

Hybrid Conference Programme

Start (GMT)	Finish (GMT)	Presenter details
Wednesday 6 November 2024		
11:30	12:45	Registration, lunch and networking
12:30	12:45	Briefing for Keynote 1 & Session 1 speakers, microphone runners, chair, moderator & committee - Auditorium
12:45	13:00	Welcome
12:45	12:50	Welcome Connecting Science: Jane Murphy, Wellcome Connecting Science, UK
12:50	13:00	Scientific Programme Committee: Kari Galambosi, Johns Hopkins University, USA Christina Havel, Harvard University, USA Nick Loman, University of Birmingham, UK Karin Lythgoe, University of Oxford, UK
13:00	13:50	Keynote 1
		Chair: Nick Loman, University of Birmingham, UK Moderator: Katrina Lythgoe, University of Oxford, UK
13:00	13:50	Effective global genomic surveillance - what will it take? Alexa Chand, UK Health Security Agency, UK
13:50	13:55	Comfort break
13:55	15:25	Session 1: Vaccines and treatments
		Chair: David Robertson, University of Glasgow, UK Moderator: Kate Grabowski, Johns Hopkins University, USA
13:55	14:25	On the trail of SARS-CoV-2 cryptic wastewater lineages Thomas Peacock, The Pirbright Institute, UK
14:25	14:55	Human papillomavirus (HPV) genital infections in young women: viral load, immune, and evolutionary dynamics Samuel Alizon, CNRS, Paris, France
14:55	15:10	Forecasting H5N1 evolution for vaccine design Thomas Grunby, Massachusetts Institute of Technology, USA
15:10	15:25	From restrictions to vaccinations: Phylogenetic and phylogeographic analysis of disrupted RSV circulation in the UK Kate Duigan, University of Edinburgh, UK
15:25	16:05	Refreshment break and networking
15:50	16:05	Briefing for Session 2 speakers, chair & moderator - Auditorium
16:05	17:50	Session 2: Animals and zoonoses
		Chair: C. Jessica E Metcalf, Princeton University, USA Moderator: Nick Loman, University of Birmingham, UK
16:05	16:35	Using serologic cohorts to understand hepatitis B spillovers in Bangladesh Emily Dudgeon, Johns Hopkins Bloomberg School of Public Health, USA
16:35	17:05	Epidemiology and evolution of whisties in Atlantic salmon Sarah Hill, Royal Veterinary College, UK
17:05	17:20	Genomic epidemiology of Pasteurella bovis unravels different genotype circulation dynamics in France Claire Lescocat, INRAE, France
17:20	17:35	Quantifying the drivers of Usutu virus introduction and dispersal in Europe James Baxter, Roslin Institute, UK
17:35	17:50	Isolation and characterisation of an infectious mammalian chikungunya-like virus from Tasmanian devil tumor cells Julien Métais, The University of Sydney, Australia
17:50	18:30	Poster pitch talks for odd number posters
18:30	19:30	Poster session 1 - odd number posters
19:30	21:00	Dinner
19:30		Bar open (card payments only)

Thursday 7 November 2024		
09:15	09:30	Briefing for Session 3 speakers, chair & moderator – Auditorium
09:30	11:00	Session 3: Epidemics and Outbreaks
		Chair: Emma Hodcroft, University of Basel, Switzerland Moderator: Kate Grabowski, Johns Hopkins University, USA
09:30	09:45	The emergence and evolution of H5N1 in dairy cattle in the United States Jonathan Parker, University of Edinburgh, UK
09:45	10:00	Exploring density and distance effects on HPAI spread using a Bayesian phylodynamic framework Claire Guinat, INRAE, France
10:00	10:30	Advancing Viral Outbreak Surveillance in Brazil through Rapid and Cost-Efficient Nanopore Sequencing Strategies Ana Muniz Chen, University of São Paulo (USP), Brazil
10:30	10:45	The global and regional spread of dengue virus Vertiv Hill, Yale University, USA
10:45	11:00	Genomic Epidemiology Reveals Persistent Zoonotic and Human Transmission of Mox in West Africa Reviel Omah, University of Edinburgh, UK
11:00	11:40	Refreshment break and networking
11:25	11:40	Briefing for Session 4 speakers, chair & moderator – Auditorium
11:40	13:10	Session 4: Viruses in the changing world
		Chair: Tanja Stadler, ETH Zürich, Switzerland Moderator: Nick Loman, University of Birmingham, UK
11:40	12:10	Will there be a warning for the next pandemic? Identifying viral targets of concern C. Ableseth E. Ikenstad, Princeton University, USA
12:10	12:40	Tracking Viral Ecology and Evolution in a Freshwater Lake Over Three Decades Gerrit Auerbach, University of Minnesota, Madison, USA
12:40	12:55	Structural phylogenetics uncover the ancient evolution of Flaviviridae glycoproteins Soyoung Lyess, The University of Tokyo, Japan
12:55	13:10	How fast are viruses spreading in the wild? Simon Dullcour, University of Brussels (ULB), Belgium
13:10	14:30	Lunch and networking

14:15	14:30	Briefing for Session 5 speakers, chair & moderator - Auditorium
14:30	16:15	Session 5: Adaptation and Evolution: Virus dynamics within and between hosts
		Chair: Sarah Hill, Royal Veterinary College, UK Moderator: Kate Gubowski, Johns Hopkins University, USA
14:30	15:00	Diverse patterns of intra-host genetic diversity in chronically infected SARS-CoV-2 patients Julie Stern, Tel Aviv University, Israel
15:00	15:30	Assessing virus evolution with protein language models David Robertson, University of Glasgow, UK
15:30	15:45	CTL Escape and Reversion in HIV-1 Transmission Pairs: Direct Evidence of Host-Specific Adaptation Henriet Longley, University of Oxford, UK
15:45	16:00	Rapid global population dynamics and fast surface protein evolution imply a venerate host for a prevalent mosquito Gytis Dudaš, Vilnius University, Lithuania
18:00	16:15	Evolutionary insights into persistent infections and reinfections across different major lineages of SARS-CoV-2: findings from three years of community surveillance Mehar Ghafari, University Of Oxford, UK
16:15	16:55	Refreshment break and networking

16:40	16:55	Briefing for Session 6 speakers, chair & moderator - Auditorium
16:55	17:40	Session 6: Challenging the paradigm in viral genomics Chair: Kate Grabowski, Johns Hopkins University, USA Moderator: Nick Loman, University of Birmingham, UK
16:55	17:10	Pathoplaxis: A Community-Driven Solution for Transparent and Equitable Viral Genomic Data Sharing Emma Hodoroff, University of Basel, Switzerland
17:10	17:25	The clocks were wrong: decades of biased phylogenetic branch length estimates for viral pathogens, and the consequences for time tree analysis Matthew Hill, University of Oxford, UK
17:25	17:40	Dalphy: Fast, scalable, accurate and accessible Bayesian phylogenetics Patrick Varilly, Broad Institute of MIT And Harvard, USA
17:40	18:20	Poster pitch talks for even number posters
18:20	19:20	Poster session 2 - even number posters
19:20	21:00	Dinner
19:20		Bar open (card payments only)

Friday 8 November 2024	
09:15	09:30 Briefing for Session 7 speakers, chair & moderator - Auditorium
09:30	11:00 Session 7: Applied bioinformatics for public health
	Chair: Thomas Peacock, The Pirbright Institute, UK Moderator: Nick Loman, University of Birmingham, UK
09:30	10:00 Capturing the diversity of co-circulating pathogens Tanya Golubchik, University of Sydney, Australia
10:00	10:30 Making surveillance metagenomics a reality Barclay Crabb, University of Edinburgh, UK
10:30	10:45 Unsupervised generative model of viral antibody escape for the design and testing of variant-proof vaccines Noor Yousef, Harvard Medical School, USA
10:45	11:00 Agnostic identification of pathogen lineages and estimation of fitness dynamics Noémie Lefrançois, ETH Zürich, Switzerland
11:00	11:15 A protein language model for exploring viral antigenicity evolution Shusuke Kawakubo, The University of Tokyo, Japan
11:15	11:55 Refreshment break and networking
11:40	11:55 Briefing for Keynote 2, chair, moderator & committee - Auditorium
11:55	12:45 Keynote 2
	Chair: Katrina Lythgoe, University of Oxford, UK Moderator: Kate Gubowski, Johns Hopkins University, USA
11:55	12:45 Leveraging pathogen sequencing and statistical analysis to inform public health - past, present and future Tanya Stadler, ETH Zürich, Switzerland
12:45	13:00 Closing remarks and prize presentation
	Scientific Programme Committee: Kate Gubowski, Johns Hopkins University, USA Christian Huber, Harvard University, USA Nick Loman, University of Birmingham, UK Katrina Lythgoe, University of Oxford, UK
13:00	14:00 Lunch and departures
14:00	Coach departures for Stansted and Heathrow airports
14:10	Coach departures for Cambridge train station and city centre