

Hybrid Conference Programme

Start (GMT)	Finish (GMT)	Presenter details	Location
Wednesday, 11 November 2026			
12:00	13:00	Registration, lunch and networking	
12:45		Briefing for keynote speaker, Session 1 speakers, microphone runners, chair, moderator and committee	Auditorium
13:00	13:15	Welcome and introductions Wellcome Sanger Institute Lia Barbara Amadi, Wellcome Sanger Institute, United Kingdom Scientific programme committee: Deogratius Ssemwanga, LSHTM and MRC-UVRI, Uganda Kate Grabowski, Johns Hopkins University, United States of America Marten Koopmans, Erasmus University Medical Centre, Netherlands Nick Loman, University of Birmingham, United Kingdom SecureBio: sponsored 'AI-enabled Biological Risk' Workshop pitch	Auditorium
13:15	14:05	Opening keynote Chair: Nick Loman Moderator: Kate Grabowski	Auditorium
13:15	14:05	Viral surveillance at the human animal interface: from response to prediction? Marten Koopmans, Erasmus University Medical Centre, Netherlands	
14:05	14:10	Comfort break	
14:10	15:55	Session 1: Animals and zoonoses Chair: Deogratius Ssemwanga Moderator: Nick Loman	Auditorium
14:10	14:40	Ecology and evolution of North American H5Nx viruses Louise Morin, University of Pennsylvania, United States of America	
14:40	15:10	Sequencing at the Source: Moving Viral Detection into the Field Erik Katsone, Institut Pasteur du Cameroun, Cameroun	
15:10	15:25	From Regional Epidemics to Global Pandemics: Spatiotemporal Reassortment Patterns of H5 HPAI Across Flyways at the Qinghai-Tibet Plateau James Baxter, Roslin Institute, The University of Edinburgh, United Kingdom	
15:25	15:40	Cryptic invasion and transmission dynamics of peste des petits ruminants virus across Europe Claire Guinat, INRAE, France	
15:40	15:55	Reconstructing the hidden evolutionary history of Andes virus from patchy genomic surveillance Mahan Ghafari, University Of Oxford, United Kingdom	
15:55	16:40	Refreshment break and networking	Event Space
16:25	16:40	Briefing for Session 2 speakers, chair and moderator	Auditorium
16:40	17:40	Session 2: Epidemics and outbreaks Chair: Kate Grabowski Moderator: Deogratius Ssemwanga	Auditorium
16:40	17:10	From Pairs to Populations Christophe Fraser, University of Oxford, United Kingdom	
17:10	17:25	Phylogenetic comparison of co-circulating Clade I mpox lineages in Kinshasa suggests similar transmissibility and virulence Kieran Chopra, Imperial College London, United Kingdom	
17:25	17:40	Phylogenetic reconstruction of Crimean-Congo haemorrhagic fever virus characterizes ecological and anthropogenic drivers across multiple centuries Ellie Bourgeois, University of Oxford, United Kingdom	
17:40	18:20	Poster pitch talks for odd number posters	Auditorium
18:20	19:20	Poster session 1 (odd number posters) and networking reception	Event Space
19:20	21:30	Dinner Bar open (card payments only)	Hindon Hall Restaurant Graham Cameron Bar

Thursday 12 November 2026			
09:15		Briefing for Session 3 speakers, chair and moderator	Auditorium
09:30	10:30	Session 3: Vaccines and treatment	Auditorium
		Chair: Deogratius Ssemwanga Moderator: Nick Loman	
09:30	10:00	Longitudinal studies of changing susceptibility to emerging and re-emerging viruses Emily Toth Martin, University of Michigan, USA	
10:00	10:15	Quantifying uncertainty in HIV-1 transmission risk from persons with low-level viremia Michael Martin, Johns Hopkins University, United States of America	
10:15	10:30	Predicting the antigenic evolution of seasonal influenza viruses by measuring phylogenetic convergence Samuel Turner, University Of Cambridge, United Kingdom	
10:30	11:15	Refreshment break and networking	Event Space
11:00		Briefing for Session 4 speakers, chair and moderator	Auditorium
11:15	12:45	Session 4: Viral metagenomics and microbiome	Auditorium
		Chair: Nick Loman Moderator: Deogratius Ssemwanga	
11:15	11:45	Sequencing viruses the ARTIC way Joshua Quick, University of Birmingham, United Kingdom	
11:45	12:15	The richness of the human virome Evelien Adenomon, Qvadrant Institute Bioscience, United Kingdom	
12:15	12:30	Beyond Mpx: Metagenomic Identification of Concurrent Viral Detections in Children with Clade Ib Mpx in Eastern Democratic Republic of the Congo Ashuza Shemamba Guillaume, Université Catholique De Bukavu, Congo (the Democratic Republic of the)	
12:30	12:45	Expanding the diversity and host range of the Sarthoviridae Kafe Van Brussel, University Of Sydney, Australia	
12:45	14:15	Lunch and networking	Event Space
12:45	14:15	Lunchtime SecureBio sponsored 'AI-enabled Biological Risk' Workshop <i>In-person attendees only</i>	Barbara McClintock Pavilion
14:00		Briefing for Session 5 speakers, chair and moderator	Auditorium
14:15	16:00	Session 5: Adaptation and evolution: virus dynamics within and between hosts	Auditorium
		Chair: Kate Grabowski Moderator: Nick Loman	
14:15	14:45	The antigenic and genetic evolution of dengue virus Henrik Salje, University of Cambridge, United Kingdom	
14:45	15:00	Revealing the deep evolutionary history of orthohepaciviruses Jonathon Mfsud, KU Leuven, Belgium	
15:00	15:15	SARS-CoV-2 saltational events are recurrent and trace to persistent human infections Cécile Tran Kiem, Imperial College London, United Kingdom	
15:15	15:30	Beyond variant calling: phylogenetic models reveal evolutionary insights from within-host diversity JT McCrone, Fred Hutch Cancer Center, United States of America	
15:30	15:45	Compositional diversity and evolutionary dynamics of accessory proteins across the family Coronaviridae Ash Porter, Dalhousie University, Canada	
15:45	16:00	One Host, Two Lineages: Population-Scale Detection of SARS-CoV-2 Coinfections Rosario Evans Pena, University Of Oxford, United Kingdom	
16:00	16:45	Refreshment break and networking	Event Space
16:00	16:45	Breaktime SecureBio sponsored 'AI-enabled Biological Risk' Workshop <i>In-person attendees only</i>	Barbara McClintock Pavilion

16:30		Briefing for Session 6 speakers, chair and moderator	Auditorium
16:45	18:00	Session 6: Bioinformatics, machine learning and AI Chair: Nick Loman Moderator: Deogratius Ssemwanga	Auditorium
16:45	17:15	AI for modeling infectious disease outbreaks Moltz Kraemer, University of Oxford, United Kingdom	
17:15	17:30	Prediction of antigenic evolution from single virus sequences using an epistasis-aware protein language model approach Rubayet Alam, University Of Glasgow, United Kingdom	
17:30	17:45	Quantum Approximation in Phylogenetic tree Construction Yeuko Manganyi, University Of Cape Town, South Africa	
17:45	18:00	How can we make better phylogenetic tree visualisations? Gytis Dudas, Vilnius University, Lithuania	
18:00	18:40	Poster pitch talks for even number posters	Auditorium
18:40	19:40	Poster session 2 (even number posters) and networking reception	Event Space
19:40	22:00	Dinner	Hinton Hall Restaurant
19:40		Bar open (card payments only)	Graham Cameron Bar
Friday 13 November 2026			
09:15		Briefing for Session 7 speakers, chair and moderator	Auditorium
09:30	10:45	Session 7: Viral genomics and public health Chair: Deogratius Ssemwanga Moderator: Kate Grabowski	Auditorium
09:30	10:00	Operational perspectives on genomic surveillance of viral pathogens in field settings Sophie Duerfouer, Bernhard Nocht Institute for Tropical Medicine, Germany	
10:00	10:15	Targeted metagenomic sequencing of respiratory infections from UK healthcare workers in the SIREN study Marissa Knoll, Wellcome Sanger Institute, United Kingdom	
10:15	10:30	Estimating epidemic success of viral lineages from population-level wastewater surveillance data Anika John, ETH Zurich, Switzerland	
10:30	10:45	Evolutionary promiscuity in norovirus emergence: hidden diversity and multiple routes to persistence and spread Damien Tully, London School Of Hygiene And Tropical Medicine, United Kingdom	
10:45	11:30	Refreshment break and networking	Event Space
11:15		Briefing for keynote, chair, moderator and committee	Auditorium
11:30	12:20	Closing keynote Chair: Kate Grabowski Moderator: Nick Loman	Auditorium
11:30	12:20	Impact of host and pathogen heterogeneities on the epidemiology and phylodynamics of acute viral Ryan Greshell, Princeton University, United States of America	
12:20	12:35	Closing remarks	Auditorium
		Scientific Programme Committee: Deogratius Ssemwanga, IAHM and MSC-UDV, Uganda Kate Grabowski, Johns Hopkins University, United States of America Nick Loman, University of Birmingham, United Kingdom	
12:35	13:40	Lunch	Hinton Hall Restaurant
13:45		Coach departure for Stansted and Heathrow airports	Main entrance
13:55		Coach departure for Cambridge train station and city centre	Main entrance