Modelling in Animal Health – ModAH conference
Nantes – School of architecture

As part of: MiHMESS Project

Funded by: ANR, INRA, INRAE, CNRS, IRT, et al.
Committees

Scientific committee


Local organising committee

Myriam Amami – Pauline Ezanno – Mily Leblanc-Maridor – Luyuan Qi

Funders

Partners
Abstracts from oral communications listed by session according to the programme order

Session 1: Host-parasite interactions
Session 2: Regional epidemiological modelling
Session 3: Control strategies and economics
Session 4: Epidemiological networks
Session 1 : Host-parasite interactions
Understanding transmission patterns of animal infections using pathogen sequence data and phylodynamics

Dr Samantha Lycett

\textsuperscript{a} Roslin Institute, University of Edinburgh

* Samantha.Lycett@ed.ac.uk

Sequencing pathogens from infected animals during outbreaks and in endemic disease settings has become much more affordable and widespread in recent years. This means that there is a growing corpus of animal pathogen sequences spanning several countries and years, and these sequences can be used to derive insights into national and international disease transmission patterns. Pathogen sequences accumulate mutations over time and using molecular clock models, time scaled trees can be created in order to track the spread of infection. By including host-type or location information as a trait, phylogeographic models can be inferred enabling quantitative transmission patterns to be estimated.

Here I will describe the use of phylodynamic techniques, especially Bayesian time resolved phylogenies together with discrete or continuous locations for modelling the spread of viral pathogens in animal populations. The amount of sequence variation between samples influences the scale at which transmission patterns can be inferred, and I will describe ways in which whole genomes or short regions are being used for analysing epidemic and endemic situations, including their potential role in disease eradication programmes. Additionally using data from highly pathogenic avian influenza outbreaks, I will show the how the effects of transmission in different host populations on the global spread and generation of new subtypes can be analysed. By considering the spread of bovine viral diarrhoea virus into and around Scotland, I will also show how predictors of transmission patterns can be identified using phylodynamics with model selection and generalized linear modelling frameworks, and describe how the relative importance of local spatial spread vs transmission due to animal movements in a trade network can be estimated.
Predicting Dynamics of Extended-Spectrum Beta Lactamase producing \textit{E. coli} in broilers

Fischer EA\textsuperscript{a,}*, Ceccarelli D\textsuperscript{b}, Dame-Korevaar MA\textsuperscript{a}, Dierikx C\textsuperscript{c}, Klinkenberg D\textsuperscript{c}, Mevius D\textsuperscript{a,}\textsuperscript{b}, Van der Goot JA\textsuperscript{b}

\textsuperscript{a} Faculty of Veterinary Science, Utrecht University, The Netherlands
\textsuperscript{b} Wageningen Bioveterinary Research, The Netherlands
\textsuperscript{c} National Institute for Public Health and the Environment, The Netherlands

* e.a.j.fischer@uu.nl

Extended-spectrum Beta lactamase (ESBL) genes, located on a transferable plasmid, encode for an enzyme able to hydrolize beta-lactam antimicrobials. The prevalence of ESBL producing bacteria in poultry is high, raising concerns for a spill-over to humans. A ban on specific antimicrobials selecting for ESBL producing bacteria in poultry production mitigates the prevalence of ESBL producing bacteria. Chickens ceased to excrete ESBL producing \textit{E. coli} within 20 weeks in one occasion [1], but on another organic farm were still present at slaughter [2]. Here we present a series of experimental and modelling studies to predict dynamics of ESBL producing bacteria in poultry in the absence of selective antimicrobials.

In \textit{in vitro} experiments, no competitive disadvantage could be found between \textit{E. coli} and the same \textit{E. coli} containing an ESBL-gene. Lotka-Volterra based models, in which we added plasmid transfer, were fitted to the growth curves of these experiments [3]. Extrapolating these findings for densities of \textit{E. coli} realistic to the chicken gut, we predicted that a minor and \textit{in vitro} unmeasurable competitive disadvantage was shown to lead to extinction of ESBL producing bacteria within the time-scale of a broiler production round (Klinkenberg et al. in prep.).

\textit{In vivo} challenge experiments were conducted to study the competition in a realistic system. Broilers were inoculated with mixed cultures of \textit{E. coli} with and without ESBL genes. We observed large differences in the dynamics of the same \textit{E. coli} carrying the same ESBL genes in different groups of broilers, and were able to apply our mathematical models to distinguish between (Fischer et al. in prep).

In conclusion, the interaction between experiments and mathematical modelling has supplied model-systems for within-host dynamics of ESBL producing bacteria. These model systems are currently extended to provide insight in dose-response and transmission dynamics of ESBL producing bacteria (Dame-Korevaar et al. in prep.).

Neutralising antibodies prevent PRRS viremia rebound: evidence from a data-supported model of immune response

Natacha Go\textsuperscript{a,b,c\*}, Suzanne Touzeau\textsuperscript{c,d}, Catherine Bello\textsuperscript{a}, Andrea Doeschl-Wilson\textsuperscript{c}

\textsuperscript{a} UMR1300 BioEpAR, INRA, Oniris, CS 40706, 44307 NANTES Cedex 3, France
\textsuperscript{b} BIOCORE, Inria, CNRS, UPMC Univ Paris 06, Université Côte d’Azur, France
\textsuperscript{c} Division of Genetics and Genomics, The Roslin Institute, Midlothian, UK
\textsuperscript{d} ISA, INRA, CNRS, Université Côte d’Azur, France

\* natacha.go@laposte.net

Understanding the mechanisms determining the variability in infection dynamics between hosts or strains for a given pathogen is a key issue to better understand and control infection spread. In particular, effective and constant reduction in pathogen load is desirable over infection profiles exhibiting rebounds for the health of the infected individuals and the entire herd. In this context, PRRS virus is of a particular interest. Indeed, (i) infection profiles either with or without rebound have been reported for various viral strains and host breeds; (ii) mechanisms responsible for the emergence of rebounds are unclear; (iii) PRRS virus infections are associated with highly variable global immune responses and mechanisms responsible for the infection dynamics are still poorly understood.

We aimed at identifying immune mechanisms that could explain PRRS\textsubscript{v} infection rebounds using a mathematical modelling approach of the within-host dynamics. Compared to published immunological models, our model provides both an integrative and detailed view of the immune response, representing the mechanisms at the between-cell scale. We fitted the model to a set of viremia data following an experimental challenge of 240 pigs with the same dose of a virulent PRRS virus strain resulting in both rebounder (109) and non-rebounder (131) profiles. Within a profile, experimental data exhibited a wide between-host variability in infection dynamics. Between both profiles, the variability in infection dynamics preceding the rebound (i.e. during the first 20 days of the 42-day post inoculation observation period) was similar. We compared, between rebounders and non-rebounders, the set of estimated parameter values, the resulting immune dynamics and the activation levels of the underlying immune mechanisms. The activation levels were quantified by the cumulated number of viral particles or infected cells that were created or destroyed over the infection time (i.e. the flows) by mechanisms of interest: viral replication, phagocytosis of viral particles, cell infection, viral neutralisation, cytolysis (by natural killers and cytotoxic lymphocytes) and apoptosis (by TNF\textsubscript{\alpha} antiviral cytokine) of infected cells.

Compared to non-rebounders, rebounders were characterised by a higher level of immune response activation, due to higher rates of cell infection. They also exhibited higher flows of infected cell cytolysis and apoptosis, but similar viral neutralisation flows despite higher infection and viral replication flows. This points out an inadequate production of neutralising antibodies.

These results would suggest that vaccines or genetic selection promoting a strong neutralising response, ideally associated with strong antiviral and cytolytic responses, should prevent against infection with rebound.
Modelling the Innate Immune Response against Avian Influenza Virus in Chicken

T.J. Hagenaars\textsuperscript{a*}, E.A.J. Fischer\textsuperscript{a,e}, C.A. Jansen\textsuperscript{b}, J.M.J. Rebel\textsuperscript{a,f}, D. Spekreijse\textsuperscript{c,g}, L. Vervelde\textsuperscript{b,h}, J.A. Backer\textsuperscript{a,i}, M.C.M. de Jong\textsuperscript{d}, A.P. Koets\textsuperscript{b,h,c}

\textsuperscript{a} Central Veterinary Institute, part of Wageningen UR, Lelystad, The Netherlands,
\textsuperscript{b} Department of Infectious Diseases and Immunology, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands,
\textsuperscript{c} Department of Farm Animal Health, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands,
\textsuperscript{d} Quantitative Veterinary Epidemiology, Wageningen University, Wageningen, The Netherlands
\textsuperscript{e} Current address: Department of Farm Animal Health, Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands
\textsuperscript{f} Current address: Wageningen UR Livestock Research, Wageningen, The Netherlands
\textsuperscript{g} Current address: Boehringer-Ingelheim Animal Health Operations bv, Weesp, The Netherlands
\textsuperscript{h} Current address: The Roslin Institute and R(D)SVS, University of Edinburgh, Edinburgh, United Kingdom
\textsuperscript{i} Current address: Centre for Infectious Disease Control, National Institute for Public Health and the Environment, Bilthoven, The Netherlands

\* thomas.hagenaars@wur.nl

At present there is limited understanding of the host immune response to (low pathogenic) avian Influenza virus infections in poultry. Here we develop a mathematical model for the innate immune response to avian influenza virus in chicken lung, describing the dynamics of viral load, interferon-\(\alpha\), interferon-\(\beta\) and interferon-\(\gamma\), lung (i.e. pulmonary) cells and Natural Killer cells [1]. We use recent results from experimentally infected chickens to validate some of the model predictions. The model includes an initial exponential increase of the viral load, which we show to be consistent with experimental data. Using this exponential growth model we show that the duration until a given viral load is reached in experiments with different inoculation doses is consistent with a model assuming a linear relationship between initial viral load and inoculation dose. Subsequent to the exponential-growth phase, the model results show a decline in viral load caused by both target-cell limitation as well as the innate immune response. The model results suggest that the temporal viral load pattern in the lungs displayed in experimental data cannot be explained by target-cell limitation alone. For biologically plausible parameter values the model is able to qualitatively match to data on viral load in chicken lungs up until approximately 4 days post infection. Comparison of model predictions with data on CD107-mediated degranulation of Natural Killer cells yields some discrepancy also for earlier days post infection.

Hindcasting historical trends of endemic Foot-and-mouth disease from cross-sectional data by leveraging within-host dynamics

Gustaf Rydevika, Mark Bronsvoorta

a Roslin Institute, Edinburgh University, Easter Bush, EH25 9RG, UK

* gustaf.rydevik@roslin.ed.ac.uk

When managing infectious diseases, it is crucial to be aware of how the incidence trend is developing, both to be able to act on unexpected increases, and to evaluate the effect of any implemented control measures. However, in many settings and for many diseases, there is at most limited surveillance data with which to track incidence trends. Being able to recover information on disease trends from limited data has major implications for the management and control of infectious diseases.

A quantitative diagnostic test measuring e.g. a specific immune response can be used as an indication of the state of the ongoing dynamic infection process within the host. Combining two or more tests can give a unique signature for each stage of the disease process, and can be used to estimate the time since infection. On a population level, it is then possible to estimate the overall distribution of infection times, as well as any increasing or decreasing trend.

We have developed a Bayesian methodology for hindcasting infectious diseases (i.e. reconstructing historical trends from currently available data) based on cross-sectional diagnostic test data, collected at a limited number of timepoints. The hindcasting framework leverages published information from e.g. experimental infection studies that describe how a diagnostic test responds in different phases of the host-pathogen interaction. This information is integrated in a statistical model of quantitative diagnostic test results collected from infected animals. We have previously published a paper[1] describing this framework for an epidemic setting and how it can hindcast the trajectory of a disease epidemic before the time of detection.

In this talk, we will present how the framework can be extended to an endemic setting, and describe how it was used to analyze a large dataset on the distribution of Foot-and-Mouth Disease (FMD) infection in 147 randomly selected herds from the Adamawa region of Cameroon [2]. Each animal had been tested for FMD with multiple different diagnostic tests, including different antibody ELISA tests, virus neutralization tests, and cell culture.

We identified a number of existing studies with records of the development of diagnostic test responses following FMD infection, and used these to construct a statistical model that describe the expected distribution of the different tests conditional on a given time since infection. The statistical model for the conditional distribution of test results was then combined with the individual test results, to provide an estimate for if and when the different herds had been infected with FMD, and estimates of the overall disease trends. Finally, the estimated times since infection were compared with information collected from herdsman that had been asked to recall the most recent FMD incursion for each herd. While such information is naturally uncertain, the correspondence between incursion estimates provided by the herdsman and estimates generated by the hindcasting framework support the reliability of the framework. This first demonstration of recovering dynamic trends of an economically important disease in a livestock setting, using cross-sectional data shows the considerable potential of leveraging within-host dynamics for infectious disease epidemiology.

Pig-to-pig direct transmission of Japanese encephalitis: its importance in two pig cohorts in Cambodia.

Alpha Oumar Il Diallo\textsuperscript{a,b,*}, Véronique Chevalier\textsuperscript{a,b}, Julien Cappelle\textsuperscript{a,b}, Didier Fontenille\textsuperscript{b}, Raphaël Duboz\textsuperscript{a,b}

\textsuperscript{a} CIRAD, UMR ASTRE, Montpellier, France
\textsuperscript{b} Institut Pasteur du Cambodge (IPC), Epidemiology and Public Health unit

* alpha-oumar.diallo@cirad.fr

Japanese Encephalitis (JE) is the most important cause of human encephalitis in several Asian regions and the Pacific. While JE is a vector-borne disease, Ricklin et al (Ricklin et al., 2016) recently demonstrated experimentally that transmission between pigs can occur via direct contact. Whether pig-to-pig transmission plays a role in the natural epidemiological cycle of JE remains unknown. To assess whether direct transmission between pigs may occur in farms we built two mathematical models of JE transmission taking into account either vector-borne transmission alone or a combination of vector-borne and direct transmission. We used Markov Chain Monte Carlos (MCMC) techniques to estimate the different parameters of the models. We fitted the models to serological data collected during two periods of four months in a farm located in the outskirt of Phnom-Penh, Cambodia. We selected the model that best explains the data i.e. the model that minimizes the sum of squares error by using the least squares criterion. Results show that the model with the combination of both vector-borne and direct transmission better explains the data. We used this model and the next generation matrix approach to determine the basic reproduction number $R_0$ as well as the vector-borne reproduction number $R_{pv}$ and the direct transmission reproduction number $R_{pp}$. Then, we determined the contribution of direct transmission versus vector-borne transmission on $R_0$ for the two cohorts. According to our results, the existence of pig-to-pig transmission is coherent with observed serological data. It may contribute to JE epidemiological cycle in our pilot study area. However, direct transmission may not sustain an outbreak without vector-borne transmission. Surprisingly, results show that the importance of pig-to-pig and vector-borne transmission are linked. It could be explained mechanistically. When one transmission mode first occurs for an individual, this individual can not be infected via the other transmission mode anymore. In the two periods of our study we observed a high density of mosquitoes around the pig farm. High density of mosquitoes with a high proportion of infectious mosquitoes could explain the fact that vector-borne transmission is the main transmission process of JE virus and the fact that pig-to-pig transmission passes unnoticed. These results need to be confirmed in other eco-climatic settings, in particular in temperate areas where pig-to-pig transmission may allow JE virus persistence during cold seasons.

**Key Words**: Japanese Encephalitis (JE), pig-to-pig transmission, MCMC, Cambodia.

Session 2 : Regional epidemiological modelling
The majority of Animal Health problems have a regional dimension. Hence, a variety of epidemiological models explicitly focuses spatial transmission beyond the local context of the farm. However, these studies often lack adequate or timely data or build their prediction on one particular realization of the associated regional spread. Facing these limitations in representativeness, still regional modelling in Animal Health can strengthen decisions and elicit purposeful scenarios for action. Selected examples of such models then often involve efforts to demonstrate credibility of the model to evaluate management activities. Confronting the model implications post-hoc with real-world outcomes of the regional spread of a pathogen contributes to this credibility. However, what if the model failed? What if the subsequent decision were only marginally successful? Are modelers prepared for their model-based conclusions failing? Surely, we will not be able to solve this problem in completeness. But multiple uses of regional models for decision support urges to reflect more about the issue of failing. This is the main objective of this presentation. The methods are non-systematic use of available applications of models to advice animal health activities. The proposed outcome will be identified challenges, possible dangers and useful look-after in the process of Animal Health applications of regional epidemiological models.
Spatio-temporal modelling of VTEC O157 in cattle in Sweden: Exploring options for control

Stefan Widgren\textsuperscript{a*}, Stefan Engblom\textsuperscript{b}, Ulf Emanuelson\textsuperscript{c}, Ann Lindberg\textsuperscript{a}

\textsuperscript{a} Department of Disease Control and Epidemiology, National Veterinary Institute, Sweden.
\textsuperscript{b} Department of Information Technology, Uppsala University, Sweden.
\textsuperscript{c} Department of Clinical Sciences, Swedish University of Agricultural Sciences, Sweden.

\* Stefan.widgren@sva.se

Verotoxigenic \textit{Escherichia coli} O157:H7 (VTEC O157) is an important zoonotic pathogen capable of causing infections in humans, sometimes with severe symptoms such as haemorrhagic colitis and haemolytic uremic syndrome (HUS). Cattle are considered to be the main reservoir of VTEC O157 and infected animals shed the bacteria in their faeces, which could subsequently infect humans through for example contamination of the environment, food and water. Introduction of animals and proximity to VTEC O157 infected farms \cite{1, 2} are associated with an increased risk for VTEC O157 infection in cattle herds. Moreover, seasonal variation in ambient temperature could have a considerable effect on the survival and growth of VTEC O157 in the environment and consequently on the indirect transmission dynamics \cite{3}.

In this work we present a spatial data-driven stochastic model that was developed in the SimInf R package \cite{4, 5, 6} to explore the spread of VTEC O157 by livestock movements and local transmission among proximal holdings in the complete Swedish cattle population. All Swedish livestock data 2005-2013 was incorporated to model the time-varying contact network between holdings and the population demographics. Meteorological data were used to model the spatio-temporal seasonal variation at the geographical location of each holding. The model was fitted against observed longitudinal data \cite{2} and extensive numerical experiments were conducted to investigate the model's response to a change in parameters reflecting a reduced shedding and susceptibility, and to targeted control actions informed by the temporal network measures: indegree, outdegree, ingoing-and outgoing contact chain.

The model identified the location of the geographical regions with the most pronounced clustering of infected holdings as in agreement with previously reported prevalence studies. Interestingly, this was regardless of whether spread between local farms was included or not. Simulated control measures based on reducing the between-herd VTEC O157 transmission by animal movements and spread between local farms, had marginal effect on the prevalence. On the other hand, control measures based on reducing the shedding and susceptibility, were efficient in decreasing the prevalence of VTEC O157 in the Swedish cattle population.

Complex dynamic model fitting to test Animal Health contingency plans in wildlife

Martin Lange*ª, Hans-Hermann Thulkeª
ªHelmholtz Centre for Environmental Research Leipzig – UFZ, Dept. Ecological Modelling

* martin.lange@ufz.de

The management of emerging diseases suffers high uncertainties due to a lack of previous experience. A highly topical example is African swine fever (ASF) in Eastern Europe. The presented study combines an individual-based, spatially explicit model of ASF in wild boar populations with an innovative approach for the comparison of point patterns, to reduce uncertainties regarding ASF infection mechanisms. The two most sensitive and uncertain parameters of the model, describing virus transmission by infectious carcasses, were systematically varied. Simulation results were compared to real-world case data of a region in Eastern Europe for which dissemination by domestic pigs can be excluded. For comparison of simulated and real-world point patterns, we developed an approach based on the full spatial and temporal information provided by case notifications. We project simulated and real-world data into the 3-dimensional space comprising location and time of the event points. The resulting 3-dimensional point clouds are buffered to obtain volumes, and set theory methods are applied to quantify their similarity. The approach allows for a spatially and temporally explicit comparison of model outcomes with real-world data, which is robust towards sampling biases like over-reporting or gaps in the data. The parameter combinations producing the highest similarity to the underlying real-world dataset suggest a high potential for the contact between wild boar and their conspecific’s carcasses, but sporadic realization of contact and transmission. The successful implementation of the procedure allows for more transparent parameterisation of the model. Clear insights about useful parameter ranges facilitate exhaustive model testing in order to support Animal Health decision making planned to combat the infection in wildlife.
Modelling BVD through farm productive compartments

Bryan Iotti\textsuperscript{a}, Eugenio Valdano\textsuperscript{b}, Mario Giacobini\textsuperscript{a}*, Lara Savini\textsuperscript{c}, Armando Giovannini\textsuperscript{c}, Sergio Rosati\textsuperscript{a}, Vittoria Colizza\textsuperscript{d,e}, Luca Candeloro\textsuperscript{c}

\textsuperscript{a} Department of Veterinary Sciences, University of Turin, Torino, Italy
\textsuperscript{b} Departament d’Enginyeria Informàtica i Matemàtiques, Universitat Rovira i Virgili, Tarragona, Spain
\textsuperscript{c} Istituto Zooprofilattico Sperimentale dell’Abruzzo e del Molise G. Caporale, Teramo, Italy
\textsuperscript{d} Sorbonne Universités, UPMC Univ Paris 06, Institut Pierre Louis d’Épidémiologie et de Santé Publique, Paris, France
\textsuperscript{e} ISI Foundation, Torino, Italy

* mario.giacobini@unito.it

The application of network science to the analysis of bovine movement networks showed that farms were exposed to different risk levels based on the intensity of their network activity and their role within the network itself [1-2]. We propose that farms exhibit different epidemiological behaviours depending on the productive compartment they belong to within the network. We use data of the Italian bovine movement network from January 1st 2014 to December 31st 2014, comprising around 8 million movements between 150000 active nodes in the network. We aggregate the dataset over each link between farms on a weekly basis to obtain a weighted directed graph. Each farm hosts three compartments, healthy and susceptible, persistently infected (PI), and persistently infected (latent) animals (PIL). The latter represents dams carrying a calf that was infected in utero and will become a PI. In this stage, the calf is not infective and is very difficult to detect immunologically, but can be moved between farms freely before birth, after which it will become extremely infective with serious epidemiological consequences. The model represents this as a transition from PIL to PI that occurs with a simple probability $\varphi$. PIs can be eliminated at a rate imposed by the free parameter $\mu$, or they can generate PILs at a rate $\varepsilon = \varepsilon(\alpha N - PIL)$, where $\varepsilon$ governs infection spreading and $\alpha$ is the percentage of females in that compartment, calculated from the original movement data. Total clearance of PI and PIL within a farm may occur with probability $M$ due to the insurgence of the fatal mucosal disease. Movements may include PIs and PILs proportional to their prevalence. To create plausible starting conditions, 1% of all farms was seeded randomly with 1 PI animal. We repeated the year’s movements 60 times, keeping the order of the weeks while applying constant-prevalence rescaling to the numerosities every 52 weeks, thus stabilizing the number of heads in the system since sales, births, deaths, and slaughterhouses are still present. Simulations were run for different values of the $\varepsilon$ parameter, ranging from 1/3 to 2x $\mu$ in increments of 1/3 and for 50 runs each. We consider four different productive compartments: beef cattle without reproduction (AL-C), beef cattle with on-farm reproduction (AL-CS), dairy cattle with reproduction (AL-LS), mixed attitude farms with reproduction (AL-MS). The ability to examine each productive compartment separately allows the identification of markedly different behaviours and prevalence levels for each of the productive compartments. These results may be used for planning more efficient control programs.

A meta-population model for the transmission of *peste des petits ruminants* virus in West Africa

Andrea Apolloni*a,b,c, Caroline Costea*b, Renaud Lancelot*a,b, Pachka Hammami*a,b, Marius Gilbert*, Gaëlle Nicolas*c, Mamadou Ciss*d, Yves Amevoïne*d, Bezeid ould elMameye, Barry Yahya*e, Ismaila Seck*e

*a French Agricultural Research for Development (CIRAD), UMR 117 Astre, Campus International de Baillarguet, 34398 Montpellier, France

*b French National Institute for Agricultural Research (INRA), UMR Astre, Campus International de Baillarguet, 34398 Montpellier, France

*c Université Libre de Bruxelles, Spatial epidemiology Lab., 1050 Brussels, Belgium

*d Institut Sénégalais de Recherches Agricoles, Laboratoire National d’Elevage et de Recherche Vétérinaire, Parc Scientifique de Hann, Dakar, Sénégal

*e Centre National d’Elevage et de Recherches Vétérinaires, Service de Pathologie Infectieuse, BP 167 Nouakchott, Mauritania

* andrea.apolloni@cirad.fr

*Peste des petits ruminants* (PPR) is caused by a *Morbillivirus* (Paramyxoviridae) that infects mostly goats and sheep. Discovered in Ivory Coast in 1942, this disease is now endemic in most African countries and has spread in Asia as far as India and China. In immunologically naïve small ruminant populations, mortality rate is around 90% among younger animals, whilst it has milder effects on older ones. PPR has a devastating effect on the economies of low-income families. A live attenuated vaccine was developed in the 1980’s, providing a life-long immunity after a single injection. The global eradication of PPR is now on the agenda of the Food and Agricultural Organisation of the United Nations (FAO) and World Animal Health Organisation (OIE) who play a pivotal role as they aim to reach this goal before 2030.

Mobility of live animals is the most important factors in the diffusion and in maintaining the disease endemic in West Africa. It is a complex phenomenon involving different types of movements: small ruminants’ trade among Western Africa countries (http://faostat.fao.org/); transhumance from arid areas of the North to greener areas in the South and sometimes crossing frontiers; religious festivity, like Tabaski during which millions of sheep are slaughtered. With this respect, Senegal and Mauritania have developed a system of animal health certificates to track livestock movements. These data allow researchers to re-construct the mobility network at the country level, and provides hint about animal movements across their borders.

To describe PPR diffusion patterns, estimate its infectious burden, and assess the effects of PPR vaccination strategies we have been developing a metapopulation model for PPR in Mauritania and Senegal. We consider a network whose nodes correspond to administrative districts, and whose links represent the animal movements between two of them. The model couples the virus transmission and small ruminant population dynamics occurring at the local (within-district) level, with the virus diffusion due to livestock mobility.

The model uses different data sources. The mobility network is built on the data collected by the Mauritanian and Senegalese Veterinary Services. Small ruminant population dynamics is calibrated on the data from previous follow-up studies implemented in Senegal. PPR prevalence and epidemiological data are taken from the VACNADA project (http://au-ibar.org/vacnada).
We briefly present the analysis of the different data sources to provide a panoramic view of the situation in West Africa. We then present some of the results of the model, focusing on the conditions that could lead to PPR outbreaks, maintain its endemcity, or stop the epidemics.

Inference in a metapopulation model of paratuberculosis in cattle via a composite-likelihood approximation

Beaunée G.*a,b, Ezanno P. b, Joly A. c, Nicolas P. a,*, Vergu E. a,#

a MaIAGE, INRA, Université Paris-Saclay, 78350, Jouy-en-Josas, France;
b Bioepar, INRA, Oniris, CS40706, 44307, Nantes, France;
c GDS Bretagne, France;
# These authors contributed equally to this work
*gael.beaunee@inra.fr

Processes related to the spatio-temporal spread of pathogens in metapopulations are most often partially observed, especially for long-lasting endemic diseases. Bovine paratuberculosis (agent Mycobacterium avium subsp. paratuberculosis – Map) is a worldwide enzootic disease of economic importance for dairy cattle producers. Its screening in the field is difficult due to long incubation period and low sensitivity of routine diagnostic tests. Our objective was to estimate key parameters of a multiscale dynamical model of Map spread from longitudinal disease-related data to learn more about the infection dynamics of this disease.

Our approach is based on a mechanistic simulation model of Map spread between dairy herds, accounting for stochastic within-herd demography and infection dynamics, and animal trade between farms. Simulations were done at a regional scale and included a total of 12,857 dairy herds in Brittany (France), for which comprehensive data on cattle trade and partial data on animal infection status (2013 herds sampled from 2005 to 2013) were available.

Five key parameters of this model are: the proportion of initially infected herds, the within-herd initial prevalence in infected herds, the probability of purchasing infected cattle from outside the metapopulation, the local indirect transmission rate, and the sensitivity of the diagnostic test.

Since a diversity of metrics could be envisioned to evaluate the distance between observations and simulations, we compared the behavior of many of these metrics in an exploratory numerical study based on a grid of parameter values associated with simulated data sets. The most promising performances were obtained with metric built as a Monte-Carlo approximation of a composite likelihood accounting for correlation between consecutive sampling points. Inference was then conducted by coupling this composite likelihood approximation with a numerical optimization algorithm (Nelder-Mead).

After validation of the inference algorithm on simulated data sets, we estimated previously unknown key parameters of the model thereby providing new insights on Map spread at regional scale.
MODELLING LA-MRSA SPREAD BETWEEN DANISH PIG HERDS

Jana Schulz*, Anette Boklund³, Nils Toft³, Tariq Halasa³

* Technical University of Denmark, National Veterinary Institute, Bülowsvej 27, 1870 Frederiksberg C, Denmark

Livestock associated Methicillin-resistant Staphylococcus aureus (LA-MRSA) of the type CC398 was first described by Voss et al. in The Netherlands in 2005 [1]. Since 2005, LA-MRSA was found in humans, pigs as well as in other animal species. A survey by the European Food Safety Authority (EFSA) in 2008 found 0% of the Danish breeding herds and 3% of the Danish pig production herds positive for LA-MRSA of type CC398 [2]. However, surveys conducted in 2014 showed an increase in the prevalence to 63% in breeding herds and 68% in slaughter pig herds [3].

Main drivers for LA-MRSA spread between pig holdings are believed to be transmission via animal movements and during pig transport [4]. Since the EU regulations require identification and registration of animals, data on animal movements are available on large scale and thus could be used as input in disease spread models. We developed a simulation model to quantify the role of the Danish pig movement network in the spread of LA-MRSA. We aimed (1) to assess whether transmission of LA-MRSA via pig movements alone can account for the observed pattern of the increase in prevalence in Denmark, and (2) to evaluate the effect of other transmission mechanisms. Herd information and movement data from 1 Jan 2006 to 31 Dec 2015 were used as basis for modelling. Within-herd dynamics were modelled as three compartment SIS model with different transmission rates within the three compartments of sows, weaners and finishers and with high and low risk transmission routes between these compartments. We developed stochastic and time-discrete simulation processes to mimic the cleaning of pigs from LA-MRSA, within-herd dynamics, transmission of LA-MRSA via pig movements and other transmission routes such as environmental transmission and indirect herd contact via humans or trucks. Several scenarios mimicking the introduction of LA-MRSA to Denmark were modelled taking into account the results of the EFSA survey in 2008. We compared the model outcome to the results of later LA-MRSA surveys conducted in Denmark. An extensive sensitivity analysis was performed to study the effect of uncertainty of model parameters.

In the future, control options such as trade restrictions will be implemented to test consequences of these control programs as well as options for eradication.

Modeling Bovine Viral Diarrhea Virus (BVDV) Spread between Dairy Cattle Farms at a Regional Scale

Luyuan Qi*a, Elisabeta Vergu*b, Pauline Ezanno*a
a BioEpAR, INRA, 44307 Nantes, France
b MaiAGE, INRA, Université Paris-Saclay, 78350 Jouy-en-Josas, France

In a region, cattle farming systems are heterogeneous in size and production, and various between-herd interactions such as animal movements (MV) and neighboring contacts (NB) exist. In order to explore pathogen spread and evaluate control strategies at a regional scale, modeling is a pertinent approach, especially when complicated heterogeneity and interactions should be incorporated and biological mechanism of the system is not sufficiently acknowledged.

Bovine Virus Diarrhea is a widespread endemic disease of cattle that is recognized as a significant economic burden in the majority of countries throughout the world. Bovine Viral Diarrhea Virus (BVDV) is transmitted through both horizontal and vertical pathways. Animals exposed to BVDV are either persistently (PI) or transiently (TI) infected. PI animals are the most important sources of the virus because they continuously shed BVDV throughout their lifetime [1]. Infected animals in one herd could spread BVDV to other herds when between-herd interactions exist. Thus, interacted herds might be repeatedly infected, leading to high prevalence and long persistence of virus at both herd and regional scales. Therefore, a better understanding of BVDV spread mechanism at a regional scale is crucial for guiding eradication of BVDV. And the evaluation of collective control schemes before applying them to farms is expected by animal health managers and authorities. Both aspects motivated this study.

To achieve our intentions, a novel stochastic multiscale epidemiological model in discrete time including both within and between-herd transmission processes was developed. The within-herd dynamics consisted of horizontal and vertical transmissions, diseases progression and herd specific demography. BVDV vertical transmission parameters were calibrated based on limited information from field data. Parameters required for demography such as birth and outgoing rates were calibrated on a comprehensive database on French cattle life trajectories. MV which was entirely data-driven and NB were taken into account when modeling between-herd transmissions. NB were defined within circular neighborhoods of fixed radius and contributed to the infection process during pasturing seasons. The model was developed in C++.

Intensive simulations of BVDV spread in a metapopulation of 12,750 dairy herds (with more than 10 female adults) located in Brittany (France) were carried out from the developed model. We initially introduced one PI cow into 10% randomly selected herds, and ran the model for 9 years of observations by using moderate epidemiological parameters and neighbor contacts. It was found that NB and MV contributed to BVDV spread with different perspectives. NB brought periodic effects to both regional prevalence (number of infected herds in the region) and incidence (number of newly infected herds) over time, with higher values during pasture seasons. NB contributed more than 70% to the cumulated incidence over 9 years. The within-herd infections caused by NB tended to extinct faster and lead to a lower number of infected animals. The developed model was highly sensitive to between-neighbor transmission rate, and the sensitivity to neighborhood radius varied with the between-neighbor transmission rate, being weak for small between-neighbor transmission rates. Additional study will be carried out within the proposed model framework addressing fitting the developed model to epidemiological data of BVDV.

Predicting range expansion of the invasive yellow-legged hornet, *Vespa velutina*, in France and the effects of control measures

Christelle SUPPO*, Christelle ROBINET, Eric DARROUZET

* Institut de Recherche sur la Biologie de l’Insecte, UMR 7261, CNRS – Université François-Rabelais de Tours, F-37200 Tours, France

b INRA, UR633 Zoologie Forestière, F-45075 Orléans, France

* christelle.suppo@univ-tours.fr

The invasive yellow-legged hornet, *Vespa velutina*, is native to Asia and was first discovered in Europe in 2005, in south-western France. Since then, it has established and spread very rapidly throughout France and neighboring countries. The Asian hornet causes serious ecological and economic problems as it kills domestic honeybees, and it can also impact human health because of possible allergic reactions following the insect sting. It is thus very important to understand the spread mechanism and contain its range expansion.

Rapid spread of invasive species is usually attributed to accidental transportation with human activities. Here, we present a model that describes the spread of this Asian hornet accounting for active dispersal of the species, long distance jumps, and also the effects of control measures. This model combines a reaction-diffusion model with the population growth rate related to the local climate, and a stochastic long-distance dispersal model. A mortality rate was included in the model to simulate the nests destruction. This model was calibrated on the invasion history in France between 2005 and 2009 and was validated on observations done in 2013.

Following these simulations, we conclude that this rapid spread does not necessarily imply long distance jumps due to human activities since the Asian hornet has very high dispersal capabilities by itself. Although it would be difficult to slow the spread of this invasive species, it would be possible at least to reduce the population level and thus reduce the ecological and sanitary impacts when increasing the control measures (e.g., nest removal).
Session 3 : Control strategies and economics
Broadening the Role and Relevance of Economics in Farmed Animal Health Management

David A. Hennessy

Department of Agriculture, Food & Resource Economics, Michigan State University, United States of America

hennes64@msu.edu

Health management is about protecting valuable assets. Economics is about understanding how resources are actually used and about how they might be better used to meet certain goals. When, as is always the case, resources are limited then economic considerations must be contemplated. Ethical considerations regarding decisions on life quality have obscured the goals for use of resources in human healthcare. Even so, the economics of human health is a large and expanding sub-field of economics. If anything, economic objectives when seeking to manage the health of farmed animals are less controversial. And yet economics play very limited roles in designing animal health management policy.

Cost-benefit analysis, decision analysis under risk, supply and demand analysis, trade impact welfare surplus assessments, willingness to pay methods and several other approaches are widely applied in animal health economics. Less developed are ways to understand and modify decisions regarding infectious diseases. Infectious diseases present distinctive management problems because herd owners may not be well-incentivized to make decisions that are consistent with maintaining and improving returns on other herds. For example, an owner may choose not to vaccinate against a disease if she believes that a sufficient number of herd owners in the area will do so. If all herd owners think like this then the general vaccination rate may be too low for the public good and disease may enter/spread in a region. The public animal health sector was created to address problems such as this and yet ways to inform public animal health managers on how to do so are not well developed. Empirical evidence also indicates that people are not very good at updating information, at addressing low-probability events, or at dealing with the possibility of drastic loss. Thus we may also be poorly equipped to deal with many infectious disease management problems.

This presentation will suggest that there is much to be gained if economists, and perhaps also other social scientists, devote more time to addressing such issues at a simple and foundational level. But to do so they will have to collaborate more effectively with epidemiologists, veterinarians and others who may be better positioned to understand how animal health decisions are made, and also what the consequences of these decisions are. Case studies will be used, where one is that of motivations for the use of antibiotics in production agriculture.
Foot and mouth disease (FMD) presents an ongoing threat to livestock industries in countries where the disease is non-endemic. For countries that are disease free without vaccination, potential outbreak size and duration have a large impact on trade restrictions and the final economic cost of an outbreak. Emergency vaccination, although increasingly recognised as a potentially important strategy for bringing FMD outbreaks under control, adds liabilities and cost and needs to be applied early for large outbreaks to achieve the best result. This study attempts to identify early decision indicators (EDIs) of outbreak severity which can then be used to inform the timing of the most effective and appropriate control methods.

FMD models from Australia, New Zealand, Canada, USA, UK and Sweden were used to create a database of simulated FMD outbreaks for each country covering a range of starting conditions. Indicators known or available to disease managers early in an FMD outbreak including farm, animal and human population density at the site of the index case and the number of IPs at days 7, 14 and 21, were assessed as predictors of final outbreak size and duration and the area under control. In this presentation, we will discuss the performance of selected EDIs available at days 7, 14, and 21 of an FMD control program as predictors of final outbreak size, duration and the total area under control. It will also be of benefit to investigate the circumstances around the iterations where the EDIs fail to correctly predict the severity of the outbreak. These iterations may give insight into factors that are important to policy makers when making decisions to include emergency vaccination as an additional response tool in the early days of an FMD outbreak.
An integrated epidemio-economic modelling framework of the complex interplay between pathogen spread and disease management: control of BVD within beef herds as a case study

Laguzet L.*, Rault A., Picault S., Arnoux S., Krebs S., Ezanno P.

*BIOEPAR, INRA, Oniris, 44307 NANTES, France

The dynamics of animal diseases is usually modelled thanks to an epidemiological modelling framework where on-farm health practices are omitted. Optimal control decisions are mainly drawn by modelling the effect of mandatory practices, which is of public interest for the control and eradication of major epidemic diseases. However, most endemic infectious animal diseases do not rely on public health control, although generating significant adverse economic consequences in livestock. Pathogen spread and the magnitude of associated economic consequences are directly linked to efforts undertaken by farmers themselves.

Our objective was to propose a mathematical modelling framework integrating individual health decisions into dynamic stochastic epidemiological models, in order to highlight the feedback loops occurring between the modification over time of the epidemiological situation and farmers’ decision process. These feedback loops exist for a single herd, but also more widely for a group of herds interacting at a regional level. This work is applied to the control of Bovine Viral Diarrhea at the scale of a beef cattle herd, using an existing epidemiological model [1] and considering vaccination as control measure. We represented decision at each time step (here of one year) as a balance between expected farm income when performing vs. not performing vaccination. Since the epidemiological model is stochastic, a methodology was needed to compare model outcomes in both cases. We simulated a sufficient number of repetitions for each scenario to compare predictions using Wilcoxon-Mann-Whitney statistical test, which allows comparing mean values without normality assumptions on the tested variable. To account for the limited information available to farmer about the subsequent actual realization, one of the simulated repetitions was assumed to truly occur. Therefore, predicted farm health decisions are not necessarily optimal. The vaccination choice performed on time \( t \) influences epidemiological dynamics between \( t \) and \( t+1 \), and thus the next decision to be made on time \( t+1 \).

The proposed approach makes it possible to characterize the dynamics in terms of vaccination decisions (existence of vaccination cycle), as well as disease dynamics at the farm level. Simulation results reveal that BVD epidemiological dynamics at farm level highly depends on farmers’ health choices over time, as well as on the randomness of biological processes.

How to avoid degradation of paratuberculosis prevalence in dairy cattle herd? An individual-based modelling approach

Guillaume Camanes*\textsuperscript{a,b}, Alain Joly\textsuperscript{a}, Racem Ben Romdhane\textsuperscript{b}, Pauline Ezanno\textsuperscript{b}
\textsuperscript{a} Groupement de Défense Sanitaire de Bretagne, 56019 Vannes, France
\textsuperscript{b} BioEpAR INRA, ONIRIS, 44307 Nantes, France

*guillaume.camanes@oniris-nantes.fr

Paratuberculosis is an infectious gastrointestinal disease of cattle worldwide [1, 2]. Caused by \textit{Mycobacterium avium} subsp. \textit{paratuberculosis} (\textit{Map}) [3], it can lead to emaciation, profuse diarrhoea, decreased milk production, and early culling of animals [4]. Several measures are available to control Map spread: to improve calf rearing, to separate as soon as possible calves from their dam, and to cull quickly high shedders [5, 6]. However, measure efficiency is not very well established and might depend on the prevalence of infection in the herd at the start of measure implementation.

Our objective was to determine which control measures and which minimal level of implementation were needed to avoid degrading prevalence of infected adults within dairy cattle herds according to the starting adult prevalence of infection. We evaluated three situations with contrasted levels of prevalence representing realistic ranges observed in dairy cattle herds in Brittany (France). We developed an original individual-based model of Map spread within a dairy cattle herd, and use this model to assess the effect of control measures on adult prevalence variations. We considered 388 strategies based mostly on reducing exposure of young animals to adult environment and on test-and-cull measures. The model includes 6 age groups (from new-borns to adults), 6 health states (susceptible, no more susceptible, transiently infectious, latently infected, moderately infectious, and highly infectious), and all of the described transmission routes (in utero, faecal-oral, milk and colostrum ingestion). The individual-based paradigm allows following the evolution of animal characteristics over time, and thus to evaluate precise test-and-cull measures with the model.

We demonstrated that, irrespective of the initial adult prevalence, both control measures should be combined to avoid degrading adult prevalence in dairy cattle herds. Reducing calf exposure to adult environment was the most important lever to reach a higher probability of prevalence maintenance or decrease. For intermediate prevalence (from 7% to 21%), we showed that it was difficult to avoid degrading prevalence even with a high level implementation of control measures, this probability ranging from 25% to 50% after 5 years of control implementation.

Our results showed that combining control measures is required to avoid degrading the prevalence of infected adults in dairy cattle herds, but that similar options are relevant irrespective of the prevalence at the start of control implementation. This result will simplify advices to be provided by Animal Health Services to farmers to help controlling Map spread at local scale.

EMuLSion, a generic simulation framework in animal epidemiology based on multi-level multi-agent modelling.

Picault S. ab*, Huang Y.-L. a, Sicard V. a, Beaudeau F. a, Ezanno P a.

a BIOEPAR, INRA, Oniris, 44307 NANTES, France
b CRIStAL, Univ. Lille, 59000 LILLE, France

* sebastien.picault@oniris-nantes.fr

To recommend better control measures in public or animal health, epidemiologists incorporate ever-finer details in their models, from individual diversity to public policies, which often involve several observation scales. Due to the variety of modelling paradigms, it becomes more and more difficult to compare hypotheses and outcomes, or explore new assumptions or scenarios, especially since the increased complexity of simulation programs is not yet counterbalanced by design principles nor by software engineering methods. Thus, any change in the model often induces a substantial coding effort.

The EMuLSion framework, developed within the MIHMES project, rely upon the multi-level agent-based paradigm to integrate existing methods within a common interface, provide a separation between concerns and reduce the part of code devoted to model designers. Multi-agent systems are composed of interacting autonomous entities (agents) endowed with behaviors, and are quite flexible since an agent can be used to model any kind of entity. Especially, in multi-level agent-based systems [1], agents can represent several organization or observation levels, from individuals to metapopulations. Thus, multi-level agent-based systems are a convenient way to encompass classical modelling paradigms used in epidemiology (e.g. compartments, IBM, metapopulations).

We also advocate for a strong separation of concerns, i.e. a clear separation between a generic simulation engine (code) on the one hand, and an explicit, human-readable and highly modular description of the model structure, parameters and assumptions on the other hand. Thanks to this approach, the EMuLSion framework is able to process epidemiological models with very little specific code development, allowing for quick model refactoring, alternative hypotheses assessment, and objective model comparison. Models can involve several modelling paradigms at the same time, and the framework also provides efficient individual grouping methods to benefit from the detail level of IBM without excessive performance degradation.

We illustrate our approach with an application to the Q fever disease in cattle, first to reproduce a within-herd model developed previously [2], study possible simplifications of assumptions, and extend it to the between-herd level.

Control of Nematodes at Different Life Stages, which stage should we target?

Mathieu Bonneau*, Jean-Christophe Bamboua, Maurice Mahieua Rémy Arquetb, Harry Archimèdea, Gisèle Alexandrea, Nathalie Mandonneta, Carine Marie-Magdeleine-Chevrya, Valérie Angeona

a INRA Antilles-Guyane, Zootechnique Research, Domaine Duclos, 97170 Petit-Bourg (Guadeloupe) – French West Indies
b INRA, Domaine Gardel, 97129 Moule, (Guadeloupe) – French West Indies

* mathieu.bonneau@inra.fr

Gastro-Intestinal nematodes are responsible for severe yield loss in grazing herbivores farming and are even responsible for the loss of animals in some cases. Nematodes life-cycle is composed of a free living stage, where the nematodes evolved from eggs to infective L3 larvae within the pasture. Once ingested by the grazing animals, the L3 can continue their growth to adult reproductive larvae inside their host, this is the parasitic stage. During this stage, the nematodes population is naturally controlled by the host immune system, with more or less success depending on the host’s resistance. Most commonly, the action of the immune system has to be completed in order to maintain the flock to a healthy state. There exists a range of different control actions, such that anthelminthic treatment, genetic selection, optimized nutrition or rotational grazing. The different control methods all focus their action at particular stages of the nematodes life-cycle. To date, there exist no fully efficient method in the long term and research aims at improving the current method, as well as proposing new one.

Beside the inherent efficacy of control methods, nematodes control at different stages can potentially impact the adult larvae population in different proportion. In this work, we consider several key stages of the nematode life cycles (eggs, infective L3 on pasture, established L4 and adult worms), as well as two key parameters of their life cycle (establishment rate and adult fecundity). We ask the following question: if nematodes can be control at different removal rates at each of these stages, which stage will have the largest impact on the flock's adult nematodes population? This question is particularly interesting in order to discuss the most promising research direction in terms of nematode control.

We propose a simulation framework, based on a matrix population model, particularly common in Ecology. In a matrix population model, the population is separated into stages (here egg, L3, L4 and adult) and the number of individuals in each stage is studied. At a daily time step, the individuals transition to the next stage, until reaching an upper stage (adult). At each transition, some individuals are removed due to the natural population mortality. This type of model suits well to the nematode life cycle and allows a compact representation of the nematode population dynamic. We use [1] to parameterize this model for *Teladorsagia circumcincta* and [2] to model the action of the host immune system. The model is sufficiently general to be adapted to other nematodes population. We use this model to simulate a flock of 35 individuals grazing on a rotation of 5 pastures. We use the model to estimate the average worm burden of the flock over a period of 200 days, when the nematode population is controlled at different life stages, with different removal rates. Each control scenario is then compared based on the estimated worm burden of the flock. With our particular parameterization, we show that focusing control inside the host (i.e., L4 or adult) allows the most significant impact. We challenged this conclusion by performing a sensitivity analysis. ModAH 2017 - Nantes, France
A stochastic metapopulation model to assess the drivers of swine influenza viruses persistence in farrow-to-finish pig farms

Charlie Cador*a, Mathieu Andraudb, Lander Willemc, Nicolas Roseb

a FarmApro, 6A Parc d’activité, Zone de Penthièvre, 22640 Plestan, France
b Swine epidemiology and welfare research unit, French Agency for Food, Environmental and Occupational Health & Safety (ANSES), BP 53, 22440 Ploufragan, France
c Centre for Health Economics Research & Modeling Infectious Diseases, Vaccine and Infectious Disease Institute, University of Antwerp, Antwerp, Belgium

* ccador@farmapro.fr

Swine influenza viruses (swIAVs) are known to persist endemically in farrow-to-finish pig farms, leading to repeated swine flu outbreaks in successive batches of pigs at a similar age. This persistence in European swine herds involves swIAVs from European lineages including H1avN1, H1huN2, H3N2, the 2009 H1N1 pandemic virus and their reassortants, potentially threatening for both animal and public health. The specific population dynamics of farrow-to-finish pig farms, the immune status of the animals at infection-time, the co-circulation of distinct subtypes leading to consecutive or concomitant infections have been evidenced as factors favouring swIAV persistence within herds. Understanding the drivers of swIAV persistence in pig herds is crucial to establish adequate control measures.

We developed a stochastic metapopulation multi-strain model representing the co-circulation of two distinct swIAVs within a typical farrow-to-finish pig herd to evaluate the risk of reassortant viruses generation due to co-infection events. Control strategies related to herd management (between-batch intervals) and/or vaccination schemes (batch-to-batch or mass vaccination of the sows and/or growing pigs) were then implemented to assess their relative efficacy.

The daily probability to observe a co-infection event in a single animal, possibly leading to reassortment, was evaluated to 16.7%. A quasi-systematic swIAV persistence in herds managed with short between-batch intervals has been observed. However in all cases, the viruses were found to persist up to three years after introduction with a probability greater than 75%. The export of piglets batches was identified as the most efficient measure facilitating swIAV infection fade-out. Although some vaccination schemes had a beneficial effect in breeding sows by reducing the persistence of swIAVs within this subpopulation, none of vaccination strategies achieved swIAVs fade-out within the entire farrow-to-finish pig herd.
Session 4: Epidemiological networks
Parameter inference and modelling the spread of bovine Tuberculosis at the national level using individual cattle life histories

Rowland R. Kao*a, Thomas Doherty*a, Oliver Tearne*b, Ellen Brooks-Pollock*c, Andrew J. Conlan*d, Michael Deason*a, James L. N. Wood*d, Mark Arnold*b

*a Institute for Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow G61 1QH, UK
*b Department of Epidemiological Sciences, Animal and Plant Health Agency, Weybridge, KT15 3NB UK
*c School of Social and Community Medicine, University of Bristol, Bristol, BS8 2PS, UK
*d Department of Veterinary Medicine, University of Cambridge, CB3 0E, UK

* rowland.kao@glasgow.ac.uk

Livestock movements in Europe are exceptionally well characterised; for example in Great Britain, a consistent, national record of daily cattle movements extends back almost 15 years. Such data provide a unique opportunity to understand the role of livestock movements in the spread of disease. In this presentation, I shall provide a brief overview of the modelling of detailed livestock networks. I shall then describe an ongoing project to use such data in order to fit a model of the bovine tuberculosis (bTB) epidemic in Great Britain. We build on previous approaches that have exploited the equally exceptional record of bTB testing in British cattle [1,2], extending in particular [2] to directly utilise the data as recorded at the individual animal level. This allows us to consider the role of life and disease testing histories to better understand disease dynamics while also potentially exploiting individual-level targeted control programmes. Posteriors for the parameters in our model are inferred using novel metrics in an Approximate Bayesian Computation (ABC) framework; I shall demonstrate the fit of our model to the epidemic in both time and space and illustrate its value in the context of predicting the impact of potential cattle vaccination strategies against bTB. While most ‘big data’ analytical approaches use purely statistical models that do not embed explicit dynamical processes, this work demonstrates the potential for computationally challenging approaches based on process models in this context.

Cattle trade networks in Europe

Eugenio Valdano\textsuperscript{a*}, Luca Ferreri\textsuperscript{b}, Alexandre Darbon\textsuperscript{c}, Chiara Poletto\textsuperscript{c}, Lara Savini\textsuperscript{d}, Carla Ippoliti\textsuperscript{d}, Armando Giovannini\textsuperscript{d}, Peter Brommesson\textsuperscript{e}, Stefan Sellmann\textsuperscript{e}, Uno Wennergren\textsuperscript{e}, Andreas Koher\textsuperscript{f}, Jason Basset\textsuperscript{f}, Hartmut H K Lentz\textsuperscript{g}, Vitaly Hövel\textsuperscript{h}, Ákos Józwiak\textsuperscript{i}, Jessica Enright\textsuperscript{j}, Rowland R. Kao\textsuperscript{j}, Pauline Ezanno\textsuperscript{k}, Gaël Beaunéel\textsuperscript{k}, Elisabeta Vergu\textsuperscript{l}, Reinhard Fuchs\textsuperscript{m}, Klemens Fuchs\textsuperscript{m}, Beatriz Vidondo\textsuperscript{n}, Ana Pascual\textsuperscript{o}, Emily Courciero\textsuperscript{o}, Vittoria Colizza\textsuperscript{p}, Jessica Enright\textsuperscript{j}, Rowland R. Kao\textsuperscript{j}, Pauline Ezanno\textsuperscript{k}, Gaël Beaunéel\textsuperscript{k}, Elisabeta Vergu\textsuperscript{l}, Reinhard Fuchs\textsuperscript{m}, Klemens Fuchs\textsuperscript{m}, Beatriz Vidondo\textsuperscript{n}, Ana Pascual\textsuperscript{o}, Emily Courciero\textsuperscript{o}, Vittoria Colizza\textsuperscript{p}

\textsuperscript{a}Departament d’Enginyeria Informàtica i Matemàtiques, Universitat Rovira i Virgili, 43007 Tarragona, Spain

\textsuperscript{b}aizoOn - Technology Consulting, Data Driven Innovation, Torino, Italy

\textsuperscript{c}Sorbonne Universités, UPMC Univ Paris 06, INSERM, Institut Pierre Louis d’Épidémiologie et de Santé Publique (IPLESP UMRS 1136), F75012, Paris, France

\textsuperscript{d}Istituto Zooprofilattico Sperimentale Abruzzo-Molise G. Caporale, Campo Boario, 64100 Teramo, Italy

\textsuperscript{e}Linköping University, Linköping, Sweden

\textsuperscript{f}Institut für Theoretische Physik, Technische Universität, Berlin, Germany

\textsuperscript{g}Friedrich-Loeffler-Institute, Institute of Epidemiology, Germany

\textsuperscript{h}Freie Universität Berlin, Institute for Veterinary Epidemiology and Biostatistics, Germany

\textsuperscript{i}National Food Chain Safety Office, Budapest, Hungary

\textsuperscript{j}Boyd Orr Centre, Institute of Biodiversity, Animal Health, and Comparative Medicine, University of Glasgow, Glasgow, United Kingdom

\textsuperscript{k}Bioepar, INRA, Oniris, CS40706, 44307 Nantes, France

\textsuperscript{l}MaIAGE, INRA, Université Paris-Saclay, 78350, Jouy-en-Josas, France

\textsuperscript{m}Austrian Agency for Health and Food Safety, Austria

\textsuperscript{n}Veterinary Public Health Institute, University of Bern, Switzerland

\textsuperscript{o}Department of Agriculture Environment and Rural Affairs, Belfast, United Kingdom

\textsuperscript{p}ISI Foundation, Torino, Italy

* eugenio.valdano@gmail.com

Diseases affecting farmed cattle compromise both human and animal health and welfare, and represent a major cause of loss in economic revenue. Their spread is known to be driven, or at least facilitated, by animal displacements among livestock holdings, both within and across countries. As a result, studying the networks of animal movements is a key step in devising new prevention and containment strategies. Past works have already analyzed cattle networks in several European countries, highlighting complex interactions between topology, function and dynamics at different spatial and time resolutions. A comprehensive study, showing the impact of country-specific driving factors on network evolution and topology, is however still missing. By using data from several European countries, and focusing on the features relevant for the spread of infections, we perform a comparative analysis to highlight both general and country-specific patterns. We find that coarse-graining the structure into statistical distributions of centrality measures is an effective way to highlight the properties shared by all networks, which represent the fingerprint of a livestock market. The situation dramatically changes when we zoom in to the microscopic structure, as we find several country-specific characteristics, especially in temporal evolution. This twofold behavior suggests that on one hand it is possible to identify several global patterns in the ways animal disease spread, which can then be applied to countries for which data are unavailable, or incomplete. On the other hand,
resolved country-specific data are needed when devising tailored and targeted intervention strategies.
Livestock disease spread through animal movements: a temporal network approach

Hartmut H. K. Lentz*a, Andreas Koherb, Philipp Hövelb, Thomas Selhorstc, Franz J. Conraths

a Institute of Epidemiology, Friedrich-Loeffler-Institute, Greifswald, Germany
b Institute of Theoretical Physics, TU Berlin, Berlin, Germany
c Unit Epidemiology, Statistics and Mathematical Modelling, Federal Institute for Risk Assessment, Berlin, Germany

* hartmut.lentz@fli.de

Livestock trade forms a network of agricultural holdings connected via trade of live animals. These networks are often treated as static objects, although trade is in fact strongly time-dependent. This has a dramatic impact on the possible spreading patterns for infectious diseases.

A static (aggregated) trade network is constructed as follows: if two nodes are connected directly to each other in a time-dependent network, the same connection is present in the static network. A fundamental difference between the static and the time dependent view however, is the consideration of paths, i.e. indirect connections over more than one edge. Concerning paths, the causality of the edges used plays an essential role. In an aggregated network, paths can seem causal, although they do not follow a time-respecting sequence of edges in the real system. This leads to a systematic overestimation of outbreak sizes, if trade networks are treated as static.

We introduce a new method, which allows for the computation of the total causal path structure of a temporal network (represented by its accessibility graph) using the adjacency matrices of its snapshots. In addition, information about the timescales required for path traversal can be derived from the step-by-step derivation of the accessibility graph of the network. This procedure directly yields the distribution of shortest path durations in a temporal network. In addition, we define the new measure causal fidelity that compares the number of paths in a temporal network with its aggregated counterpart. This measure allows a quantitative assessment of how well a temporal network can be approximated by a static aggregated one.

The methods presented here require only basic knowledge linear algebra and can be implemented efficiently. Their capability is demonstrated for a livestock trade network in Germany.

**Analysis and prediction of the cattle trade network in France to inform epidemiological risk**

Vergu E.*a, Beaunée G.*a,b, Ezanno P. b, and Members of MIHMES and CADENCE Projects

*aMaIAGE, INRA, Université Paris-Saclay, 78350, Jouy-en-Josas, France; bINRA, LUNAM Université, Oniris, UMR1300 BioEpAR, CS40706, F-44307, Nantes, France;

*elisabeta.vergu@inra.fr

Effective control of livestock infectious diseases is a major issue for sustainable animal farming and competitive agri-food chains, as well as for public health. Livestock trade movements is one of the most important pathways for pathogen transmission between holdings. Therefore, it is crucial to understand and be able to predict the temporal evolution of the network of animal movements, and assess the risk related to epidemics unfolding on this network.

Here, we focus on the study of cattle trade network in France, based on a fully detailed dataset spanning over several years, extracted from the French database of cattle movements, which records life histories of all French cattle from birth to death.

If time permits, results on two aspects, i.e. prediction of the temporal dynamics of cattle movements and assessment of epidemiological risk, will be presented. On the first axis, performances of statistical models predicting the occurrence of transactions between holdings based on their characteristics as covariates, on one hand, and of a microeconomic model incorporating generic components for trade of cattle at the holding level, on the other hand, will be discussed. On the second axis, proxies for pathogen spread, such as percolation and reachability ratio, accounting for network time-varying properties and for simple epidemiological assumptions on transmission probability and epidemic dynamics, and computed using efficient algorithms of network exploration will be provided.

*This work was supported by the Agence Nationale de la Recherche (grants MIHMES ANR-10-BINF-07 and CADENCE ANR-16-CE32-0007) and the INRA Métaprogramme GISA (grant PREDICATT).*
Manipulation of contact network structure and the impact on FMD disease transmission

Sibylle Mohr*, Michael Deason*, Thomas Doherty*, Mikhail Churakovb,c,d, Rowland Kao*

*Boyd Orr Centre for Population and Ecosystem Health, Institute of Biodiversity, Animal Health and Comparative Medicine, College of Medical, Veterinary and Life Sciences, University of Glasgow, 464 Bearsden Road, Glasgow, G61 1QH, UK
b Mathematical Modelling of Infectious Diseases Unit, Institut Pasteur, Paris, 75015, France
c CNRS, URA3012, Paris, 75015, France
d Center of Bioinformatics, Biostatistics and Integrative Biology, Institut Pasteur, Paris, 75015, France

*Sibylle.Mohr@glasgow.ac.uk

The movements of livestock between individual premises and markets can be characterised as a dynamic network where the structure of the network itself can critically impact the transmission dynamics of many infectious diseases. As evidenced by the 2001 Foot-and-Mouth disease (FMD) epidemic in the UK, this can involve transmission over large geographical distances and can result in major economic loss [1,2]. Following the end of the outbreak, mandatory livestock movement restrictions were introduced as a biosecurity measure: a 13-day standstill in Scotland for cattle and sheep after moving livestock onto a farm (with certain exemptions) and a 6-day standstill for cattle and sheep in England and Wales from 2003 (without any exemptions). An important consideration when contemplating legislative changes such as movement restrictions is the knock-on effect these could have on the emergent properties of the system, i.e. the network structure itself. In this study, we investigate how disease dynamics change when the local contact structure of the recorded livestock movement network in Scotland is altered through rewiring movements between premises. The network rewiring algorithm used here changes the structure of the recorded livestock movement network through a combination of altered movement restrictions and redirection of movements between holdings and markets to avoid nonsensical activity (e.g. movements to markets on days when they are inactive) while conserving key characteristics (e.g. movement date and market sales of the correct animal production type).

There is obvious benefit from rewiring, resulting in networks with higher clustering coefficients and lower density, both decreasing the number of susceptible contacts compared to the recorded movement network. The rewired networks were then investigated for their impact on simulated Foot-and-Mouth disease outbreaks in Scotland. Using an adaption of a well-established simulation model [3] we simulated the spread of FMD through animal movements and local spatial spread. Stochastic model simulations were performed for scenarios with and without exemptions to the standstill rules. As expected, rewiring leads to a decrease in outbreak size and - if standstill exemptions are prohibited – higher probability of smaller outbreaks. Without exemptions, a short 6-day movement standstill is almost as effective as a long standstill period of 13-days. Overall, a simpler biosecurity system with shorter standstills but no exemptions, which would likely be easier to legislate for and monitor, would offer no substantial additional risk for FMD. These results suggest that explicitly manipulating the contact network structure in a sensible way has the potential to significantly impact disease control.

VULNERABILITY OF ITALIAN CATTLE SYSTEM TO BRUCELLOSIS

Alexandre Darbona, Eugenio Valdano, Chiara Poletto, Lara Savini, Luca Candeloro, Armando Giovannini, Vittoria Colizza*

a INSERM U1136, Pierre Louis Institute of Epidemiology and Public Health, Paris, France
b Istituto Zooprofilattico Sperimentale Abruzzo-Molise G. Caporale, Teramo, Italy
c ISI Foundation, Torino, Italy

* vittoria.colizza@inserm.fr

Livestock disease management and control aim to reduce epidemic risks and prevent large economical losses. Mathematical models integrating data on animal populations and movements and parameterized to specific diseases were shown to provide important contributions to reach this objective. Here we focus on the case study of bovine Brucellosis in the Italian cattle trade system, for which long historical time series are available. We introduce the infection propagator approach, a theoretical framework for the assessment of the degree of vulnerability of a host population to epidemics. By reinterpreting the tensor formalism of multi-layer networks, this approach allows the analytical computation of the epidemic threshold for an arbitrary time-varying network, i.e. the critical pathogen transmissibility above which large-scale propagation occurs. Applied to our case study and driven by the empirical data on Brucellosis epidemics and cattle trade movements, the approach provides concrete insights into Brucellosis prevention and control in a realistic setting.

USING AN AGENT-BASED MODEL TO DESCRIBE THE POTENTIAL SPREAD OF EQUINE INFLUENZA WITHIN A NETWORK OF HORSES ATTENDING AN EQUESTRIAN SHOW

Kelsey L. Spence*, Terri L. O’Sullivan a, Zvonimir Poljak a, Amy L. Greer a

a Department of Population Medicine, University of Guelph, 50 Stone Rd E, Guelph, ON, Canada, N1G 2W1

* kspenc04@uoguelph.ca

Horses attending equestrian shows form a contact network where opportunities exist for disease introduction and spread. The influence of this contact network on the potential for disease spread in the population can be described using simulation models. The objectives of this study were to describe the potential spread of equine influenza (EI) in a network of horses attending a 2-day equestrian show in Ontario, Canada, and to evaluate the effect of population-level infection control interventions on the model-projected clinical attack rate.

Horse show participants completed a questionnaire about their horse (e.g. vaccine status, age, etc.) and horses stabled at their respective home facilities. These data were used to construct a contact network of horses at multiple home facilities, which was represented using an agent-based model. In each model iteration, a random horse was infected with EI before travelling to the show and disease spread within the network was simulated. The intervention scenarios examined in the model included (1) isolation of horses attending the show upon return to their home facility, and (2) targeted increases in facility-level vaccine coverage before the occurrence of the outbreak. The model outcomes of interest included the attack rate (the number of infected horses / total population) and the average outbreak duration. The model was run for 1000 iterations per intervention scenario.

The network consisted of 765 horses (55 horses attending the show and 710 secondary contacts) at 38 home facilities. In the absence of interventions other than baseline levels of EI vaccination, the average EI attack rate was 4.2% (SD = 3.8%; range = 0.1 – 20.8%) and the average outbreak duration was 19.6 days (SD = 4.3 days; range = 7 – 39 days). The results of the intervention scenarios demonstrated that isolation of travelling horses for 14 days upon return to their home facilities was the most effective intervention, resulting in an average attack rate of 0.3% (SD = 0.1%; range = 0.1 – 0.8%) and an average outbreak duration of 7.6 days (SD = 0.7 days; range = 7 – 10 days). The most effective vaccination scenario was to target barns with 4 or more owners pre-outbreak and increase their facility-level vaccine coverage to 75%. This resulted in a lower average attack rate compared to the base scenario (3.0%; SD = 3.0%; range = 0.1 – 22.5%) and a longer average outbreak duration of 21.0 days (SD = 7.5 days; range = 7 – 59 days).

These results provide insight into effective disease control strategies to prevent and control an EI outbreak where the initial introduction of the pathogen into the population occurs before a horse show. Simulation models provide an opportunity to improve our understanding of disease transmission opportunities and examine a variety of “what-if” scenarios in order to identify improvements to existing infection control strategies.
Abstracts from posters listed in alphabetical order (according to last name of presenting authors)
A COMPARTMENTAL MODEL FOR CONTAGIOUS CAPRINE PLEUROPNEUMONIA IN A HERD OF SAND GAZELLE: FIRST ESTIMATES OF THE BASIC REPRODUCTIVE RATIO R0 IN A CONTROLLED ENVIRONMENT

Louis Lignereux a,b, Andrea Apolloni c,d *, Anne-Lise Chaber b,e, Lucía Manso Silván c, Armelle Peyraud c, Claude Saegerman b, François Thiaucourt c

a Environment Agency Abu Dhabi, Terrestrial and Marine Biodiversity, P.O. Box 45553, Al Mamoura Building, Abu Dhabi, United Arab Emirates
b Faculty of Veterinary Medicine, University of Liège, Epidemiology and risk analysis applied to veterinary sciences, Fundamental and Applied Research for Animal and Health (FARAH) Center, Quartier Vallée 2, Avenue de Cureghem 7A, Bât. B42, B---4000 Liège, Belgium
c French National Agricultural Research Center for International Development (CIRAD), UMR ASTRE, F-34398 Montpellier, France.
d Institut Sénégalais de Recherches Agricoles, Laboratoire National de l’Elevage et de Recherche Vétérinaire, Parc Scientifique de Hann, Dakar, Sénégal
e Wildlife Consultant L.L.C, Al Ain, United Arab Emirates

*andrea.apolloni@cirad.fr

Contagious caprine pleuropneumonia (CCPP), caused by Mycoplasma capricolum subsp. capripneumoniae (MCCp)(1), was long considered a goat---specific disease but the strict specificity of MCCp has been challenged recently and since 2007(2) there has been a growing number of reports of CCPP affecting wild ungulates, either held in captivity or free ranging.

We report here a CCPP outbreak that occurred in a captive population of 3355 sand gazelles (Gazella marica) held in the United Arab Emirates. The course of the disease was comprehensively recorded and its spread within and among the various pens could be deduced from observations made during this outbreak. These observations were used to validate the parameters of an in-silico transmission model.

We used a modified SEIR model, where animals can either be in one of the following states: Susceptible (S), Exposed but not infectious yet (E), Infectious (I), Recovered (R) or Dead (D). This compartmental model was calibrated after applying a Monte Carlo---Markov Chain (MCMC) procedure to the daily mortality data recorded for one specific pen. The results of this calibration allowed us to estimate both the infection transmissibility ($\beta$) and the infection---induced mortality rate ($p$). We used the procedure from Diekmann et al. (3) to provide first estimates of the basic Reproductive ratio $R_0$ for this disease in this setup.

We present results from this model, focusing on the estimation of $R_0$ and the infection---induced mortality rate, and comparing results from other models. We highlight the practical implications by providing therapeutic and preventive recommendations to support control measures.

Spread of West Nile Virus in Germany, A Modelling Endeavour

Suman Bhowmick**, Hartmut H. K. Lentz*, Philipp Lorenz, Philipp Hövel (Calibri 12)

* Institut für Epidemiologie, Bundesforschungsinstitut für Tiergesundheit
  Federal Research Institute for Animal Health
  Südufer 10 | 17493 Greifswald - Insel RiemsFriedrich-Loeffler-Institut

** Institut für Theoretische Physik Technische Universität Berlin
  Hardenbergstr. 36
  D-10623 Berlin

* suman.bhowmick@fli.de

West Nile virus (WNV) is an arthropod-borne virus (arbovirus) spreading in transmission cycle between mosquitoes and birds. In addition, horses and human are also the victims of WNV, infected by blood feeding mosquitoes. In our current endeavour, a dynamic model devised to decipher the intricacy of the spreading dynamics of the West Nile virus.

The model, which is of SEIR (susceptible-exposed-infected-removed) type, comprises of 19 compartments. In this model, we tried to couple the terrestrial and aqueous stages of mosquitoes through a single ODE, for the simplicity. In addition to the local spreading dynamics, spatial spread through aerial movement (diffusion) and bird migration shall be included in the model.

As results, we will present solutions of the local infection model as well as an analytical expression for the basic reproduction number $R_0$. The seasonal and environmental impacts are also included into the considerations. The associated map of the basic reproduction number $R_0$ shall be investigated further along with the ODE coupled with network in the future work.

Controlling the spatio-temporal population dynamics of tsetse flies, vectors of nagana disease, in a cattle breeding region of Senegal

Hélène Cecilia*a, Ahmadou Dickob, Sandie Arnouxa, Sébastien Picaulta,c, Augustin Bancéd, Jérémy Bouyerb,e, Pauline Ezannoa

a Bioepar, INRA, Oniris, La Chantrerie, 44307 Nantes, France,
b UMR CMAE, CIRAD, Campus International de Baillarguet, Montpellier, France,
c Univ. Lille, CNRS, Centrale, Lille, UMR 9189 – CRISTAL, F-59000, Lille, France,
d CIRDES, Bobo-Dioulasso, Burkina Faso, e Institut Sénégalais de Recherches Agricoles, Laboratoire National d’Élevage et de Recherches Vétérinaires, Hann, Dakar, Sénégal

* helene.cecilia@oniris-nantes.fr

The tsetse fly complex (Glossina spp.) transmits the parasite responsible for African Animal Trypanosomiasis (AAT), or nagana, which is the most economically important livestock disease in Africa. The challenge of the last decades was to design programs that could sustainably control fly populations in different regions of the continent. Given the contrasted outcomes of these programs, there is still a need for a better understanding of the spatio-temporal dynamics of this vector.

Mathematical models and computer-based simulations are relevant to assess which control measures should be used and when, accounting for the ecological complexity of the target pest and territorial specificities of the controlled area. They provide a useful tool, complementary to field observations and experiments, to suggest efficient vector management strategies.

We developed a deterministic and mechanistic spatio-temporal model of the population dynamics of tsetse flies, structured by sex and age (pupae, teneral and non-teneral adults). Temperature and fly density influenced the life-cycle, while spatial diffusion depended on density and relative quality of neighbouring locations. We applied the model on populations of Glossina palpalis gambiensis in the Niayes area of Senegal, for which biological and landscape data were available. The landscape was divided into 250m x 250m cells of heterogeneous carrying capacity, estimated by habitat suitability models. We transformed observed temperatures into “perceived” ones, to account for micro-environments where flies live. Dispersal, mortality, and development rates were calibrated on laboratory data, experts’ opinions and literature.

The sensitivity analysis of the model identified the biological and environmental parameters influencing the most population dynamics. We showed that the mortality and development of adult females, along with temperature, were the key drivers of population persistence. Our predictions suggested that combining techniques to both increase mortality and decrease fecundity would be optimal to eradicate tsetse flies in targeted zones. Sequential aerosol technique (SAT), traps and targets (TT) and insecticide-treated livestock (ITL) increase daily mortality rates, whereas the sterile insect technique (SIT), by preventing egg-laying, slows down the development rate of the population. Furthermore, our results highlighted the need for more biological insights to achieve accurate model predictions. Additional field work and experiments are necessary to better infer the relationship between adult mortality and temperature, as well as differences between temperatures from weather stations and temperatures in tsetse fly resting places.
EXODIS-FMD: A MICRO SIMULATION MODEL OF FOOT AND MOUTH DISEASE IN LIVESTOCK POPULATIONS IN GREAT BRITAIN

C. Cook*¹, C. Birch¹, R. Moir², J. Pocock³, E. Baker³

¹Department of Epidemiological Sciences, Animal and Plant Health Agency, New Haw, Addlestone, Surrey, KT15 3NB, UK

²Epidemiology and Risk Policy Advice, Animal and Plant Health Agency, Nobel House, 17 Smith Square, London, SW1P 3JR, UK

³Risk Solutions, Dallam Court, Dallam Lane, Warrington, WA2 7LT, UK

*charlotte.cook@apha.gsi.gov.uk

Foot and Mouth disease (FMD) presents an ongoing risk to the UK livestock industry due to the high impact of disease incursions. As well as having a high animal welfare impact, any disease incursion will result in domestic and international trade restrictions that have substantial economic costs to industry and government.

Exodis-FMD is a spatially explicit, stochastic simulation model for simulating the control of FMD in Great Britain (GB) at a holding level resolution with daily time steps. The requirement for a complex simulation model of FMD was driven by the needs of policy makers to investigate the wide range of possible effects of different disease management policies, including resource logistics and economic consequences. A simulation modelling approach in this situation is ideal due to the limited observational data from a small number of FMD outbreaks in GB.

We describe Exodis-FMD, the model structure, function and applications in the context of its role as a tool to support policy advice and outbreak response. The data sets that are required for a complete simulation are based on administrative data collected on a regular basis or from visits during an outbreak. The parameters required by the model are described but detailed parameter information is not included, as Exodis-FMD is designed to allow extensive parameter modification for scenario exploration.

The model is currently used for policy evaluation and it also has the capability to be used to provide supporting evidence for contingency planning. The model and its documentation has also become a valuable description of the GB FMD response plan.
SOBOL GLOBAL SENSITIVITY ANALYSIS EMPLOYED FOR A RABIES TRANSMISSION MODEL IN NORTHERN AUSTRALIA

Beatriz Vidondo, Victoria Brookes, Michael P. Ward, Salome Dürr

* Veterinary Public Health Institute, University of Bern, Switzerland
b Sydney School of Veterinary Science, The University of Sydney, Australia

* salome.duerr@vetsuisse.unibe.ch

Sensitivity analysis (SA) is commonly used to investigate the influence of input parameter values on simulation model outcomes. In contrast with univariate SA, global SA (GSA) accounts for interactions and non-linear relationships between input parameters. An example is Sobol GSA, a variance-based GSA, rarely used for epidemiological models. Total and first effects Sobol indices (SI, [0,1]) are computed, describing the influence of input parameters with and without parameters interaction.

We applied Sobol GSA to an agent-based, spatially explicit, stochastic rabies outbreak simulation model developed for a small free-roaming dog population in Northern Australia. Vaccination, culling and dog confinement were included as control strategies. We investigated the sensitivity of three model outcomes (outbreak size: number of rabid dogs (NRD) and number of dead dogs (died from rabies or culled, NDD); and outbreak duration (OD)) to core model parameters and parameters specifying control interventions.

Twenty-seven different scenarios were considered including: non-intervention; single and combined application of preventive vaccination (PV, coverage 40-80%); reactive vaccination (RC, coverage 40-80%); targeted culling of known exposed dogs (CC, level 50-90%); random culling (RC, level 10-50%); and restrictions of dog movements between (MBBH) and within (MBWC) communities with compliance levels of 70-95% and 50-95%, respectively. Sobol GSA was undertaken (R package sensitivity, function sobolmartinez) using 12000-34000 iterations per scenario, and parallel runs on a high performance cluster computer.

In the non-intervention scenario, the NRD was most sensitive to the incubation period (SI=0.69), the bite probability given a contact (SI=0.86) and the rate of permanent movements between communities (SI=0.81). For most intervention scenarios, the NRD and OD were most sensitive to incubation period (mean SI=0.41) and detection delay (mean SI=0.44). Additionally, the NRD was sensitive to vaccination coverage (mean SI= 0.53, PV scenarios) and culling level (mean SI= 0.21, CC and RC scenarios). For PV scenarios, the NDD was mostly sensitive to vaccination coverage (mean SI= 0.50) and, when combined with culling strategies, whether or not to cull vaccinated dogs (mean SI= 0.53). For RC scenarios, the NDD was highly sensitive to whether to cull dogs in the affected community only or in the entire region after detection of the outbreak (mean SI= 0.40).

GSA helped to identify the parameters to which model outputs are most sensitive, i.e. from which more information is needed to increase the accuracy of models’ predictions (reducing uncertainty), or by which decision-makers may reach greatest effect in disease control (reducing variability). Based on our results, improving surveillance or increasing disease awareness in order to reduce detection delay would be well invested resources. Additional information on the incubation period, bite probability given a contact and rate of permanent movements of dogs between communities might be obtained from a systematic literature review, outbreak reports, expert opinion or field data collected in specific regions, e.g. via long term monitoring programs. Although challenges of the Sobol GSA were encountered (e.g. requiring of large iteration numbers and centered model outputs...
with a minimum of variability), it is a powerful tool for both improving the design of the model and of the intervention strategies, thus contributing to better preparedness planning
Developing a framework for quantifying real-time contact patterns in agricultural animals using OpenBeacon proximity sensing hardware.

Joel Cummings\(^a\), Alexander Olpina\(^b\), Rachael Milwid\(^b\), Marek Laskowski\(^c\), Zvonimir Poljak\(^b\), Terri L. O’Sullivan\(^b\), and Amy L. Greer*\(^b\)

\(^a\) Department of Computer Science, University of Guelph, ON, Canada
\(^b\) Department of Population Medicine, University of Guelph, Guelph, ON, Canada
\(^c\) Department of Mathematics and Statistics, York University, Toronto, ON, Canada

* agreer@uoguelph.ca

Mathematical disease transmission models often make a variety of simplifying assumptions regarding the number and duration of contacts that occur between individuals within a host population. However, it is unclear to what extent these assumptions align with true contact patterns. The contact network structure used in disease transmission models has important implications for evaluating the risk of pathogen introduction and subsequent spread as well as for understanding the impact and relative effectiveness of different interventions. Tools for real-time sensing of contact patterns and proximity logging that have been deployed in human populations have primarily focused on institutional settings (e.g. hospitals, and schools), where access to Wi-Fi signals, power outlets, and harsh environmental conditions are not limiting factors. Quantifying contact networks within agricultural settings has proven more difficult. Our objective was to develop a framework to enable the collection of time-varying network data from agricultural animals using OpenBeacon hardware. In addition, our framework needed to remove the necessity of data receiving base stations which are impractical for agricultural settings as they require a power source, and/or a Wi-Fi connection.

OpenBeacon tags are small, lightweight, powered by a coin battery, and less costly than other types of animal tracking tools. In our set-up, each OpenBeacon tag has a unique ID. When another tag is encountered, each tag records the ID of the encountered tag and records the time at which the interaction began. When a tag leaves the proximity of the contacted tag, the tag ID and time at which the interaction ends is recorded. This allows for the calculation of total interaction time for each unique proximity tag interaction. All ID and time stamp data is logged to an 8MB flash memory chip on the tag which allows for the offline logging of contacts without requiring base station readers. Each interaction requires 16 bytes of storage space on the chip. Based on the 8MB flash memory, this means that in our tag set-up, each tag can store more than 500,000 individual interactions. This is an important aspect of our data collection framework because it allows for long term deployments in dense agricultural populations where the number of potential contacts may be large. At the completion of the tag deployment, tags are collected and data is transferred off of the proximity tags and into a MySQL database using a USB connection.

Our framework for the collection of contact network data from agricultural populations is relatively cheap, and easy to deploy. Examples of data outputs include the time varying network diagrams, and heat maps showing the duration of contact between each pair of individuals at any time scale of interest. The ability to directly quantify the number, and duration of direct contacts between agricultural animals is an important step for improving our understanding of the generalizability of animal contact networks. Data obtained using this method will enable decisions regarding the parameterization of disease transmission models for agricultural host-pathogen systems to be informed by empirical data.
Between-group pathogen transmission: from processes to modelling

Thierry Hoch1*, Suzanne Touzeau2,3, Anne-France Viet1, Pauline Ezanno1

1 INRA, Oniris, BIOEPAR, Nantes, France
2 Université Côte d’Azur, INRA, CNRS, ISA, France
3 Université Côte d’Azur, Inria, INRA, CNRS, UPMC Univ Paris 06, BIOCORE, France

* thierry.hoch@inra.fr

Pathogen transmission is a key process in epidemiology and its mathematical form plays a pivotal role when modelling pathogen spread. Much work has been devoted to the transmission function applied to a homogeneous population structure [1, 2, 3]. However, modelling between-group transmission, required when different groups can be identified on account of a distinct epidemiological risk, is less documented. The aim of this study is to detail the mathematical form of the between-group transmission functions encountered in the literature and to assess its influence on the results of a theoretical epidemiological model.

Five transmission functions were identified and chosen based on their biological relevance. To assess their effect on the behaviour of a SIR model, simulations were carried out considering a population with two groups of distinct sizes and for various values of three parameters: the basic reproduction number, the proportion of the total transmission due to between-group transmission and the ratio of group sizes. Pathogen spread simulations highlighted differences in prevalence among four of the five tested transmission functions (frequency-dependent, density-dependent and functions representing either a temporary mixing or a proportion of visitors exposed to infectious individuals). The fifth function, representing limited interactions at a gate, was shown to be equivalent to the density-dependent function in our parametrization. The differences could be seen in both long-term and transient simulated dynamics.

This work highlights the need to carefully define the between-group transmission function when modelling pathogen spread in a heterogeneous structure. It brings insight into the biological grounds that could guide the choice of such a function.

Using Lambda-coalescents in phylodynamical analysis of viral genetic samples.

Patrick Hoscheita, * Oliver Pybusb

aMaIAGE, INRA, Université Paris-Saclay, 78350, Jouy-en-Josas, France;
bDept. of Zoology, University of Oxford

*patrick.hoscheit@inra.fr

Over the last decade, the use of phylogenetic methods in infectious disease epidemiology has become widespread. The increasing availability of large databases of pathogen genome sequences requires the development of mathematical frameworks that integrate different features of pathogen evolution. Existing mathematical models for phylogenies were invented with the evolution of animal and plant species in mind. However, in the case of rapidly-evolving viruses, many common assumptions concerning the diversification process are no longer valid: in particular, the population dynamics of the virus are constrained by its epidemiology, and different viral strains are under strong selection due to host immune responses. Further, the heterogeneous nature of viral transmission raises the question of whether neutral models based on binary trees models (such as the Kingman coalescent) are adequate to represent viral evolution.

In this work, we use Lambda-coalescent processes (e.g. Beta(2-a,a)-coalescents) to model large-sample phylogenies of viral populations. These processes have been identified as correctly taking into account the dynamics of repeated selective sweeps that are typical of the evolution of pathogens such as the HIV and influenza A viruses. Their most important feature is that they are in general non-binary, and can thus represent heterogeneity in transmission dynamics, which is a common phenomenon in the epidemiology of viral animal disease. We present a method that takes this heterogeneity into account when estimating past demographic shifts in viral population dynamics (the Lambda-skyline plot), and apply this method to a large-scale sample of the 2014-2015 West African Ebola outbreak.
Defining sentinels for outbreak detection in livestock-trade networks

Philipp Hövel*, Frederik Schirdewahn†, Andreas Koher§, Vitaly Belik¶, Hartmut H. K. Lentz, Vittoria Colizza

* Institute of Theoretical Physics, Technische Universität Berlin, Hardenbergstr. 36, 10623 Berlin, Germany
† Institute for Veterinary Epidemiology and Biostatistics, Freie Universität Berlin, Königsweg 67, 14163 Berlin, Germany
§ Institute of Epidemiology, Friedrich-Loeffler-Institut, Südufer 10, 17493 Greifswald - Insel Riems, Germany
¶ Sorbonne Universités, UPMC Univ Paris 06, INSERM, Institut Pierre Louis d’Épidémiologie et de Santé Publique (IPLESP UMRS 1136), 75012 Paris, France

* phoevel@physik.tu-berlin.de

We analyse a temporal network of livestock trade and present results of numerical simulations of epidemiological dynamics. The considered network is the backbone of the pig trade in Germany [1], which forms a major route of disease spreading between agricultural premises. The network is comprised of farms connected by a link, if animals are traded between them. We propose a concept for epidemic surveillance generally performed on a subset of the system due to limited resources. The goal is to identify agricultural holdings that are more likely to be infected during the early phase of an epidemic outbreak. These farms, which we call sentinels [2], are excellent candidates to monitor the whole network. To identify potential sentinel nodes, we determine most probable transmission routes by calculating functional clusters. These clusters are formed by nodes that have similar invasion paths. Then, we select sentinels by choosing nodes out of every cluster. We find that any epidemic outbreak can be reliably detected at an early stage by monitoring a small number of those sentinels [3].

Considering a susceptible-infected-recovered model, we show that an outbreak can be detected with only 18 sentinels out of almost 100,000 farms with a probability of 65% in approximately 13 days after first infection. This finding can be further improved by including nodes with the largest in-component (highest vulnerability), which increases the detection probability to 86% with 8 days after first occurrence of the disease.

MODELLING THE SPREAD OF BLUETONGUE IN SLOVENIA

Tanja Knific* a, Tadej Malovrh b, Marko Potočnik b, Matija Pretnar c, Milica Krković c, Aljoša Vodopija c, Jasna Prezelj c,d

a Veterinary faculty, University of Ljubljana, Gerbičeva 60, 1000 Ljubljana, Slovenia
b Administration of the Republic of Slovenia for Food Safety, Veterinary Sector and Plant Protection, Dunajska cesta 22, 1000 Ljubljana, Slovenia
c Faculty of Mathematics and Physics, University of Ljubljana, Jadranska 19, 1000 Ljubljana, Slovenia
d Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska, Glagoljaška 8, 6000 Koper, Slovenia

* tanja.knific@vf.uni-lj.si

The first occurrence of bluetongue (BT) in Slovenia was detected on 18th November 2015 in two bovine animals. Despite the immediate introduction of the prescribed measures, eight outbreaks were documented in the following year. The disease has considerable economic impact on the cattle industry; mostly due to trade restrictions and decreased milk production. In order to assess the risk of disease spread the purpose of this project was to develop a mathematical model that could sufficiently describe the spread of a BT outbreak in Slovenia.

In accordance with the nature of the disease, we redesigned a basic “Susceptible-Infectious-Recovered” (SIR) model. We were modelling the change in the health status of cattle and small ruminants, as well as the horizontal and vertical transmission of BT virus in vector midges of the genus Culicoides spp. One of the key components of the model are environmental conditions for which data, specific for our area, were collected. Information on the epidemiological characteristics of the agent and the spread of the disease were obtained from published literature. These data are usually estimated for the area the study refers to; therefore, we adjusted and weighted certain values using expert opinions. The system is described with locally correlated difference equations, wherein we took into account different boundary and initial conditions. We made the assumption that hosts populations are constant, whereas the vector population is modelled on each square kilometre depending on the density of hosts, the terrain and the direction and strength of the wind. Growth factor of the vector population is adjustable and time dependent. The number of simulated steps depends on observational time of infection and the wind speed.

Notably, the end user can modify the main influential factors in the model through the graphical user interface. This allows the simulation of the disease spread with different initial outbreak areas, weather and other conditions. The results of simulations are displayed on the map of Slovenia. On each square kilometre, we can follow the number of healthy and infected vectors and the number of healthy and infected hosts. Thus, we can estimate the direction and speed of the disease spread. When interpreting the results, we have to consider the underlying assumptions and the values of adjustable parameters. Nevertheless, in combination with an economic analysis, the developed model could provide evaluation of the impact of a potential BT outbreak and useful additional information for decision making on disease control measures.

Modelling brucellosis in a heterogeneous wild population of Alpine ibex
(Capra ibex)

S. Lambert*\(^a\), S. Rossi\(^b\), C. Toïgo\(^c\), E. Gilot\(^a,d\), A. Thébault\(^e\)

\(^a\) Université Lyon1, UMR CNRS 5558 Laboratoire de Biométrie et Biologie Evolutive, Villeurbanne, France
\(^b\) Unité Sanitaire de la Faune, Office National de la Chasse et de la Faune Sauvage, Gap, France
\(^c\) Unité Faune de Montage, Office National de la Chasse et de la Faune Sauvage, Gières, France
\(^d\) VetAgro Sup, Marcy l’Etoile, France
\(^e\) Agence Nationale de Sécurité Sanitaire, de l’environnement et du travail, Maisons-Alfort, France

* sebastien.lambert@univ-lyon1.fr

Ecological characteristics of the host are important drivers of pathogen spread and persistence in wild populations. If the complex interplay between host ecology and pathogen dynamics is not accounted for, naïve management strategies can have counter-intuitive effects. For instance, by interacting with density-dependent parameters such as survival and fertility rates [1] or with spatial heterogeneity [2], management may increase the number of susceptible hosts and thus promote pathogen transmission.

While France is officially free of brucellosis since 2005, one cattle herd infected with Brucella melitensis was detected in 2012 in the French Alps (Bargy massif). This outbreak probably originated from the local Alpine ibex population [3], in which high seroprevalences have been found since then (38 % in 2012-2013) [4]. This is the first case of B. melitensis persistence in European wildlife. In this context, a modelling approach is relevant to investigate the plausibility of different routes of transmission of Brucella within this population and to identify ecological factors influencing the persistence of B. melitensis in this population, in order to evaluate various management strategies.

A stochastic individual-based model was developed in 2014-2015 [5,6]. This model integrated several ecological characteristics of the Alpine ibex population of the Bargy massif, such as density-dependent demographic processes, seasonality of mating and births periods, characteristics of male behaviour during mating and changes in contact structure due to social segregation. The main hypothesis of the model was that, except for those factors, the contacts were homogeneous inside this closed population. However, new data are not in agreement with this hypothesis but suggest spatial as well as individual heterogeneity [7,8].

Here, we present and discuss the possible ways to incorporate these heterogeneities in the model. The first source of heterogeneity is in space use, especially among females, which is related to marked differences in seroprevalence [7] and could be accounted for using metapopulation, lattice or network models. The second source of heterogeneity is concerning both susceptibility and excretion, due to age and immunogenetic factors [8]. This model will then be numerically implemented and used to better understand transmission processes in the population and to evaluate management strategies.

USE OF PROXIMITY LOGGERS TO QUANTIFY CONTACT PATTERNS WITHIN AN ONTARIO EQUINE FACILITY

Rachael Milwid*a, Terri L. O’Sullivan*a, Zvonimir Poljak*b, Marek Laskowski*a,b, Amy L. Greer*a

*a Department of Population Medicine, University of Guelph, Guelph, ON, Canada
*b Department of Mathematics and Statistics, York University, Toronto, ON, Canada

*Disease transmission models often make simplifying assumptions regarding the contact that is sufficient for disease transmission between individuals. Further refinement of these models requires more detailed information about the contact patterns of individuals (e.g. frequency and duration) and the implications of realistic contact patterns. Our objective was to use proximity logging technology to better understand contact patterns within Ontario equine facilities. We present a methodology for using radio frequency identification (RFID) proximity loggers to record contact that occurs when two individuals wearing tags come within a pre-determined distance of each other. We analyze data collected over a seven-day period in order to quantify contact patterns. The utility of these data for providing a detailed description of time-varying contact patterns between individuals is discussed.

A pilot study was conducted within an Ontario equine facility with nine horses. Loggers were attached to the horses’ halters which were kept with the horse at all times during a week-long study period. Staff at the facility carried out the usual schedule for each participating horse (e.g. turnout, training). The loggers recorded the ID of the horses that came within two meters of each other, as well as the time and duration of each individual contact over a seven-day period. Surveys completed by the facility manager provided horse-level information such as sex and breed, as well as routine daily activities. Data on the horse’s pasture and stall locations were recorded. The resulting contact data were used to describe and compare contact networks for each day of the study.

Results included an analysis of visual representations of the daily networks, as well as each node’s degree, and the consistency of contacts throughout the study period. Visually, the general contact patterns were similar each day reflecting the daily schedule of the facility, with contact similarities based on horses being turned out in the same pasture, as well as horses in the same barn aisle. While this general pattern of contacts is obvious, it is also clear that the network degree, individuals in contact, and the contact between the various wings of the barn changed from day to day. The mean unweighted network degree was 4.7 for the week. Each horse had contact with up to 8 other horses per day. The horse with the highest daily degree centrality changed depending on the day of the study period. The Jaccard’s difference index indicated that the most similar days had ~74% identical contacts and the least similar days shared ~55% of identical contacts (with the exception of day 5).

This work serves as a pilot study to quantify the variability in contact patterns between horses over time. This heterogeneity in contacts can help understand the disease transmission potential within an equine facility.

Transmission dynamics of lumpy skin disease in Ethiopia

W. Molla\(^{a,b,*}\), K. Franken\(^a\), M.C.M. de Jong\(^a\)

\(^a\) Quantitative Veterinary Epidemiology, Wageningen University & Research, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands
\(^b\) Faculty of Veterinary Medicine, University of Gondar, P.O. Box 196, Gondar, Ethiopia

* wassie.abebe@wur.nl/Mollawassie@yahoo.com

Lumpy skin disease (LSD) is a severe disease of cattle caused by a \textit{capripoxvirus} and often causes regional epidemics in African countries, also in Ethiopia. The study was carried out in central and north-western part of Ethiopia with the objectives to understand LSD outbreak dynamics, to quantify the transmission between animals and herds and to estimate the disease reproduction ratio in predominantly mixed crop-livestock system (considered as one large population of several small herds) and in intensive commercial herd types (considered as separate populations). The transmission parameters were estimated based on a SIR epidemic model. For this, the infection chains were followed over time and the numbers of susceptible, infectious and recovered animals as well as new cases were recorded.

Generalized linear model with a complementary-log–log link function and log ((number of infectious animals or herds + the amount of virus in the environment)/total number of animals or herds) as offset variable was used to estimate the regression coefficient (intercept) and then the transmission parameter \(\beta\) by exponentiation of this coefficient. The reproduction ratio was obtained by multiplying \(\beta\) with the average length of LSD infectious period. A higher morbidity was recorded in infected crop-livestock mixed production system herds (24.1%) than in infected intensive system herds (17.5%) whereas mortality among those that were infected were 1.5% and 4.0% respectively. The transmission rate parameters between herds and among animals were 0.038 (95% CI: 0.036-0.041) and 0.043 (95% CI: 0.040-0.045) per day, respectively in the crop-livestock production system whereas the transmission rate among animals in intensive production system was 0.045 (95% CI: 0.041-0.051) per day. The overall transmission rate among animals in both production systems was 0.043 (95% CI: 0.041-0.045) per day. The transmission rates did not significantly vary between production systems and herd sizes. The reproduction ratio (R) of LSD between herds in the crop-livestock production system was 1.24 and 1.07 among animals, the same R was estimated among animals in intensive production system. Estimates of R can now be used to compare between situations with different interventions.
Treatment strategies for sheep scab: An economic model of farmer behaviour

Emily J. Nixon, Hannah Rose Vineer, Richard Wall

Veterinary Parasitology and Ecology Group, University of Bristol, Bristol Life Sciences Building, 24 Tyndall Avenue, Bristol, BS8 1TQ, United Kingdom

*emily.nixon@bristol.ac.uk

Ovine psoroptic mange (sheep scab) is a debilitating and damaging condition caused by a hypersensitivity reaction to the faecal material of the parasitic mite *Psoroptes ovis*. Farmers incur costs from the use of prophylactic acaricides and, if their sheep become infected, they incur the costs of therapeutic treatment plus the economic loss from reduced stock growth, lower reproductive rate, wool loss and hide damage. The unwillingness of farmers to use routine prophylactic treatment has been cited as a primary cause of the growing incidence of sheep scab in the United Kingdom (UK) since the disease was deregulated in 1992. However, if farmers behave rationally from an economic perspective, the optimum strategy that they should adopt will depend on the risk of infection and the relative costs of prophylactic versus therapeutic treatment, plus potential losses. This calculation is also complicated by the fact that the risk of infection is increased if neighbours have scab and reduced if neighbours treat prophylactically. Hence, for any farmer, the risk of infection and optimum approach to treatment is also contingent on the behaviour of neighbours, particularly when common grazing is used. Here, the relative economic costs of different prophylactic treatment strategies are calculated for upland and lowland farmers and a game theory model is used to evaluate the relative costs for a farmer and his/her neighbour under different risk scenarios. The analysis shows that prophylaxis with organophosphate (OP) dipping is a cost effective strategy, but only for upland farmers where the risk of infection is high. In all other circumstances prophylaxis is not cost effective relative to reliance on reactive (therapeutic) treatment. Hence, farmers adopting a reactive treatment policy only, are behaving in an economically rational manner. Prophylaxis and cooperation only become economically rational if the risk of scab infection is considerably higher than the current national average, or the cost of treatment is lower. Should policy makers wish to reduce the national prevalence of scab, economic incentives such as subsidising the cost of acaricides or rigorously applied financial penalties, would be required to make prophylactic treatment economically appealing to individual farmers. However, such options incur their own infrastructure and implementation costs for central government.
WHAT REALLY CAUSES FOOTROT IN SHEEP: A NATIONAL COHORT STUDY OF THE MICROBIAL DIVERSITY OF *DICHEROBACTER NODOSUS* IN SHEEP IN SICKNESS AND IN HEALTH

Naomi Prosser*, Professor Laura Green*, Dr Kevin Purdy*

*School of Life Sciences, Gibbet Hill Campus, University of Warwick, Coventry, CV4 7AL

* N.Prosser@warwick.ac.uk

Footrot is a disease of sheep that costs the UK industry an estimated £80 million per annum [1]. It is also a welfare concern. There are two clinical presentations, interdigital dermatitis and severe footrot, that affect almost all flocks in the UK, with a mean prevalence of lesions of 4.5% and 3.1% respectively [2]. The causal agent of footrot, *Dichelobacter nodosus*, has ten serogroups. In the UK, there is one licensed multivalent vaccine containing 9/10 serogroup antigens which reduces lameness by approximately 20% [2]. This limited efficacy is possibly due to antigenic competition between serogroups. Autogenous mono/bivalent vaccines are more effective [3].

A total of 169 farmers from across England have completed three questionnaires over a three-year period on prevalence of lameness and management of lameness in their flock. These farmers have provided eight swabs from the interdigital skin of sheep feet; overall, 40% were from severe footrot, 35% from interdigital dermatitis, 7% from healthy feet and 20% were from other foot lesions. 2% of swabs were from feet with more than one lesion. A multiplex PCR is being used to identify the serogroups present on each swab. Statistical models combining the management data and serogroup data will be used to test the hypotheses that serogroup diversity and distribution differ by region and flock management, that vaccination reduces serogroup diversity, and that tailored flock specific vaccines with fewer serogroups could be more successful at controlling footrot in England.

Intramammary infections (IMI) are the most frequent and important diseases of dairy cows. It is a significant animal and economic issue in the dairy farming, and affects both milk production and milk quality [1]. Intramammary infections (IMI) caused by bacterial infection is routinely diagnosed through bacterial culture. *Corynebacterium spp.* are considered to be minor udder pathogens [2].

The development of decision support tools for the detection and management of IMI remains the subject of extensive research. IMI with *Corynebacterium spp.* are generally mild causing limited loss in milk production. However, significant elevation of somatic cell count (SCC) has been observed. Pathogen-specific transmission patterns have been described for other major and minor mastitis pathogens but not for *Corynebacterium spp.* [3]. This has motivated us to construct a model of the transmission dynamics of *Corynebacterium spp.* IMI throughout the lactation period.

Mathematical models are desirable to enhance the identification and understanding of factors that affect pathogen specific IMI dynamics. Longitudinal transmission models are valuable for predicting infection outbreak risk, quantifying the effectiveness of response tactics and performing response planning.

In this work, we focus on the modelling of *Corynebacterium spp.* by using a compartmental model. We have established a new *Corynebacterium spp.* SISw (naive susceptible-Infectious-susceptible within) model. We have simulated the model numerically by using parameters obtained through real data fitting procedure using nonlinear least squares method for nonlinear ordinary differential equations (ODEs). The real data were collected from a 13-month longitudinal observational study in one commercial dairy herd in New York, US. The transmission dynamics were further evaluated by the basic reproduction number $R_0$, which is defined as the expected number of secondary cases that arises per infectious individual in a fully susceptible population.

DECISION SUPPORT SYSTEMS FOR PARASITE CONTROL IN LIVESTOCK

Eric Morgan*a, Jan van Dijkb, Siân Mitchellc, Hannah Rose Vineera

a Veterinary Parasitology & Ecology, School of Veterinary Sciences, University of Bristol, UK
b Epidemiology and Population Health, Institute of Infection and Global Health, University of Liverpool, UK
c Animal and Plant Health Agency, UK

* Hannah.rosebristol.ac.uk

Parasitic disease epidemiology is often heavily dependent on the impact of weather on the free-living stages of the parasite’s life cycle. In these cases, weather-dependent models of parasite infection dynamics can help determine the optimal treatment strategy to prevent infection and disease and mitigate negative impacts of climate change and inter-annual weather variability on disease risk.

The gastrointestinal nematode Nematodirus battus is a significant cause of morbidity and mortality in young lambs in the United Kingdom due to the mass emergence of infective larvae in spring. Due to the unpredictable onset of spring in recent years, treating according to a traditional timetable to prevent infection has become largely ineffective. A spatial decision support system (‘risk map’) was developed [1] in collaboration with a UK sheep industry-led organisation, Sustainable Control of Parasites in Sheep (SCOPS) to allow farmers to make informed risk assessments for their flock and treat according to risk. User feedback indicates that the model has been successful in preventing infection, reducing clinical signs of disease and preventing lamb deaths.

Mathematical models predicting the population dynamics [2] and basic reproductive quotient (Q0) [3] of other gastrointestinal parasites infecting livestock such as Haemonchus contortus have also been developed, and their use as part of a decision support system to determine the optimal timing of treatment is currently being evaluated in the UK, Cuba and Botswana [4].

The effect of shared pastures on the between-herd spread of bovine Tuberculosis

Gianluigi Rossi*a, Rebecca L. Smitha

a Department of Pathobiology, University of Illinois, Urbana, 61801 IL, USA

* grossi@illinois.edu

Shared pastures are a common practice for many livestock industries, including cattle, horses, sheep, and goats. This practice is widespread in several countries, and in many of those it consists in allocating lands in which animals from different herds can graze during the summer season1,2. However, from an epidemiological point of view, mixing animals from different herds could enhance the spread of infectious diseases, because it creates the between-herds potential infectious contacts2,3. This represents a problem in particular for slow-spreading diseases, such as bovine tuberculosis (bTB), in which the signs of pathogen shedding individuals are not be evident, and thus a farmer might not be suddenly aware of an herd infection4.

The main objective of this study is to understand the risk of bTB spread among cow-calf operations that share pastures1. Our approach is quantitative, as we use a stochastic meta-population model able to represent: (i) the herds demographic, (ii) the within- and between-herd bTB epidemic dynamics, and (iii) the surveillance system in place (i.e. slaughterhouse inspection, and skin test follow-up). Each herd population is divided into 4 categories of animals (cows, heifers, bulls, and calves), and 4 potential disease status are considered (Susceptible, Occult to skin-test, Reactive to skin test, and Infectious)5. Our main assumption is that during the winter season (November to May), infectious contacts might occur only within an already infected herd. However, during the summer season (June to October), as a part of each herd is moved to a shared pasture land, contacts might also occur between them1. In this case, the between-herd infectious rate ($\beta_B$) is calculated by scaling the within-herd infectious rate ($\beta_w$) by a factor $\phi$ which quantifies the between-herd mixing during pastures (i.e. no mixing for $\phi = 0$, complete mixing for $\phi = 1$).

Our goal is to provide an estimate of (i) the time to first detection, (ii) the probability of other herds being infected at first detection, and (iii) the amount of testing necessary to clear out other herds. All this estimation are done for different values of $\phi$.

Results of this model could have several important implications. On one hand, it can provide insights on the best bTB surveillance6 and eradication7 methods in livestock industries for developed countries. On the other hand, it can also suggest the best control strategies for bTB in smaller herds, such as those common in developing countries, where this disease represents a threat for human, as well as animal health3,4.
Pathogen spread between farms results from the interaction between epidemiological characteristics of the infectious agents and the contact structure between holdings. In this context, the analysis of animal movements at national scale appears pivotal to understand the contribution of the contact network to the spread of diseases. Pig movements have been recorded in France since 2010 and stored in the National Swine Identification Database handled by a professional association (BDPORC), offering the opportunity to explore the contact network. In this study, we modelled pig movements in France based on two different hypotheses to define actual infectious contacts.

(i) In the first network model, links between holdings represented movements of animals being unloaded in farms, intermediate transit movements of a truck in a farm without unloading any animal being neglected. This model is relevant for pathogens that spread between farms only through the introduction of animals in farms (i.e. diseases for which the indirect transmission route is negligible).

(ii) In the second network model, links between holdings represented both movements of animals and the transit of the truck in a farm without any unloading event. This model could be applied for pathogens spreading not only with the introduction of animals in farms but also through the transit of trucks in farms even without any animal introduction (i.e. diseases for which indirect transmission occurs).

These two approaches were used to model pig movement data recorded in France from June 2012 to December 2014, aggregated on a six-month basis. For each type of model, we calculated network descriptive statistics (size, average degree, average path length, diameter, density, clustering coefficient, Jaccard similarity coefficient, assortativity degree, reciprocity ratio, closeness and betweenness centralities). We also looked for weakly and strongly connected components (WCCs and SCCs) and we explored communities at different scales (entire network, network of breeding farms or of production farms only).

Whatever the model, the heavy-tailed node degree distributions suggested a scale-free structure. In the first model, nucleus, multiplication and post-weaning farms had higher values for degree and betweenness centrality, showing their expected key role in the spread of a disease transmitted exclusively by infected animals. In the second model, farrowing and farrow-to-finish herds presented higher values for in-degree centrality and they therefore appear more vulnerable to the introduction of infectious diseases through indirect contacts (trucks as mechanical vectors). In both models, few WCCs were detected, the largest one gathering at least 90% of holdings. In the first model, a high number of SCCs was found, the largest one containing less than 1% of farms. On the contrary, the network modelled with the second approach was less fragmented, with a lower number of SCCs and the detection of a giant SCC containing more than 70% of pig herds. The topology of network communities also varied with the modelling assumptions: in the first approach, a huge geographically dispersed community was found, whereas the second model highlighted several small geographically clustered communities. These results underline the relevance to develop network models corresponding to the pathogen features and the need to target specific type of holdings and areas for surveillance and control depending on the epidemiological context.
NETWORK ANALYSIS OF PIG MOVEMENTS: LOYALTY PATTERNS AND CONTACT CHAINS OF DIFFERENT HERD TYPES IN DENMARK

Jana Schulz*, Anette Boklund, Tariq Halasa, Nils Toft, Hartmut Lentz

* Technical University of Denmark, National Veterinary Institute, Bülow'svej 27, 1870 Frederiksberg C, Denmark
** Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Südufer 10, 17439 Greifswald – Insel Riems, Germany

*janson@vet.dtu.dk

Understanding animal movements is an important factor for the development of meaningful surveillance and control programs, but also for the development of disease spread models. We analysed the Danish pig movement network using static and temporal network analysis tools to provide deeper insight in the connection between holdings dealing with pigs, such as production herds, slaughterhouses or traders.

Pig movements, which occurred between 1 Jan 2006 and 31 Dec 2015 in Denmark, were summarized to investigate temporal trends such as the development of the number of active holdings, the number of registered movements and the number of pigs moved.

To identify holdings and holding types with potentially higher risk for introduction or spread of diseases via pig movements, we calculated the holding’s in- and out-loyalty as a local measure of its tendency to maintain contacts with the same holdings over time [1]. Furthermore, we determined network components to identify subsets of holdings where connectedness is particularly high and the holding types within connected components [2]. Finally, we evaluated the size of the in-going and out-going contact chain for each holding by tracing back and forward all direct and indirect contacts within yearly snap shots [3].

The total number of active holdings as well as the number of pig movements decreased during the study period while the holding sizes increased. Around 60 – 90% of connections between two pig holdings were present in two consecutive years and around one third of the connections persisted within the considered time period of 10 years.

Breeding and multiplier herds could be confirmed to have a higher risk of spreading a pathogen via pig movements based on their higher sizes of out-going contact chains compared to other holding types. Production herds showed a highly variable risk of spreading and receiving infections via pig movements which could be explained by variations in the holding management. The yearly components indicate circular connections between holdings that might support pathogen perpetuation. Loyalty patterns vary among holding types, with e.g. high in-loyalty for production and weaner herds and high out-loyalty for e.g. production herds and boar stations.


Salah Uddin Khan\textsuperscript{a}, Terri O’Sullivan\textsuperscript{a}, Zvonimir Poljak\textsuperscript{a}, Janet Alsop\textsuperscript{b}, Amy Greer\textsuperscript{a}

\textsuperscript{a}Department of Population Medicine, Ontario Veterinary College, University of Guelph
\textsuperscript{b}Ontario Ministry of Agriculture, Food, and Rural Affairs

* sukhanbd@uoguelph.ca, agreer@uoguelph.ca

\textbf{Background:} Infectious diseases in farmed animals have economic, social, and public health consequences [1]. Foreign animal diseases (FAD) of swine are of significant concern [2]. Mathematical models are often used to simulate FAD outbreaks and best practices for control [3]. However, simulation outcomes are sensitive to the population structure used. Within Canada, access to individual swine farm population data with which to parameterize models is a challenge because of privacy concerns. Our objective was to develop a methodology to generate a synthetic population of swine farms in Ontario, Canada that could represent the existing population structure and improve the efficacy of simulation models.

\textbf{Methods and Results:} We used multiple data processing steps to develop a synthetic swine farm population. We identified geographical information system data on factors such as facilities supporting farm infrastructure, land availability, zoning and local regulations, and natural geographic barriers that could affect swine farming in Ontario. We defined the relative importance of each of the factors and generated an algorithm to produce a combined likelihood score for swine farming. We then assigned probability scores to one square kilometer geospatial grids throughout the province and generated random farm locations on the probability surface. Assigned farm locations were proportional to the swine farm density described in the 2011 Canadian Census of Agriculture suggesting that our algorithm generated a reasonable approximation of the farm locations at the county level. Farms were then randomly assigned to farm types proportional to the existing swine herd types. The sensitivity of the synthetic population model is currently being validated against a known database of swine farm locations in Ontario.

\textbf{Conclusion :} In the absence of a full, identifiable population structure dataset, incorporating a synthetic population that captures key characteristics of the observed population structure while protecting privacy concerns is an important methodological advancement and will be useful for individuals interested in modeling the spread of pathogens between farms across a landscape and using models to evaluate disease control strategies.

Coordination of individual decisions – a Leader-Follower Markov Decision Process (LF-MDP) approach

Viet A.F.*, a Belloc C., a, Sabbadin R.b

a UMR1300 BioEpAR, INRA, Oniris, CS 40706, 44307 NANTES Cedex 3, France

b UR875 MIAT, INRA, CS52627, 31326 CASTANET TOLOSAN Cedex, France

* anne-france.viet@oniris-nantes.fr

Animal disease management often requires to design and implement control policies at the collective scale. However, for endemic non notifiable diseases, individual farmers are responsible for the adoption and the compliance of control policies at the farm scale. Organizations (groups of farmers, health institutions...) may try to influence farmers’ control actions through incentives, in order to improve the health and economical situation in a group of farms. The problem of endemic disease control can be seen as a form of multi-agent sequential decision problem under uncertainty. Indeed, farmers (followers) try to maximize their profit by deciding when and how to apply control actions within their herds, while the organization (leader) has for objective to minimize the disease consequences, by giving incentives to farmers. Published studies in animal health defined various scenarios of incentives and evaluated their consequences by simulation. The focus of these studies were individual decision, pathogen spread within an area [1] or only the leader decision [2]. Instead, we were interested in optimising the organisation decision together with the individual decisions. To do so, we used a Leader-Follower Markov Decision Processes (LF-MDP) framework [3] that combines Markov Decision Processes and stochastic games. We considered that farms are separated into groups based on their disease status. We proposed an original algorithm to solve the LF-MDP model under this assumption [4]. For problems with more than 20 followers, we proposed an approximation algorithm. We instantiated our approach on the problem of controlling the spread of the Porcine Reproductive and Respiratory Syndrome, a key issue in pig production. We validated our approximation method by comparison with the optimal resolution approach on problems with few followers. Our approximate algorithm currently allows us to solve problems with up to 100 followers.

References
Factors associated with between-herds movements of cows and heifers in France

Pierre Villard*,ab, Carole Salaa, Jean-Luc Vinarda, Didier Calavas, Viviane Hénaux

a Université de Lyon, ANSES - Laboratoire de Lyon, Unité Epidémiologie, 31 avenue Tony Garnier, 69007 Lyon
b UMR CIRAD-INRA Animal, Santé, Territoires, Risques, Écosystèmes (ASTRE) CIRAD Chemin de Baillarguet, 34980 Montferrier-sur-Lez

* pierre.villard@anses.fr

Cattle movements between herds are a major driver of infectious agent spread in the network of susceptible herds. The identification of factors influencing the decisions of farmers to buy or sell bovines is essential to predict those movements and thereby orient policies to control disease diffusion. The purpose of this study was to identify key herd characteristics influencing sales and purchases of reproductive females and replacement heifers in dairy herds.

We applied a hurdle model to identify factors associated to the act of selling or buying (with a binomial regression) and to the numbers of sales or purchases when appropriate (with a zero-truncated Poisson regression) for two periods without major cattle epidemics in France – therefore without movement restrictions – 2010-2011 and 2013-2014. We tested a set of variables describing herd management practices (presence of a feedlot, number of fattening bovines, herd size, three-year trend in herd size) and herd performances (annual mortality rates, three-year trend in mortality rates, average calving interval, turn-over rate) computed from the French National Cattle Register. We also included in our models a cluster variable obtained from a herd classification approach based on social network indicators (betweenness, in-closeness, out-closeness and closeness). We used this social network approach because each purchase for a herd corresponds to a sale for another. Moreover, from an epidemiological point of view, it is rather different if one herd sells ten bovines to a single herd, or if it sells one bovine to ten herds.

Overall, the results are consistent for the two periods. They showed that the purchase decision was favoured by a three-year increase trend in herd size and a high mortality rate for calves; for the number of purchases, a high number of purchases was associated with a three-year increase trend in herd size, a high turn-over rate and with the most connected cluster. For the sale model, we evidenced that farmers with herds without a feedlot and having a low turn-over rate are more likely to sell; but for those who sale, herds with a feedlot and a high turn-over rate sale more than the others.

Even if the role of most of these factors was already well-known, our study allows quantifying their effect. As we selected two study periods without movement restriction policy, our models could be used to predict sales and purchases in “normal” conditions. They could also be used as a standard to investigate movement restriction policies effects on sales and purchases.
Emergent and re-emergent infectious diseases are known to be a global public health problem [1]. Taylor et al. (2001) estimated that sixty percent of human pathogens are zoonotic and a large majority of emerging infectious diseases are associated with zoonotic pathogens [2]. Zoonotic diseases are originated from a primary reservoir where the pathogens are persistent. One of the most important reservoir is bats where many of terrible diseases are caused by viruses originated from these primary reservoir, such as Ebolavirus, Marburg, SARS coronavirus, MERS coronavirus, Nipah virus and Hendra virus [3]. Outbreaks of diseases mentioned above are associated with outbreaks in animal population originated from primary reservoir. For example, Ebola virus caused major outbreaks in nonhuman primates and in the same way Nipah virus is responsible for outbreaks in pig farms [4]. The emergence and the epidemic dynamics are mostly associated with the recurrent introduction of the pathogen into the target population through primary reservoir spillover. The dynamic of an emergent disease in a target population is not well understood this is why an epidemiologic stochastic model can be needed. We propose a simple Susceptible-Infected-Recovered model with recurrent introduction of the infection into the population. The reservoir is defined as a compartment where the pathogen is persistently maintained in the population and this pathogen is considered as endemic. The dynamic in the target population is analyzed and depend on the effect of the reservoir through the spillover process and the direct transmission between individuals.