enzootic circulation for early warning in public health. Here, we combined serocatalytic models with latent class approaches to quantify the relationship between the force of infection (FOI) in wild birds and in humans for both USUV and WNV, explicitly accounting for imperfect serological assays. We analysed serological data collected between 2016 and 2023 in the Netherlands, including human sera (n = 4,209) collected from a population-based biobank, and bird sera (n = 4,042) collected from a USUV/WNV surveillance programme. Samples were screened using an NS1-based protein microarray, with reactive bird sera confirmed by focus reduction neutralization tests, and reactive human sera confirmed by plaque reduction neutralization tests. We estimated the FOI and quantified the spillover rates of USUV and WNV in humans in the Netherlands by fitting Bayesian serocatalytic models to seroprevalence data of both birds and humans simultaneously. We explicitly accounted for uncertainties in the diagnostic accuracy of serological test outcomes using Bayesian latent class analysis. We further validated our spillover estimates by transforming the annual FOI into seasonal prevalence estimates that were subsequently compared to results from PCR testing in bloodbank samples. The estimated FOIs varied across years and were around seven times and twenty times higher in birds compared to humans for WNV and USUV respectively, indicating a greater spillover potential for WNV than USUV. Reconstructed seasonal prevalence patterns generally showed good consistency with external human bloodbank PCR samples. In addition, the modelled seroincidence estimates in humans exceeded the number of reported cases. Our findings therefore indicate that a large proportion of spillover infections is currently unobserved, suggesting that the public health burden of these arboviruses might be larger than previously thought. Future research into drivers of heterogeneity in spillover could further enhance the value of ecological surveillance for assessing public health risks.

Selective culling and the potential persistence of lumpy skin disease in cattle herds: insights from a mechanistic transmission model

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On June 29, 2025, France reported its first outbreak of lumpy skin disease (LSD) on a cattle farm in Savoie, likely resulting from viral introduction from Sardinia, Italy. LSD spread rapidly, with 117 outbreaks detected in 2025. This vector-borne disease affecting cattle is highly contagious and requires strict measures for its eradication. In France, emergency vaccination and a ban on animal movements around detected outbreaks were implemented, combined with total depopulation of the affected herds, leading to the culling of more than 3,000 cattle. During the outbreak, the total depopulation of affected herds became increasingly unacceptable to cattle farmers, as these measures were perceived as unnecessary, leading to major protests across the country. In this context, mathematical models calibrated using experimental and field data can be used to compare intra-farm transmission dynamics under different management strategies, such as the selective culling of animals diagnosed as infected versus the total depopulation of the farm. In this study, we propose a compartmental model of intra-farm transmission. This model allows us to represent transmission dynamics by taking into account cattle and vector (Stomoxys calcitrans) populations. Transmission dynamics are reconstructed in two parts: the first, without intervention, until the outbreak is detected when the first symptomatic animal appears; and the second, where a testing and selective culling strategy is implemented. The strategy relies on diagnostic tests capable of detecting infection in asymptomatic cattle, and different sensitivities and timeliness of the tests are examined. Finally, we consider a vector control strategy aimed at reducing the vector population, testing several levels of efficacy. For each scenario, the selective culling strategy is evaluated based on the virus persistence time in the herd, prevalence, and the number of animals culled to eradicate the virus. Our model shows that selective culling cannot eradicate the virus within 30 days, even with a hypothetical diagnostic test that is more than 50% effective at detecting infected animals 5 days before they become infectious. Given that current tests have a sensitivity of 30% for subclinical animals and a detection window of 2 to 3 days prior to the onset of infectiousness, the predicted eradication time is 53 days, with 93% of the herd's cattle infected, representing a moderate advantage over a total depopulation strategy. However, the results of this study are limited by the parameter uncertainty, and the findings should be interpreted with caution. Furthermore, the model is limited to intra-herd transmission and does not assess the risk of transmission to other herds. Future studies will integrate these results into an inter-herd transmission model to evaluate the consequences of a selective culling strategy on the risks of contamination of other herds.

The HPAI Modelling Challenge: A global initiative to improve animal health epidemic preparedness and response

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Highly pathogenic avian influenza continues to pose a major challenge to animal health authorities, due both to its epidemiological complexity as well as the limited availability of validated modelling frameworks that are ready to be deployed during outbreaks. While a wide range of mathematical and statistical methods exist to analyse epidemic dynamics, the models employing these methods can differ substantially in their underlying transmission and control assumptions. Such structural differences can result in mixed or conflicting policy guidance, further complicating the decision process. To strengthen modelling preparedness and to support evidence-based decision-making, we organised the HPAI Modelling Challenge ("the Challenge")—an international collaborative modelling exercise designed to broaden the range of HPAI models while fostering transparency and cross-team exchange. The Challenge is built around a single synthetic fully-reproducible epidemic scenario, generated in-silico, simulating HPAI-like spread across a heterogenous multispecies poultry population of over 9000 farms and five production types, with explicit surveillance and control mechanisms. Epidemic scenarios, contextual datasets (i.e. population, farm activity, animal movements, outbreaks, and preventive culls), and policy-oriented questions were released to participating teams over three phases aligned with epidemic onset, peak, and resolution in pseudo-real-time. Spanning five continents, 46 modelling teams participated with 26 completing at least one phase and providing model-based recommendations on different management approaches. As teams were unconstrained in their methodologies, a diverse array of approaches was observed. These outputs were then used to construct ensemble predictions of forecasts and scenario projections, and evaluate the performance of different approaches. Here we discuss the motivation and development of the Challenge, present preliminary ensemble analyses, and discuss lessons learnt in running such an event that contributes to improved global preparedness for emerging health threats.

The Trojan Boar: modelling vaccine-derived ASF emergence under discontinuous live attenuated vaccination campaigns in wild boar

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Live attenuated vaccines represent one of the most promising control strategies for African swine fever (ASF) in wild boar populations, given the absence of effective commercial alternatives. However, their deployment may entail an underexplored risk: the progressive evolution of the attenuated strain through transmission and mutation, potentially giving rise to vaccine-derived viral lineages. We investigate this process using SWIFCO, an individual-based spatio-temporal model of ASF dynamics in wild boar. The model explicitly represents strain evolution along a reversion continuum, in which the vaccine strain accumulates mutations across transmission events, progressively restoring pathogenic properties, and incorporates discontinuous vaccination campaigns with varying coverage and duration. We analyze how mutation accumulation, transmission dynamics, and vaccination protocols interact to shape epidemiological outcomes, including persistence, spatial spread, and the emergence of virulent strains. Our results show that the attenuated vaccine strain can progressively evolve along transmission chains and, eventually result in strains with restored virulence. These vaccine-derived lineages co-exist with the original strain in the population. Rather than leading to immediate large-scale outbreaks, this mechanism sustains a repeated, transient circulation of the evolved strains. The silent persistence emerges as a direct consequence of the vaccination protocol. In particular, coverage and campaign duration jointly determine the opportunities for mutation accumulation and transmission renewal, thereby structuring long-term epidemiological dynamics.

Timing matters: modelling the interplay among maternally derived antibodies, prevalence of infection and pcv2 vaccination in swine

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Introduction and Objectives Porcine circovirus 2 (PCV2) continues to represent a major endemic challenge for pig production worldwide. Although vaccination of piglets is routinely applied, vaccine performance may vary depending on the level of maternally derived antibodies (MDA) and the timing at which pigs become naturally infected. The objective of this study was to develop a modelling framework to assess how MDA levels and infection pressure influence PCV2 transmission dynamics, and to determine the most suitable vaccination timing under different epidemiological scenarios. Materials and Methods A stochastic individual-based model was implemented in the EMULSION framework to reproduce a single production batch in a farrow-to-finish system. The model incorporated horizontal PCV2 transmission, age-related MDA waning, vaccine-induced humoral immunity, and disease outcomes, including PCV2 subclinical infection (PCV2-SI) and PCV2 systemic disease (PCV2-SD), together with their impact on growth performance. Four MDA distributions at weaning, classified as low, medium, high and very high, were combined with three PCV2 prevalence levels at nursery entry: 1%, 5% and 10%. These conditions were evaluated under six intervention strategies: no vaccination (NV) and vaccination at 14, 21, 28, 35 or 42 days of age. Overall, 72 epidemiological scenarios were simulated, with ten stochastic replicates per scenario. Model parameters were derived from published literature. The main outputs included PCV2-SI and PCV2-SD prevalence, viraemia dynamics, growth performance and economic indicators. Results and Discussion In the absence of vaccination, higher MDA levels postponed the onset of PCV2 infection, while greater PCV2 prevalence at weaning led to earlier viral circulation. The effectiveness of vaccination was markedly dependent on the MDA profile. In scenarios with low, medium or high MDA levels, vaccination at 14–21 days of age provided the greatest benefit, minimizing PCV2-SI occurrence and optimizing growth performance. Under these conditions, PCV2-SI and PCV2-SD were reduced by up to 94% and 97%, respectively. Conversely, when MDA levels were very high, later vaccination between 28 and 42 days of age was required to reduce potential immune interference. Across simulated scenarios, NV pigs showed an approximate 5 kg reduction in final body weight, whereas optimal vaccination improved economic margin by 0.05–0.10 €/kg live weight. Conclusion This modelling approach offers a useful framework to guide evidence-based decisions on PCV2 vaccination timing. The combined use of serological information, particularly MDA levels, and virological data, such as PCV2 prevalence at weaning, may support the design of vaccination strategies adapted to the epidemiological context of each farm.

Posters

Agent-based modelling to investigate the impact of herd structure and preventive measures on Porcine Reproductive and Respiratory Syndrome transmission dynamics

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Porcine Reproductive and Respiratory Syndrome virus (PRRSV) is a viral enzootic disease of primary economic importance for the swine industry worldwide. Understanding within-herd PRRSV dynamics opens up a wide range of challenges, reflecting the epidemiological complexity of infection control at the farm level. Vertical transmission can result in heterogeneous infectious statuses among piglets at birth, while sow immunization through vaccination clearly helps reduce clinical signs and likely slows down virus transmission among breeding animals. However, transmission still occurs and could be a pivotal factor in persistence at the herd level. Meanwhile, newborn piglets acquire maternally derived antibodies through colostrum intake, which may delay infection dynamics at the batch level and paradoxically favour transmission between batches when vaccinated. Airborne transmission remains uncertain for PRRSV-1 circulation in Europe, although it is well documented for PRRSV-2 strains in North America. Altogether, modelling these processes relies on an accurate representation of demographic dynamics, the structure of batch-rearing systems and robust epidemiological parameterisation. Recent developments in agent-based modelling allowed for detailed representations of intensive production systems where herd organisation and batch-rearing systems play a central role in shaping contact patterns and, consequently, virus spread. This approach offers valuable insights into the conditions under which PRRSV can persist within herds. The objective of this study was to assess the impact of herd structure on PRRSV transmission by comparing batch-rearing systems representative of French pig production. We also evaluated the effectiveness of preventive measures, with a particular focus on vaccination. To this end, we developed an agent-based, stochastic, discrete-time model using the EMULSION framework, which facilitates model design, the representation of contrasting organisation settings and effective communication among collaborators. The model explicitly represents individual animals and their interactions while capturing herd-level processes. Key attributes, such as animal category, health state, physiological stage, gestating and vaccination status, were dynamically tracked throughout the simulations. This modelling framework provides a robust tool to investigate how batch-rearing organisation and preventive strategies shape PRRSV transmission dynamics and to support the design of tailored control strategies for farrow-to-finish herds.

Analyzing the impact of control measures on the transmission patterns of African swine fever within commercial swine farms

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African swine fever (ASF) is a highly contagious disease and a major threat to the U.S. swine industry. Despite progress in modeling ASF transmission dynamics, it remains necessary to determine which control interventions could contain or eradicate the virus in commercial swine barns. We created a dynamic transmission model that simulates the spread of ASF within pens, barns, farms, and pixels using population and movement data from 18,000 barns across the U.S. We estimated the number of pig depopulation units (CO2 trailer chambers) required for scenarios involving either whole-farm depopulation or depopulation of only infected barns or pens. The simulated outputs for different depopulation scenarios were benchmarked by: 1) reduction in the number of infected animals, and 2) fewer pens exposed to the virus. We also tested preventive vaccination before the epidemic began and reactive vaccination after the premises became infected to measure the effect of vaccination on the spread of infection. Our model accounted for different levels of vaccine efficacy and trailer capacities. Our results showed that increasing the number of trailers used for depopulation by 10 reduced the number of infected farms by 0% (IQR: 0%-9%). Compared to having no control measures, all depopulation strategies reduced the number of infected animals by at least 50% with adequate trailer availability. Farm depopulation was the most effective (95% reduction; IQR: 78%–99%), followed by barn-level (92%; IQR: 63%-97%), neighboring pens (90%; IQR: 51%-93%), and individual pen depopulation (91%; IQR: 52%-96%). Preventive vaccination with 90% efficacy reduced the number of infected animals by 45% (IQR: 42%-67%), and reactive vaccination reduced them by 4% (IQR: 2%-6%). While preventive vaccination provides a foundational layer of defense, depopulation of infected animals, even at the pen level, remains the most significant factor in limiting the disease spread between farms.

Bayesian frameworks for Bovine Viral Diarrhoea targeted surveillance

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In the absence of a gold standard test, traditional Bayesian frameworks for assessment of diagnostic performance use test results based on cut-offs (+ve/-ve). By utilizing all the information captured in test results without the need to translate them into binary outcomes, we furthered that approach. Building on bulk-milk test results from three European countries with varying Bovine Viral Diarrhoea (BVD) prevalence, Sweden, France and UK, our Bayesian mixture model allowed us to derive revised estimates of distributions for multiple parameters. Not only did we estimate diagnostic performance (Sensitivity and Specificity) but also per country prevalence, test correlation and data distribution parameters. Importantly, by extending our Bayesian framework we also derived farm-level probability of exposure to BVD virus based on actual test results and prevalence values. The latter tangible outcome of our approach has definite potential to be used for targeted surveillance. For instance, a farm-level probability of exposure dashboard based on bulk-milk diagnostic results could be deployed to identify herds with high probability of exposure and values close to the cut-off, which would have been otherwise classified as negative by traditional methods. Given the significant reproductive and productive losses of this widespread, highly contagious and persistent livestock disease, we recommend exploring the potential of enhanced Bayesian frameworks to revise and tailor BVD surveillance efforts to their specific context.

Branching Process Models of Sub-Critical FMD Transmission: Inference, Control, and Surveillance Design in Karnataka, India

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Effective control of livestock diseases often produces a sub-critical phase – outbreaks occur but die out before becoming epidemic – in which standard epidemic models are poorly suited to characterising transmission dynamics. Foot-and-Mouth Disease (FMD) in India offers a clear example: national control programs have been in place and intensifying since 2012, yet the disease persists across multiple states, including Karnataka. Branching processes are a natural framework for this disease regime, capturing the stochastic extinction dynamics that define sub-critical spread. We fit a branching process model to FMD outbreak data from Karnataka, using the offspring distribution to characterise how transmission intensity and individual-level variation have changed under successive control policies. Our best-fit model implies substantially smaller outbreak sizes and reduced variance in transmission compared to the pre-control period, consistent with a population-level reduction in R below 1. We further apply this model to derive the minimally-sufficient surveillance effort required to detect transient outbreaks before fade-out, with implications for establishing eradication and designing post-control monitoring programs.

Comparing Between-Farm HPAI Transmission Kernels Across Epidemics in France

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Introduction: Highly pathogenic avian influenza (HPAI) has caused repeated epidemics in France since 2020, particularly affecting duck production systems. Outbreak numbers have decreased since the introduction of a nationwide duck vaccination program, but infections in vaccinated flocks still occur. Spatial mechanistic models of HPAI spread are useful for estimating between-farm transmission risk and exploring alternative control strategies, but it remains unclear whether risk estimates from one subtype-year can be generalised to another. Our aim was to fit an existing spatial kernel model to estimate and compare between-farm transmission risk during the 2020–2021 H5N8 and 2021–2022 H5N1 epidemics. Methods: We first created a comprehensive georeferenced national poultry population dataset for all farms that were active during that period. This dataset was built by harmonising imperfect population records with outbreak line lists, culling records, daily movement data and records indicating which establishments were operational during each epidemic year. We reconstructed infectious periods for each outbreak farm while accounting for detection method. Currently we are estimating transmission kernels for the 2020–2021 epidemic using three candidate models: a basic distance-only model, a partial model, and a full model including distance, relative infectiousness and susceptibility by poultry type, and farm-size effects. Model selection will be performed using AIC. Estimated parameters will be compared to those obtained from an existing model fitted to the 2021–2022 H5N1 epidemic. Results: Expected results include the selection of the best fitting model for the H5N8 epidemic. We will compare relative infectivity and susceptibility parameters of different species-production types across epidemics. Similar parameter estimates would suggest that between-farm transmission risk is primarily driven by host and spatial factors rather than virus subtype, whereas differences would indicate subtype-specific transmission dynamics requiring distinct parameterisation. Conclusion: This research will show how comparative spatial kernel modelling can be used to assess whether HPAI transmission risk estimates are robust across subtype-years. The results will inform whether a single parameterisation can be applied across subtype-years or whether epidemic-specific models are required for risk assessment and scenario modelling. Future work will build on these fitted models to explore counterfactual scenarios, including species-targeted vaccination strategies.

Comparing epidemics and cost-benefits of control measures for salmonid diseases using network modelling

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Infectious diseases pose a significant challenge to aquaculture systems, where high connectivity between aquaculture sites can enable the rapid spread of pathogens. The effectiveness and economic impact of control strategies such as contact tracing, culling and fallowing depend on disease-specific transmission dynamics and the connectivity of the site at which infection is introduced. Understanding how pathogen biology influences epidemic behaviour within aquaculture networks is therefore critical for proportionate and effective disease preparedness. Here, a network-based epidemiological modelling framework, called AquaNet-Mod, was used to compare the epidemiological and economic impacts of two major salmonid viral diseases, infectious hematopoietic necrosis (IHN) and viral haemorrhagic septicaemia (VHS) under different control scenarios. Simulations were conducted representing transmission through river connectivity and live fish movements across salmonid farms and fisheries in England and Wales. Model parameterisation was informed by literature review and expert elicitation, incorporating disease-specific characteristics such as seasonality and environmental persistence. Epidemic size, duration and economic cost were compared under baseline and alternative control strategies. Both random and deterministic infection seeding approaches were used to compare average epidemic outcomes with those arising from high-risk introduction sites. Results indicate that IHN outbreaks are consistently larger and more costly than VHS outbreaks within the same network, with average total costs approximately 26% higher under baseline controls. Current interventions were effective for both diseases, substantially reducing epidemic size and duration. High-risk sites of initial infection resulted in larger and longer epidemics, demonstrating the importance of the index case on the epidemic's outcome. Overall, this study highlights how pathogen-specific characteristics shape epidemic outcomes and influence the effectiveness of control strategies. The findings demonstrate the value of network-based modelling for supporting evidence-based decision-making in animal health, particularly for tailoring disease preparedness and optimising resource allocation across different epidemiological contexts.

Decoding the spread: Ecological clustering and metapopulation modelling to better understanding HPAI risk

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Background. Due to the complex migration, rapid turnover, and multi-species interactions of wild birds, HPAI have been showing a heterogenous spread across boarders. We combined ecological, epidemiological, and geographic information to reconstruct the dynamics of disease spread in wild bird populations. Methods. We synthesised open-source data from WOAH-WAHIS (43 regions, 263 species) and GBIF appearance records. Using multiple correspondence analysis (MCA) and hierarchical clustering on 154 species which were kept after matching two databases, we categorised birds by migration directions, habitat, taxonomy, and abundance. Next, we aggregated all bird populations and developed a deterministic spatially explicit metapopulation ODE model across 43 connected patches, with susceptible-infected-recovered (SIR) compartments in each patch and coupling through an adjacency-based contact network. Transmission is represented as both local within-patch infection and between-patch spillover, while a time-varying migration-risk multiplier monitor transmission intensity seasonally for each patch. Patch-specific initialization takes into account bird abundance and WAHIS-reported case totals over the year, and demographic turnover and disease mortality are explicitly included to capture rapid population renewal in wild bird systems. Simulations were solved with deSolve (lsoda) under daily time steps to evaluate short-term epidemic trajectories under heterogeneous movements. Results. Clustering identified six distinct species categories (with four outliers excluded), providing the demographic basis for a local point-process model under development. The metapopulation model reproduces hidden HPAI circulation over one month, demonstrating how ecological connectivity enabled transboundary spread even during periods of low local prevalence. This framework identifies critical spatiotemporal windows for HPAI transmission, providing a robust tool for risk-informed surveillance and the integration of movement ecology into wildlife disease forecasting.

Discrete-time survival analysis of risk factors for recurrent bovine tuberculosis outbreaks in Irish cattle herds

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Bovine tuberculosis (bTB) incidence has risen among Irish cattle in recent years, with recurrent outbreaks being a major obstacle in controlling the disease. Recurrence reflects a mixture of residual infection and re-infection, influenced by herd-level factors such as management practices and biosecurity. Previous studies have examined risk factors for recurrent bTB outbreaks using either fixed-horizon logistic regression or continuous-time survival analysis. However, fixed-horizon approaches do not account for variations in follow-up testing, while continuous-time survival models may not align with the discrete testing process through which bTB outbreaks are detected. In this study, we investigated the risk factors for recurrent bTB outbreaks in 26,737 Irish cattle herds with at least one recorded outbreak that derestricted between 2012 and 2023. We used a Bayesian discrete-time survival model, implemented as a mixed-effects complementary log-log regression, to model recurrence across successive follow-up whole-herd skin tests. The model identified increased recurrence hazard associated with herd size, inward movement, neighbourhood infection pressure, and previous outbreak history, consistent with existing findings. It also characterised how recurrence hazard changed over repeated negative whole-herd skin tests: compared with the first follow-up test, the hazard declined substantially at the second follow-up test (hazard ratio [HR] 0.75; 95% credible interval [CrI]: 0.71-0.78) and again at the fourth follow-up test (HR 0.60; 95% CrI: 0.57-0.64). Allowing time-varying effects further showed that the contribution of some risk factors can change across follow-up testing. Persistent outbreak history was associated with higher risk at the first follow-up test (HR 1.47; 95% CrI: 1.27-1.68), but this association weakened by the fourth follow-up test (HR 1.18; 95% CrI: 0.95-1.48). Receiving gamma interferon (GIF) testing was associated with lower recurrence hazard at the first follow-up test (HR 0.88; 95% CrI: 0.77-1.00), but the association shifted towards higher hazard by the fourth follow-up test (HR 1.16; 95% CrI: 0.97-1.37), showing both the possible protective effect of GIF testing and its preferential application on higher-risk herds. Overall, a discrete-time survival model gives interpretable hazard ratios comparable to continuous-time survival models while more closely matching the discrete, test-based data-generating process. The approach provides a more detailed picture of how bTB recurrence risk evolves during post-outbreak surveillance in Ireland, and it may be adaptable to other diseases involving discrete, uneven follow-up processes.

Do epidemiological data combined with whole genome sequencing data allow for the reconstruction of the transmission history of the SB0999 genotype of Mycobacterium bovis in south-western France?

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Bovine Tuberculosis (bTB) is a chronic disease caused by Mycobacterium bovis which can infect various hosts species, including cattle among domestic species as well as badgers and wild boar among wild species. BTB can be transmitted from one farm to another through various routes, such as cattle trade, contacts on pastures, or via wildlife. Our aim was to study how epidemiological data and whole genome sequencing of M. bovis strains can be used to reconstruct the transmission history of the SB0999 genotype, which has been detected in southwestern France. To this end, we used various types of data to identify epidemiological links between farms and construct contact networks with herds as nodes. We used the national database of identification to trace the movements of cattle present on an infected farm between the date of confirmation of infection and nine years before. We looked into the national land registry to identify farms having neighboring pastures to infected farms. We used indicators of badger presence, developed in a previous study and based on spatial and vegetation data, to analyze the role of wildlife in disease transmission. In addition, we defined intermediate farms as farms that were not identified as infected but may have played a role in disease transmission by having epidemiological links (movement, pasture, or wildlife) with infected farms. For these intermediate farms, we defined different levels based on their proximity to infected farms: level 0 farms are in direct contact with infected farms, level 1 farms are in direct contact with level 0 farms, and so on. All these links were used to construct a directed and temporal network. Besides epidemiological data represented by this network, we used whole genome sequences provided by the national reference laboratory. SNPs allowed us to construct a phylogenetic tree using BEAST2 and to calculate pairwise evolutionary distances. The last step in this study will involve combining evolutionary distances and the contact network to construct a transmission tree that will provide a better understanding of the transmission dynamics of the SB0999 genotype of M. bovis. The next stage of this project will be to extend this methodology to the other genotypes identified in France.

Ecological and structural determinants of avian influenza virus diversity in live bird market trade networks in Cambodia

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In Southeast Asia, where avian influenza viruses (AIVs) are endemic, live bird markets (LBMs) have been identified as key settings that facilitate viral circulation and persistence. In Cambodia, previous studies revealed the co-circulation of multiple AIV subtypes across and within LBMs, as well as co-infections within individual bird hosts, creating opportunities for viral reassortment and emergence of new strains. However, these patterns likely emerge from the combined effects of multiple interrelated factors rather than isolated. The objective of this study is to disentangle the ecological and structural determinants of AIV diversity within a complex LBM trade network in Cambodia. In 2025, a cross-sectional study was conducted across 188 poultry premises in 8 provinces of Cambodia. A total of 12,502 samples were collected and 346 questionnaires were conducted, exploring poultry management practices, biosecurity, and poultry trade. Samples were tested by RT-PCR and sequenced. Premises typology was first identified using multivariate and clustering analyses. Combined with the AIV infection status of each premises and by using generalized linear models, the types that are the most at risk were identified. Then, to further identify specific practices associated with AIV subtype circulation, co-circulation and co-infection, Additive Bayesian Networks (ABN) were used to explore the network of relationships between all the variables. The results show that three main poultry premises types were identified (LBMs, slaughterhouses and farms), each with specific characteristics. Viral detection was the highest in slaughterhouses (85%, 61/71) and LBMs (73%, 19/26), characterized by high poultry turnover, slaughtering and multiple species, compared to farms (13%, 12/91). Among positive premises, 47% (43/92) exhibited co-circulation of at least two subtypes, mostly LBMs and slaughterhouses, and 63% (27/43) included at least one co-infected bird. Results also reveal that slaughtering, overnight storage and mixing different poultry species are significantly associated with AIV detection, which is consecutively associated with co-circulation of multiple strains, and co-infection in some birds. Overall, this cross-sectional study shows that AIV diversity is shaped by a combination of interdependent practices and structural features, providing a more comprehensive understanding of viral ecology and supporting the design and implementation of integrated interventions to reduce viral circulation and emergence.

Effect of host-antibodies on arboviral transmission

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Antibodies produced by birds infected with WNV can prevent subsequent infections. However, breakthrough infections do occur. How much these infections contribute to onward transmission is unknown. To address this knowledge gap, we investigated the effect of preexisting antibodies on transmission from host to mosquito, as well as on dissemination within the mosquito. We performed a series of membrane feeding experiments, using bloodmeals with controlled levels of virus and antibodies, to evaluate the effect of preexisting antibodies on host infectiousness. The resulting dose-response curves showed a clear significant relation between viral dose (TCID50) and infection probability. Notably, the curves show that mosquitos can already get infected at lower viral titers than commonly assumed. We also found a significant positive effect of dose on the proportion of mosquitos becoming infectious. This could be explained by a dose dependent duration of the extrinsic incubation period (EIP). We found no additional inhibitory effect of unbound antibodies on mosquito infection once ingested, indicating the concentration of infectious virus is the primary driver of host infectiousness. Collectively, this work gains valuable insight on host infectiousness, how this relates to different measures of viremia and the relation between viral load and EIP. These findings will help improve the reliability of epidemiological models for arboviruses.

Estimating the relative risk of HPAI presence in wild birds and spillover to commercial poultry farms in Norway: a spatiotemporal risk mapping approach

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Highly pathogenic avian influenza (HPAI) poses an increasing threat to commercial poultry production across Europe. In Norway, six outbreaks in commercial flocks have been recorded since 2021, most in the poultry-dense region of Rogaland county. Despite increased surveillance activities, Norway currently lacks quantitative spatial estimates of HPAI introduction risk to commercial poultry. This study aims to produce a high-resolution, season-specific relative risk map of HPAI presence in wild birds and subsequent spillover risk to commercial poultry farms in Norway. Risk factors were identified through a scoping literature review and assessed for relevance to the Norwegian context in consultation with specialist veterinarians and international collaborators. Risk factor weights were derived using the Best-Worst Method (BWM), a structured expert elicitation approach that enables efficient and consistent pairwise comparisons. Spatial risk layers were constructed at 5x5 km resolution across mainland Norway, including composite seasonal abundance of wild waterfowl and seabirds (based on citizen science data), CORINE land cover classes, human population density, poultry farm and bird density, and historical HPAI detection data. Layers were combined as a weighted mean, producing risk maps for winter, spring, summer, and autumn. Sensitivity to weight uncertainty was assessed through a weight-perturbation approach, and maps were validated against historical HPAI confirmations in wild birds and the locations of the commercial farm outbreaks. The seasonal framework captures the shifting distribution of reservoir host species across Norway's broad latitudinal range. The resulting maps provide a decision-support tool for targeted surveillance prioritisation and biosecurity interventions, and demonstrate how expert-weighted spatial models can be applied in data-limited settings where outbreak frequency is insufficient for purely statistical approaches.

Estimating the sampling and laboratory testing requirements for the transmission of African swine fever within US commercial swine barns

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African swine fever (ASF) remains a formidable threat to the US swine industry due to its high contagion and the potential for economic devastation. Although advances in modeling transmission dynamics have been significant, quantifying the exact sampling and diagnostic requirements for efficient surveillance and containment remains a critical gap. We developed a multi-scale dynamic transmission model to simulate ASF propagation across pens, barns, individual premises, and geographic pixels. Our model accounted for complex transmission pathways, including: 1) within-pen and between-pen fecal and aerosol transmission, 2) pig and truck movement, 3) human mediated transmission between barns, and 4) inter-pixel airborne dispersal. To evaluate diagnostic performance, we integrated data from 52 facilities in the National Animal Health Laboratory Network (NAHLN) into our model. We estimated: 1) the ideal number of sample collectors for 10,000 breeding and growing commercial swine farms in the US, 2) the number of samples needed to be diverted to other laboratories when laboratory capacity is exceeded, and 3) the amount of materials needed for sampling during 100-day epidemics. Our results showed that a total of 14 sample collectors (99% CI: 0-1,143) was sufficient to perform sampling without delays across all scenarios. North Carolina exhibited the highest diagnostic demand, processing 35,185 samples in the worst-case scenario. The state required the most significant redistribution of resources, with 23% of simulations exceeding local laboratory processing capacity, and 20,121 samples being diverted to out-of-state facilities in the worst-case scenario. Finisher farms necessitated the highest daily resource allocation with a median of 5 (99% CI: 1–184) collectors, followed by nursery farms (4 collectors, 99% CI: 1–44) and sow farms (2 collectors, 99% CI: 1–44). The total number of needles and tubes used for sampling reached a median of 59,753 units (99% CI: 14,880–417,806) by the conclusion of the 100-day outbreak. These results underscore the critical need for robust logistical planning and scalable diagnostics. Our findings provide a data-driven framework for stakeholders to ensure that sampling and testing infrastructure can maintain pace with viral transmission, thereby facilitating timely detection and effective containment.

FAO's Risk Monitor: Early Warning System to Reduce Food Security Impacts

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In 2025, the Food and Agriculture Organization of the United Nations launched the Risk Monitor, a new early warning system aimed at addressing food insecurity risks. Designed to empower anticipatory action, rapid-response financing, and potentially, insurance payouts, to mitigate the impact of acute food insecurity, the FAO Risk Monitor platform combines live data, expert analysis, and automated alerts to help decision-makers detect risks early and respond before they escalate. The tool tracks a wide range of risks that are known to drive food insecurity, from natural hazards like droughts, floods, tropical cyclones, and heatwaves, to human-made threats such as conflict and political instability. The data powering the Risk Monitor comes from a wide range of trusted sources, including FAO, other international organizations such as the World Bank, academic institutions like the Peace Research Institute Oslo (PRIO) and Uppsala Conflict Data Program (UCDP), and private-sector partners such as Raincoat. A robust data engineering pipeline ensures the accuracy, timeliness, and completeness of the information, providing a solid foundation for early warning and response. FAO is now working to better incorporate pest and disease events, as well as their early warning systems and forecasts into the system. This effort has highlighted challenges and opportunities in advancing the application of animal health models to support anticipatory action and reduce food insecurity. This talk will present the work that FAO has done to develop the Risk Monitor, including advances in reference data services and pipelines, while highlighting areas where more collaboration with the animal health modeling community would be beneficial, particularly as the Risk Monitor continues to evolve.

Genetic parameter estimation for susceptibility to Mycobacterium avium subsp. paratuberculosis (MAP) under simulated dairy herd transmission

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Introduction Paratuberculosis (Johne's disease), caused by Mycobacterium avium subspecies paratuberculosis (MAP), remains a persistent challenge in dairy production. Selective breeding for reduced susceptibility has been proposed as a promising control strategy. However, accurately estimating and evaluating the genetic parameters of susceptibility remains challenging because key components of the transmission process, particularly exposure level and time of infection, are not directly observable in field data. Methods In this study, we developed a stochastic agent-based transmission model incorporating simulated host genomes and MAP transmission within a commercial dairy herd system. Observations were generated by sampling the simulated herds under different testing frequencies (annual, seasonal, and monthly), from which infection histories and environmental exposure were reconstructed. These infection outcomes and reconstructed exposures, together with pedigree and genotype information, were analyzed using a generalized linear mixed model (GLMM), a linear mixed model (LMM) and an extended LMM including exposure as a covariate. For each model, both animal and sire models were fitted using pedigree-based (ABLUP) and genomic-based (GBLUP) relationship matrices. These analyzes provided estimates of genetic variance, transmission-related parameters, and estimated breeding values (EBVs) for log-susceptibility. The objective was to simulate MAP transmission in a realistic herd setting and assess to what extent underlying genetic variation in log-susceptibility can be recovered from imperfect field data under different surveillance scenarios. Results Results showed relatively high prediction accuracies for EBVs for the susceptibility trait. Cow accuracies ranged from 0.35–0.45 using ABLUP and 0.55–0.65 using GBLUP, while sire accuracies were substantially higher (0.80–0.90). The GLMM achieved slightly higher accuracies than LMM-based approaches (i.e., 0.45 vs. 0.38–0.40 for cows under monthly testing with ABLUP). Testing frequency (monthly, seasonal, annual) had only a minor effect on prediction accuracy, but more strongly affected estimation of genetic variance and transmission-related parameters. Animal and sire models showed comparable performance. Overall, we developed an innovative approach that incorporates genetic heterogeneity into transmission models and compared six genetic statistical models across three testing frequencies for evaluating the infectious disease related trait. Among all tested models, the main benefit of the GLMM is that it provides epidemiologically interpretable estimates of genetic variance and breeding values, making them meaningful for predicting response to selection.

How mechanistic modelling of intra-vector viral dynamics can help explore arbovirus transmission across scales

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Arboviruses, transmitted between vertebrate hosts through the bite of arthropod vectors, are expanding worldwide, making them a threat to both public and animal health. In this context, epidemiological modelling is an important tool to better understand the transmission mechanisms of these arboviruses and to guide surveillance and control strategies. Among the key components of vector-borne transmission models is the extrinsic incubation period (EIP), which is directly linked to intra-vector viral infection dynamics (IVD). This important step in arbovirus transmission is rarely represented explicitly in vector-borne transmission models. The objective of this work is to study, through a modelling approach, the variability of IVD in human and zoonotic arboviruses and its impact on vector-borne transmission at the population level. To address this, we use a mechanistic modelling framework of intra-vector viral dynamics as a central tool to (i) characterize within-vector variability and its underlying mechanisms, (ii) quantify its impact on population-level transmission, and (iii) inform the design of vector competence experiments. The development of this generic compartmental model of IVD, combined with data driven inference from vector competence experiments, enabled the characterization of variability in IVD for chikungunya virus (CHIKV), dengue virus (DENV), Zika virus (ZIKV), West Nile virus (WNV), and Rift Valley fever virus (RVFV). This challenged the common assumption that the EIP follows an exponential distribution suggesting that more flexible distributions, notably the beta distribution, better capture the observed dynamics. The introduction of a mechanism allowing exit from the infectious state made it possible to question the assumption of a persistent infectious state, under certain experimental conditions for CHIKV. Coupling the IVD model with a DENV transmission model allowed us to assess the impact of the EIP distribution on epidemic dynamics in humans. This mainly affects the timing and intensity of epidemics, with later, lower, and slightly longer-lasting peaks when the distribution is informed by experimental data rather than assumed to be exponential. The impact of this distribution varies depending on the epidemiological context. The analysis of the inference quality of the IVD model also enabled the exploration of its use to guide the choice of the number and timing of observation points in vector competence experiments. Overall, this work illustrates how modelling intra-vector viral dynamics can contribute to a better understanding of arbovirus transmission across scales.

Long-term and short-term causes of West Nile virus circulation in Europe: a spatiotemporal model accounting for under-reporting

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Background. West Nile virus (WNV) is a vector-borne pathogen transmitted between reservoir birds and Culex mosquitoes. It can also affect mammals such as horses and humans, where infection may result in "dengue-like" symptoms or, more rarely, in potentially lethal neurological symptoms. It is important to understand the virus' spatial distribution, despite infections being often missed by the human and animal health surveillance systems. Here, we had the objectives to map WNV occurrence in the bird reservoir across Europe, while accounting for cases under-reporting, and to assess the relative impact on it of both long-term (structural) and short-term (conjectural) drivers. Methods. We collated data on WNV human cases notified to ECDC (European Centre for Disease Prevention and Control) and on WNV equine cases notified to WAHIS (World Animal Health Information System), between 2010 and 2024, aggregated at the month and European NUTS region scales. We built an occupancy model with (i) a "Reservoir" component, quantifying the probability of WNV (unobserved) circulation in the bird reservoir, and (ii) a "Reporting" component representing the probability of human or equine case reporting, given reservoir circulation. We proposed a Directed Acyclic Graph to determine "Reservoir" predictors, including monthly weather variables (absolute temperatures and anomalies in temperature and in the Modified Normalized Difference Water Index, MNDWI), a structural variable related to the landscape's suitability to reservoir birds (Bird Risk Index, BRI), and spatial (Besag-York-Mollie 2) and temporal (random walk) autocorrelation terms. We ran two versions of the model, depending on the cases data, either human or equine, used in the “Reporting” component. Results. The effects found for some conjectural weather variables (including the temperature anomaly on month m-2) on WNV occurrence in the bird reservoir were consistent in both models. For other variables, including the BRI, the effect depended on the model. This may reflect that host jump conditions are different between wild birds and horses than between wild birds and humans. Given WNV circulation in the reservoir, we estimated the subsequent reporting of human cases to be higher in more populated and less urban regions. These variables likely reflect the level of human exposure to mosquitoes that bit birds. We also found the reporting of equine cases to be associated with the equine population in the region, and to depend on the country. Conclusions. In our model, we partitioned the effects of environmental variables on WNV occurrence from its spatiotemporal autocorrelation, and from the effects of socio-economic variables on WNV case reporting. Our results suggest that this virus has the potential to affect most parts of Europe.

Long-term spatial social network analysis of large herbivore species in an African savanna landscape

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Interspecific social networks are an essential part of the structure and functions of many communities and understanding the formation is critical to natural resource management and conservation. These networks can determine how herbivore populations and communities grow, function and respond to environmental changes. Our study draws on five decades of monitoring the 8500 square-kilometre Amboseli ecosystem in southern Kenya, to present a multi-species social network analysis of twenty large herbivores modelled within a 5 by 5 KM grid system. The analysis is implemented using machine learning schemes. The species include wild and domestic herbivores comprising of grazers, browsers and mixed feeders. Herbivores can group for reasons ranging from seasonal resource selectivity based on quality and quantity, to predator avoidance. The results point to interspecies social network connections that are likely to change with increased human influence shaping the ecosystem. The multispecies network model also provides a strong basis for mapping long-term animal characteristics that eventually leads to deeper understanding of species behavior, disease risks and the significance of space and mobility in alleviating the ecological disruption of compressed populations.

Modeling direct cross-transmission of antibiotic-resistant bacteria at the animal–human interface: case studies on pig and chicken production in high and low/middle income countries.

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Scope: Antimicrobial resistance (AMR) is a growing threat to public health. Occupational settings involving close and repeated contact with livestock are of particular concern. While foodborne transmission pathways have been widely studied, the mechanisms governing AMR transmission through direct human–animal contact remain insufficiently understood. It is complex and bidirectional, depending on bacterial species (e.g., airborne, cutaneous, hand-to-mouth transmission) and farming conditions (e.g., biosecurity, contact frequency). Existing work is largely anthropocentric, focusing on humans as the primary recipients of AMR exposure. Contribution: This work proposes a compartmental epidemiological model that explicitly implements a bidirectional AMR transmission between humans and livestock within a One Health framework. The model captures both the occupational AMR acquisition risk of livestock-exposed workers such as farmers and veterinarians, and the potential for spillover back into the animal reservoir, enabling the analysis of feedback dynamics across the human and animal populations. The proposed framework is flexible and can be adapted to different animal systems, bacterial species, and socio-economic contexts (e.g., Low- and Middle-Income Countries (LMICs) and High-Income Countries (HICs)). It allows the comparison of different intervention and biosecurity scenarios, including changes in human-animal contact frequency, infection prevention measures and antimicrobial stewardship policies in both populations. Presentation: This presentation aims to describe the structure and assumptions of the epidemiological model, with particular emphasis on the mechanisms of bidirectional transmission across human and animal compartments. The presentation will demonstrate the application of the model using parameter estimates from the literature on two case studies: livestock associated methicillin-resistant Staphylococcus aureus (MRSA) in pig production systems in a HIC context (e.g., Brittany, France), and extended-spectrum beta-lactamase (ESBL)-producing Escherichia coli in chicken production in a LMIC context (e.g., Vietnam). Results from a global sensitivity analysis will be presented to identify which parameters most strongly drive variability in AMR colonization outcomes, alongside key data gaps highlighted during model parametrization. Funding: This work is financially supported by the French Priority Research Programme on Antimicrobial Resistance (PPR Antibiorésistance), coordinated by Inserm and funded by the Secrétariat général pour l'investissement (SGPI).

Modeling the population dynamics of Culex pipiens and Culex modestus mosquitoes across the rural-urban gradient around Lyon, France, to assess the risk of West Nile and Usutu virus spread

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Mosquitoes of the Culex genus are the main vectors of West Nile and Usutu virus, which represent an emerging threat to human and animal health across Europe. With their opportunistic feeding behavior, Culex mosquitoes act as bridge vectors between birds, horses and humans. Rising temperatures, resulting from climate change, are expanding favorable conditions for these mosquitoes in France and thus increasing the risk of outbreaks beyond historically endemic areas like Camargue. This study aims to model the population dynamics of two key vector species, the ubiquitous Culex pipiens and the understudied Culex modestus, in the Rhône department. We adapted an existing mechanistic, climate-driven compartmental model based on ordinary differential equations. The model is adjusted to the specificities of the Culex genus. It incorporates winter diapause and divides the life cycle into aquatic (eggs, larvae, pupae) and adult female stages (emerging, host-seeking, engorged and ovipositing). Transition and mortality rates within the model are dependant on daily temperatures. The model will be fitted to field captures of adult mosquitoes conducted in and around Lyon through the MASCARA network from 2022 to 2025. Preliminary analyses focus on identifying how environmental conditions differently affect the population dynamics of Cx. pipiens and Cx. modestus. As a ubiquitous species, Cx. pipiens is expected to exhibit high adaptability across diverse habitats. On the other hand, initial capture results suggest that Cx. modestus favors rural over urban environments. To account for these ecological differences, species-specific adjustments are being implemented into the model framework. Additionally, the spatial distribution of local water bodies is expected to play a major role in defining the environmental carrying capacity. This mechanistic approach to the ecology Cx. modestus and Cx. pipiens already provides a robust baseline for future research. While future data collection will allow for continuous model refinement, this framework is already designed to be geographically transposable to other regions of France, such as Loire-Atlantique where mosquito collection is currently being implemented. Ultimately, once coupled with epidemiological models to simulate virus circulation, it could serve as a valuable tool to support public health decision-making and raise awareness about emerging vector-borne diseases.

Modeling the spillover risk of highly pathogenic avian influenza from wild birds to cattle in Denmark

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Since early 2024, highly pathogenic avian influenza virus (HPAIV) H5N1 of clade 2.3.4.4b has spilled over from wild birds to dairy cattle in the United States (U.S.), spreading to more than 1000 herds and threatening both animal and public health. Denmark's location along major migratory flyways and the lack of active HPAIV surveillance in cattle underscore the need to assess potential spillover risk from wild birds to cattle to strengthen preparedness. A quantitative spillover risk assessment model was developed to integrate data from Bird Flu Radar, eBird, and cattle density to estimate the weekly probability of HPAIV introduction from wild birds to cattle. The model was calibrated using observed U.S. spillover data and extrapolated to Denmark under the assumption of a comparable transmission rate parameter. Under the frequency-dependent model, the expected HPAIV introductions to Danish cattle via wild birds remain below 0.35 cases per week, with the highest temporal risk from December to March. High-risk areas were concentrated along the Danish coastline and near the German border. In contrast, applying a density-dependent model shifted the spatial risk toward regions with higher cattle densities, while the high-risk temporal periods remained unchanged. Overall, the results indicate a spatially and temporally variable risk of HPAIV spillover from wild birds to cattle in Denmark. The model establishes a data-driven framework to strengthen early warning and guide targeted surveillance efforts in high-risk regions.

Modelling Dynamic Interspecific Contact Networks at the Wildlife–Livestock Interface in Amboseli Ecosystem,Kenya

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Seasonal drought in the Amboseli ecosystem in Kenya concentrates wildlife and livestock around limited water and grazing resources, increasing interspecific contact and the risk of pathogen spillover. Environmental variability strongly shapes these dynamic, multi-host interactions, yet remains difficult to represent accurately in animal health models. This study develops a spatially explicit modelling framework to simulate interspecific contact networks using Ocelet, a domain-specific language (DSL) for modelling spatial dynamics based on the concept of Interaction Graph. The model focuses on African elephants (Loxodonta africana), wildebeest (Connochaetes taurinus), plains zebras (Equus quagga), and cattle (Bos indicus). It integrates aerial animal census data with remotely sensed environmental variables, including Copernicus Sentinel-2-derived vegetation and surface water indices, 2-m air temperature (ERA5-Land), precipitation (CHIRPS version 3), and human infrastructure, to represent the influence of seasonal landscape dynamics on host movement and interactions. Simulation results identify persistent dry-season hotspots driven by vegetation contraction and aggregation around water points, where network connectivity across species may increase substantially. These areas may represent elevated-risk zones for interactions between domestic and wild animals, with potential for increased transmission of multi-host pathogens under intensified resource competition. The framework captures the temporal evolution of interspecific contact networks and provides a reproducible approach to identify high-risk locations and periods. Its application can support targeted surveillance and management strategies at wildlife–livestock interfaces under environmental change and increasing anthropogenic pressure.

Multiple pathway risk assessment in animal health with R

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Real-world quantitative risk assessment often requires models with multiple transmission pathways, multiple scenarios, and hierarchical data structures. However, existing R tools such as mc2d are built around single pathways with aligned inputs, which hinders their application to more complex scenarios involving multiple transmission pathways, such as disease introduction via live animal movements, animal products, and fomites. These difficulties particularly arise when pathway inputs are indexed at different, non-aligned levels (for example, when the set of countries and species differs across pathways). In practice, analysts may address this by either oversimplifying the model or writing overly complex code, both of which can reduce transparency, validation and communication. To overcome this limitation, we propose mcmodule, an R package that extends mc2d (Pouillot, 2010) to support modular, multi-pathway Monte Carlo risk modelling. mcmodule organises stochastic parameters into metadata-rich modules, where each module is defined by explicit probability-step expressions evaluated using stochastic inputs drawn from data tables. Inputs and outputs carry provenance metadata and data keys (e.g., country, species, commodity, scenario). This design supports safe alignment across mismatched pathway components and consistent aggregation across hierarchical levels. The framework also supports automated node creation from data frames, scenario comparison, interactive risk network visualisation, and diagnostics for convergence, uncertainty decomposition, and sensitivity analysis (including Morris and Sobol' indices). We showcase mcmodule using a sheep pox virus introduction risk assessment for Spain based on small-ruminant import data (2023–2025). The model represents live animal imports and animal products in separate modules, computing risk for each type of import. It aggregates across multiple species, type of products, and countries of origin and compares the risk of introduction under the baseline surveillance with enhanced testing scenarios. Compared with standard mc2d code, mcmodule reduces redundancy by using reusable components that can be developed in parallel and validated independently. Interactive visualisation supports traceability from inputs (e.g., country prevalence) through intermediate steps (e.g., failure to detect infection at border inspection) to the final output, the annual risk of sheep pox virus introduction. Integrated diagnostics identify influential parameters through sensitivity analysis and decompose output uncertainty by input parameters. This package addresses limitations of existing quantitative risk analysis workflows in R and reduces the effort required to build detailed pathogen introduction risk analyses. mcmodule is available on CRAN, with documentation at nataliaciria.github.io/mcmodule.

Obtaining clues on distance-dependent transmission routes by fitting transmission kernels

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Quantifying between-farm transmission kernels is a powerful instrument for reconstructing epidemic spread and assessing the likely impact of control measures in livestock outbreaks. Beyond disease-specific estimates, comparisons across outbreaks can reveal generic spatial patterns in transmission that may be shared across pathogen-host systems [1]. In this presentation, we therefore focus on the spatial transmission kernel as a summary of distance-dependent between-farm spread and examine whether its shape displays universal features, with a special emphasis on Bluetongue outbreaks.Previous analysis of bluetongue virus serotype 8 (BTV-8) transmission in ruminants in Northwestern Europe in 2006–2007 showed that the spatial transmission kernel has a long-tailed form of Lévy-walk-type. In that setting, interventions such as movement bans and zoning appear to shape the kernel in a characteristic and broadly universal manner. More recent kernel estimates for the 2023 BTV-3 epidemic in the Netherlands show a similarly long-distance spatial range, extending over tens of kilometers, and are consistent with the BTV-8 kernel estimates reported earlier [2]. The long-range tail suggests that short-distance midge dispersal alone is insufficient to explain the observed spread, implying that additional mechanisms such as livestock movement likely contributed to transmission.Overall, the comparison between transmission kernels estimated for different epidemics of BTV and other livestock diseases supports the use of transmission-kernel analysis as a generic tool not only for quantifying between-farm transmission, but also for supporting the formation of hypotheses on transmission routes, and for detecting the effect of movements bans and zoning on transmission.
[1]. Gert Jan Boender and Thomas J. Hagenaars. Common features in spatial livestock disease transmission parameters. Scientific Reports (2023) 13:3550. https://doi.org/10.1038/s41598-023-30230-w[2]. Boender, G.-J.; Hagenaars, T.J.; Holwerda, M.; Spierenburg, M.A.H.; van Rijn, P.A.; van der Spek, A.N.; Elbers, A.R.W. Spatial Transmission Characteristics of the Bluetongue Virus Serotype 3 Epidemic in The Netherlands, 2023. Viruses 2024, 16, 625. https://doi.org/10.3390/v16040625

Oh No Phylo: bonding epidemiological and evolutionary research for phylogenetic analysis

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Background: A phylogenetic tree is a graphical representation of the evolutionary relationships between biological entities, usually sequences or species. Phylogenetic trees help us understand species evolution (macro-evolution) and, on a much shorter time scale, molecular evolution in cancer and pathogen transmission (e.g., SARS-CoV-2). Phylodynamics uses phylogenetic trees to characterize the population dynamics of species or pathogens from genetic data. Unfortunately, there is a limited transfer of knowledge between macroevolution and infectious disease epidemiology. This resulted in the separate development of concepts, nomenclature, methods, and algorithms that could nonetheless be applied to multiple problems. Additionally, new methods are often developed for technical or research purposes and may not always be applicable to real data. Methods: All available software packages for analyzing viral genomic data will be put in an overview and their use cases will be investigated. Furthermore, the most important research questions in epidemiological (animal) and evolutionary research are identified, together with the main quantities that can be estimated throught phylogenetic analysis. (Conceptual) Results: We will have a clear overview of the methods and software resources, a list of research questions, and a flowchart to guide researchers on how to start a phylogenetic or phylodynamic analysis and to choose the right tool.

PARAMETRA: a parameter database for livestock disease modelling

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Livestock infectious diseases models support policy and decision-making, but parameterisation is still a challenge for their development. Parameter values are dispersed across heterogeneous sources, reported with inconsistent metadata, and difficult to reuse, which leads to duplicated effort and limits reproducibility. PARAMETRA is an open-source, curated database for animal disease modelling that compiles transmission model parameters and aims to serve as a practical resource for the animal health modelling community. The initial release (Antonopoulos, 2025) was populated through a semi-systematic literature review and includes over 2,000 parameter values for 20 priority livestock pathogens covering: transmission (e.g., R0, transmission coefficients, infection probabilities), infectious, latent and incubation periods, pathogen survival and disinfection efficacy, diagnostic test sensitivity and specificity, prevalences and control plans, and regional biosecurity practices. Each entry links a parameter, pathogen, and reference, with additional information (where available) such as host species, study type and uncertainty bounds. The database is intended as a living resource that will be continuously expanded and updated through community contributions. Ongoing developments include adding a vaccination parameters table and implementing a curation pipeline to support long-term maintenance and alignment with FAIR data principles. PARAMETRA is currently available at https://biosecure-eu.github.io/parametra/ and can be accessed as an Excel workbook, an R package (GitHub), and CSV files for direct import into R or Python. Future work will include a proper online platform for browsing the database. Feedback and contributions (https://ec.europa.eu/eusurvey/runner/parametra-submission) are welcomed to make PARAMETRA a sustainable, useful resource for the animal health modelling community. References Antonopoulos, A., Ciria, N., Regan, Á., Tubay, J., Ciaravino, G., Hayes, B., Lambert, S., Vergne, T., Velkers, F., Biebaut, E., Viltrop, A., Dewulf, J., Charlier, J., Fischer, E., & Palau, A. A. (2025). PARAMETRA: A transmission modelling database for livestock diseases. Preventive Veterinary Medicine, 245, 106668. https://doi.org/10.1016/j.prevetmed.2025.106668

Potential of accelerometer collars as a source of data for syndromic surveillance of emerging infectious diseases in dairy cattle

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Introduction: Precision livestock farming is the collection and analysis of sensor-derived data to improve production and monitor the health and welfare of farm animals. These data are typically collected, analyzed, and interpreted at the level of individual animals or herds. However, such data may also have high potential for population-level surveillance, particularly syndromic surveillance, defined as the monitoring of non-specific indicators or symptoms in real-time or near real-time. Here, we aimed to assess whether behavioural data from accelerometer collars could provide an early warning signal of emerging infectious disease at the population level, using the emergence of bluetongue virus in Brittany in summer 2025 as a case study. Methods: We used behavioural data from accelerometers collars fitted to 16,967 dairy cows on 196 farms in three departments in Brittany, France from 2020-2025. We analyzed two behaviors, as classified by the collars: time spent eating and time spent resting. We first modelled the baseline daily for each of these two behaviors by fitting a linear mixed model with nested random effects for individual cow and farm, thereby accounting for both individual-level variation and farm-level practices. We then compared the recorded time spent eating or resting to the expected time for each cow each day. Individual-level alerts were defined as a day on which recorded time eating or resting time differed significantly from the model prediction, based on the 95% confidence interval. Because some deviations from expectations are expected under baseline conditions, we aggregated these individual alerts into a time series representing the daily proportion of cows with an alert. We then applied the Shewhart algorithm to detect unusual increases in this proportion. Results and Discussion: Our analyses of both behaviors generated alerts in late June, approximately two weeks before the bluetongue virus outbreak was detected in the region. However, for eating the signal was limited to a single day, with an immediate return to baseline levels, suggesting that it should be interpreted with caution. Analysis of the resting produced several groups of signals over consecutive days during the time period although the first signals are earlier than expected for bluetongue virus. The analysis further highlights several limits for the real-world deployment of such technologies on working farms to contribute to the surveillance of emerging infectious diseases.

Predicting Species-Specific Avian Influenza Pathogenesis using Within-Host Modelling

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The clinical severity and infectiousness of avian influenza A virus infection (AIV) varies considerably between bird species. While historically AIV presents as a low severity gastrointestinal infection in water birds, modern agricultural practices have led to seasonal mass epizootics of highly pathogenic AIV in farmed poultry, causing considerable economic loss and threatening spillover into other domesticated livestock species and humans. The species-specific effect of AIV infection is a result of multiple interacting biochemical systems at the host-pathogen interface. For example, different tissues in different species vary in their expression of influenza receptor isomers (sialylated glycans) and in the initial immunogenic response to the presence of AIV. To understand the complex dynamics of AIV infection within-host in different bird species, we will construct stochastic compartmental models to represent the network of interacting biochemical systems and tissue structures that to contribute to disease severity. These models will be parameterised withh Bayesian inference methods using data produced by naïve control animals from vaccination challenge trials, viral biochemical assays and tissue composition experimentation. By using experimental data, we demonstrate that it is possible to replicate disease outcomes and pathologies given a pre-specified host species and AIV subtype to produce an estimation of the likelihood of any given outcome. In the future, these models could be included in a multiscale nested population model, providing a more biologically representative approach to AIV epidemiology, as well as simulating new viral characteristics and biological risk factors at the zoonotic interface.

Proximity sensed social contact networks of white-tailed deer (Odocoileus virginianus) provide insight into disease transmission risks

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Background. Social interactions between white-tailed deer (Odocoileus virginianus) are influenced by demographic, environmental, and human factors. For directly transmitted pathogens, close contact between deer increases the risk of disease transmission but is challenging to quantify. Methods. Contacts between deer in Ontario, Canada (2022-2023) were recorded using proximity devices. The resulting data were used to construct contact networks. We contextualized the networks using genotype data and locations obtained from global positioning system (GPS) radio collars. Results. Deer of all ages, sexes, and relatedness were in direct contact with one another in 2022 and 2023. Approximately 70% of the collared deer in each year were represented in the network. Annual networks contained well-connected clusters with a substantial percentage of the collared deer in the network (2022: 67%; 2023: 92%). Assortativity coefficients, which measure the tendency for individuals to preferentially associate with like individuals, were low for sex (2022: 0.03; 2023: 0.08) and age (2022: 0.03; 2023: 0.03). The networks were largest and most connected in winter and early spring. The proportion of contacts between unrelated deer (2022: 49.15%; 2023: 73.44%) was equal to or greater than related deer (2022: 50.85%; 2023: 26.56%), but the maximum cumulative duration of contact was shorter between unrelated individuals (2022: 8.41; 2023: 6.06 days) than related individuals (2022: 10.62 hours; 2023: 12.80 hours). The location of the contacts aligned with known habitat utilization and migration patterns. Only 2.06% of all contacts occurred within 100 meters of a supplemental feeder provided by local residents of the area. Conclusions. Our results suggest that targeting subgroups of deer populations may fail to control disease transmission should a pathogen be introduced. This is especially applicable to chronic wasting disease (CWD) and bovine tuberculosis (bTB), which can persist for years before being detected. Our study underscores the importance of understanding deer behaviours that influence contact patterns and the associated risk of disease transmission.

Quantifying environmental and epidemiological drivers of African Swine Fever occurrence and persistence across European countries

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Introduction African swine fever (ASF) continues to cause major ecological and economic impacts across Europe, affecting both wild boar and domestic pigs. Occurrence and persistence are driven by direct and carcass-mediated transmission and are influenced by host density, movement, management, and environmental conditions. Climate and human activities further shape host ecology, virus survival, and detection patterns. The European Food Safety Authority emphasizes that ASF transmission patterns are driven by interactions between habitat, climate, and environmental suitability rather than host density alone. Cross-country spatial analyses remain limited. This study's main goal was to quantify environmental and epidemiological drivers of ASF occurrence and persistence across Europe. Materials and Methods A total of 24,171 ASF-positive wild boar cases (2016–2024) from six European countries at 10×10 km resolution were analyzed, considering 2- and 5-year infection periods. Predictors included forest structure, human footprint, wild boar density, and climate variables. ASF occurrence was defined as the proportion of positive PCR tests, while persistence was defined as the proportion of ASF-positive months per spatial unit. Models were fitted using INLA with a logit link. After univariate screening and correlation checks, forward selection (WAIC-guided) was used to identify significant predictors for the response variable. Three models were applied: (1) hierarchical with country random effects and spatial structure (Besag), (2) spatial without country effects, and (3) country-specific spatial models. Results For the occurrence models 1 and 2, the forest proportion and the average temperature were selected as predictors, showing a positive and negative association, respectively, with the proportion of PCR-positive tests. For the persistence model over 2 years, no predictors were retained in models 1–2 or most country analyses. For 5 years, the human footprint index was significant, showing a negative association with persistence (~2.7–3.1% decrease in odds per unit). Model 1 revealed unexplained between-country variation, with higher persistence in Latvia and Slovakia, intermediate in Hungary, and lower in Italy and Lithuania. However, heterogeneous predictors were selected for country-specific models, reflecting the diversity of settings across Europe. For instance, precipitation reduced persistence in Lithuania, while temperature effects varied (negative in Latvia, positive in Slovakia). Conclusion Few consistent predictors of ASF occurrence and persistence were identified, especially for a 2-year infectious period. Over longer periods, the human footprint showed a consistent negative association, and context-dependent climatic effects highlighted the importance of local factors in shaping ASF occurrence and persistence.

Rapid response modelling to support evidence-based decisions: The HASTE project

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Outbreaks of emergency animal diseases present significant threats to Australia's livestock industries, food security, trade access, and biodiversity. These events can disrupt supply chains, halt livestock movements, and damage international market confidence, leading to long-lasting economic, environmental, and social consequences. The impact on animal welfare is also considerable, with potential suffering for affected animals, while community wellbeing can be closely tied to the health of animals and the local economy, especially in regional areas. The HASTE project aims to improve Australia's biosecurity response to rapidly emerging threats by creating a framework to test, evaluate and improve epidemiological modelling to support decision-making. In doing so, we are developing rapid modelling tools to minimise the negative impacts and prepare and empower decision makers to use these tools in animal biosecurity emergency outbreaks. In this presentation I will give an overview of the HASTE project, with a focus on simulation exercises. During HASTE we developed a new approach to simulation exercises, which involves workshop participants interacting with a simulated outbreak, live during the workshop. Outbreak management decisions were made in real-time and covered surveillance, destruction and control areas. The simulation also output data that was fed into government dashboards, descriptive epidemiology visualisations and into forecasting tools to support decision-making in the room. As a result, decision-makers were able to use forecasting and decision tools, outside of a real outbreak to practice decision-making and build collaborations across organisations.

What makes African swine fever endemic in wild boars?

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African Swine Fever (ASF) is a highly fatal viral disease affecting both wild and domestic suids. Since 2007, the virus largely spread through Europe and Asia, with significant food security and economic impacts. With no vaccine currently available, the spread of the virus among wild and domestic populations rises multiple questions ranging from conservation biology to animal welfare. Wild boars are a key component in the introduction of the virus in Europe and its persistence in the environment, yet little is known about the mechanisms at play in the transmission, spread and maintenance of ASF in natural wild boar populations. Here, we aimed to identify the main epidemiological mechanisms driving the risk of ASF to become endemic after introduction events. To achieve this objective, we extended a stochastic agent-based model of ASF transmission dynamics in a natural wild boar population from France to account for its spatial structure and diversity of transmission pathways. We found that both the spatial circulation and dynamics - rather than a simple increase in the density of hosts - and the timing of introduction events are key drivers for endemicity. Notably, we found higher risk of endemicity for summer introduction events, when the population is renewed by spring births and suffers low hunting pressure. Our findings further highlight the major role of infected carcasses in maintaining the virus in the environment, regardless of the season, and in contrast to transmission from direct contacts and through infected faeces. These results are key information for improving the preparedness of the French pig industry to ASF threats.

Within and between farm modelling to investigate policies regarding aviary influenza and changes in agricultural practice

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Every year, the Netherlands experiences several outbreaks of highly pathogenic avian influenza (HPAI) in commercial poultry, even on farms with tight biosecurity. Two key developments are changing the epidemiology of HPAI outbreaks. First, there is a growing trend toward outdoor, free-range poultry production. Currently, 46% of layer farms are free-range, a shift that may increase both the number of introductions and the risk of transmission. Currently this risk is mitigated by obligatory indoor housing during times with enhanced circulation. Second, new vaccines are being developed that can protect poultry but do not completely prevent transmission. Mechanistic models are ideally suited to investigate these changes. In this presentation, we will discuss our work addressing three main questions related to these developments: 1)The impact of increasing outdoor poultry farms without mitigating measures, 2) Surveillance strategies given the vaccination of poultry, and 3) Human exposure to HPAI in the context of poultry vaccination. For each question, we use the same set of within-farm and between-farm transmission models. For the within-farm model, we used a stochastic two-type SIR model, in which we distinguish between low and high titre response to vaccination. Birds with a high titre response have a reduced reproduction number and strongly reduced mortality. Birds with a low titre only have a reduced mortality with the same transmission rate as unvaccinated birds. The outcomes of the within-farm SIR models were used to inform the infectious period of the between-farm models. Between-farm transmission is based on distance via an existing transmission kernel recalibrated assuming a increased susceptibility of outdoor farms without mitigation by obligatory indoor housing during periods of enhanced circulation. Our findings indicate that more outdoor poultry farms without mitigation increases both the risk of outbreaks and the number of farms affected during an epidemic. If outdoor farms are randomly distributed in space, the outbreak sizes are almost linearly increasing with the fraction of outdoor farms. Clustering of outdoor farms results in a rapid increase of epidemic size at around 50% of farms. Vaccination causes smaller within-farm outbreak sizes and increases the risk of non-detection. We demonstrate that vaccination—even with prolonged outbreaks—reduces human exposure to HPAI. Furthermore, vaccination decreases the fraction of major outbreaks and by additional active surveillance increased risk of non-detection can be mitigated. This work is based on projects across work for a private-public partnership, a research consortium, and a policy-report and thus serves as a showcase of research conducted for and with policymakers, which aligns with the work group on the modeling-policy nexus of the ModAH-hub.

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