ModAH
Conf
2024

3rd Modelling in Animal Health conference

27-29 August
Nantes - France

Conference Booklet

ModAH Conf

The conference on Modelling in Animal Health aims to bring together scientists from all over the world around one theme, in order to open new avenues of research and international collaborations.

The main topics of the conference cover a broad spectrum of animal health modeling, including but not limited to: intra-host/intra-vector modeling, genomic and phylodynamic models, large-scale epidemiological networks and models, domestic/wildlife interfaces, the use of models to evaluate control strategies and guide policy decisions

Scientific committee

Gaël Beaunée
Katharine Rose Dean
Jana Schulz
Rowland Kao
Patrick Hoscheit
Pauline Ezanno

Timetable

Tuesday, 27 of August

13:00 14:00		**Registration**	
14:00 14:10		**Welcome remarks**	
14:10 15:00	KL	**Quirine ten Bosch** Wageningen University & Research	Silent transmission in vector-borne diseases – combining field and lab data to shed light on epidemiological dark matter.
15:00 15:20	CT	**Simon Firestone** The University of Melbourne	Modelling workflows for rapid outbreak appraisal, decision- and policy-support in Australia
15:20 15:40	CT	**Mariken de Wit** Wageningen University & Research	Characterising the role of the silent reservoir in shaping vector-borne disease emergence
15:40 16:40		**Coffee break & poster session**	
16:40 17:00	CT	**Aeron Sanchez** Roslin Institute, University of Edinburgh	Using machine learning with wild bird reporting data to produce risk maps of Highly Pathogenic Avian Influenza in Britain and determine possible biases in the wild bird reporting
17:00 17:20	CT	**Maryem Ben Salem** ANSES	Perception, Behaviour and Transmission: Insights from an agent-based model on HPAI epidemiology
17:20 17:40	CT	**Facundo Muñoz** Cirad	Modelling dispersal, survival and trapping in SIT trials
19:00 21:00		**Junior Researcher networking event**	

Wednesday, 28 of August

09:00 09:20	CT	**Luca Martelli** Istituto Zooprofilattico Sperimentale delle Venezie	Unraveling the Role of Wild-Domestic Interface in the Spread of High Pathogenicity Avian Influenza
09:20 09:40	CT	**Emma L. Fairbanks** University of Warwick	Assessing the impact of host clustering and control strategies on African horse sickness virus transmission: A simulation-based analysis
09:40 10:00	CT	**Sébastien Picault** INRAE	From mechanistic models to decision-support tools: generating user-friendly web application from artificial intelligence and software engineering methods
10:00 10:20	CT	**Glen Guyver-Fletcher** University of Warwick	Using a multi-species epidemiological model to assess optimal FMD vaccine allocations across India
10:20 11:00	**Coffee break & poster session**		
11:00 11:20	CT	**Laetitia Canini** Anses	Outbreak reconstruction with a slowly evolving multi-host pathogen: a comparative study of three existing methods on Mycobacterium bovis outbreaks
11:20 11:40	CT	**Rémi Fay** Université Lyon 1	Methodological challenges in estimating brucellosis transmission risk in an Alpine ibex population using approximate Bayesian computation
11:40 12:00	CT	**Clara Delecroix** Wageningen University & Research	A novel machine learning approach to anticipate vector-borne disease outbreaks
12:00 12:20	CT	**Egil A.J. Fischer** Utrecht University	SUMMERFAIR – combining data science and infection models for estimating transmission parameters
12:20 13:50	**Lunch**		
13:50 14:40	KL	**Mike Tildesley** University of Warwick	Modelling optimal intervention strategies for animal diseases in data poor settings
14:40 15:00	CT	**Brandon Hayes** INRAE - ENVT	Quantifying the influence of wild boar density on African swine fever spread in wild boar populations, Italy, 2022-2023
15:00 15:20	CT	**Anna Gamza** Roslin Institute, University of Edinburgh	Spatial scales of interactions driving spread of Highly Pathogenic Avian Influenza in Great Britain
15:20 16:20	**Coffee break & poster session**		
16:20 16:40	CT	**Hélène Cecilia** New Mexico State University	Quantifying the relationship between within-host viral dynamics and transmission to mosquitoes: the case of Zika virus in two monkey species

16:40 17:00	CT	**Jonathan Bastard** Anses	Reconstructing West Nile virus dynamics in a tropical island using sentinel serological data
17:00 17:20	CT	**Vianney Sicard** UFZ – Helmholtz Centre for Environmental Research	Modeling Vaccination Strategies for African Swine Fever Control Among Wild Boars: A Computational Approach
17:20 17:40	CT	**Gustavo Machado** North Carolina State University	Mitigating between-farm disease transmission through simulating vehicle rerouting and enhanced cleaning and disinfection protocols
20:00	**Conference Dinner**		

Thursday, 29 of August

09:00 09:20	CT	**Amandine Bibard** Boehringer Ingelheim Animal Health France	Windborne dispersal of Culicoides midges in Europe: Case study with epizootic hemorrhagic disease virus in France
09:20 09:40	CT	**Alfredo Acosta** Swedish Veterinary Agency	Modelling phage therapy dynamics of MRSA on ex vivo pig skin experiments
09:40 10:00	CT	**Baptiste Sorin-Dupont** INRAE	Better targeting treatments against Bovine Respiratory Disease by combining dynamic generalized linear models and mechanistic modelling
10:00 10:20	CT	**Chris Banks** Roslin Institute, University of Edinburgh	Machine learning augmented diagnostic testing to identify sources of variability in test performance
10:20 11:00	**Coffee break & poster session**		
11:00 11:20	CT	**Hélène Duault** INRAE	Could ship movements transmit Infectious Salmon Anemia Virus between Norwegian fish farms ?
11:20 11:40	CT	**Oriane Ploquin** IRD	The role of wildlife diversity and contacts in the circulation of infectious diseases: an integrated monitoring of a human/livestock/wildlife interface in sub-saharan savanna
11:40 12:00	CT	**Thomas Hagenaars** Wageningen Bioveterinary Research	Evaluating control measures against Highly Pathogenic Avian Influenza spread between Dutch poultry farms: preventive culling and bucket sampling
12:00 12:40	IT	**Pauline Ezanno** INRAE	ModAH-HUB: an new international network in modelling in animal health
12:40 12:50	**Conclusion**		

KL: Keynote Lecture, CT: Contributed Talk, IT: Invited Talk.

List of Abstracts – Talks

Tuesday 20th

K1 - Silent transmission in vector-borne diseases – combining field and lab data to shed light on epidemiological dark matter

Q. ten Bosch

KL

Wageningen University & Research

Vector-borne diseases continue to cause major health burden to humans and animals worldwide. While they are responsible for massive, widespread outbreaks in some cases, transmission often remains unnoticed. This can be due to transmission in reservoirs that are not affected by the pathogen itself, or by large proportions of asymptomatic infections in commonly affected species. Such silent transmission can cause great challenges to surveillance and control efforts, as well as the planning of trials for new interventions. We will dive into the epidemiological dark matter of vector-borne disease transmission and explore how models, combined with experimental and field data, can contribute to a better understanding of what goes on under the radar of our surveillance systems.

O01 - Modelling workflows for rapid outbreak appraisal, decision- and policy-support in Australia

S. Firestone[1]***, C. M. Baker***[1]***, S. Roche***[5]***, S. Lee***[1]***, M. Theng***[2]***, E. Sellens***[5]***, M. A. Stevenson***[1]***, R. N. Hall***[6]***, A. Gohil***[1]***, A. C. Breed***[5]

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In the early stages of outbreaks, modelling and other epidemiological analyses can provide vital decision-support. This project aimed to develop decision-support tools including epidemiological models for use during animal disease outbreaks in Australia. A workshop of experts and stakeholders was convened to reach agreement on national priorities and actions, and to inform the development of modelling tools and workflows for rapid outbreak appraisal and decision-support. Needs were considered within a national framework of key questions, tools and human resources. Based on the outputs of the workshop and further stakeholder consultation, planning and development of tools and a workflow was undertaken and tested on real and simulated outbreak datasets. Specific questions that modelling could help answer related to outbreak origin, scale, spread, severity, populations at risk, impacts/costs, early disease indicators that warrant policy changes, resource allocation, impacts assessment and cost-benefit analysis of control options. A comprehensive modelling workflow plan was developed including modules for: descriptive/spatiotemporal analyses, dynamic transmission modelling/forecasting, ecological niche modelling (for diseases involving vectors and/or wildlife), phylogenetic modelling and airborne dispersal modelling. The outputs intended to guide rapid appraisal, risk assessment and policy development early in outbreak response. The descriptive/spatiotemporal and dynamic transmission modelling/forecasting modules have been developed and implemented. Their outputs have been integrated into an interactive user interface and their accuracy and usefulness tested at early stages based on time-slices of datasets from the outbreaks of foot-and-mouth disease (FMD) in the United Kingdom (2001) and equine influenza in Australia (2007). The provided figure shows temporal and spatial projections based on data available 21 days after detection in the Cumbria cluster of the 2001 FMD outbreak by fitting a parsimonious deterministic within- and stochastic between-herd SEIR agent-based model with an Approximate Bayesian Computation Sequential Monte Carlo (ABC-SMC) algorithm. This project has identified critical modelling questions to enable decision-support during the early phase of animal disease outbreaks, planned a comprehensive workflow of modelling tools, developed and tested key modules. Further work will involve working on additional outbreak datasets and with the wider network of stakeholders to address critical modelling gaps in preparedness for outbreaks.

O02 - Characterising the role of the silent reservoir in shaping vector-borne disease emergence

M.M. d. Wit[1]***, G. Beaunée***[2]***, M. Dellar***[3,4]***, L. Krol***[3]***, E. Münger***[5]***, N. Atama***[5]***, H. v. d. Jeugd***[6]***, M. Koopmans***[5]***, M.C.M. d. Jong***[1]***, R. Sikkema***[5]***, Q. t. Bosch***[1]

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Disentangling contributions of different host types to disease emergence and transmission is highly complex, but critical to improve preparedness, prediction, and response. Especially for emerging wildlife diseases, our ability to unravel these contributions is often hampered by the lack of high-quality information on population distributions and patterns of disease occurrence as well as computational tools to integrate a wide range of data sources. Here, we illustrate that by jointly analysing several sources of surveillance data coupled with a mechanistic transmission model, it was possible to quantify unobserved drivers of transmission for an emerging, multi-host, wildlife disease. We used five sources of blackbird surveillance data that captured the emergence of Usutu virus in the Netherlands between 2016-2022. These were used to calibrate single- and multi-host mechanistic transmission models of Usutu virus using Approximate Bayesian Computation. These transmission models included information on mosquito and bird abundance and population dynamics, bird dispersal, and local temperature. We explored the characteristics of a potential additional reservoir host through model comparison, while simultaneously estimating unknown parameters. Using the best-fitting model we reconstructed the outbreak over time and space and quantified each host type's contribution to transmission. We found that while blackbirds were most impacted by the virus, they could not, by themselves, contribute sufficiently to the population-level build-up of immunity needed to explain the spatial and multi-annual patterns that characterised its emergence. We characterised the unobserved reservoir species as having a longer lifespan, little disease-induced mortality, and a larger home range than blackbirds. Basic reproduction numbers differed between years, but tended to peak between late July to late August. The difference between the basic and effective reproduction number was largest in August. The estimated large contribution of alternative host species implies that also regions with low blackbird density might be suitable for Usutu virus transmission if other reservoir species are present, but surveillance schemes other than trends in dead birds would be required to detect circulation. Our results highlight the importance of considering multiple host species when designing intervention strategies, surveillance schemes, or future predictions as disease impact and contributions to transmission vary strongly

O03 - Using machine learning with wild bird reporting data to produce risk maps of Highly Pathogenic Avian Influenza in Britain and determine possible biases in the wild bird reporting

***A. Sanchez*, R. Kao, A. Mastin, S. Vickers**

Roslin Institute, University of Edinburgh

Highly Pathogenic Avian Influenza (HPAI) is a current global concern with implications for wildlife and domesticated poultry and with the potential for becoming a human pandemic. Ascertainment of case locations is crucial but in Great Britain as elsewhere, locations of wild bird cases are highly dependent on voluntary submissions of dead birds. Here we aim to combine the data from wild bird testing along with other data sources and use machine learning methods to map the prevalence of high path HPAI in wild bird populations across the UK, while also accounting for ascertainment biases in the reporting data. We were also able evaluate the factors affecting the biases in wild bird reporting. The wild bird testing data was combined with several other data sources such as, wild bird populations, land usage, human populations, etc., to provide further information to the ML models. The ascertainment biases were determined by generating a number of false cases using randomly selected locations, dates and species, combining it with the real reported wild bird data and then training a model to classify the reports as a real reported bird or a randomly generated report. From the trained model we were able to determine which parameters are important in classifying the real reports, giving us an idea into what factors result in biases in reporting as well as looking which geographic locations are likely affected by under reporting. To map the risk of AI we trained an ML model to predict whether a reported wild bird that was sampled ended up testing positive or negative. By passing random data points into the trained model, we can then get a probability of testing positive for a given date, location and species, this is used as a proxy for presence/risk of HPAI for the corresponding inputs. These predictions can be used to generate a geo-temporal risk map of HPAI across Britain. This work can provide a better geo-temporal risk map of HPAI in the UK which could be useful for better targeting of surveillance and prevention measures. We also aim to use the results from this in future simulation projects.

O04 - Perception, Behaviour and Transmission: Insights from an agent-based model on HPAI epidemiology

M. B. Salem[1]***, A. Scoizec***[1]***, S. L. Bouquin***[1]***, M. Salines***[1]***, V. Allain***[1]***, S. Bougeard***[1]***, R. Thomas***[1]***, M. Baudrin***[2]***, F. Debil***[2]***, K. Fiore***[2]***, L. Saint-Cyr***[2]***, M. Andraud***[1]

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Since 2015, the French poultry industry has been facing considerable challenges due to recurring outbreaks of high pathogenicity Avian Influenza (HPAI). These outbreaks highlight the need for a deeper understanding of the virus's transmission mechanisms and an optimsation of control measures. This project addresses these needs by integrating socio-economic factors, environmental factors and epidemiological processes into a single model. Recognised as essential in humanhealth issues, the dynamic integration of socio-economic considerations into epidemiological models for animal diseases remains sparse. However, agent-based models are gaining popularity for their ability to dynamically represent host populations and individual behaviours, and to facilitate the integration of interdisciplinary inputs. Using agent-based modelling, poultry farms will be represented as agents with specific characteristics, including species, flock size, biosecurity measures and farmers' perception of HPAI risk, which can evolve over time (figure 1). The agents' environment will incorporate geographical, epidemiological, sociological, economic, and environmental information. Geographically, the model integrates a spatial dimension through the use of Geographic Information System (GIS) data, enabling the representation of farms' locations and between-farm movements. Agents will modulate the risk of introduction and spread of the infection through their actions or reactions, based on their perception of the information in their environment. This, in turn, will impact the environment, including other agents. Therefore, agents' perceptions and actions/reactions will retroactively feed into each other, modifying the epidemic landscape and social network structure. Agentspecific socio-economic factors will be integrated at the agent level as attributes, while factors affecting all agents will be represented as components of the environment. For the environmental factors, an analysis of the 2022-2023 outbreaks identified variables, such as closeness to particular risk zones, as important in the occurrence of the outbreaks. The socio-economic and epidemiological components are ongoing, drawing on both literature data and a field study involving interviews with concerned stakeholders. Our results are expected to enhance the understanding of HPAI dynamics and to facilitate the identification of optimal control strategies. Additionally, this project will contribute to a paradigm shift in infectious animal disease modelling, moving from simplistic epidemiological models to more complex systems that better reflect field realities.

O05 - Modelling dispersal, survival and trapping in SIT trials

***F. Muñoz*, A. Capel**

UMR ASTRE, Cirad

The sterile insect technique (SIT) is widely used as a tool for biological control or eradication of insect populations by releasing large numbers of sterile males into a target area where they mate with wild females, causing the population to decline. The release frequency, volume and the temporal and spatial coverage must be adapted to each target environment to ensure effectiveness, which requires a series of preliminary trials in order to understand the dispersal and survival of the released individuals in those specific conditions. The relevant parameters must be estimated from the number of sterile males caught in a battery of traps deployed throughout the region. These parameters are usually estimated independently of each other, using simple linear regressions with unrealistic hypotheses that neglect their interdependence and the influence of the specific spatial location of the traps. We present a probabilistic model for the number of captures in each trap, which improves the accuracy and precision of the estimates, while properly accounting for the associated uncertainty. We demonstrate the results with simulated and real data and discuss both frequentist and Bayesian estimation approaches.

Wednesday 21st

O06 - Unraveling the Role of Wild-Domestic Interface in the Spread of High Pathogenicity Avian Influenza

***L. Martelli*[1], D. Fornasiero[1], J. A. Martínez-Lanfranco[2], A. Spada[3], A. Franzoso[1], F. Scarton[4], F. Scolamacchia[1], G. Manca[1], P. Mulatti[1]**

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Wild birds are crucial in maintaining High Pathogenicity Avian Influenza (HPAI) viruses, acting as transmission vectors to poultry. However, the dynamics at the wilddomestic interface are poorly known. Advancing the understanding of the association between geographical distributions of key wild bird species and occurrence of HPAI outbreaks in poultry during 2017-2018 epidemic in Northern Italy might significantly enhance HPAI prevention and surveillance protocols. A Bayesian Adaptive Regression Trees (BART) approach was used to develop a series of Species Distribution Models (SDMs) of 40 bird species camera-trapped at 10 poultry farms in Northeastern Italy, constructed on eBird data as input occurrences and a suite of bioclimatic spatial layers as predictors. The predicted bird occurrences were used to parametrize HPAI outbreaks models. To identify redundant information within the species, a Cluster Analysis (CA) was used to group them based on spatial congruence of their predicted occurrences. The outbreak modelling consisted of an ensemble approach with five methodologies: Generalized Linear Model, Generalized Additive Model, Boosted Regression Trees, Random Forest, and Maximum entropy. The framework included single species univariable models, followed by a final multivariable model using the best predictors from each cluster. Based on the performance of BART models and CA of prediction similarities, 22 wild bird species grouped in seven clusters were selected for further analyses. The cluster including most of the observed Ardeidae species resulted the most important variable in explaining the probability of HPAI outbreaks (importance = 28%), showing a positive association with outbreaks, highlighting a potential bridging role for this species group. Birds historically associated with avian influenza (i.e. Order Anseriformes and Charadriiformes) were included in a separate cluster (importance = 17%), and a positive correlation with the outbreaks occurrences suggested their role in the disease ecology. These results underline the complex role of the wilddomestic interface in the epidemiology of HPAI, suggesting that a broader range of species than what is typically considered might be involved in HPAI virus ecology. Including these groups of species in passive surveillance programs would help in prioritizing sampling efforts, and identifying early warning signals of possible transmission to poultry holdings.

O07 - Assessing the impact of host clustering and control strategies on African horse sickness virus transmission: A simulation-based analysis

***E. L. Fairbanks**, J. M. Daly, M. J. Tildesley*

University of Warwick, University of Nottingham

African horse sickness virus (AHSV), a Culicoides-borne virus, causes high morbidity in naïve horse populations. Approval has recently been given for the recommencement of direct horse movements from AHSV-endemic South Africa to the European Union. Current attenuated or inactivated whole virus AHSV vaccines, unable to differentiate between infected and vaccinated animals (DIVA), risk a country's disease-free status if used, potentially impacting equine industry economies. New vaccines are in development; meanwhile some governments suggest the use of stable netting, to block access of horses to Culicoides. First, we develop a novel model evaluating the impact of climate and vector control on vectorial capacity, comparing the transmissibility of AHSV with other pathogens previously observed in Europe spread by the same vector. Then, we integrate this with a stochastic model for the spatial transmission of AHSV between premises, using parameterisations from Morocco when AHSV emerged in 1989. Using the UK as an example, we use previous estimates for the number of horses in 5km x 5km grids. In each simulation, equines in each grid are distributed into premises according to one of two distributions: Moroccan AHSV-affected premises sizes (1989) or UK premises sizes (inferred from equine influenza outbreak data 2010-present). The effectiveness of ring vaccination and vector control strategies are assessed. Applying the vectorial capacity model, we show that AHSV has a higher peak predicted vectorial capacity than bluetongue virus (BTV), Schmallenberg virus (SBV) and epizootic haemorrhagic disease virus (EHDV). For the spatial transmission model, simulations using Moroccan AHSV premises sizes resulted in a handful of infected premises. In contrast, the larger predicted UK premises sizes led to outbreaks affecting thousands of premises and, in some cases, hundreds of thousands of horses. The potential of interventions to mitigate this is dependent on their coverage. Insecticide-treated stable netting is shown to significantly reduce transmission even at low coverage levels. However, untreated stable netting is likely to have limited impact. The success of vector-control tools and vaccines depends heavily on horse owners' willingness to adopt these strategies and adhere to regulations.

O08 - From mechanistic models to decision-support tools: generating user-friendly web application from artificial intelligence and software engineering methods

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Mechanistic epidemiological modelling is often used in the detection and prevention of livestock diseases, accounting for realistic farming practices. It helps understand the spread of pathogens and compare intervention scenarios. However, it is difficult for decision makers to manipulate mechanistic models and interpret outputs by themselves. To overcome this obstacle, artificial intelligence and software engineering techniques can make mechanistic epidemiological models more accessible to farmers and veterinarians, by transforming such models into user-friendly decision-support tools (DST). To facilitate the co-construction of DSTs, we have established a domain-specific language to specify model components as well as tool features through a textual formalization and automatic code generation. This helps nonmodeller stakeholders to read, assess, and revise the model assumptions or scenarios and the tool structure at any moment, making the whole process more collaborative and accessible. We have illustrated this approach using an epidemiological model of Bovine Respiratory Disease (BRD) in fattening farms. This disease affects young bulls shortly after being allocated into pens. BRD is often difficult to anticipate and control because it is a multi-factorial and multi-pathogen disease, which leads to massive use of antimicrobials. The decision-support tool developed from an existing mechanistic BRD model allows users (farmers, veterinarians...) to describe their farm conditions, possible pathogens, and configure different intervention scenarios. Based on that, they can evaluate the epidemiological and economics outcomes associated with different farming practices, and finally decide how to balance the reduction of disease impact and the reduction of antimicrobial usage. As these methods are generic, they can apply to various infectious diseases and farming practices. Additionally, they require little coding (usually none at all), which is likely to foster a broader use of mechanistic models in veterinary epidemiology in general, and more specifically their further use to support decision-making in practical situations by farmers, veterinarians, or other stakeholders.

O09 - Using a multi-species epidemiological model to assess optimal FMD vaccine allocations across India

G. Guyver-Fletcher, D. Bhatia, M. Ferrari, M. Tildesley

University of Warwick, UK; Penn State University, USA

Foot-and-Mouth Disease (FMD) is a virulent livestock disease which is endemic in much of Africa and Asia. Although it can infect all cloven-hoofed animals, the prime livestock species of concern are cattle, buffalo, and pigs. the disease presents an economic burden both directly, through reduced yields, and indirectly, through reduced access to trade. India is interested in controlling and eradicating the disease and has exerted significant effort over the past 2 decades building a country-wide FMD-control apparatus. Circulation of FMD has declined substantially, but the disease remains endemic. We develop a multi-species mechanistic model of FMD virus transmission for India, incorporating between-species contacts, virus seasonality, vaccination, and waning immunity. We combine this with publicly available data on livestock headcounts and serological surveys to explore the efficacy of different vaccine allocations, both across species and across different states. Results suggest that current levels of vaccination may not be sufficient to lead to eradication, and that increasing the current levels of vaccine coverage are required for the eradication of the disease. The addition of pigs to the prophylactic mass vaccination campaigns could avert a high number of infections per vaccine dose used. However, only some regions in India contain swine populations sufficient for this to affect circulation greatly. Assessing the allocation of vaccine doses on a species-wise and state-wise basis indicates that it may be necessary to vaccinate sheep and goats in addition to buffalo, cattle, and pigs. Our work and results suggest that additional vaccination of sheep or goats can further reduce prevalence, and thus help to facilitate progress towards FMD elimination in India in the future.

O10 - Outbreak reconstruction with a slowly evolving multi-host pathogen: a comparative study of three existing methods on Mycobacterium bovis outbreaks

***L. Canini**, H. Duault, B. Durand*

Anses - Laboratoire de Santé Animale - EpiMIM

In a multi-host system, understanding host-species contribution to transmission is key to appropriately targeting control and preventive measures. Outbreak reconstruction methods aiming to identify who-infectedwhom by combining epidemiological and genetic data could contribute to achieving this goal. However, the majority of these methods remain untested on realistic simulated multi-host data. Mycobacterium bovis is a slowly evolving multi-host pathogen and previous studies on outbreaks involving both cattle and wildlife have identified observation biases. Indeed, contrary to cattle, sampling wildlife is difficult. The aim of our study was to evaluate and compare the performances of three existing outbreak reconstruction methods (seqTrack, outbreaker2 and TransPhylo) on M. bovis multi-host data simulated with and without biases. Extending an existing transmission model, we simulated 30 bTB outbreaks involving cattle, badgers and wild boars and defined six sampling schemes mimicking observation biases. We estimated general and specific to multi-host systems epidemiological indicators. We tested four alternative transmission scenarios changing the mutation rate or the composition of the epidemiological system. The reconstruction of who-infected-whom was sensitive to the mutation rate and seqTrack reconstructed prolific super-spreaders. TransPhylo and outbreaker2 poorly estimated the contribution of each host-species and could not reconstruct the presence of a dead-end epidemiological host. However, the host-species of cattle (but not badger) index cases was correctly reconstructed by seqTrack and outbreaker2. These two specific indicators improved when considering an observation bias. We found an overall poor performance for the three methods on simulated biased and unbiased bTB data. This seemed partly attributable to the low evolutionary rate characteristic of M. bovis leading to insufficient genetic information, but also to the complexity of the simulated multi-host system. This study highlights the importance of an integrated approach and the need to develop new outbreak reconstruction methods adapted to complex epidemiological systems and tested on realistic multihost data.

O11 - Methodological challenges in estimating brucellosis transmission risk in an Alpine ibex population using approximate Bayesian computation

R. Fay[1]***, S. Lambert***[2]***, A. Thébault***[3]***, P. Marchand***[4]***, A. Payne***[5]***, E. Petit***[6]***, C. Toïgo***[7]***, E. Gilot-Fromont***[1]

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Estimating pathogen transmission risk is a central issue in epidemiology. Estimating transmission risk could be particularly challenging when available epidemiological information is limited, as it is often the case in wildlife populations, and could be complexified by the existence of multiple transmission routes. Difficulties also arise when fitting complex epidemiological models (e.g. individual-based model) to empirical data. Here, we aim to estimate transmission risk of brucellosis in a wild Alpine ibex population. Transmission between animals occur via two main transmission routes: (i) exposure to infectious births/abortions and (ii) venereal transmission. We develop an individual-based model (IBM) providing a mechanistic description of this ecological system. This model includes a spatially explicit demographic model describing the ibex population dynamics, and an epidemiological model based on the classical SEIR framework. While parameters of the ibex model (demographic rates, reproduction behavior, spatial ecology) can be informed by previous studies, transmission parameters are unknown for this species. We thus estimate these parameters by fitting our IBM to field data collected during the epidemiological surveys using Approximate Bayesian Computation (ABC). ABC method allows simple and intuitive way to estimate unknown parameters by first simulating new datasets based on set of candidate parameters, and second, selecting parameters allowing to reproduce the observed data. While intuitive, the performances of this method rests on choices concerning summary statistics computed from the simulated data, range of values used for candidate parameters, and the type of ABC algorithm to be applied. We show how these choices affect the estimation of the risk of pathogen transmission in our study case, and provide general lessons that can be learned.

O12 - A novel machine learning approach to anticipate vector-borne disease outbreaks

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West Nile virus is an arbovirus causing repeated outbreaks in North America, Europe, and Africa. It infects mosquitoes and birds, but also humans and horses as dead-end hosts. As treatments and diagnostic tests for humans are still under research, current measures to halt the transmission of West Nile Virus are mostly preventive. These preventive interventions mainly target the vector populations and are only effective if implemented in a timely fashion. Thus, signalling when an outbreak is about to start is crucial to effectively prevent the transmission. Here, we investigate the use of machine learning approaches to signal upcoming WNV outbreaks. Our algorithm uses time series of incidence and seroprevalence in multiple vector and host species to predict whether an epidemic is approaching. Each of these time series is encoded into an image. These image representations of the time series are used to leverage image description models. Public image description models (i.e., VGG16, ResNet, XEfficient) were employed to extract informative features in images which enhance the learning capability of machine learning approaches. This novel approach was compared to traditional machine learning approaches to analyse time series, such as CNN or LSTM. As the large data requirements to train a machine learning algorithm are hardly met, a synthetic dataset was created for training. The synthetic dataset consists of time series generated using a library of randomly generated stochastic dynamic models of vector-borne diseases. To ensure enough diversity in the dataset, each model is based on a unique set of assumptions and parameter values, randomly selected from a diverse set of predefined assumptions. Preliminary results suggest that this novel approach can accurately predict upcoming outbreaks of West Nile Virus. Encoding the data into images improved the prediction performance compared to conventional machine learning approaches to analyse time series. Real-world data sets will be used to confirm these findings. As the training dataset is generic, we will test whether these results hold for other vector-borne diseases in the next stage of the project. This approach could provide accurate early warnings to guide policymakers in implementing prevention measures.

O13 - SUMMERFAIR – combining data science and infection models for estimating transmission parameters

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The quantification of transmission parameters is crucial for the parameterization of infectious disease models and quantification of the effects of interventions in experimental settings. New infectious disease models and estimation procedures are developed and existing data could be reused in these models, but also existing data can lead to new models and methods. Currently, the reuse of observational and experimental data for transmission of infections is often hampered by a lack of standardization of data. Furthermore reanalysis with different sets of underlying assumptions or models is time-demanding. Here we present the SUMMERFAIR frame work that includes a data-standard based on an existing ontology (Infection Transmission Ontology) and an analysis pipeline with steps to interpret data, apply different estimation procedures including different underlying infectious disease dynamics (e.g. indirect versus direct transmission). The framework is flexible and will automatically produce a data quality report and documentation of assumptions underlying the interpretation of data. The data processing is programmed in Python and the data analysis in R. Due to standardization of data the method can also be used easily for meta-analyses. We will show demonstrate the framework on existing data.

K2 - Modelling optimal intervention strategies for animal diseases in data poor settings

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Emerging diseases of livestock can devastate the agricultural industry and have a severe impact upon livestock exports. It is therefore vital to provide tools to assess the risk associated with infectious diseases and establish surveillance and intervention protocols that will reduce the cost of such outbreaks in the future. In this presentation, I will discuss the role of infectious disease models in supporting contingency planning for livestock disease outbreaks. These models typically require data on locations, sizes and species compositions of farms, as well as detailed information on any animals that are infected with the disease. However, in many settings such data are not available. I will therefore demonstrate how models can support infectious disease control in settings where such detailed data are not accessible and how surveillance resources should be targeted to reduce model uncertainty and provide accurate predictions regarding the future spread of disease.

O14 - Quantifying the influence of wild boar density on African swine fever spread in wild boar populations, Italy, 2022-2023

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African swine fever (ASF) continues to threaten the swine industry and wild boar populations, both globally and within the European Union. Elucidating the drivers of ASF virus transmission remains a high priority to predict disease spread, inform risk management, and support biosecurity measures. Wild boar density is considered to play a central role in shaping observed transmission patterns, though its contribution has been observed to vary across the few epidemic scenarios in which it was assessed. To provide quantitative estimates of the influence of wild boar density on ASF spread, a spatially-explicit mechanistic SEIR model of ASF transmission between density-explicit wild boar habitats was developed and parameterized to observed epidemic data in Northern Italy, from 2022 through the end of 2023. Average duration of infectious periods, local prevalence at time of first detection, detection rate, and recovery rate parameters were estimated directly from surveillance data. Wild boar species density estimates at 4 km2 were generated by the ENETWILD consortium and provided by EFSA. Four models were constructed utilizing linear relationships between habitat infectivity and susceptibility and wild boar density. The betweenhabitat transmission rate was considered either constant or seasonal, yielding a final total of eight different models. Between-habitat transmission rate, relative infectivity and relative susceptibility were estimated by fitting each model to the observed epidemic through sequential Monte Carlo approximate Bayesian computation (ABC-SMC). The best-fit model utilized seasonal transmission rates and accounted for densityrelated differences in susceptibility and infectivity of wild boar habitat. We estimated ASF transmission rates of 1.2 (95% credible interval [CI95]: 0.3 – 2.8) cells per week in the winter and 0.4 (CI95 0.09–0.9) cells per week in the summer. Cells with an estimated density greater than 4 wild boar/km2 were slightly more infectious and susceptible (1.2 and 1.1 times, respectively) than cells with a density less than 4 boar/km2 in 2022, though in 2023 the relative susceptibility and infectivity was much more pronounced (1.9 and 2.5 times, respectively). These results demonstrate the role that wild boar density played in ASF propagation in Northern Italy and can be used to inform wild boar management strategies.

O15 - Spatial scales of interactions driving spread of Highly Pathogenic Avian Influenza in Great Britain

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The geographical spread of infectious diseases informs the development of intervention strategies aiming at stopping this spread. The need to understand the spatiotemporal dynamic of transmission better is particularly acute for Highly Pathogenic Avian Influenza (HPAI), which has recently moved in Europe from seasonal introductions to more endemic situation. As such there is an urgent need to understand spatiotemporal patterns of circulation, in order to inform our understanding of the long-term impact of the virus, and tailor efficient intervention strategies. The combination of infection and bird populations data aggregated on various geographical scales with phylogenetic data from British HPAI outbreaks offers a rare opportunity to quantify the scales of potentially infectious interactions that drive HPAI. As the genetic proximity implies the close connection on transmission tree, the genetic relationships between sequences and variables describing places they come from indicate the scale and resolution of interactions driving transmission. We use the genetic distance between sequenced HPAI cases in Great Britain together with the set of other variables (i.e. number of registered cases, wild bird abundance and poultry farms count) calculated over various geographical scales. Our analyses show that HPAI case data and wild bird abundance, but not farm count, are more predictive of genetic distances between sequenced viruses when aggregated over grid-based areas compared to administrative areas that are inherently adjusted for human population density. The geographical scale of interactions seems to be the smallest for wild birds' abundance (area size approx. 80 km2), medium for poultry cases (area size approx. 660 km2), and bigger for wild bird cases (area size approx. 2780 km2). The farm count data were the most indicative for smaller human population-based geographies of approx. 500-1000 people. Our study indicates that the scale of geographical aggregation and/or extrapolation that should be considered is variable dependent and reflects the scale of processes it indicates. In the future our findings may be used to provide geographical scales that are the most useful to studying dynamics of HPAI spread and the reach of intervention strategies.

O16 - Quantifying the relationship between within-host viral dynamics and transmission to mosquitoes: the case of Zika virus in two monkey species

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Zika virus (ZIKV) is maintained in sylvatic cycles between monkeys and arboreal mosquitoes in the Old World and has spilled over to establish a humanendemic transmission cycle. ZIKV was recently introduced to South America; whether ZIKV can establish a sylvatic transmission cycle there is an open and urgent question. Key determinants of transmission in a novel environment are within-host replication dynamics in novel hosts and the impact of these dynamics on transmission to vectors. We used phenomenological modeling to obtain estimates of ZIKV infectiousness for both Old World (cynomolgus macaques) and New World (squirrel monkey) monkey species from experimental data. We used Aedes albopictus mosquitoes to infect monkey hosts with a sylvatic or human-endemic strain of ZIKV, and monitored host viremia and transmission to mosquitoes over the course of infection. We used a non-linear mixed effect model to describe within-host viral dynamics and assessed the impact of host species, virus strain, and inter-individual variability (Figure). Host species did not significantly impact viral dynamics, whereas in macaques, the human-endemic strain of ZIKV induced significantly lower and later peak titers than the sylvatic strain. Both monkey species, when infected with the sylvatic strain of ZIKV, infected mosquitoes which in turn became saliva-positive (infectious). We fitted doseresponse relationships to describe i) the association between host viral titer and the probability of disseminated infection in mosquitoes, ii) the heterogeneity of mosquito leg titers, and iii) the association between mosquito leg titer and the probability of being infectious. Combined, these steps allowed us to derive an estimation of monkey infectiousness over time. Both species are most infectious at day 4 post-infection, with an average probability of infecting mosquitoes just above 0.5. Importantly, the infectious period is longer in squirrel monkeys than cynomolgus macaques. Our results suggest that a ZIKV sylvatic cycle could be established in neotropical monkey species. Future population-level mechanistic models will benefit from accurate estimations of host-to-vector transmission, a critical parameter often oversimplified. Such models will be needed as they combine individual-level transmission potential with ecological factors (e.g. the densities and contact structure of hosts and vectors), to properly assess sylvatic ZIKV epidemic potential in the neotropics.

O17 - Reconstructing West Nile virus dynamics in a tropical island using sentinel serological data

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West Nile virus (WNV) is a mosquito-borne virus present in almost all continents, including in the Caribbean. Its reservoir hosts are birds, and it can spread to "dead-end hosts", including horses and humans, in whom the infection can be fatal. However, it often remains undetected in humans, leading to risks for blood and organ donations. The multi-host (and essentially wildlife) nature of WNV epidemiological system makes monitoring its circulation a complex task. In Guadeloupe island, longitudinal sampling was performed in sentinel horses starting in 2002 and in sentinel chickens starting in 2013. Over the whole study period, between 2 and 11 sera samples were taken in each of the 203 sentinel horses, and between 2 and 44 samples in each of the 244 sentinel chickens. Sera samples were analyzed for the presence of IgG antibodies against WNV using ELISA, and virus neutralization tests were performed on positive samples. We then built a model of the seasonal dynamics of WNV force of infection (FOI) and fitted it to the serological data using Markov Chains Monte Carlo. We found that the weekly FOI in horses could reach a maximum of 0.007 (95% Credible Interval: [0.006; 0.008]) around the month of October. This FOI was multiplied by 0.1 [0.0004; 0.3] in chickens, which can be explained by their smaller size. We estimated a weekly sero-reversion rate of 0.0005 [0.0001; 0.001], which is consistent with a long-term persistence of WNV IgG antibodies in infected individuals. To conclude, the collection of longitudinal data in sentinel animals allowed us to reconstruct seasonal variations in the FOI over 15 years in Guadeloupe island.

O18 - Modeling Vaccination Strategies for African Swine Fever Control Among Wild Boars: A Computational Approach

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African swine fever (ASF) is a deadly infectious disease that affects domestic pigs and wild boars. Since its entry into the eastern part of the EU in early 2014, ASF has spread locally among the wild boar population, posing a high risk of infection to domestic pigs and causing significant economic losses to pig farms. The main affected countries in the eastern EU

include Poland, Lithuania, Latvia, and Estonia. Due to its shared borders with Poland, the spread of ASF is a significant concern for Germany, particularly in Saxony. Current control measures include preventive culling in defined areas, known as 'white zones' (WZ), which are fenced off. Another control strategy is vaccinating the population, which for wild boars involves the use of an oral vaccine. However, representing and modeling oral vaccination processes and their impact on spread dynamics in the wild boar population remain challenging. We propose a representation of the oral vaccination process and its implementation in an existing computational spatiotemporal stochastic model (Swifco). The model considered each stage of the vaccine's effect, from bait consumption to the loss of protection, as well as the different levels of protection provided by the vaccine (protection from infection and protection against spreading the infection). We considered a theoretical imperfect vaccine, that is, not providing full protection against becoming infected or transmitting the infection. The model took into account geographies landscape of wild boar habitat together with the explicit spatial distribution of vaccine baits. We estimate how various scenarios of vaccine deficits will change the control efficiency on the level of wild boar populations compared to perfect but theoretical vaccination. Hence, we present the informed recommendation to qualify the registration of an ASF vaccine minimum standard.

O19 - Mitigating between-farm disease transmission through simulating vehicle rerouting and enhanced cleaning and disinfection protocols

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The role of contaminated vehicles in spreading infectious diseases among commercial swine farms, including African swine fever, is still largely unexplored. Vehicle cleaning and disinfection (C&D) is the primary control strategy to reduce the likelihood of transmission through indirect contact between farms via vehicle movements. However, C&D effectiveness remains unknown, and the role of vehicles in disease transmission cannot be ruled out. This study aimed to reduce the risk of between-farm transmission through vehicle contacts by rerouting vehicles while considering C&D events and effectiveness. Vehicles were ranked based on rules, including disease status of visited farms, vehicle contact network communities, C&D events, and shipment time efficiency. The rerouting system showed that, even when C&D was utterly inefficient, it reduced up to 42% of contacts between infected and uninfected farms via vehicle movements and 17% of the total number of interactions between farms from distinct network communities. The rerouting efficacy increased with a C&D effectiveness of 100%, reducing up to 100% contacts between infected and uninfected farms and between farms from distinct network communities. Despite the potential benefit of preventing disease dissemination among the farms, the rerouting system increased by up to 81% in C&D visits and up to 54% in distance traveled per vehicle. Ultimately, we have demonstrated that a rerouting vehicle system holds potential as an additional strategic tool for preventing and controlling the spread of diseases among farms through vehicle movements.

Thursday 22nd

O20 - Windborne dispersal of Culicoides midges in Europe: Case study with epizootic hemorrhagic disease virus in France

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The epizootic hemorrhagic disease virus (EHDV) is a novel emerging threat for the European livestock sector. First detected in Sardinia and southern Spain at the end of 2022, this transboundary disease emerged in France in September 2023 despite restrictions on animal movement and enhanced surveillance protocols. Although virus spread is believed to be mediated by the dispersal of Culicoides vectors by the wind, prediction is difficult due to the large number of meteorological parameters that must be considered. Using simulations of atmospheric trajectories, we developed a model to investigate the long-distance dispersal risk zone of Culicoides in Europe, starting from different source zones. Our model predicted with good sensitivity the newly EHDV-infected areas in France over a period of 5 weeks after its first introduction in the country. Prospectively, we predicted that the midge dispersal zone of early 2024 could expand towards most of the western half of France and could sporadically reach new countries under favorable spring conditions. The wind dispersal risk maps provided are intended to support better preparedness and response to Culicoides-borne diseases.

O21 - Modelling phage therapy dynamics of MRSA on ex vivo pig skin experiments

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Introduction: The Phage-EX project aims to determine if phage therapy is a viable strategy to reduce the transmission of livestock-associated methicillin resistant Staphylococcus aureus (LA-MRSA) within and between pig herds and in turn mitigate public health risks. Ex vivo pig skin experiments were used to refine the understanding of bacteria-phage population dynamics on pig skin by fitting an infectious disease model to the experimental data. Methods: Fifteen pig skin samples were inoculated with an LA-MRSA ST398 strain isolated from a pig farm and SA-podovirus phage isolated from pig slaughter wastewater at bacterial concentrations (MOI) of 0.1, 1, and 10. Enumeration of LA-MRSA and phages on the skin was done at regular time intervals, up to 24 hours. An SIR+Phage model of bacteria and phage population dynamics over time was fitted by Approximate Bayesian Computation (ABC) (SimInf in R) followed by a sensitivity analysis (PRCC). Results: The most influential parameters were the binding rate of phages (0.703h-1), and the growth rate of bacteria (0.021h-1). ABC optimization enhanced the fitted model; however, partially account for the differences in the dynamics of the bacteria-phage at differing MOI. New insights into parameters like burst size (58-200) and phage decay (0.006h-1) will inform phage-therapy experimental trials. Discussion: The biological mechanism of bacteria-phage interactions on pig skin warrants further exploration. The model could not entirely fit the differences in MOI by only the starting condition of the experiment indicating that a more realistic model includes other pathways. This may relate to non-specific binding of phages supposedly dependent on the MOI. In the current project, this relationship will be further investigated prior to live animal experiments to identify candidate MOI for effective phage therapy. Conclusions: The findings enhance understanding of the bacteria/phage population dynamics on pig skin and will guide the development of phage therapy for LA-MRSA.

O22 - Better targeting treatments against Bovine Respiratory Disease by combining dynamic generalized linear models and mechanistic modelling

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Bovine Respiratory Disease (BRD) is a major health challenge for young bulls. To minimize economic losses, collective treatments have been widely adopted. Nevertheless, performing collective treatment involves a trade-off between BRD cumulative incidence and severity, and antimicrobial usage (AMU). This raises the question about the optimal timing for treatment. To overcome this challenge, we propose a proof of concept of a decision support tool aimed at helping farmers and veterinarians make informed decisions about the appropriate timing for performing collective treatment for BRD. The proposed framework integrates a mechanistic stochastic simulation engine for modelling the spread of a BRD pathogen (Mannheimia haemolytica), and a hierarchical multivariate binomial dynamic generalized linear model (DGLM). The latter provides early warnings based on the estimated risk of infection. In total, we studied 48 scenarios, using synthetic data, involving two batch sizes (small and large), four farm risk levels of BRD (low, medium, balanced, and high), two allocation systems in batches (sorted by risk level or randomly allocated), and three treatment intervention types (individual, conventional collective, and collective triggered by the DGLM early warnings). In most scenarios, collective treatments triggered by the DGLM were associated with a reduction of the cumulative incidence and severity of BRD cases. Collective treatments triggered by early warnings typically exhibited either lower or equivalent AMU compared to conventional collective treatments. However, in the Low and Balanced-risk scenarios, the use of DGLM-based collective treatments did not provide an added advantage. Additionally, the DGLM estimates of the risks of infection performed well in the first time steps of the simulation when compared to the true empirical risks. Our findings highlight the potential of the proposed decision support tool in providing valuable guidance for improving animal welfare and AMU. Further validation through real-world data collected from on-farm situations is necessary.

O23 - Machine learning augmented diagnostic testing to identify sources of variability in test performance

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Background & aims of study The Single Intradermal Comparative Cervical Tuberculin (SICCT) or skin test is widely used as a diagnostic test for bovine Tuberculosis (bTB). The test itself is highly specific, with few false positives, but has a low sensitivity, meaning that many infections are missed; this leads to a greater likelihood of larger outbreaks and to increased farm-to-farm transmission as a result of cattle movement. There are many potential sources of error in testing, contributing to low test sensitivity, and other surrounding factors that may increase the risk of bTB infection. The relationship between these factors is complex and often highly correlated. In this work we use a machine learning model to integrate a number of these risk factors and error sources with the goal of improving the interpretation of a skin test result. * Methods & results Using a Boosted Regression Tree model, we incorporate risk factors including location, testing history, previous disease status, and veterinary practice and tuberculin batch information, among others. The model is trained on historical data, validated against a reserved proportion of the data, and the trained model improves herd-level test performance (HTP). Whilst maintaining the prior level of HTP specificity, using the model to augment a test result achieves a greater than 10% improvement in HTP sensitivity. We also show that the model effectively reduces the variation in testing accuracy between veterinary practices. Then using a simulation model of bTB transmission in the UK cattle network, we show a reduction in farm ”breakdowns” resulting from the augmented HTP sensitivity provided by the combination of test and diagnostic model. * Implications Greater sensitivity in testing will result in more timely intervention in the case of an outbreak, and thus will have the effect of reduced onward transmission of the disease. This technique is also generalisable to any low sensitivity disease diagnostic testing setting (animal or human) with sufficient available risk data.

O24 - Could ship movements transmit Infectious Salmon Anemia Virus between Norwegian fish farms ?

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In Norway, Infectious Salmon Anemia (ISA) is a notifiable and economically important disease. Accurately understanding between-farm transmission by disentangling the role of human activities, especially ship movements, remains essential for ISA control and prevention. Using a network approach, our objective was to assess the possible contribution of ship movements to ISA virus (ISAV) transmission between farms. We analyzed open-access Barentswatch data

on fish health and ship tracks from 2021 to 2023. We described yearly static networks reconstructed according to ship type (all ships or well boats) and timeframe ($\Delta = 1$, 8 and 15 days between visits). We assessed the relevance of salmon production areas as subdivisions of the network. Finally, we identified ship movements that could have resulted in ISAV transmission between confirmed ISA cases and explored whether the network was associated with the spatiotemporal distribution of these cases using a permutation test. Connectivity was high in yearly networks, with the largest strongly connected component encompassing ≥ 72% of farms. Farms' locations in the same or different production areas influenced their likelihood of being connected, however increasing Δ enabled the connection of distant regions. Even when controlling for farms' locations, the number of possible transmission events identified in the all-ships networks was significantly greater than expected by chance ($p < 0.03$). Ship movements were associated with the distribution of ISA cases, and are, therefore potential viral transmission pathways between farms. While the network was well structured by salmon production areas, inadequate disinfection of ships could lead to longer ISAV survival times, thus resulting in long-distance ISAV transmission events throughout the country. This study highlighted the need to further investigate the role of ships in fish disease spread and the use of genetic data could provide additional insights.

O25 - The role of wildlife diversity and contacts in the circulation of infectious diseases: an integrated monitoring of a human/livestock/wildlife interface in sub-saharan savanna

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In sub-Saharan Africa, the sharing of vital resources like water and grazing among human, wild, and domestic animal populations near unfenced national parks is heavily influenced by strong seasonal variations exacerbated by climate change. Understanding the dynamics of interactions among these populations and their implications for pathogen transmission is imperative for stakeholders. This study focuses on the foot-andmouth disease (FMD) virus as a transmission marker. In Zimbabwe, particularly around its largest national park, Hwange, the porous interface between FMD reservoir hosts like the buffalo, other wildlife, and livestock offers a unique setting to understand each species' role in transmission. Over a span of 1.5 years, a longitudinal survey was conducted on livestock populations residing at the periphery of protected areas, serving as sentinel populations to illustrate FMD dynamics at the interface. Simultaneously, we monitored wildlife community contact and biodiversity in neighboring PAs, especially around surface water bodies, using camera traps and GPS tracking protocols. Host interactions were classified based on their potential role in FMD epidemiology (maintenance, bridge, dead-end), network analyses were employed to reveal potential spatial and temporal heterogeneity of contacts between key species. This study notably marks the first longitudinal survey on goats in Zimbabwe, where vaccination strategies primarily target cattle. Different spatial patterns of disease circulation were observed in both domestic species, indicating distinct epidemiological functions. Intraspecific transmission was more likely in goats than in cattle, with serodynamics in cattle influenced by proximity to specific wildlife communities. At water points, interaction networks at risk of spillover in wildlife were found to be driven by the presence of megaherbivores, regardless of whether they were hosts for FMD. This research, made possible by close collaboration with local stakeholders, integrated extensive ecological and epidemiological surveys to elucidate the link between biodiversity and disease circulation. Through in-depth modeling implementing social network analysis in Capture-Mark-Recapture models, the study demonstrates how pathogen spillover risks are closely tied to the management of protected and communal areas, leading to nuanced spatial patterns rather than broad seasonal ones. Such a community-wide approach remains crucial for addressing ecosystem health and the dilution effect in biodiversity hotspots.

O26 - Evaluating control measures against Highly Pathogenic Avian Influenza spread between Dutch poultry farms: preventive culling and bucket sampling

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Problem Statement: Back in 2003, between-farm transmission of highly pathogenic avian influenza (HPAI) caused a large epidemic in Dutch poultry. Based on current (2024) farm densities and farm sizes, an epidemiological model predicts that current risks of between-farm spread are much lower than in 2003. On the one hand, still one area is identified where sustained between-farm transmission is expected if only minimum European control measures are applied. On the other hand, future epidemics in this high-risk area are predicted to be much smaller than the 2003 epidemic. Over the period September 2021 to September 2022, 57 HPAI outbreaks occurred in commercial poultry in The Netherlands. Fourteen of these outbreaks occurred within the high-risk area, and around most of these outbreaks, 1-km preventive ring culling was applied. The pattern of occurrence of the 57 outbreaks turned out to be compatible with the model predictions. Policy makers asked the following two questions: 1. According to the epidemiological model, what is the currently expected effect of preventive culling within a radius of 1 km in the high-risk area? 2. To what extent could the sampling of dead poultry (bucket sampling) in a zone around outbreak farms, speed up the detection of outbreaks and thus reduce transmission risks compared to the existing, mainly passive, surveillance? Method: Each one of the two questions required its own type of modelling analysis: 1. Model simulation of between-farm transmission for different control scenarios.

2. Modelling within-farm HPAI spread and detection. Results: 1. The model predicts that preventive culling within 1 km in the high-risk area will reduce the average duration of an epidemic of between-farm transmission from 51.4 to 43.9 days and the average total number of outbreak farms from 14.6 to 9.7. However, this comes at a price, as the expected total number of culled farms is 44.8 with preventive culling, compared to 14.6 farms without preventive culling. 2. Bucket sampling on poultry farms can detect an HPAI outbreak on the farm earlier than the existing surveillance system. The predicted reduction in the average time between introduction and detection is approximately 30 percent.

IT1 - ModAH-HUB: a new international network in modelling in animal health

P. Ezanno[1]

[1] Oniris, INRAE, BIOEPAR, Nantes, France

The modeller community in animal health needs to share good modelling practices, develop new methods to face current modelling challenges, work on solutions for simpler and better data access, facilitate model comparison and ensemble modelling, and enhance interactions with end-users and stakeholders. To that end, we propose to federate the scientific community working on epidemiological modelling in animal health in a new international network: the ModAH-HUB. We propose to start with concrete priority actions built upon existing projects, giving progressively room to new ideas and actions. Working groups will concern transversal topics as well as case studies on specific diseases or groups of diseases. To ease model storage, sharing, search and reuse, we also propose to build an extensive and open inventory of animal health models: the ModAH-collection. This talk is a unique occasion to discuss together of this initiative, which aims to be as open and representative of the community as possible.

List of Posters

P01 - Participatory Modelling meets African Swine Fever - Systems Thinking in Action

***J. Schulz**, L. Rogoll, C. Sauter-Louis, K. Schulz*

Friedrich-Loeffler-Institut, Institute of Epidemiology, Greifswald / Insel Riems, Germany

P02 - Epidemiogenetic Modelling for Enhanced Coccidiosis Management in Poultry

***M. Ithurbide**[1], F. Calenge[1], M. Pinard[1], Doeschl-Wilson[2]*

[1] GABI, INRAE, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France.
[2] The Roslin Institute, University of Edinburgh, Easter Bush, Roslin, Edinburgh, UK.

P03 - Revisiting the representation of extrinsic incubation period: finding from modelling within-vector viral dynamics for major arboviruses: Dengue, Zika, and Chikungunya

***L. Loisel**[1], P. Ezanno[2], V. Raquin[2], M. Ratinier[2], G. Beaunée[1]*

[1] Oniris, INRAE, BIOEPAR, 44300 Nantes
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P04 - Inference of a Bovine Respiratory Disease mechanistic model

***H. Farchati**, P. Ezanno, G. Beaunée*

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P05 - Stakeholders' behaviour and public policies: feedback across the farming industry

***M. Roustit**, P. Ezanno, A. Rault*

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P06 - Exposure-induced individual-level heterogeneity as a possible cause of silent transmission of vector-borne diseases

***L. Rongen**, Q. t. Bosch*

Quantitative Veterinary Epidemiology, Wageningen University & Research, the Netherlands

P07 - Modelling the effect of genotype (PRNP) on chronic wasting disease transmission and population dynamics of reindeer

M. N. Osnes[1,2]***, A. Mysterud***[3,4]***, K. R. Dean***[1]***, S. Widgren***[5]***, H. Viljugrein***[1,3]

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[3] Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences, University of Oslo, P.O. Box 1066 Blindern, NO-0316 Oslo, Norway.
[4] Norwegian Institute for Nature Research (NINA), P. O. Box 5685 Sluppen, NO-7485 Trondheim, Norway.
[5] Department of Disease Control and Epidemiology, Swedish Veterinary Agency, P.O. Box 12709, SE-751 89 Uppsala, Sweden.

P08 - Quantification of human exposure to antimicrobial resistant E. coli using a farm-to-fork model in broiler chicken production

S. Basak[1]***, N. Sarnino***[2]***, R. Merle***[2]***, L. Collineau***[1]

[1] ANSES
[2] FU Berlin

P09 - Modelling the spread of Mycoplasmopsis bovis in Sweden using the SimInf framework

I. R. Ewerlöf[1,2]***, T. Rosendal***[1]***, J. Frössling***[1,2]***, S. Gunnarsson***[2]***, E. Hurri***[3]***, L. Stengärde***[4]***, M. Tråven***[5]***, S. Widgren***[1]

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[5] Department of Clinical Sciences, Swedish University of Agricultural Sciences (SLU), SE-750 07 Uppsala, Sweden.

P10 - Investigating domestic-feral pig interactions at an Australian piggery for the purposes of epidemiological modelling

M. Oberin[1]***, V. Brookes***[2]***, M. Stevenson***[1]***, R. Bradhurst***[3]***, S. Firestone***[1]

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tralia.
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P11 - Phylogenetic analysis of swine influenza A: investigating the probability of a new introduced strain in the Netherlands via import from neighboring countries

G. R. Lagerweij, B. R. v. d. Roest, E. A.J. Fischer

Faculty of Veterinary Medicine, Department of Farm Animal Health, Utrecht University, Utrecht, The Netherlands

P12 - The HPAI Modelling Challenge

B. H. Hayes[1], G. Beaunée[2], S. Lambert[1], T. Vergne[1]

[1] IHAP, University of Toulouse, INRAE, ENVT, Toulouse, France.
[2] Oniris, INRAE, BIOEPAR, 44300 Nantes

P13 - The ModAH Hub initiative

G. Beaunée, P. Ezanno

Oniris, INRAE, BIOEPAR, 44300 Nantes

P14 - ModAH Collection: an extensive inventory of animal health models

G. Beaunée, P. Ezanno

Oniris, INRAE, BIOEPAR, 44300 Nantes

List of Participants

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Jonathan Bastard	ANSES
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Useful Information

The conference will take place on the ″Ile de Nantes″, in the **Halle 6 Ouest** - 42 Rue la Tour d’Auvergne, 44200 Nantes, France.

Talks will be held in the conference hall of the *Hall 6 Ouest*. It is situated in the west part of the Agora, behind the poster and break area..

Coffee breaks and lunches will be offered in the east part of the Agora in front of the main entrance of the *Hall 6 Ouest*.

The **poster session** will be held throughout the conference, from Tuesday to Thursday, in the **east part of the Agora** (same location as coffee breaks).

Wi-Fi will be available during the conference, under the name ″tiers-lieux nantes-univ″.

The **conference dinner** will be held in a boat on the river Erdre, departing from the pier at Place Waldeck Rousseau, Quai de la Motte Rouge, 44008 Nantes.

Partner Institutions

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- Nantes Métropole