

Tuesday 28th November 2023

15:00-17:30	Registration Main Entrance Hall
17:30-19:00	Welcome Reception and Poster Session 1 Europa Foyer & Italia Foyer

Wednesday 29th November 2023

08:30-10:30	Opening Session Room: Europa Auditorium Session Chairs: Katrina Lythgoe, Cecile Viboud, Joseph Wu
08:30-08:40	Welcome and Opening Remarks Katrina Lythgoe, Cecile Viboud, Joseph Wu & Joanna Aldred, <i>Publisher, Elsevier, The Netherlands</i>
08:40-09:10	[INV01] Strengthening the use of epidemiological modelling Yot Teerawattananon, Health Intervention and Technology Assessment Program (HITAP), Thai Ministry of Public Health, Thailand
09:10-09:50	[INV02] Impacts of vaccinating against influenza Sarah Cobey, University of Chicago, USA
09:50-10:30	[INV03] The rocky road to global polio eradication: Can we deliver on a 35-year-old commitment? Nicholas Grassly, Imperial College London, UK

10:30-11:00	Refreshment Break Foyer Europa
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	Session 1: Vector-borne 1 Room: Europa Auditorium Session Chair: Alex Perkins	Session 2: Methods Room: Italia Session Chair: Kaiyuan Sun	Session 3: Animal diseases 1 Room 7 Modules Session Chair: Gavin Smith
11:00-12:40	11:00 - 11:20 [O1.1] Targeting vector control for dengue control: A modelling assessment of alternative approaches 11:20 - 11:40 [O1.2] Modeling the West Nile virus force of infection in the avian host population in Northern Italy 11:40 - 12:00 [O1.3] Uncovering mechanisms behind the spatial-temp emergence of Usutu virus in the Netherlands 12:00 - 12:20 [O1.4] Linking antigenic diversity to dengue disease risk 12:20 - 12:40 [O1.5] Estimating the efficacy and likely population impact of TAK-003, a second-generation dengue vaccine	11:00 - 11:20 [O2.1] The omnipotent butterfly effect: strict counterfactual scenarios in stochastic simulations using a counter-based pseudorandom number generator 11:20 - 11:40 [O2.2] Disentangling the dynamics of cross-reacting pathogens in serological studies 11:40 - 12:00 [O2.3] Jointly estimating household secondary attack risk and heterogeneity between individuals: biases and considerations for study design 12:00 - 12:20 [O2.4] Estimating the epidemic reproduction number from temply aggregated incidence data: a statistical modelling approach and software tool 12:20 - 12:40 [O2.5] Capturing partnership heterogeneity and concurrency in heterosexual network models	11:00 - 11:20 [O3.1] Episodic resurgence of highly pathogenic avian influenza H5 virus 11:20 - 11:40 [O3.2] Phylogenetic analysis of A(H5N1) highly pathogenic avian influenza viruses reveals reassortment dynamics and diversification of host specificity 11:40 - 12:00 [O3.3] Phylogenetics combined with longitudinal infection data demonstrate feasibility of hepatitis E virus control in pig farms 12:00 - 12:20 [O3.4] Efficient Bayesian modelling of infectious diseases in wildlife: an application to bovine tuberculosis in badgers 12:20 - 12:40 [O3.5] Uncovering the contribution of ecological and environmental traits to predicted avian influenza risks in wild birds across Europe

12:40-13:40	Lunch Room: Foyer Europa	Author Workshop Room: Italia
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	Session 4: COVID 1 Room: Europa Auditorium Session Chair: Sen Pei	Session 5: Childhood Room: Italia Session Chair: Rosalind Eggo	Session 6: Genomics 1 Room 7 Modules Session Chair: Trevor Bedford
13:40-15:40	13:40 - 14:00 [O4.1] Effect of superspreading and disease outreach on temp networks 14:00 - 14:20 [O4.2] Are changes in population mobility predictive of respiratory virus transmission? Insights from high	13:40 - 14:00 [O5.1] Understanding the relative role of viral-viral interference and non-pharmaceutical interventions in shaping RSV epidemics: a modeling study 14:00 - 14:20 [O5.2] Comparison of static and dynamic transmission models for	13:40 - 14:00 [O6.1] Combining epidemiologic and genomic data to define epidemiologically-relevant units of cholera transmission in Africa

	<p>resolution mobile phone data in the pre- and post-COVID-19 pandemic periods in Seattle, Washington</p> <p>14:20 - 14:40 [O4.3] Epidemiological insights from digital contact tracing as a tool to reduce and understand the transmission of respiratory pathogens</p> <p>14:40 - 15:00 [O4.4] Contact behaviour before, during and after the COVID-19 pandemic in the Netherlands</p> <p>15:00 - 15:20 [O4.5] Modelling the potential impact of 100 Days Mission and broader investments on the COVID-19 pandemic</p> <p>15:20 - 15:40 [O4.6] How to describe, compare, and select assumptions about self-protective behavior in models of disease-dynamics?</p>	<p>respiratory syncytial virus intervention programs for infants in England and Wales</p> <p>14:20 - 14:40 [O5.3] Delineating the seasonality of varicella and its association with climate in the tropical country of Colombia</p> <p>14:40 - 15:00 [O5.4] Tracking progress to measles elimination using routinely collected subnational surveillance data: A case study from Nigeria</p> <p>15:00 - 15:20 [O5.5] A quantitative simulation-based evaluation of the early detection of poliovirus using environmental surveillance</p> <p>15:20 - 15:40 [O5.6] Age-time-specific transmission pattern of 4 serotypes of Hand Foot Mouth Disease in Ho Chi Minh City, Vietnam: A Bayesian catalytic model with maternal immunity</p>	<p>14:00 - 14:20 [O6.2] Historical and current spatiotemp patterns of poliovirus spread</p> <p>14:20 - 14:40 [O6.3] Characterizing the social and spatial determinants of SARS-CoV-2 transmission from pairs of identical genome sequences</p> <p>14:40 - 15:00 [O6.4] From geno to pheno: Reconstructing Influenza antigenic maps through Natural Language approaches to HA protein sequences</p> <p>15:00 - 15:20 [O6.5] Estimating between-country migration of the global opportunistic pathogen <i>Streptococcus pneumoniae</i></p> <p>15:20 - 15:40 [O6.6] Population heterogeneity in within-host evolution: consequences for vaccine escape</p>
15:40-16:10	<p>Refreshment Break Room: Foyer Europa</p>		
16:10-17:50	<p>Session 7: Vaccination 1 Room: Europa Auditorium Session Chair: Katy Gaythorpe</p>	<p>Session 8: Chronic Room: Italia Session Chair: Alex Cook</p>	<p>Session 9: Within host Room 7 Modules Session Chair: Rustom Antia</p>
16:10-17:50	<p>16:10 - 16:30 [O7.1] Maternal immunization and the blunting of pertussis vaccines in infants: Too early to tell</p> <p>16:30 - 16:50 [O7.2] Retrospective analysis of equity-based optimization for COVID-19 vaccine allocation</p> <p>16:50 - 17:10 [O7.3] Should we use the 4CMenB (Bexsero) meningitis vaccine to protect men who have sex with men (MSM) in England against gonorrhoea? A model based analysis of impact and cost effectiveness</p> <p>17:10 - 17:30 [O7.4] Bridging the gap between efficacy trials and mathematical models: Improving vaccine descriptions in prospective impact evaluations of new tuberculosis vaccines</p> <p>17:30 - 17:50 [O7.5] Understanding the key determinants of an HPV therapeutic vaccine: A modeling analysis</p>	<p>16:10 - 16:30 [O8.1] Population-level effectiveness of pre-exposure prophylaxis for HIV prevention among men who have sex with men in Montréal, Canada: a modelling study using surveillance and survey data</p> <p>16:30 - 16:50 [O8.2] Using multiple contact networks in an agent-based model to track hepatitis C elimination in an ongoing pandemic era</p> <p>16:50 - 17:10 [O8.3] Modelling the impact of targeted testing in early HIV infection on the HIV epidemic among men who have sex with men in the Netherlands</p> <p>17:10 - 17:30 [O8.4] Population mobility and the development of Botswana's generalized HIV epidemic: a network analysis</p> <p>17:30 - 17:50 [O8.5] The frequency and implications of HIV dual infection</p>	<p>16:10 - 16:30 [O9.1] Comparative antibody breadth of influenza A in ferrets and humans: implications for susceptibility and reinfection intervals</p> <p>16:30 - 16:50 [O9.2] Mechanisms of persistence of Kaposi's sarcoma-associated herpesvirus</p> <p>16:50 - 17:10 [O9.3] Quantitative analysis of the antiviral effect of mucosal antibodies to suppress infectious SARS-CoV-2 shedding</p> <p>17:10 - 17:30 [O9.4] Viral and immune kinetics of HPV genital infections in young adult women</p> <p>17:30 - 17:50 [O9.5] Dynamics of anti-SARS-CoV-2 antibody titers and its protection against the confirmed Omicron BA.5 infections: using a community-based prospective cohort in Korea</p>
17:50-19:20	<p>Poster Session 2 Room: Foyer Italia</p>		

Thursday 30th November 2023

08:30-10:30	INV04, INV05, INV06 Room: Europa Auditorium Session Chair: Adam Kucharski		
08:30-09:10	[INV04] SARS-CoV-2 transmission in the night town Hiroshi Nishiura, Kyoto University Graduate School of Medicine Faculty of Medicine, Kyoto, Japan		
09:10-09:50	[INV05] From promise to realization: Sequencing and surveillance for the future Emma Hodcroft, Swiss Tropical and Public Health Institute, Basel, Switzerland		
09:50-10:30	[INV06] SIR... or MADAM? The impact of privilege on careers in epidemic modelling SIR... or MADAM? The impact of privilege on careers in epidemic modelling Anne Cori, Imperial College London, UK		
10:30-11:00	Refreshment Break Foyer Europa		
11:00-12:40	Session 10: Vector Borne 2 Room: Europa Session Chair: Lucy Okell	Session 11: AMR Room: Italia Session Chair: Lulla Opatowski	Session 12: Genomics 2 Room 7 Modules Session Chair: Luca Ferretti
11:00-12:40	<p>11:00 - 11:20 [O10.1] Modeling the intra-vector arboviral dynamics challenges the exponential assumption used for the distribution of the extrinsic incubation period in mosquitoes</p> <p>11:20 - 11:40 [O10.2] Assessing yellow fever outbreak potential and implications for vaccine strategy</p> <p>11:40 - 12:00 [O10.3] Public health impact of age-expansion of perennial malaria chemoprevention: a modelling study</p> <p>12:00 - 12:20 [O10.4] Shifting patterns of dengue three years after Zika virus emergence in Brazil</p> <p>12:20 - 12:40 [O10.5] Multi-objective calibration of the agent-based malaria transmission model, EMOD, to detailed symptom, parasite, gametocyte, and infectiousness data from a trial of asymptomatic screening in Sapone, Burkina Faso</p>	<p>11:00 - 11:20 [O11.1] How do substandard and falsified antimicrobials affect the emergence of antimicrobial resistance?</p> <p>11:20 - 11:40 [O11.2] Inference of asymptomatic carriers of antimicrobial-resistant organisms in healthcare settings using multitype observations</p> <p>11:40 - 12:00 [O11.3] Taxation of veterinary antibiotics to reduce antimicrobial resistance</p> <p>12:00 - 12:20 [O11.4] Estimating and improving identifiability for an agent-based model of infectious disease transmission in a hospital setting</p> <p>12:20 - 12:40 [O11.5] Impact of the COVID-19 pandemic responses on the community transmission of antibiotic resistance</p>	<p>11:00 - 11:20 [O12.1] Harmonizing time series data and genetic sequences in a dynamic transmission forest</p> <p>11:20 - 11:40 [O12.2] Community structure and temp dynamics of SARS-CoV-2 coordinated substitution networks allow for early detection of emerging variants with altered phenotypes</p> <p>11:40 - 12:00 [O12.3] Using single-nucleotide polymorphisms to estimate concordance of transmission pairs from household vs. non-household contacts in an on-going pandemic outbreak</p> <p>12:00 - 12:20 [O12.4] VILOCA: Local haplotype reconstruction and mutation calling for short- and long-read sequencing data</p> <p>12:20 - 12:40 [O12.5] Lineage frequency time series reveal elevated levels of genetic drift in SARS-CoV-2 transmission in England</p>
12:40-13:40	Lunch Foyer Europa		
13:40-15:40	Session 13: COVID 2 Room: Europa Auditorium Session Chair: Andrew Azman	Session 14: Phylodynamics Room: Italia Session Chair: Tanja Stadler	Session 15: Surveillance Room 7 Modules Session Chair: Paolo Bosetti
13:40-15:40	<p>13:40 - 14:00 [O13.1] The net benefits and return-on-investment of pandemic preparedness measures: a multi-country scenario analysis</p> <p>14:00 - 14:20 [O13.2] Novel epidemiological household models applied to SARS-CoV-2 data from over 15,000 households in Utah: insights into transmission variability and age effects</p>	<p>13:40 - 14:00 [O14.1] Spread.gl: visualising pathogen dispersal in a high-performance browser application</p> <p>14:00 - 14:20 [O14.2] Agnostic identification of pathogen lineages and estimation of fitness dynamics</p> <p>14:20 - 14:40 [O14.3] Reconstructing the spatio-temp spread of serotype 1 wild poliovirus in Pakistan</p>	<p>13:40 - 14:00 [O15.1] Generative Bayesian modeling to nowcast the effective reproduction number from line list data with missing symptom onset dates</p> <p>14:00 - 14:20 [O15.2] District-level forecasting of elimination of trachoma as a public health problem by 2030</p>

	<p>14:20 - 14:40 [O13.3] Advancing the use of infectious disease modelling in national and international outbreak response: A global analysis</p> <p>14:40 - 15:00 [O13.4] Setting-specific transmission heterogeneities of COVID-19 in Hong Kong</p> <p>15:00 - 15:20 [O13.5] Bayesian reconstruction of SARS-CoV-2 transmissions highlights substantial proportion of negative serial intervals</p> <p>15:20 - 15:40 [O13.6] Predicting the features and spreading patterns of SARS-CoV-2 variants of concern as they unfolded. A retrospective analysis</p>	<p>and Afghanistan from VP1 sequence data (2012-2022)</p> <p>14:40 - 15:00 [O14.4] Joint inference of the effective reproduction number by integrating phylodynamic and epidemiological modelling with particle filtering</p> <p>15:00 - 15:20 [O14.5] Scalable and robust mechanistic integration of epidemiological and genomic data for phylodynamic inference</p> <p>15:20 - 15:40 [O14.6] Quantifying the value of viral genomics when inferring who infected whom in the 2014–16 Ebola virus outbreak in Guinea</p>	<p>14:20 - 14:40 [O15.3] Epidemic surveillance and nowcasting using RT-qPCR cycle threshold values</p> <p>14:40 - 15:00 [O15.4] Informing pandemic response in the face of uncertainty: An evaluation of the US COVID-19 Scenario Modeling Hub</p> <p>15:00 - 15:20 [O15.5] Identifying signature features of epidemic diseases in 19th century all-cause mortality data</p> <p>15:20 - 15:40 [O15.6] Heterogeneous epidemic forecast: From renewal equation to reproduction matrix</p>
15:40-17:10	<p>Poster Session 3, with Refreshment Break & Meet the Editor Session Room: Foyer Europa</p>		
17:10-18:30	<p>Session 16: Vaccination 2 Room: Europa Auditorium Session Chair: Corey Peak</p>	<p>Session 17: Wastewater Surveillance Room: Italia Session Chair: Kathy Leung</p>	<p>Session 18: Mpox Room 7 Modules Session Chair: Jantien Backer</p>
17:10-18:30	<p>17:10 - 17:30 [O16.1] Individual variation in vaccine immune response can produce bimodal distributions of protection</p> <p>17:30 - 17:50 [O16.2] Assessing population-level target product profiles of broadly-protective human influenza a vaccines</p> <p>17:50 - 18:10 [O16.3] The role and influence of perceived experts in an anti-vaccine community on Twitter</p> <p>18:10 - 18:30 [O16.4] Statistical and mathematical details of trials for estimating vaccine effectiveness for emerging infectious disease threats</p>	<p>17:10 - 17:30 [O17.1] Estimating the net reproduction number (R_w) of SARS-CoV-2 infections using wastewater data</p> <p>17:30 - 17:50 [O17.2] Establishing a wastewater global surveillance network at airports for early detection of emerging pathogens: A modeling study</p> <p>17:50 - 18:10 [O17.3] Modeling SARS-CoV-2 in wastewater: Inference of virus loads and relation to hospital admissions</p> <p>18:10 - 18:30 [O17.4] Non-daily sampling, dilution, degradation, and measurement noise: Improving wastewater-based epidemiology by modeling the sampling process</p>	<p>17:10 - 17:30 [O18.1] Modelling the transmission dynamics and impact of control measures on the 2022 outbreak of mpox among gay, bisexual and other men who have sex with men in England</p> <p>17:30 - 17:50 [O18.2] The fading of the mpox outbreak among MSM in the Netherlands: a mathematical modelling study</p> <p>17:50 - 18:10 [O18.3] Evaluating the decline of the mpox epidemic in Italy: the role of behavior changes and control strategies</p> <p>18:10 - 18:30 [O18.4] Characteristics of the sexual networks of gay, bisexual, and other men who have sex with men in Montréal, Toronto, and Vancouver: Implications for the transmission and control of mpox in Canada</p>
19:30-22:00	<p>Conference Networking Reception (tickets to be purchased) Bologna Congress Centre</p>		

Friday 1st December 2023

8:30-09:50	INV07, INV08 Room: Europa Auditorium , Session Chair: Katia Koelle		
08:30-09:10	[INV07] Antigenic diversity of pathogens Henrik Salje, University of Cambridge, UK		
09:10-09:50	[INV08] Under siege, not the movie: A tale of response to frequent and multiple disease outbreaks, lessons learnt, and, future strategies Ifedayo Adetifa, Nigeria Centre for Disease Control and Prevention, Nigeria		
09:50-10:20	Refreshment Break Foyer Europa		
10:20-12:00	Session 19: Vector Borne 3 Room: Europa Auditorium Session Chair: Emma Davis	Session 20: Animal Diseases 2 Room: Italia Session Chair: Eric Lofgren	Session 21: Immunity Room 7 Modules Session Chair: Saki Takahashi
10:20-12:00	<p>10:20 - 10:40 [O19.1] Synthetic control methods for infectious disease epidemiology: applications to Wolbachia interventions</p> <p>10:40 - 11:00 [O19.2] Modelling <i>P. vivax</i> and <i>P. falciparum</i> co-infections with heterogeneity in mosquito biting exposure</p> <p>11:00 - 11:20 [O19.3] Using particle Markov Chain Monte Carlo to translate continuously collected antenatal care malaria prevalence into trends of community transmission — Burkina Faso, Mozambique, and Nigeria, 2020–2022</p> <p>11:20 - 11:40 [O19.4] Plotting a path through the <i>P. vivax</i> treatment dilemma: a modelling study integrating individual-level observations from primaquine trials and population-level treatment effects</p>	<p>10:20 - 10:40 [O20.1] One health strategies for rabies management programmes: integrating epidemiological and health dynamics of zoonotic systems</p> <p>10:40 - 11:00 [O20.2] Disentangling the role of direct and indirect effects of vaccination against Marek's disease: a path analysis modelling approach</p> <p>11:00 - 11:20 [O20.3] Pseudonymising livestock movement data: why it matters how you do it</p> <p>11:20 - 11:40 [O20.4] Modelling the interplay between demography and epidemiology dynamics: The case of African swine fever in wild boar</p> <p>11:40 - 12:00 [O20.5] Quantifying fitness effects of resistance genes using phylodynamic multi-type birth-death models among <i>Campylobacter coli</i> from conventional and antibiotic-free agricultural swine populations</p>	<p>10:20 - 10:40 [O21.1] How immunity shapes the long-term dynamics of seasonal influenza</p> <p>10:40 - 11:00 [O21.2] Revisiting modelling assumptions on the regulating mechanisms for the transmission dynamics of <i>Shistosoma mansoni</i></p> <p>11:00 - 11:20 [O21.3] Dynamics of two competing SARS-CoV-2 variants, Mu and Gamma, during Bogotá's largest COVID-19 wave in Colombia: A modeling study</p> <p>11:20 - 11:40 [O21.4] Conceptual models of cross-immunity, and practical applications</p> <p>11:40 - 12:00 [O21.5] A unifying framework for infectious disease dynamics inference from serological data</p>
12:00-12:40	Room: Europa Session Chair: Alex Cook [INV09] Could we prevent the next pandemic by stopping pathogen spillover? Raina K. Plowright, College of Veterinary Medicine, Cornell University, USA		
12:40-13:00	Conference Closing: Katia Koelle, Katrina Lythgoe, Cecile Viboud, Joseph Wu, Joanna Aldred Room: Europa		