

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	Wellcome Connecting Science: Jane Murphy, Wellcome Connecting Science, UK
12:50	13:00	Scientific Programme Committee: Kate Grabowski, Johns Hopkins University, USA Christian Happi, Harvard University, USA Nick Loman, University of Birmingham, UK Katrina 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? Meera Chand, Public Health England, 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 Tomas Grudny, Massachusetts Institute of Technology, USA
15:10	15:25	Title TBC TBC
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 henipavirus spillovers in Bangladesh Emily Gurley, Johns Hopkins Bloomberg School of Public Health, USA
16:35	17:05	Title TBC Sarah Hill, Royal Veterinary College, UK
17:05	17:20	Genomic epidemiology of Pestivirus bovis unravels different genotype circulation dynamics in France Claire Lescoat, 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 characterization of an infectious mammalian chu-like virus from Tasmanian devil tumor cells Julien Melade, 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 10:00 Rapid Virus Genomics for Outbreak Investigation: Feasibility and Added Value in Kenya
[George Githinji, KEMRI | Wellcome Trust, Kenya](#)

10:00 10:30 Advancing Viral Outbreak Surveillance in Brazil through Rapid and Cost-Efficient Nanopore Sequencing Strategies
[Ingra Moraes Claro, University of São Paulo \(USP\), Brazil](#)

10:30 10:45 The global and regional spread of dengue virus
Verity Hill, Yale University, USA

10:45 11:00 Genomic Epidemiology Reveals Persistent Zoonotic and Human Transmission of Mpox in West Africa
Ifeanyi 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. Jessica E Metcalf, Princeton University, USA](#)

12:10 12:40 Tracking Viral Ecology and Evolution in a Freshwater Lake Over Three Decades
[Karthik Anantharaman, University of Wisconsin-Madison, USA](#)

12:40 12:55 Structural phylogenetics uncover the ancient evolution of Flaviviridae glycoproteins
Spyros Lytras, The University of Tokyo, Japan

12:55 13:10 How fast are viruses spreading in the wild?
Simon Dellicour, 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 Grabowski, Johns Hopkins University, USA

14:30 15:00 Diverse patterns of intra-host genetic diversity in chronically infected SARS-CoV-2 patients
[Adi 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
Harriet Longley, University of Oxford, UK

15:45 16:00 Rapid global population dynamics and fast surface protein evolution imply a vertebrate host for a prevalent mosquito orthomyxovirus
Gytis Dudas, Vilnius University, Lithuania

16:00 16:15 Evolutionary insights into persistent infections and reinfections across different major lineages of SARS-CoV-2: findings from three years of community surveillance
Mahan 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 Pathoplexus: A Community-Driven Solution for Transparent and Equitable Viral Genomic Data Sharing
Emma Hodcroft, 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 Hall, University of Oxford, UK

17:25 17:40 Delphy: 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
[Rachel Colquhoun, 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 Youssef, 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 Grabowski, Johns Hopkins University, USA

11:55 12:45 Leveraging pathogen sequencing and statistical analysis to inform public health - past, present and future
[Tanja Stadler, ETH Zürich, Switzerland](#)

12:45 13:00 Closing remarks and prize presentation

Scientific Programme Committee:

[Kate Grabowski, Johns Hopkins University, USA](#)

[Christian Happi, 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