ModAH 2024 – Program

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

Tuesday, 27 of August

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

Wednesday, 28 of August

09:00–09:20	CT	**Luca Martelli** Istituto Zooprofilattico Sperimentale delle Venezie	Unraveling the Role of Wild-Domestic Interface in the Spread of High Pathogenicity Avian Influenza
09:20–09:40	CT	**Emma L. Fairbanks** University of Warwick	Assessing the impact of host clustering and control strategies on African horse sickness virus transmission: A simulation-based analysis
09:40–10:00	CT	**Sébastien Picault** INRAE	From mechanistic models to decision-support tools: generating user-friendly web application from artificial intelligence and software engineering methods
10:00–10:20	CT	**Glen Guyver-Fletcher** University of Warwick	Using a multi-species epidemiological model to assess optimal FMD vaccine allocations across India
10:20–11:00	**Coffee break & poster session**		
11:00–11:20	CT	**Laetitia Canini** Anses	Outbreak reconstruction with a slowly evolving multi-host pathogen: a comparative study of three existing methods on Mycobacterium bovis outbreaks
11:20–11:40	CT	**Rémi Fay** Université Lyon 1	Methodological challenges in estimating brucellosis transmission risk in an Alpine ibex population using approximate Bayesian computation
11:40–12:00	CT	**Clara Delecroix** Wageningen University & Research	A novel machine learning approach to anticipate vector-borne disease outbreaks
12:00–12:20	CT	**Egil A.J. Fischer** Utrecht University	SUMMERFAIR – combining data science and infection models for estimating transmission parameters
12:20–13:50	**Lunch**		
13:50–14:40	KL	**Mike Tildesley** University of Warwick	Modelling optimal intervention strategies for animal diseases in data poor settings
14:40–15:00	CT	**Brandon Hayes** INRAE - ENVT	Quantifying the influence of wild boar density on African swine fever spread in wild boar populations, Italy, 2022-2023
15:00–15:20	CT	**Anna Gamza** Roslin Institute, University of Edinburgh	Spatial scales of interactions driving spread of Highly Pathogenic Avian Influenza in Great Britain
15:20–16:20	**Coffee break & poster session**		
16:20–16:40	CT	**Hélène Cecilia** New Mexico State University	Quantifying the relationship between within-host viral dynamics and transmission to mosquitoes: the case of Zika virus in two monkey species
16:40–17:00	CT	**Jonathan Bastard** Anses	Reconstructing West Nile virus dynamics in a tropical island using sentinel serological data
17:00–17:20	CT	**Vianney Sicard** UFZ – Helmholtz Centre for Environmental Research	Modeling Vaccination Strategies for African Swine Fever Control Among Wild Boars: A Computational Approach
17:20–17:40	CT	**Gustavo Machado** North Carolina State University	Mitigating between-farm disease transmission through simulating vehicle rerouting and enhanced cleaning and disinfection protocols
20:00	Conference Dinner		

Thursday, 29 of August

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