30th Nov 2021

	Column 1	Column 2	Column 3
09:00-09:10	**Welcome and opening remarks by conference chairs/Epidemics Editors-in-chief** Plenary Session		
09:10-10:10	**Session 01: Statistical/mathematical methods 1** Anne Cori Oral Session	**Session 02: Pandemic preparedness 1** Ben Cowling Oral Session	**Session 03: Phylodynamics 1** Louis du Plessis Oral Session

Session 01: Statistical/mathematical methods 1

09:10-09:25 [O01.1]
Using next generation matrices to estimate the proportion of cases that are not detected in an outbreak
H Juliette T Unwin[1], Anne Cori[1], Natsuko Imai[1], Katy Gaythorpe[1], Sangeeta Bhatia[1], Lorenzo Cattarino[1], Christl Donnelly[1,2], Neil Ferguson[1], Marc Baguelin[1,3]
[1]*Imperial College, London, UK.* [2]*University of Oxford, UK.* [3]*London School of Hygiene and Tropical Medicine, UK*

09:25-09:40 [O01.2]
A spatiotemporal model that captures the emergence and spread of drug resistance
Tamsin Lee
Swiss Tropical and Public Health Institute, Switzerland. University of Basel, Switzerland

09:40-09:55 [O01.3]
The odin.dust computational and statistical framework opens up new possibilities for real-time modelling by enabling many-compartment stochastic models
John Lees, Marc Baguelin, Richard FitzJohn
Imperial College London, UK
09:55-10:10
Q&A Panel discussion

Session 02: Pandemic preparedness 1

09:10-09:25 [O02.1]
Effects of international travel restrictions on COVID-19 importation risk
Jessica Liebig[1], Kamran Najeebullah[1], Raja Jurdak[2,1], Ahmad El Shoghri[3,2], Dean Paini[1]
[1]*Commonwealth Scientific and Industrial Research Organisation, Australia.* [2]*Queensland University of Technology, Australia.* [3]*University of New South Wales, Australia*

09:25-09:40 [O02.2]
Quantifying the timeliness of a disease surveillance system
Kamran Najeebullah[1], Jessica Liebig[1], Jonathan Darbro[2], Raja Jurdak[3], Dean Paini[1]
[1]*Commonwealth Scientific and Industrial Research Organisation, Australia.* [2]*Metro North Public Health Unit, Queensland Health, Brisbane, Queensland, Australia.* [3]*Queensland University of Technology, Brisbane, Australia*

09:40-09:55 [O02.3]
Preparedness for novel outbreaks using models and value of information analysis
Peter U. Eze[1], Nicholas Geard[2], Christopher M. Baker[3], Patricia Campbell[4,5], Iadine Chades[6]
[1]*The University of Melbourne, University Of Melbourne, Australia.* [2]*University of Melbourne, Melbourne, Australia.* [3]*The University of Melbourne, Melbourne, Australia.* [4]*Peter Doherty Institute for Infection and Immunity, The Royal Melbourne Hospital and The University of Melbourne, Australia, Melbourne, Australia.* [5]*University of Melbourne, Australia.* [6]*CSIRO Land and Water Dutton Park, Brisbane, Australia*
09:55-10:10
Q&A Panel discussion

Session 03: Phylodynamics 1

09:10-09:25 [O03.1]
Impact and mitigation of reporting bias in discrete phylogeography inference: a simulation study applied to rabies in Morocco
Maylis Layan[1,2], Simon Dellicour[3,4], Nicola De Maio[5], Hervé Bourhy[1], Guy Baele[4], Simon Cauchemez[1]
[1]*Institut Pasteur, France.* [2]*Sorbonne Université, France.* [3]*Université Libre de Bruxelles, Belgium.* [4]*Rega Institute, KU Leuven, Belgium.* [5]*European Bioinformatics Institute (EMBL-EBI), Wellcome Genome Campus, UK*

09:25-09:40 [O03.2]
Phylogenetic inference of the transmission direction of pneumococcal infections, a validation study
Jada Hackman[1], Carmen Sheppard[2], Jody Phelan[1], Sonal Shah[1], David Litt[2], Norman K. Fry[2], Martin Hibberd[1], Elizabeth Miller[1], Stefan Flasche[1], Stéphane Hué[1]
[1]*London School of Hygiene and Tropical Medicine, UK.* [2]*Public Health England, UK*

09:40-09:55 [O03.3]
Estimating global spatial dynamics and vaccine-induced fitness changes of *Bordetella pertussis*
Noémie Lefrancq[1,2], Valérie Bouchez[2], Nadia Fernandez[2], Nathalie Armatys[2], Annie Landier[2], Sophie Guillot[2], Julie Toubiana[2], Simon Cauchemez[2], Henrik Salje[1,2], Sylvain Brisse[2]
[1]*University of Cambridge, UK.* [2]*Institut Pasteur, France*
09:55-10:10
Q&A Panel discussion

10:10-10:30	**Break** Break and Social Events		
10:30-11:30	**Session 04: Statistical/mathematical methods 2** Simon Cauchemez Oral Session	**Session 05: Antimicrobial resistance 1** Laura Temime Oral Session	**Session 06: Dynamics of infections in animal populations 1** Simon Dellicour Oral Session

Session 04: Statistical/mathematical methods 2

10:30-10:45 [O04.1]
Real-time surveillance of SARS-CoV2 infection from a longitudinal household study
Thomas House[1], ONS CIS Team[2]
[1]*University of Manchester, UK.* [2]*Office for National Statistics, UK*

Session 05: Antimicrobial resistance 1

10:30-10:45 [O05.1]
Microbiome-pathogen interactions drive epidemiological dynamics of antibiotic resistance: modelling insights for infection control
David Smith[1,2,3,4], Laura Temime[4], Lulla Opatowski[1,2,3]
[1]*Institut Pasteur, France.* [2]*Université Paris Saclay, France.* [3]*INSERM, France.* [4]*Conservatoire National des Arts et Métiers, France*

Session 06: Dynamics of infections in animal populations 1

10:30-10:45 [O06.1]
Disentangling the role of poultry and wild birds in the spread of highly pathogenic avian influenza virus H5N8 in Europe
Claire Guinat[1,2], Cecilia Valenzuela Agui[1,2], Jeremie Scire[1,2], Tim Vaughan[1,2], Anne Pohlmann[3], Christoph Staubach[3], Edyta Swieton[4], Mariette Ducatez[5], Tanja Stadler[1,2]

[1]ETH Zurich, Switzerland. [2]SIB, Switzerland. [3]FLI, Germany. [4]NVRI, Poland. [5]ENVT-INRAE, France

10:45-11:00 [O04.2]
Inferring the relationship between viral load and infectiousness using contact tracing data
Martyn Fyles[1,2], Elizabeth Fearon[3], Joshua Blake[4], Thomas House[1,2,5,6], Lorenzo Pellis[1,2,5], Ian Hall[1,2,5,7]
[1]University of Manchester, UK. [2]The Alan Turing Institute, UK. [3]London School of Hygiene and Tropical Medicine, UK. [4]University of Cambdrige, UK. [5]JUNIPER Consortium, UK. [6]IBM Research, Hartree Centre, UK. [7]PHE, UK

11:00-11:15 [O04.3]
Extending EpiEstim to estimate the transmission advantage of new variants in real-time
Sangeeta Bhatia[1], Rebecca Nash[1], Jack Wardle[1], Edward Knock[1], Neil Ferguson[1], Pierre Nouvellet[2,1], Anne Cori[1]
[1]Imperial College London, UK. [2]University of Sussex, UK
11:15-11:30
Q&A Panel discussion

10:45-11:00 [O05.2]
Does plasmid-based beta-lactam resistance increase *E. coli* infections: Modelling addition and replacement mechanisms
Noortje G. Godijk[1], Martin C.J. Bootsma[1,2], Henri C. van Werkhoven[1], Valentijn A. Schweitzer[1], Sabine C. de Greeff[3], Annelot F. Schoffelen[3], Marc J.M. Bonten[1]
[1]Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, Utrecht University, Utrecht, The Netherlands. [2]Department of Mathematics, Faculty of Sciences, Utrecht University, Utrecht, Utrecht, The Netherlands. [3]Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), Bilthoven, Utrecht, The Netherlands

11:00-11:15 [O05.3]
Worldwide antibiotic resistance dynamics: how different is it from one drug-bug pair to another?
Eve Rahbe[1], Laurence Watier[2], Philippe Glaser[3], Lulla Opatowski[2]
[1]Institut Pasteur, Université Paris-Saclay, France. [2]Institut Pasteur, INSERM, Université Versailles St-Quentin, France. [3]Institut Pasteur, France
11:15-11:30
Q&A Panel discussion

10:45-11:00 [O06.2]
Phylogeography reveals association between swine trade and the spread of porcine epidemic diarrhea virus in China and across the world
Wan-Ting He[1], Nena Bollen[2], Yi Xu[3], Simon Dellicour[2], Wenjie Gong[4], Alexander Lee[5], Marc A Suchard[6], Philippe Lemey[2], Guy Baele[2], Shuo Su[1]
[1]Nanjing Agricultural University College of Veterinary Medicine, Nanjing, China. [2]KU Leuven Rega Institute for Medical Research, Leuven, Belgium. [3]China animal disease control center, Ministry of Agriculture,, China. [4]Key Laboratory of Jilin Province for Zoonosis Prevention and Control, Institute of Military Veterinary, Academy of Military Medical Sciences, China. [5]Kentucky State University Division of Mathematics and Sciences, Frankfort, KY, USA. [6]University of California Los Angeles Department of Biostatistics, Los Angeles, CA, USA

11:00-11:15 [O06.3]
Phylodynamic investigation of the transmission and control of highly pathogenic avian influenza A (H5N8) epidemic in France in 2016-17
Debapriyo Chakraborty[1], Claire Guinat[2,3], Nicola Müller[4], Francois-Xavier Briand[5], Mathieu Andraud[5], Axelle Scoizec[5], Beatrice Grasland[5], Jean-Luc Guerin[1], Mathilde Paul[5], Timothée Vergne[1]
[1]National Veterinary School of Toulouse (ENVT), Toulouse, France. [2]2Department of Biosystems Science and Engineering, ETH Zurich, Basel, Switzerland. [3]Swiss Institute of Bioinformatics (SIB), Switzerland. [4]Fred Hutchinson Cancer Research Centre, Seattle, USA. [5]The French Agency for Food, Environmental and Occupational Health & Safety (ANSES) Laboratory of Ploufragan-Plouzané-Niort, Ploufragan, France
11:15-11:30
Q&A Panel discussion

11:30-11:40	**Break**
	Break and Social Events

11:40-12:20	**Plenary lecture 1 - Gabriel Leung, University of Hong Kong, Hong Kong**
	Vijay Dhanasekaran
	Plenary Session
	Looking forward by looking back: nowcasting lessons from COVID-19 for the next outbreak
	11:40-12:20 [PLN.01]
	Looking forward by looking back: nowcasting lessons from COVID-19 for the next outbreak
	Gabriel Leung
	University of Hong Kong, Hong Kong, Hong Kong

12:20-14:00	**Poster session 1**
	Poster Session

14:00-17:00	

17:00-17:40	**Plenary lecture 2 - Isabel Rodriguez-Barraquer, University of California San Francisco, USA**
	Amy Welosowski
	Plenary Session
	17:00-17:40 [PLN.02]

Opportunities and challenges of seroepidemiology for epidemic preparedness and control
Isabel Rodríguez-Barraquer
University of California San Francisco, San Francisco, CA, USA

17:40-18:00	**Break** Break and Social Events		

18:00-19:00	**Session 07: Statistical/mathematical methods 3**	**Session 08: Pandemic preparedness 2**	**Session 09: Dynamics of infections in animal populations 2**

Session 07: Statistical/mathematical methods 3
John Drake
Oral Session

18:00-18:15 [O07.1]
A generalized differential equation compartmental model of infectious disease transmission
Scott Greenhalgh[1], Carly Rozins[2]
[1]Siena College, USA. [2]York University, Canada

18:15-18:30 [O07.2]
Evaluation of individual and ensemble probabilistic forecasts of COVID-19 mortality in the US
Estee Cramer[1], Evan Ray[1], Velma Lopez[2], Johannes Bracher[3,4], Jo Walker[2], Rachel Slayton[2], Michael Johansson[2], Matthew Biggerstaff[2], Nicholas Reich[2]
[1]University of Massachusetts, Amherst, USA. [2]Centers for Disease Control and Prevention, USA. [3]Chair of Econometrics and Statistics, Karlsruhe Institute of Technology, Germany. [4]Computational Statistics Group, Heidelberg Institute for Theoretical Studies, Germany

18:30-18:45 [O07.3]
Quantifying individual heterogeneity in transmission of SARS-CoV-2 from household studies
Anderson Thayer[1], Michael Levy[2], Alison Hill[1]
[1]Johns Hopkins University, Baltimore, MD, USA. [2]University of Pennsylvania, Philadelphia, PA, USA
18:45-19:00
Q&A Panel discussion

Session 08: Pandemic preparedness 2
Michael Johansson
Oral Session

18:00-18:15 [O08.1]
The COVID-19 Scenario Modeling Hub
Rebecca Borchering[1], Cécile Viboud[2], Emily Howerton[1], Claire Smith[3], Shaun Truelove[3], Luke Mullany[4], Michelle Qin[5], Lucie Contamin[6], Harry Hochheiser[6], Michael Runge[7], Katriona Shea[1], Justin Lessler[3]
[1]The Pennsylvania State University, USA. [2]National Institutes of Health Fogarty International Center, USA. [3]Johns Hopkins University, USA. [4]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA. [5]Harvard University, Cambridge, MA, USA. [6]University of Pittsburgh, USA. [7]U.S. Geological Survey, USA

18:15-18:30 [O08.2]
Incorporating freedom from disease principles into wastewater surveillance to improve health security: a case study of SARS-CoV-2
David A. Larsen[1], Mary B. Collins[2], Qian Du[3], Tabassum Z. Insaf[4,5], Pruthvi Kilaru[6], Brittany L. Kmush[6], Frank Middleton[7], Abigail Stamm[4], Maxwell L. Wilder[2], Teng Zeng[6]
[1]Syracuse University Department of Civil and Environmental Engineering, USA. [2]SUNY ESF, USA. [3]Quadrant Biosciences, USA. [4]New York State Department of Health Bureau of Environmental and Occupational Epidemiology, USA. [5]University at Albany, USA. [6]Syracuse University, USA. [7]SUNY Upstate, USA

18:30-18:45 [O08.3]
Estimating the effective reproductive number of SARS-CoV-2 from clinical case reports and viral concentrations in wastewater
Jana S. Huisman[1,2], Jérémie Scire[1,2], Daniel C. Angst[1], Jinzhou Li[1], Richard A. Neher[3], Marloes Maathuis[1], Christoph Ort[4], Tamar Kohn[5], Timothy R. Julian[4,6,3], Sebastian Bonhoeffer[7], Tanja Stadler[1]
[1]ETH Zurich, Switzerland. [2]Swiss Institute of Bioinformatics, Switzerland. [3]University of Basel, Switzerland. [4]EAWAG, Swiss Federal Institute of Aquatic Science and Technology, Switzerland. [5]EPFL, Switzerland. [6]Swiss Tropical and Public Health Institute, Switzerland. [7]Swiss Federal Institute of Technology, Zurich, Switzerland
18:45-19:00
Q&A Panel discussion

Session 09: Dynamics of infections in animal populations 2
Pauline Ezanno
Oral Session

18:00-18:15 [O09.1]
Integrating animal movements with phylogeography to model the spread of PRRS virus in the U.S.
Dennis Makau[1], Moh Alkhamis[2], Igor Paploski[1], Cesar Corzo[1], Samantha Lycett[3], Kimberly VanderWaal[1]
[1]Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, USA. [2]Department of Epidemiology and Biostatistics, Faculty of Public Health, Health Sciences Center, Kuwait University, Kuwait. [3]Roslin Institute, University of Edinburgh, Edinburgh, UK

18:15-18:30 [O09.2]
Tracking dispersal of foot-and-mouth disease virus across landscape gradients in Uganda using novel phylodynamic tools
Anna Munsey[1], Frank Mwiine[2], Sylvester Ochwo[2], Lauro Velazquez-Salinas[3], Zaheer Ahmed[4], Luis Rodriguez[3], Elizabeth Rieder[3], Andres Perez[1], Kimberly VanderWaal[1]
[1]University of Minnesota, USA. [2]Makerere University, Uganda. [3]USDA Agricultural Research Service, USA. [4]USDA Animal and Plant Health Inspection Services, USA

18:30-18:45 [O09.3]
Using phylogeography as a proxy for population connectivity for spatial modeling of outbreak data of Foot and Mouth Disease in Vietnam
Umanga Gunasekara[1], Miranda Bertram[2], Do.H Dung[3], Nguyen Phuong[3], Vo.V Hung[3], Nguyen V Long[3], Minh Phan[3], Andres Perez[1], Jonathan Artz[2], Kimberly VanderWaal[1]
[1]University of Minnesota, Minneapolis, MN, USA. [2]USDA-ARS, USA. [3]Department of Animal Health, Vietnam
18:45-19:00
Q&A Panel discussion

19:00-19:20	**Break** Break and Social Events		

19:20-20:20	**Session 10: Non-pharmaceutical intervention 1** David Champredon Oral Session	**Session 11: Antimicrobial resistance 2** Gwen Knight Oral Session	**Session 12: Social/spatial/network 1** Amy Welosowski Oral Session

19:20-19:35 [O10.1]
Modeling the interaction and effects of nonpharmaceutical interventions and vaccination on COVID-19 burden in California, USA
Tomás León, Jason Vargo, Erica Pan, Seema Jain, Priya Shete
California Department of Public Health, Sacramento, CA, USA

19:35-19:50 [O10.2]
Multi-modeling approach to evaluating efficacy of pharmaceutical and non-pharmaceutical interventions in influenza pandemics
Pragati V. Prasad[1], Molly Steele[1], Carrie Reed[1], Lauren Ancel Meyers[2], Zhanwei Du[2], Remy Pasco[2], Alison Galvani[3], Jorge A. Alfaro-Murillo[3], Bryan Lewis[4], Matthew Biggerstaff[1]
[1]Centers for Disease Control and Prevention, USA. [2]Section of Integrative Biology and Institute for Cellular and Molecular Biology, University of Texas at Austin, USA. [3]Department of Biostatistics & Center for Infectious Disease Modeling and Analysis (CIDMA), Yale School of Public Health, USA. [4]Biocomplexity Institute & Initiative, University of Virginia, USA

19:50-20:05 [O10.3]
Modelling the impact of non-pharmaceutical interventions and vaccination on SARS-CoV-2 transmission in Canada to support public health decisions
Victoria Ng[1], Vanessa Gabriele-Rivet[1], Kelsey Spence[2], Lisa Waddell[1], Patricia Turgeon[1], Ainsley Otten[1], Aamir Fazil[1], Nicholas Ogden[1]
[1]Public Health Agency of Canada, Canada. [2]University of Guelph, Canada
20:05-20:20
Q&A Panel discussion

19:20-19:35 [O11.1]
Identifying asymptomatic spreaders of antimicrobial-resistant pathogens in hospital settings
Sen Pei[1], Fredrik Liljeros[2], Jeffrey Shaman[1]
[1]Columbia University, USA. [2]Stockholm University, Sweden

19:35-19:50 [O11.2]
Modelling the dual nature of bacteriophage in the context of antimicrobial resistance: bacterial predation and horizontal gene transfer by transduction
Quentin Leclerc[1], Jacob Wildfire[2], Arya Gupta[3], Jodi Lindsay[2], Gwenan Knight[1]
[1]London School of Hygiene & Tropical Medicine, UK. [2]St George's University of London, UK. [3]University of Kent, UK

19:50-20:05 [O11.3]
Data-driven modeling to understand the evolutionary dynamics of ESBL resistance in E. coli over the last decade
Olivier Cotto[1], Stéphane Béchet[2], André Birgy[3,4], Stéphane Bonacorsi[3,4], Robert Cohen[2,5,6,7,8], Florence Débarre[9], Corinne Levy[10,11], François Blanquart[1,3]
[1]PSL Research University, France. [2]Association Clinique et Thérapeutique Infantile du Val-de-Marne, Créteil, France. [3]Université de Paris, France. [4]Hôpital Robert Debré, France. [5]French Pediatric Infectious Disease Group, Paris, France. [6]Centre de Recherche Clinique, Centre Hospitalier Intercommunal de Créteil, France. [7]Université Paris Est, France. [8]Centre Hospitalier Intercommunal de Créteil, France. [9]Sorbonne Université, France. [10]Association Clinique et Thérapeutique Infantile du Val-de-Marne, France. [11]French Pediatric Infectious Disease Group, France
20:05-20:20
Q&A Panel discussion

19:20-19:35 [O12.1]
Quantifying bias from differential geographic representativeness in estimates of human mobility
Taylor Chin[1], Ayesha Mahmud[2], Caroline Buckee[1]
[1]Harvard T.H. Chan School of Public Health, USA. [2]University of California, Berkeley, USA

19:35-19:50 [O12.2]
Modelling patterns in self-reported sexual age-mixing with Bayesian distributional regression in BRMS
Timothy Wolock[1], Seth Flaxman[1], Kathryn Risher[1,2], Tawanda Dadirai[3], Simon Gregson[1,3], Jeffrey Eaton[1]
[1]Imperial College London, UK. [2]London School of Hygiene & Tropical Medicine, UK. [3]Biomedical Research and Training Institute, Zimbabwe

19:50-20:05 [O12.3]
Elucidating the Spatiotemporal Dynamics of Streptococcus pneumoniae in South Africa using genetic and human mobility data
Sophie Belman[1,2], Shabir Madhi[3], Anne von Gottberg[4], Mignon du Plessis[4], Stephen Bentley[1], Henrik Salje[2]
[1]Wellcome Sanger Institute, UK. [2]University of Cambridge, UK. [3]MRC Respiratory and Meningeal Pathogens Research Unit, South Africa. [4]National Institute for Communicable Diseases, South Africa
20:05-20:20
Q&A Panel discussion

20:20-22:00	**Poster session 2** Poster Session

1st Dec 2021

	Column 1	Column 2	Column 3
09:10-10:10	**Session 13: Dynamics of infections in animals 3** Katie Hampson Oral Session **09:10-9:25 [O13.1]** **Lessons learnt from the first modelling challenge in animal health: improving preparedness to control African swine fever at the interface between livestock and wildlife** Pauline Ezanno[1,2], Timothée Vergne[1,3], Servane Bareille[1,2], Matthieu Mancini[1,2], Sébastien Picault[1,2] [1]INRAE, France. [2]Oniris, France. [3]ENVT, France **09:25-9:40 [O13.2]** **A Bayesian inference method to estimate transmission trees while allowing for multiple introductions with an application to SARS-COV2 in Dutch mink farms** B.R. Van der Roest[1], M.C.J. Bootsma[2,3], E.A.J. Fischer[3], R.S. Sikkema[4], B.B. Oude Munnink[4], F.C. Velkers[3], W.H.M. van der Poel[5], M. Spierenburg[6], D. Klinkenberg[7], M.E.E. Kretzschmar[8,7] [1]Julius Center for Health Sciences and Primary Care, UMC Utrecht, The Netherlands. [2]Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, The Netherlands. [3]Utrecht University, The Netherlands. [4]WHO Collaborating Centre for Arbovirus and Viral Hemorrhagic Fever Reference and Research, The Netherlands. [5]Wageningen Bioveterinary Research, The Netherlands. [6]Netherlands Food and Consumer Product Safety Authority (NVWA), The Netherlands. [7]National Institute for Public Health and the Environment (RIVM), The Netherlands. [8]University Medical Center Utrecht, The Netherlands **09:40-9:55 [O13.3]** **A simulation model of vaccine pressure and immune escape for RNA viruses** Daniel Balaz[1], Andrea Doeschl-Wilson[1], Rowland Kao[1], Kimberly VanderWaal[2], Samantha Lycett[1] [1]University of Edinburgh, UK. [2]University of Minnesota, USA **09:55-10:10** **Q&A Panel discussion**	**Session 14: Dynamics of various infections 1** Pascal Crépey Oral Session **09:10-9:25 [O14.1]** **Modelling scabies transmission in Monrovia, Liberia** Nefel Tellioglu[1], Rebecca H. Chisholm[2,3], Patricia T. Campbell[4], Shelui Collinson[5], Karsor Kollie[6], Jodie McVernon[7], Michael Marks[5], Nic Geard[1,8,4] [1]School of Computing and Information Systems, The University of Melbourne, Australia. [2]Department of Mathematics and Statistics, La Trobe University, Australia. [3]Centre for Epidemiology and Biostatistics, Melbourne School of Population and Global Health, The University of Melbourne, Australia. [4]Peter Doherty Institute for Infection and Immunity, The Royal Melbourne Hospital and The University of Melbourne, Australia. [5]Clinical Research Department, Faculty of Infectious and Tropical Diseases, London School of Hygiene & Tropical Medicine, UK. [6]Ministry of Health, Liberia. [7]Victorian Infectious Diseases Reference Laboratory Epidemiology Unit at the Peter Doherty Institute for Infection and Immunity, The Royal Melbourne Hospital and The University of Melbourne, Australia. [8]Melbourne School of Population and Global Health, The University of Melbourne, Australia **09:25-9:40 [O14.2]** **Changes in transmission of Enterovirus D68 (EV-D68) in England inferred from seroprevalence data** Margarita Pons-Salort[1], Ben Lambert[2], Everlyn Kamau[2], Heli Harvala[3], Peter Simmonds[2], Nicholas Grassly[1] [1]Imperial College London, UK. [2]University of Oxford, UK. [3]University College of London, UK **09:40-9:55 [O14.3]** **A new method to better predict extinction time of infectious diseases in deterministic frameworks: an example of African sleeping sickness** Maryam Aliee[1], Ching-I Huang[1], Ron E Crump[1], Erick Mwamba Miaka[2], Matt J Keeling[1], Kat S Rock[1] [1]University of Warwick, The Zeeman Institute SBIDER, UK. [2]Programme National de lutte contre la THA (PNLTHA), Democratic Republic of Congo **09:55-10:10** **Q&A Panel discussion**	**Session 15: Dynamics of Covid 1** Hiroshi Nishiura Oral Session **09:10-9:25 [O15.1]** **Demographic characteristics and overdispersion of secondary transmission of COVID-19 during the first two waves in Japan** Yura K Ko[1,2], Yuki Furuse[3,4], Kota Ninomiya[5,6], Kanako Otani[2], Mayuko Saito[1], Motoi Suzuki[2], Hitoshi Oshitani[1] [1]Department of Virology, Tohoku University Graduate School of Medicine, Sendai, Japan. [2]Center for Surveillance, Immunization, and Epidemiologic Research, National Institute of Infectious Diseases, Tokyo, Japan. [3]Institute for Frontier Life and Medical Sciences, Kyoto University, Kyoto, Japan. [4]Hakubi Center for Advanced Research, Kyoto University, Kyoto, Japan. [5]Graduate school of Pharmaceutical Sciences, the University of Tokyo, Tokyo, Japan. [6]National Institute of Public Health, Saitama, Japan **09:25-9:40 [O15.2]** **Temporal assessment of serial intervals on characterizing the transmission dynamics in four waves of COVID-19 Hong Kong** Sheikh Taslim Ali[1,2], Wey Wen Lim[1], Amy Yeung[1,2], Dongxuan Chen[1,2], Dillon C. Adam[1], Yiu Chung Lau[1,2], Jessica Y. Wong[1], Eric H. Y. Lau[1,2], Peng Wu[1,2], Benjamin J. Cowling[1,2] [1]The University of Hong Kong, Hong Kong. [2]Laboratory of Data Discovery for Health, Hong Kong **09:40-9:55 [O15.3]** **Correlation between times to SARS-CoV-2 symptom onset and secondary transmission undermines case isolation efforts** Natalie Linton[1,2], Andrei Akhmetzhanov[3], Hiroshi Nishiura[1] [1]Kyoto University, Japan. [2]Hokkaido University, Japan. [3]National Taiwan University, Taiwan **09:55-10:10** **Q&A Panel discussion**
10:10-10:30	**Break** Break and Social Events		
10:30-11:30	**Session 16: Phylodynamics 2** Vijay Dhanasekaran Oral Session **10:30-10:45 [O16.1]** **Developing a novel outbreak scanning tool and reporting system for identifying emerging SARS-CoV-2 variants of interest or concern** Olivia Boyd, Robert Johnson, Erik Volz	**Session 17: Dynamics of various infections 2** Albert Jan van Hoek Oral Session **10:30-10:45 [O17.1]** **Sub-types specified environment dependence of seasonal influenza transmission** Bing Zhang, Xiangjun Du	**Session 18: Dynamics of Covid 2** Thomas House Oral Session **10:30-10:45 [O18.1]** **Mathematical modelling of COVID-19 infection heterogeneity: Not all lockdowns are born equal, neither are vaccination policies** Jhonatan Tavori, Hanoch Levy

Imperial College London, UK

10:45-11:00 [O16.2]
Untangling introductions and persistence in COVID-19 resurgence in Europe
Philippe Lemey[1], Nick Ruktanonchai[2], Samuel Hong[1], Vittoria Colizza[3], Marion Koopmans[4], Adam Sadilek[5], Andrew Tatem[2], Guy Baele[1], Marc Suchard[6], Simon Dellicour[7]
[1]KU Leuven, Belgium. [2]University of Southampton, UK. [3]Sorbonne Université, France. [4]Department of Viroscience, WHO, The Netherlands. [5]Google, United States Minor Outlying Islands. [6]University of California, Los Angeles, Belgium. [7]Université Libre de Bruxelles, Belgium

11:00-11:15 [O16.3]
Nipah virus diversity across different spatial scales in South and Southeast Asia
Oscar Cortés Azuero[1], Birgit Nikolay[2], Noémie Lefrancq[1], Clifton McKee[3], Emily Gurley[3], Julien Capelle[4], Vibol Hul[5], Ausraful Islam[6], Veasna Duong[5], Henrik Salje[1]
[1]University of Cambridge, UK. [2]Epicentre, France. [3]Johns Hopkins Bloomberg School of Public Health, USA. [4]CIRAD, France. [5]Institut Pasteur in Cambodia, Cambodia. [6]icddr,b, Bangladesh
11:15-11:30
Q&A Panel discussion

Sun Yat-sen University, China

10:45-11:00 [O17.2]
Limits to monitoring post-vaccination dynamics of HPV genotypes: Simulations of observational study designs
Mélanie Bonneault[1,2,3], Elisabeth Delarocque-Astagneau[2], Maxime Flauder[1,2], Johannes A. Bogaards[4], Didier Guillemot[1,2,5], Lulla Opatowski[1,2], Anne CM Thiébaut[3]
[1]Epidemiology and Modelling of Antibiotic Evasion Unit, Institut Pasteur, France. [2]Université Paris-Saclay, UVSQ, Inserm, UMR 1018, AESOP team, France. [3]Université Paris-Saclay, Inserm U1018, CESP, High Dimensional Biostatistics Team, France. [4]Amsterdam University Medical Centers, Dept. Epidemiology & Data Science, The Netherlands. [5]AP-HP, Paris Saclay, Department of Public Health, Medical Information, Clinical Research, France

11:00-11:15 [O17.3]
Incorporating equity in infectious disease modeling: case study of a distributional impact framework for measles transmission
Tigist F. Menkir, Abdulrahman Jbaily, Stephane Verguet
Harvard T.H. Chan School of Public Health, USA
11:15-11:30
Q&A Panel discussion

Tel Aviv University, Israel

10:45-11:00 [O18.2]
Using viral loads to improve epidemiological surveillance
James Hay[1], Lee Kennedy-Shaffer[2,1], Brian Cleary[3], Sanjat Kanjilal[4,5], Madikay Senghore[1], David Hong[6], Stacey Gabriel[3], Marc Lipsitch[1], Aviv Regev[3,7,8], Michael Mina[1,3,4]
[1]Harvard TH Chan School of Public Health, USA. [2]Vassar College, USA. [3]Broad Institute of MIT and Harvard, USA. [4]Brigham and Women's Hospital, USA. [5]Harvard Pilgrim Health Care Institute, USA. [6]Wharton Statistics, USA. [7]Massachusetts Institute of Technology, USA. [8]Howard Hughes Medical Institute, USA

11:00-11:15 [O18.3]
Establishment and Lineage Dynamics of the First Wave of the SARS-CoV-2 Epidemic in the UK
Louis du Plessis[1,2], John T. McCrone[3], Alexander E. Zarebski[1], Verity Hill[3], Christopher Ruis[4], Bernardo Gutierrez[1], Jayna Raghwani[1], Moritz U.G. Kraemer[1], Andrew Rambaut[3], Oliver G. Pybus[1,5]
[1]University of Oxford, UK. [2]ETH Zürich, Switzerland. [3]University of Edinburgh, UK. [4]University of Cambridge, UK. [5]Royal Veterinary College, UK
11:15-11:30
Q&A Panel discussion

11:30-11:40	**Break**
	Break and Social Events

11:40-12:20	**Plenary lecture 3 - Chikwe Ihekweazu, Nigeria Centre for Disease Control, Nigeria**
	Steven Riley
	Plenary Session
	11:40-12:20 [PLN.03]
	Time to get serious about global detection, "interpretation", and response.
	Chikwe Iheweazu
	World Health Organization, Genève, Switzerland. Nigeria Centre for Disease Control, Abuja, Nigeria

12:20-14:00	**Poster session 3**
	Poster Session

14:00-16:30	

16:30-17:00	**Meet the Editors**
	Plenary Session
	Come along to meet the Editors of Elsevier's Epidemics Journal. In this session you will have the opportunity to ask the Editors directly any questions about submitting a paper, what they look for in a paper, and what trends they see both in terms of what is being submitted, and how the field is changing as a whole. The session will be moderated by Elsevier's Simon Holt

17:00-17:40	**Plenary lecture 4 - Emily Gurley, Johns Hopkins University, USA**
	Cecile Viboud
	Plenary Session
	Improving detection of zoonotic spillovers using Nipah virus as a case study: How surveillance can save the world
	17:00-17:40 [PLN.04]
	Improving detection of zoonotic spillovers using Nipah virus as a case study: How surveillance can save the world

Emily Gurley
JOHNS HOPKINS, Baltimore, MD, USA

17:40-18:00

Break
Break and Social Events

18:00-19:00

Session 19: Phylodynamics 3
Nidia Trovao
Oral Session

18:00-18:15 [O19.1]
Using genomic epidemiology of SARS-CoV-2 to support contact tracing and public health surveillance in rural Humboldt County, California
Allison Black[1], Gunnar Stoddard[2], Patrick Ayscue[3], Joseph DeRisi[3], Jeremy Corrigan[4]
[1]*The Chan Zuckerberg Initiative, Palo Alto, CA, USA.* [2]*Humboldt County Department of Health and Human Services, Eureka, CA, USA.* [3]*Chan Zuckerberg Biohub, San Francisco, CA, USA.* [4]*Humboldt County Public Health Laboratory, USA*

18:15-18:30 [O19.2]
Phylodynamic inference for emerging viruses using segregating sites
Yeongseon Park, Michael Martin, Katia Koelle
Emory University, USA

18:30-18:45 [O19.3]
Building capacity and tools for applied genomic epidemiology in local public health departments
Sidney Bell[1], Amy Kistler[2], Shannon Axelrod[1], Tony Tung[1], Allison Black[1], Dan Lu[1], Olivia Holmes[1], Kirsty Ewing[1], TJ Chen[1], Patrick Ayscue[2]
[1]*Chan Zuckerberg Initiative, USA.* [2]*Chan Zuckerberg Biohub, USA*
18:45-19:00
Q&A Panel discussion

Session 20: Social/spatial/network 2
Vittoria Colizza
Oral Session

18:00-18:15 [O20.1]
The effect of localized differences in geographic mixing and population age structure on the spatial and temporal dynamics of respiratory syncytial virus (RSV)
Tiffany Fitzpatrick[1], Daniel Weinberger[2], Virginia Pitzer[1]
[1]*Yale University School of Public Health, New Haven, CT, USA.* [2]*Yale University School of Public Health, New Haven, CT, Canada*

18:15-18:30 [O20.2]
Modeling the 2018-2020 Ebola outbreak: Insights into determinants of geographic spread
Tierney O'Sullivan[1], Andrew M. Kramer[1,2], Rebecca Merrill[3], Elvira McIntyre[4,5], Suzanne M. O'Regan[1], Dédé N. Ndungi[6], John M. Drake[1]
[1]*University of Georgia, USA.* [2]*University of South Florida, USA.* [3]*Global Border Health Team, USA.* [4]*Geospatial Research, Analysis and Services Program (GRASP), Agency for Toxic Substances and Disease Registry, Centers for Disease Control and Prevention, USA.* [5]*Perspecta Inc., USA.* [6]*République démocratique du Congo Ministère de la Santé, Democratic Republic of Congo*

18:30-18:45 [O20.3]
The seasonality of indoor social behavior and its implications for the dynamics of respiratory disease risk
Eva Rest, Zachary Susswein, Shweta Bansal
Georgetown University, Washington, DC, USA
18:45-19:00
Q&A Panel discussion

Session 21: Vaccination Covid 1
Laura Matrajt
Oral Session

18:00-18:15 [O21.1]
Factors associated with zero-dose vaccination status and implications for supplementary immunization activities
Rohan Arambepola[1], Yangyupei Yang[1], Kyle Hutchinson[2], Gloria Musukwa[3], Francis Mwansa[3], Amy Winter[1], William Moss[1], Simon Mutembo[1], Amy Wesolowski[1]
[1]*Johns Hopkins Bloomberg School of Public Health, USA.* [2]*Akros, Zambia.* [3]*Ministry of Health, Zambia*

18:15-18:30 [O21.2]
Methods and assumptions for estimating SARS-CoV-2 vaccine efficacy
Rebecca Kahn[1], Lee Kennedy-Shaffer[2], Marc Lipsitch[1]
[1]*Harvard T.H. Chan School of Public Health, USA.* [2]*Vassar College, USA*

18:30-18:45 [O21.3]
A comparison between one and two dose SARS-CoV-2 vaccine prioritisation in England for a fixed number of vaccine doses
Edward Hill, Matt Keeling
University of Warwick, UK
18:45-19:00
Q&A Panel discussion

19:00-19:20

Break
Break and Social Events

19:20-20:20

Session 22: Phylodynamics 4
Trevor Bedford
Oral Session

19:20-19:35 [O22.1]
SOPHIE: outbreak investigation and transmission history reconstruction in a joint phylogenetic and network theory framework
Pelin Icer, Fatemeh Mohebbi, Pavel Skums
Georgia State University, USA

19:35-19:50 [O22.2]
Methods combining genomic and epidemiological data in the reconstruction of transmission trees: a systematic review
Hélène Duault[1,2], Benoit Durand[1], Laetitia Canini[1]

Session 23: Dynamics of various infections 3
Steven Riley
Oral Session

19:20-19:35 [O23.1]
Re-emergence of respiratory syncytial virus following the COVID-19 pandemic in the United States: a modeling study
Zhe Zheng[1], Virginia Pitzer[1], Eugene Shapiro[2], Louis Bont[3], Daniel Weinberger[1]
[1]*Yale School of Public Health, USA.* [2]*Yale University School of Medicine, USA.* [3]*Utrecht University, The Netherlands*

19:35-19:50 [O23.2]

Session 24: Dynamics of various infections 4
Isabel Rodriguez-Barraquer
Oral Session

19:20-19:35 [O24.1]
Understanding environmental pathogen transmission by combining parsimonious mathematical models and tailor-made animal experiments
Anna Gamża[1], Thomas Hagenaars[2], Miriam Koene[2], Mart de Jong[1]
[1]*Wageningen University & Research, The Netherlands.* [2]*Wageningen Bioveterinary Research, Wageningen University & Research, The Netherlands*

19:35-19:50 [O24.2]

[1]*Paris-Est University, Laboratory for Animal Health, Anses, Maisons-Alfort, France.* [2]*Université Paris-Saclay, Faculté de médecine, Le Kremlin-Bicêtre, France*

19:50-20:05 [O22.3]
The tale of two Eastern European countries: genomic epidemiology analysis of SARS-CoV-2 transmission dynamics in Belarus and Ukraine
Alina Nemira[1], Ayotomiwa Ezekiel Adeniyi[1], Elena Gasich[2], Kirill Bulda[2], Leonid Valentovich[3], Anatoly Krasko[2], Olga Glebova[1], Alexander Kirpich[1], Pavel Skums[1]
[1]*Georgia State University, USA.* [2]*Republican Research and Practical Center for Epidemiology and Microbiology, Belarus.* [3]*Institute of Microbiology, Belarus*
20:05-20:20
Q&A Panel discussion

What can a model tell us about the role of reinfection on the risk of TB disease progression?
Laura White[1], Brooke Nichols[1], Youngji Jo[2], C Robert Horsburgh[1]
[1]*Boston University, USA.* [2]*Boston Medical Center, USA*

19:50-20:05 [O23.3]
The role of time-varying viral shedding in modeling wastewater surveillance: dynamics of the 2013 poliovirus outbreak in Israel
Andrew Brouwer[1], Marisa Eisenberg[1], Lester Shulman[2,3], Michael Famulare[4], James Koopman[1], Steve Kroiss[4], Musa Hindiyeh[2], Yossi Manor[2], Itamar Grotto[5,6], Joseph Eisenberg[1]
[1]*University of Michigan, Ann Arbor, MI, USA.* [2]*Chaim Sheba Medical Center, Tel Aviv, Israel.* [3]*Tel Aviv University Sackler Faculty of Medicine, Tel Aviv, Israel.* [4]*Institute for Disease Modeling, Bellevue, WA, USA.* [5]*Ben-Gurion University of the Negev Faculty of Health Sciences, Be'er Sheva, Israel.* [6]*State of Israel Ministry of Health, Jerusalem, Israel*
20:05-20:20
Q&A Panel discussion

Drivers of influenza seasonality in temperate zones: leveraging novel data sources to improve our understanding
Andrew Tiu, Shweta Bansal
Georgetown University, Washington, DC, USA

19:50-20:05 [O24.3]
Disentangling detection in an elimination setting: a geostatistical analysis of diagnostic delays for visceral leishmaniasis in India
Emily Nightingale, Oliver Brady, Graham Medley
London School of Hygiene and Tropical Medicine, UK
Q&A Panel discussion

| 20:20-22:00 | **Poster session 4**
Poster Session |

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	Column 1	Column 2	Column 3
09:10-10:25	**Session 25: Non-pharmaceutical intervention 2** Hannah Clapham Oral Session	**Session 26: Vaccination 1** Gabriela Gomez Oral Session	**Session 27: Social/spatial/network 3** Nim Arinaminpathy Oral Session

Column 1

Session 25: Non-pharmaceutical intervention 2
Hannah Clapham
Oral Session

09:10-09:25 [O25.1]
Determining the effect of mass-screening
Christian Berrig, Rasmus Kristoffer Pedersen, Lone Simonsen, Viggo Andreasen
PandemiX Center, Department of Science and Environment, Roskilde University, Denmark

09:25-09:40 [O25.2]
Non-pharmaceutical interventions and the emergence of pathogen variants
Ben Ashby[1], Robin Thompson[2]
[1]University of Bath, UK. [2]University of Warwick, UK

09:40-09:55 [O25.3]
The importance of sustained compliance with physical distancing during COVID-19 vaccination rollout
Alexandra Teslya[1], Ganna Rozhnova[1,2], Thi Mui Pham[1], Daphne van Wees[1], Hendrik Nunner[3], Noortje Godijk[1], Martin Bootsma[1,4], Mirjam Kretzschmar[1]
[1]Julius Center for Health Sciences and Primary Care, University Medical Center Utrecht, The Netherlands. [2]BioISI—Biosystems & Integrative Sciences Institute, Faculdade de Ciências, Universidade de Lisboa, Portugal. [3]Faculty of Social Sciences, Utrecht University, The Netherlands. [4]Mathematical Institute, Utrecht University, The Netherlands

09:55-10:10 [O25.4]
Estimating the effect of social inequalities on the mitigation of COVID-19 across communities in Santiago de Chile
Nicolò Gozzi[1], Michele Tizzoni[2], Matteo Chinazzi[3], Leo Ferres[4,5], Alessandro Vespignani[3,2], Nicola Perra[1,3]
[1]Networks and Urban Systems Centre, University of Greenwich, UK. [2]ISI Foundation, Italy. [3]Laboratory for the Modeling of Biological and Socio-technical Systems, Northeastern University, USA. [4]Data Science Institute, Universidad del Desarrollo, Chile. [5]Telefónica R&D, Chile

10:10-10:25
Q&A Panel discussion

Column 2

Session 26: Vaccination 1
Gabriela Gomez
Oral Session

09:10-09:25 [O26.1]
Modelling the relative benefits of using the measles vaccine outside cold chain for outbreak response
James Azam[1], Barbara Saitta[2], Kimberly Bonner[3], Matthew J. Ferrari[4], Juliet R.C. Pulliam[1]
[1]DSI-NRF Centre of Excellence in Epidemiological Modelling and Analysis, Stellenbosch University, Stellenbosch, South Africa. [2]Access Campaign, Médecins Sans Frontières, New York, USA. [3]University of Minnesota, Twin Cities, Minneapolis, USA. [4]d   The Center for Infectious Disease Dynamics, The Pennsylvania State University, Pennsylvania, USA

09:25-09:40 [O26.2]
Magnitude of RSV seasonality and implications for vaccination strategies
Fabienne Krauer[1], Mihaly Koltai[1], Marina Treskova-Schwarzbach[2], Stefan Flasche[1]
[1]London School of Hygiene & Tropical Medicine, UK. [2]Robert Koch Institute, Germany

09:40-09:55 [O26.3]
Optimal pneumococcal vaccination campaign strategies in humanitarian crises
Kevin van Zandvoort[1], Mohamed Bobe[2], Abdirahman Ibrahim Buqul[3], Mohammed Ismail[2], Mohamed Saed[2], Emma Diggle[4], Catherine McGowan[4,1], Rosalind M Eggo[1], Francesco Checchi[1], Stefan Flasche[1]
[1]London School of Hygiene & Tropical Medicine, UK. [2]Save the Children International, Somalia. [3]Republic of Somaliland Ministry of Health Development, Somalia. [4]Save the Children UK, UK

09:55-10:10 [O26.4]
Inferring vaccine efficacy and mode of action from human challenge studies
Fuminari Miura[1,2], Don Klinkenberg[1], Jacco Wallinga[3]
[1]National Institute for Public Health and the Environment, The Netherlands. [2]Ehime University, Japan. [3]Leiden University Medical Center, The Netherlands

10:10-10:25
Q&A Panel discussion

Column 3

Session 27: Social/spatial/network 3
Nim Arinaminpathy
Oral Session

09:10-09:25 [O27.1]
Predicting the spatial distribution of COVID-19 case incidence for outbreaks in Australian urban centres using aggregate mobile device data.
Cameron Zachreson[1], Lewis Mitchell[2], Michael Lydeamore[3,4], Nicolas Rebuli[5], Martin Tomko[1], Nicholas Geard[1]
[1]The University of Melbourne, Australia. [2]The University of Adelaide, Australia. [3]Monash University, Australia. [4]Victorian Department of Health and Human Services, Government of Victoria, Australia. [5]University of New South Wales, Australia

09:25-09:40 [O27.2]
Changes in contact patterns shape the dynamics of the COVID-19 outbreak in China
Juanjuan Zhang[1], Maria Litvinova[2], Yuxia Liang[1], Yan Wang[1], Wei Wang[1], Stefano Merler[3], Cécile Viboud[4], Alessandro Vespignani[5,6], Marco Ajelli[7,2], Hongjie Yu[8]
[1]Fudan University, China. [2]Indiana University School of Public Health, USA. [3]Bruno Kessler Foundation, Italy. [4]National Institutes of Health, USA. [5]Northeastern University, USA. [6]ISI Foundation, Italy. [7]Northeastern University, Boston, MA, USA. [8]Fudan University, Shanghai, China

09:40-09:55 [O27.3]
Social contact patterns relevant to the spread of SARS-CoV-2 and other infectious diseases in a rural sub-Saharan setting
Esther van Kleef[1], Mibyn Budiongo[2,3], Brigitte Umutoni[4], Pietro Coletti[5], Djibril Binga[2], Marianne van der Sande[1,6], Raquel Inocencio Da Luz[1], Delphin Phanzu[2,3]
[1]Institute of Tropical Medicine, Belgium. [2]Centre de Recherche en Santé de Kimpese, Democratic Republic of Congo. [3]Institut Médical Evangélique, Democratic Republic of Congo. [4]University of Hasselt, Belgium. [5]Data Science Institute, University of Hasselt, Belgium. [6]Julius Center for Health Sciences and Primary Care, Utrecht University, The Netherlands

09:55-10:10 [O27.4]
Socioeconomic determinants of mobility responses during the first wave of COVID-19 in Italy: from provinces to neighbourhoods
Laetitia Gauvin[1], Paolo Bajardi[1], Emanuele Pepe[1], Brennan Lake[2], Filippo Privitera[2], Michele Tizzoni[1]
[1]ISI Foundation, Italy. [2]Cuebiq Inc, USA

10:10-10:25
Q&A Panel discussion

| 10:25-11:40 | **Social event - Mentoring Program**
Break and Social Events
We're happy to host a mentorship program at Epidemics8. As part of this program, attendees will find opportunities to network with peers, receive mentoring from more senior scientists. |

11:40-12:20	**Plenary lecture 5 - Julia Gog, University of Cambridge, UK** Gabriela Gomez Plenary Session **11:40-12:20 [PLN.05]** **Some insights from the UK response to COVID-19** Julia Gog *University of Cambridge, Cambridge, UK. JUNIPER consortium, UK*
12:20-14:00	**Poster session 5** Poster Session
14:00-16:00	
16:00-17:00	**Social event - Mentoring Program and Career Panel** Break and Social Events We're happy to host a mentorship program and a career panel at Epidemics8. As part of this program, attendees will find opportunities to network with peers, receive mentoring from more senior scientists and hear from a panel about diverse careers in infectious disease modeling.
17:00-17:40	**Plenary lecture 6 - Trevor Bedford, Fred Hutchinson Cancer Research Center, USA** Katia Koelle Plenary Session Phylodynamics and molecular evolution of SARS-CoV-2 **17:00-17:40 [PLN.06]** **Phylodynamics and molecular evolution of SARS-CoV-2** Trevor Bedford *Fred Hutchinson Cancer Research Center, Seattle, WA, USA*
17:40-18:50	**Social event - Epidemics Pub Quiz: the ultimate test of general and highly specific knowledge** Break and Social Events Have you been feeling like there hasn't been a venue to showcase both your deep knowledge of infectious disease modeling and general knowledge such as history, geography and infamous songs from the 1980s? Do you feel like your local pub quiz hasn't focused enough on the difference between frequency versus density dependent models? Do you want to meet other random folks in the field and really be able to evaluate how well they can name that tune or put all James Bond movies in order? Here is your chance to join for the first (and possibly last ever) Epidemics Pub Quiz where teams will be random, questions will be witty, and answers will be mostly verifiable.
18:50-19:00	**Break** Break and Social Events

19:00-20:15	**Session 28: Malaria** Amy Welosowski Oral Session **19:00-19:15 [O28.1]** **Mathematical modelling of Plasmodium vivax to identify areas of residual transmission and effects of delayed treatment** Clara Champagne[1,2], Maximilian Gerhards[1,2], Justin Lana[3], Bernardo García Espinosa[3], Michael White[4], Emilie Pothin[1,2,3] [1]*Swiss Tropical and Public Health Institute, Switzerland.* [2]*University of Basel, Switzerland.* [3]*Clinton Health Access Initiative, USA.* [4]*Institut Pasteur, France* **19:15-19:30 [O28.2]** **Nordic malaria in the 19th century: could it happen again?**	**Session 29: Vaccination 2** Ben Lopman Oral Session **19:00-19:15 [O29.1]** **Effects of repeated influenza vaccination and waning protection on annual influenza vaccine effectiveness in the United States** Qifang Bi[1], Barbra Dickerman[2], Marc Lipsitch[2], Sarah Cobey[1], n/a n/a[3] [1]*University of Chicago, USA.* [2]*Harvard T.H. Chan School of Public Health, USA.* [3]*the U.S. Flu Vaccine Effectiveness Network, USA* **19:15-19:30 [O29.2]** **Vaccination schedule and maternal antibody interference: modeling population outcomes of pediatric norovirus vaccination** Elizabeth Sajewski[1], Alicia Kraay[1], Andreas Handel[2], Ben Lopman[1] [1]*Emory University, USA.* [2]*University of Georgia, USA*	**Session 30: Epidemic interaction and cocirculation 1** Cecile Viboud Oral Session **19:00-19:15 [O30.1]** **The impact of co-circulating pathogens on SARS-CoV-2/COVID-19 surveillance. How concurrent epidemics may alter surveillance** Aleksandra Kovacevic[1,2,3,4], Rosalind M. Eggo[5], Marc Baguelin[5,6], Matthieu Domenech de Cellès[7], Lulla Opatowski[1,2,3,4] [1]*Institut Pasteur, France.* [2]*University of Versailles Saint-Quentin-en-Yvelines (UVSQ), France.* [3]*CESP/INSERM, France.* [4]*University Paris-Saclay, France.* [5]*London School of Hygiene & Tropical Medicine, UK.* [6]*Imperial College London, UK.* [7]*Max Planck Institute for Infection Biology, Germany* **19:15-19:30 [O30.2]**

Mathias Mølbak Ingholt[1], Tzu Tung Chen[2], Franziska Hildebrandt[3], Rasmus Kristoffer Pedersen[1], Lone Simonsen[1]

[1]PandemiX Center, Department of Science and Environment, Roskilde University, Denmark. [2]Regional Climate Group, Department of Earth Sciences, University of Gothenburg, Sweden. [3]Stockholm University, Sweden

19:30-19:45 [O28.3]

Projected progression of antimalarial drug resistance in Burkina Faso using high resolution spatial modeling under drug policy and seasonal importation scenarios

Robert Zupko[1], Trần Đăng Nguyên[1], Thư Tran[1], Fabrice Somé[2], Jean-Bosco Ouédraogo[2], Maciej Boni[1]

[1]The Pennsylvania State University, University Park, PA, USA. [2]Institut de Recherche en Sciences de la Santé, Burkina Faso

19:45-20:00 [O28.4]

Identifying events of plasmodium falciparum transmission between humans and mosquitoes using parasite genotype data

Sophie Bérubé[1], Betsy Freedman[2], Diana Menya[3], Joseph Kipkoech[4], Lucy Abel[5], Steve Taylor[2], Wendy Prudhomme O'Meara[2,3], Andrew Obala[6], Amy Wesolowski[1]

[1]Johns Hopkins Bloomberg School of Public Health, USA. [2]Duke University, USA. [3]Moi University School of Public Health, Kenya. [4]Academic Model Providing Access to Healthcare Moi University, Kenya. [5]Academic Model Providing Access to Healthcare Moi Teaching and Referral Hospital, Kenya. [6]Moi University School of Medicine, College of Health Sciences, Kenya

20:00-20:15
Q&A Panel discussion

19:30-19:45 [O29.3]

Outbreak response for zoonotic emerging infectious diseases: projecting vaccine demand and impact for Lassa Fever, MERS, Nipah, and Rift Valley Fever

Anita Lerch[1], Quirine ten Bosch[2], Quan Tran[1], John Huber[1], Margaret Elliot[1], Molly Hartlage[1], Kathryn Strimbu[1], Magdalene Walters[1], Alex Perkins[1], Sean Moore[1]

[1]University of Notre Dame, USA. [2]Wageningen University and Research, The Netherlands

19:45-20:00 [O29.4]

Health impact of novel TB vaccines in low- and middle-income countries

Rebecca Clark[1], Christinah Mukandavire[1], Arminder Deol[1], Chathika Weerasuriya[1], Allison Portnoy[2], Matthew Quaife[1], Shelly Malhotra[3], Rebecca Harris[1,4], Nicolas Menzies[2], Richard White[1]

[1]London School of Hygiene and Tropical Medicine, UK. [2]Harvard T.H. Chan School of Public Health, USA. [3]Global Access, IAVI, USA. [4]Sanofi Pasteur, Singapore

20:00-20:15
Q&A Panel discussion

Disentangling the dynamics of cross-reacting pathogens in serological studies: a study of arbovirus transmission in Bangladesh

Megan O'Driscoll[1], Jessica Vanhomwegen[2], Damien Hoinard[2], Nathanael Hoze[2], Simon Cauchemez[2], Kishor Kumar Paul[3], Abu Mohd Naser[3], Mohammad Shafiul Alam[3], Emily Gurley[4], Henrik Salje[1]

[1]University of Cambridge, UK. [2]Institut Pasteur, France. [3]ICDDRB, Bangladesh. [4]Johns Hopkins School of Public Health, USA

19:30-19:45 [O30.3]

Modelling the impact of prevention strategies on cervical cancer incidence in South Africa

Cari van Schalkwyk[1], Jennifer Moodley[2], Alex Welte[1], Leigh Johnson[2]

[1]SACEMA, University of Stellenbosch, South Africa. [2]University of Cape Town, South Africa

19:45-20:00 [O30.4]

COVID-19 impact on vaccine preventable diseases: Assessing reductions in immunisation coverage and pathways to recovery

Jaspreet Toor[1], Susy Echeverria-Londono[1], Xiang Li[1], Kim Woodruff[1], Todi Mengistu[2], Neil M Ferguson[1], Katy AM Gaythorpe[1]

[1]Imperial College London, UK. [2]Gavi, the Vaccine Alliance, Geneva, Switzerland

20:00-20:15
Q&A Panel discussion

20:15-20:20

20:20-22:00

Poster session 6
Poster Session

[P6.01]
Inference is bliss: simulation for power estimation of a cholera outbreak intervention study

Ruwan Ratnayake[1,2,3], Francesco Checchi[1], Christopher Jarvis[1,2], John Edmunds[1,2], Flavio Finger[3]

[1]London School of Hygiene and Tropical Medicine, UK. [2]Centre for the Mathematical Modelling of Infectious Diseases, UK. [3]Epicentre, France

[P6.02]
A household-structured approach to modelling interventions during the COVID-19 pandemic

Joe Hilton[1], Robert Sawko[2], Heather Riley[3], Thomas House[3]

[1]University of Warwick, UK. [2]IBM Research, UK. [3]University of Manchester, UK

[P6.03]
Reconstructing the first six months of the COVID-19 epidemic in Delhi, India: infection attack rate and reporting of deaths

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[P6.04]
Clustering vaccine coverage and estimating the indirect benefits of immunisation

Xiang Li, Katy Gaythorpe, Susy Echeverria-Londono, Jaspreet Toor, Neil Ferguson
Imperial College London, UK

[P6.05]

Data pipelines in a pandemic: the human in the machine

Katy Gaythorpe, Rich Fitzjohn, Wes Hinsley, Natsuko Imai, Ed Knock, Pablo Perez Guzman, Imperial College Data Validation team, Marc Baguelin, Neil Ferguson

Imperial College London, UK

[P6.06]

Quantifying the spatial spread of plague (*Yersinia pestis*)—a case study of two cities in British India during the early 1900s

Warren Tennant, Simon Spencer, Mike Tildesley, Matt Keeling

University of Warwick, UK

[P6.07]

What would it take to prevent importation of COVID-19?

Samuel Clifford[1], Billy Quilty[1], Timothy Russell[1], CMMID COVID-19 Working Group[1], Yung-Wai Chan[2,1], Joseph Wu[3,4], Rui Pedro Galão[5], Rosalind Eggo[1], Stefan Flasche[1], John Edmunds[1]

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[P6.08]

Global predictions of short to medium-term COVID-19 transmission trends: a retrospective assessment

Sangeeta Bhatia[1], Kris V Parag[1], Jack Wardle[1], Natsuko Imai[1], Sabine L Van Elsland[1], Steven Riley[1], Neil Ferguson[1], Christl Donnelly[1,2], Anne Cori[1], Pierre Nouvellet[3,1]

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[P6.09]

Key issues when estimating the time-varying reproduction number in real-time

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[P6.10]

Understanding the incidence and timing of rabies cases in domestic animals and wildlife in southern Tanzania in the presence of a widespread domestic dog vaccination campaign.

Sarah Hayes[1], Kennedy Lushasi[2,3], Maganga Sambo[2], Joel Changalucha[4,5], Elaine Ferguson[5], Lwitiko Sikana[4,5], Katie Hampson[3,2], Pierre Nouvellet[6], Christl Donnelly[7,1]

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[P6.11]

Evaluation of spatio-temporal heterogeneity of dengue incidence in Colombo city, Sri Lanka : an assessment of urban risk factors and drivers using point process spatial modelling

Nayantara Wijayanandana[1], Jorge Cano Ortega[1], Ruwan Wijayamuni[2], Hasitha Tissera[3], Gabriel Ribeiro Dos Santos[4], Christian Bottomley[1], Neal Alexander[1], Henrik Salje[4]

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[P6.12]

What is the return-on-investment of pandemic preparedness?

Patrick Doohan[1], Alessandra Løchen[1], David J. Haw[1], Giovanni Forchini[1,2], Peter C. Smith[1,3], Katharina Hauck[1]

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[P6.13]

The impacts of using human mobility proxies in epidemic models

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[P6.14]

Molecular HIV Transmission Cluster Analysis in a Generalised African Epidemic.

Newton Otecko[1], Matthew Hall[1], William Probert[1], David Bonsall[1], Tanya Golubchik[1], Richard Hayes[2], Sarah Fidler[3], Helen Ayles[4,2], Lucie Abeler-Dörner[1], Christophe Fraser[1]

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[P6.15]

Evidence for Influenza and RSV interaction from 10 years of enhanced surveillance in Nha Trang, Vietnam, a modelling study.

Naomi R Waterlow[1], Michiko Toizumi[2], Edwin van Leeuwen[3], Hien-Anh Thi Nguyen[4], Lay Myint-Yoshida[5], Rosalind M Eggo[1], Stefan Flasche[1]

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[P6.17]

Anatomy of the COVID-19 Vaccination Campaign in Italy

Nicolò Gozzi[1], Matteo Chinazzi[2], Jessica T. Davis[2], Kunpeng Mu[2], Ana Pastore y Piontti[2], Marco Ajelli[3,2], Nicola Perra[1,2], Alessandro Vespignani[2,4]

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[P6.18]

Improved group testing strategy for sars-cov-2 detection from pcr tests

Leonhardt Unruh[1], Michael Crone[1], Hooman Zabeti[2], Nick Dexter[2], Ivan Lau[2], Ben Adcock[2], Paul Freemont[1], Leonid Chindelevitch[1]

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[P6.19]

Agent-Based Modelling of Strain-Vaccine-NPI Interactions in Covid-19 using OpenABM-Covid19

Robert Hinch, William Probert, Nikolas Baya, Luca Ferritti, Chris Wymant, Jasmina Panovska-Griffiths, Anel Nurtay, Lucie Abeler-Dorner, David Bonsall, Christophe Fraser

University of Oxford, UK

[P6.20]

Diversity of symptom phenotypes in SARS-CoV-2 community infections observed in multiple large datasets

Martyn Fyles[1], Karina-Doris Vihta[2], Rajenki Das[1], Caroline Jay[1], Tom Wingfield[3], Elizabeth Fearon[4], Thomas House[1], Carole Sudre[5], Harry Long[6]

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[P6.21]

Time-varying reproduction number estimation using temporal smoothers of case incidence data

Xiaoxi Pang[1], Ian Hall[1,2], Thomas House[1], Yang Han[1], Lorenzo Pellis[1]

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[P6.22]

Fitting bayesian hierarchical models to longitudinal PCR data for SARS-CoV-2: inferring individual-level dynamics of PCR positivity over the course of entire infections

Timothy Russell[1], Joel Hellewell[1], Sam Abbott[1], CMMID COVID-19 Working Group[1], Rupert Beale[2], Gavin Kelly[2], Catherine Houlihan[2], Eleni Nastouli[3], John Edmunds[1], Adam Kucharski[1]

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[P6.23]

Ensemble forecasts of COVID-19 cases and deaths in the United States

Evan Ray[1], Logan Brooks[2], Yijin Wang[1], Aaron Gerding[1], Estee Cramer[1], Jacob Bien[3], Johannes Bracher[4], Aaron Rumack[2], Matthew Biggerstaff[5], Michael Johansson[5]

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[P6.24]

Novel methods for estimating the instantaneous and overall COVID-19 case fatality ratio among care home residents in England

Christopher Overton[1], Luke Webb[1], Jo Hardstaff[2], Karthik Paranthaman[2], Heather Riley[1], James Sedgwick[2], Julia Verne[2], Ian Hall[1,2]

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[P6.25]

Sifting 'prevalence' data from major surveys for (HIV) incidence estimates

Laurette Mhlanga[1], Eduard Grebe[2,1], Alex Welte[1]

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[P6.26]

Inferring missing screening data to uncover the dynamics of *gambiense* human African trypanosomiasis in Uganda

Ron Crump[1], Simon Spencer[1], Ching-I Huang[1], Paul Bessell[2], Richard Selby[3], Albert Mugenyi[4], Paul Brown[1], Andrew Hope[3], Michelle Stanton[3], Joshua Longbottom[3]

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[P6.27]

Agent-based modeling of COVID-19 transmission and prevention

Cliff Kerr[1], Jamie Cohen[1], Robyn Stuart[2], Dina Mistry[1], Katherine Rosenfeld[1], Rafael Nunez[1], Romesh Abeysuriya[3], Jasmina Panovska-Griffiths[4], Michael Famulare[1], Daniel Klein[1]

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[P6.28]
The Models of Infectious Disease Agent Study (MIDAS) Coordinating Center: 2021 Update
Jessica Salerno[1], Stephanie Shadbolt[2], Jeremy Espino[1], John Levander[1], Jeff Stazer[1], Lucie Contamin[1], Anne Cross[1], Alice Arcury-Quandt[1], Dasha Pokutnaya[1], Harry Hochheiser[1]
[1]University of Pittsburgh, USA. [2]Fred Hutchinson Cancer Research Center, USA

[P6.31]
Estimating cholera seroincidence in partially vaccinated populations
Forrest Jones[1], Rachel Mills[2], Taufiq Bhuiyan[3], Ralph Tenier[4], Louise Ivers[2], Justin Lessler[5], Firdausi Qadri[3], Daniel Leung[6], Jason Harris[2], Andrew Azman[1]
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[P6.32]
Activity space maps: a novel human mobility data set for quantifying time spent at risk
Daniel T. Citron[1], Shankar Iyer[1], Robert C. Reiner[2], David L. Smith[2]
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[P6.33]
Cryptic transmission of SARS-CoV-2 and the first COVID-19 wave
Jessica Davis[1], Matteo Chinazzi[1], Nicola Perra[2], Kunpeng Mu[1], Ana Pastore y Piontti[1], Marco Ajelli[3], Natalie Dean[4], Kaiyuan Sun[5], Ira M. Longini Jr.[6], M. Elizabeth Halloran[7,8], Cécile Viboud[9], Alessandro Vespignani[1,10]
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[P6.34]
An evaluation of the impact of the COVID-19 pandemic on Zambia's childhood vaccination program
Amy Winter[1], Saki Takahashi[2], Andrea Carcelen[3], Kyla Hayford[3], Wilbroad Mutale[4], Francis Mwansa[5], Nyambe Sinyange[6], William Moss[3], Simon Mutembo[3]
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[P6.35]
Protecting essential food workers from COVID-19 while trading masks and physical distancing for vaccination: a novel integrated QMRA-IDT modeling approach
Elizabeth Sajewski, Julia Sobolik, Alicia Kraay, Juan Leon, Ben Lopman
Emory University, USA

[P6.36]
Assessing socio-demographic fairness of the COVID-19 forecast hub ensemble model
Ariane Stark, Dasuni Jayawardena, Nicholas Reich
University of Massachusetts Amherst, USA

[P6.37]
Optimal balance between computational cost and classification accuracy for SARS-Cov-2 lineages using Natural-Vectors-based methods
Roberto Cahuantzi[1], Matthew Hall[2], Lorenzo Pellis[1], Katrina Lythgoe[2], Thomas House[1]
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[P6.38]
Estimating risk for epidemic spread via maritime shipping networks in the context of SARS-CoV-2
Andrew Kramer, Mark Luther, Steven Meyers
University of South Florida, USA

[P6.39]
Stochastic invasion of variants of concern and border controls in a population with heterogeneous immunity.
Jacob Curran-Sebastian[1], Ian Hall[1,2,3,4], Katrina Lythgoe[5,6], Lorenzo Pellis[1,3,4], Thomas House[1,7,3,4]
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[P6.40]

Multi-scale models to infer transmission dynamics and forecast COVID-19 pandemic trends in three Latin American countries

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[P6.41]

Multi-strain dynamics of PRRSV type-2 in U.S. pig populations

Igor Paploski[1], Nakarin Pamornchainavakul[1], Albert Rovira[1], Cesar Corzo[1], Declan Schroeder[1,2], Maxim Cheeran[1], Andrea Doeschl-Wilson[3], Rowland Kao[3], Samantha Lycett[3], Kimberly VanderWaal[1]

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[P6.42]

Modelling the risks of additional COVID-19 waves in late 2021 in England under different vaccination strategies including vaccination of teenagers

Jasmina Panovska-Griffiths[1], Robyn Stuart[2], Katherine Rosenfeld[3], Cliff Kerr[3], Jamie Cohen[3], Daniel Klein[3], Robert Hinch[1], Christophe Fraser[1], Chris Bonell[4], Russell Viner[5]

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[P6.43]

Could vaccinating at-risk populations with Meningococcal B vaccine reduce incidence and antimicrobial resistance in gonococcal infections in the UK?

Segun Oke[1], Ray Borrow[2], Valerie Decraene[2], Alexander Thompson[3], Roberto Vivancos[2], Lorenzo Pellis[1,4,5], Ian Hall[1,4,5,2], Soeren Metelmann[6], Anna Donten[7]

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[P6.44]

Estimating incidence of SARS-CoV-2 infections from the UK Coronavirus Infection Survey real-time prevalence data

Joshua Blake[1], Paul Birrell[2,1], Thomas House[3], Theodore Kypraios[4], Koen Pouwels[5], Daniela De Angelis[1], Sarah Walker[5]

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[P6.45]

Evaluating the potential for vaccination in children to reduce the risk of COVID-19 outbreaks in schools during fall 2021

Guido España, Marya Poterek, Sean Cavany, Sean Moore, Alex Perkins

University of Notre Dame, USA

[P6.46]

Multifaceted adaptive landscape of toxigenic *Vibrio cholerae* during epidemic waves in the Democratic Republic of Congo associated with a novel and unique ICP1 Bacteriophage

Meer T. Alam[1,2], Taylor Paisie[1,2], Carla Mavian[1,2], Marco Salemi[1,2], Angus Angermeyer[3], Kimberley D. Seed[3,4], Andrew Camilli[5], J. Glenn Morris, Jr[1,6], Asfar Ali[1,7]

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[P6.47]

Theory of combining probabilistic projections with applications in epidemiology

Emily Howerton[1], Michael C. Runge[2], Tiffany L. Bogich[1], Rebecca K. Borchering[1], Hidetoshi Inamine[1], Justin Lessler[3], William J.M. Probert[4], Claire P. Smith[5], Shaun Truelove[5], Cécile Viboud[6]

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[P6.48]

Dynamic mapping of COVID-19 cases in the United States

Kees H. Schipper[1], Abigail L. Larson[2], Ryan B. Simpson[1], Clea H. Bell[2], James C. McCann[1], Bingjie Zhou[1], Maia C. Tarnas[1], Elena N. Naumova[1]

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[P6.49]

Planning a return to normal after the COVID-19 pandemic: identifying safe contact levels via online optimization

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[P6.50]

The contribution of hospital-acquired infections to the COVID-19 epidemic in England in the first half of 2020

Gwen Knight[1], Thi Mui Pham[2], James Stimson[3], Sebastian Funk[1], Yalda Jafari[1], Diane Pople[3], Stephanie Evans[4], Jonathan Read[5], Ben Cooper[6], Julie Robotham[4]

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[P6.52]

Investigation of COVID-19 vaccination status and hesitancy in the United States using the Household Pulse Survey (HPS) in January-May 2021

Ryan Simpson[1], James C. McCann[1], Naglaa H. El-Abbadi[1], Maia C. Tarnas[1], Ana B. Ronan[1], Clea H. Bell[2], Hebeini Wang[1], Minya Yang[1], Xuechen Pei[1], Zhongqi Fan[1]

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[P6.53]

The risk of drug resistance during long-acting antimicrobial therapy

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[P6.54]

Ensemble epidemic forecasting using vector quantile regression

Aaron Gerding

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[P6.55]

Oscillatory dynamics in the dilemma of social distancing

Alina Glaubitz, Feng Fu

Dartmouth College, Hanover, NH, USA

[P6.56]

Modeling serological testing to inform relaxation of social distancing for COVID-19 control

Kristin Nelson[1], Alicia Kraay[1], Conan Zhao[2], David Demory[2], Joshua Weitz[2], Benjamin Lopman[1]

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[P6.57]

Demonstrating the benefits of mathematical models for target product profiles in gene drive research and development

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[P6.58]

Rapid review of social contact patterns during the COVID-19 pandemic

Carol Liu[1], Juliette Berlin[1], Moses Kiti[1], Emanuele Del Fava[2], Andre Grow[2], Emilio Zagheni[2], Alessia Melegaro[3], Samuel Jenness[1], Benjamin Lopman[1], Kristin Nelson[1]

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[P6.59]

Mathematical modeling of the use of insecticide treated nets for elimination of visceral leishmaniasis in Bihar, India

Dewey Taylor[1], Jan Rychtar[1], Anna Fortunato[2], Casey Glasser[3], Joy Watson[4], Yongjin Lu[4]

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[P6.60]

A mathematical framework to predict effective PrEP on-demand strategies to prevent HIV transmission

Gulsah Yeni, Jessica Conway

The Pennsylvania State University, University Park, PA, USA

[P6.61]

An ODE model of yaws elimination in Lihir Island, Papua New Guinea

Presley Kimball[1], Jacob Levenson[2], Amy Moore[3], Jan Rychtar[4], Dewey Taylor[4]

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[P6.62]

Mobility patterns of people with tuberculosis in South Africa and implications for transmission

Abdou M. Fofana[1,2], Helen E. Jenkins[2], Jacob Bor[2], Lesly Scott[3], Graeme Dor[3], Anne Shapiro[2], Harry Moultrie[4], Sarah Leavitt[2], Beth Crankshaw[4], Karen R. Jacobson[5]

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[P6.63]

Contact patterns by age and geography with recurrent mobility: influence of relaxing assumptions

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3rd Dec 2021

	Column 1	Column 2	Column 3
09:10-10:10	**Session 31: Epidemic interaction and cocirculation 2** Matthieu Domenech Oral Session **09:10-9:25 [O31.1]** **Prediction of upcoming global influenza seasons after relaxation of COVID-19 NPIs** Sheikh Taslim Ali[1,2], Songwei Shan[1,2], Sukhyun Ryu[3], Zhanwei Du[1,2], Lin Wang[4], Jungyeon Tae[3], Peng Wu[1,2], Eric H. Y. Lau[1,2], Gabriel M. Leung[1,2], Benjamin J. Cowling[1,2] [1]*The University of Hong Kong, Hong Kong.* [2]*Laboratory of Data Discovery for Health, Hong Kong.* [3]*Konyang University College of Medicine, Republic of Korea.* [4]*University of Cambridge, UK* **09:25-9:40 [O31.2]** **The importance of supplementary immunisation activities to prevent measles outbreaks during the COVID-19 pandemic in Kenya** Caroline Mburu[1,2], John Ojal[1,2], Rose Chebet[1], Donald Akech[1], Pieter Van Gageldonk[3], LSHTM CMMID Covid-19 Working Group[2], James Nokes[1,4], Anthony Scott[2,1], Stefan Flasche[2], Ifedayo Adetifa[1] [1]*Kemri-Wellcome Trust Research Programme,Kilifi, Kenya.* [2]*London School of Hygiene and Tropical Medicine, UK.* [3]*Department of Immunosurveillance, Centre for Infectious Diseases Control, National Institute of Public Health and the Environment (RIVM, The Netherlands.* [4]*School of Life Sciences and Zeeman Institute for Systems Biology and Infectious Disease Epidemiology Research (SBIDER), University of Warwick, UK* **09:40-9:55 [O31.3]** **How immunity from and interaction with seasonal coronaviruses can shape SARS-CoV-2 epidemiology** Naomi Waterlow[1], Edwin Van Leeuwen[2,1], Nicholas G. Davies[1], Stefan Flasche[1], Rosalind Eggo[1] [1]*London School of Hygiene and Tropical Medicine, UK.* [2]*Public Health England, UK* **09:55-10:10** **Q&A Panel discussion**	**Session 32: Pandemic preparedness 3** Luca Ferretti Oral Session **09:10-9:25 [O32.1]** **An ensemble model based on early predictors to forecast COVID-19 healthcare demand in France** Juliette Paireau[1,2], Alessio Andronico[1], Nathanaël Hozé[1], Maylis Layan[1], Pascal Crépey[3], Alix Roumagnac[4], Marc Lavielle[5,6], Pierre-Yves Boëlle[7], Simon Cauchemez[1] [1]*Institut Pasteur, France.* [2]*Santé publique France, France.* [3]*EHESP, Univ. Rennes, France.* [4]*PREDICT Services, France.* [5]*INRIA, France.* [6]*Ecole Polytechnique, CNRS, France.* [7]*INSERM, France* **09:25-9:40 [O32.2]** **The epidemiological impact of digital contact tracing in England and Wales** Luca Ferretti, Chris Wymant, Christophe Fraser *University of Oxford, UK* **09:40-9:55 [O32.3]** **CoMix social contact survey: an international collaboration** Amy Gimma[1], Kerry Wong[1], Pietro Coletti[2], Kevin van Zandvoort[1], W John Edmunds[1], Christopher Jarvis[1] [1]*London School of Hygiene and Tropical Medicine, UK.* [2]*University of Hasselt, Belgium* **09:55-10:10** **Q&A Panel discussion**	**Session 33: Within-host 1** Lulla Opatowski Oral Session **09:10-9:25 [O33.1]** **Modelling the effect of within-host dynamics on the diversity of a multi-strain pathogen** Nefel Tellioglu[1], Nic Geard[1,2], Rebecca H. Chisholm[3,1] [1]*The University of Melbourne, Australia.* [2]*The Royal Melbourne Hospital and The University of Melbourne, Australia.* [3]*La Trobe University, Australia* **09:25-9:40 [O33.2]** **Timing of Natural Killer cell response leads to different disease severity in coronavirus infection** Xiaochan Xu, Kim Sneppen *Niels Bohr Institute, Denmark* **09:40-9:55 [O33.3]** **Analysing within-host phylodynamics to understand HIV transmission** Lele Zhao[1], Luca Ferretti[1], Joshua Herbeck[2], Christophe Fraser[1] [1]*University of Oxford, UK.* [2]*University of Washington, USA* **09:55-10:10** **Q&A Panel discussion**
10:10-10:30	**Break** Break and Social Events		
10:30-11:30	**Session 34: Vaccination 3** Juliet Pulliam Oral Session **10:30-10:45 [O34.1]** **Exploring the effect of spatial heterogeneity of immunisation in vaccine impact in Sub-Saharan Africa** Susy Echeverria-Londono[1], Jaspreet Toor[1], Xiang Li[1], Anna-Maria Hartner[2], Jeremy Roth[2], Kim Woodruff[1], Allison Portnoy[3], Alyssa Sbarra[4,5], Neil Ferguson[1], Katy Gaythorpe[1]	**Session 35: Dengue 1** Nick Golding Oral Session **10:30-10:45 [O35.1]** **Probabilistic dengue forecasting using Earth observations** Felipe J Colón-González[1,2], Leonardo Soares Bastos[3], Oliver J Brady[1], Rachel Lowe[1]	**Session 36: HIV** Lorenzo Pellis Oral Session **10:30-10:45 [O36.1]** **A hypervirulent strain of HIV-1 circulating in the Netherlands** Chris Wymant[1], Daniela Bezemer[2], Francois Blanquart[3], Luca Ferretti[1], Astrid Gall[4], Matthew Hall[1], Tanya Golubchik[1], Marion Cornelissen[5], Peter Reiss[2], Christophe Fraser[1]

[1]Imperial College London, UK. [2]Imperial College London, London, UK. [3]Harvard T.H. Chan School of Public Health, USA. [4]University of Washington, USA. [5]London School of Hygiene and Tropical Medicine, UK

10:45-11:00 [O34.2]
Model-based validation of a hybrid test-negative design for vaccine evaluation during outbreak response
Carl Pearson[1], Thomas Hladish[2], John Edmunds[1], Rosalind Eggo[1]
[1]London School of Hygiene & Tropical Medicine, UK. [2]University of Florida, USA

11:00-11:15 [O34.3]
Lives saved with vaccination for 10 pathogens across 112 countries in a pre-COVID-19 world
Vaccine Impact Modelling Consortium
Imperial Colllege London, UK
11:15-11:30
Q&A Panel discussion

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[1]London School of Hygiene & Tropical Medicine, UK. [2]School of Environmental Sciences, University of East Anglia, UK. [3]Programa de Computação Cientifica da Fiocruz, Brazil

10:45-11:00 [O35.2]
The role of antigenic and genetic diversity in driving the infection and disease risk of dengue virus
Lin Wang[1], Angkana Huang[2,3], Leah Katzelnick[4], Ana Coello Escoto[4], Richard Jarman[5], Stefan Fernandez[6], Simon Cauchemez[7], Irina Maljkovic Berry[5], Derek Cummings[2,3], Henrik Salje[1]
[1]Department of Genetics, University of Cambridge, UK. [2]Department of Biology, University of Florida, USA. [3]Emerging Pathogens Institute, University of Florida, USA. [4]Viral Epidemiology and Immunity Unit, NIH, USA. [5]Viral Diseases Branch, Walter Reed Army Institute of Research, USA. [6]Department of Virology, Armed Forces Research Institute of Medical Sciences, Thailand. [7]Mathematical Modelling of Infectious Diseases Unit, Institut Pasteur, France

11:00-11:15 [O35.3]
Estimating dengue transmission intensity from serological data: a comparative analysis using mixture and catalytic models
Victoria Cox[1], Megan O'Driscoll[2,1], Natsuko Imai[1], Ari Prayitno[3], Sri Rezeki Hadinegoro[3], Anne-Frieda Taurel[4], Laurent Coudeville[5], Ilaria Dorigatti[1]
[1]Imperial College London, UK. [2]University of Cambridge, UK. [3]Universitas Indonesia, Jakarta, Indonesia. [4]Sanofi Pasteur, Singapore, Singapore. [5]Sanofi Pasteur, Lyon, France
11:15-11:30
Q&A Panel discussion

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[1]University of Oxford, UK. [2]Stichting HIV Monitoring, The Netherlands. [3]College de France, France. [4]European Molecular Biology Laboratory, UK. [5]University of Amsterdam, The Netherlands

10:45-11:00 [O36.2]
Characteristics of sources and recipients in HIV transmission pairs from the PopART study
Matthew Hall[1], Tanya Golubchik[1], David Bonsall[1], William Probert[1], Newton Otecko[1], Xiaoyue Xi[2], Helen Ayles[3,4], Sarah Fidler[2], Richard Hayes[3], Christophe Fraser[1]
[1]University of Oxford, UK. [2]Imperial College London, UK. [3]London School of Hygiene and Tropical Medicine, UK. [4]Zambart, Zambia

11:00-11:15 [O36.3]
The effect of managing transmitted HIV drug resistance in HIV prevention
Ivy Kombe[1], David Bonsall[1], William Probert[1], Lucie Abeler-Dörner[1], Barry Kosloff[2,3], Mohammed Limbada[2,3], Helen Ayles[2,3], Sarah Fidler[4], Richard Hayes[3], Christophe Fraser[1]
[1]Big Data Institute, University of Oxford, UK. [2]Zambart, Zambia. [3]London School of Hygiene and Tropical Medicine, UK. [4]Imperial College, UK
11:15-11:30
Q&A Panel discussion

| 11:30-11:40 | **Break** |
| | Break and Social Events |

| 17:00-17:40 | (see below) |

11:40-12:20

Plenary lecture 7 - Nim Arinaminpathy, Imperial College London, UK
Juliet Pulliam
Plenary Session
Short-term shocks with long-lasting effects: How COVID-19 has affected the global TB response

11:40-12:20 [PLN.07]
Short-term shocks with long-lasting effects: How COVID-19 has affected the global TB response
Nim Arinaminpathy
Imperial College London, London, UK

| 12:20-16:00 | |

| 16:00-17:00 | **CDC session** |

17:00-17:40

Plenary lecture 8 - Katie Hampson, University of Glasgow, UK
Shweta Bansal
Plenary Session

17:00-17:40 [PLN.08]
Dissecting rabies transmission dynamics: from endemic persistence to elimination
Katie Hampson
University of Glasgow, Glasgow, UK

17:40-17:50	**Break** Break and Social Events		

| 17:50-18:50 | **Session 37: Dengue 2** Derek Cummings Oral Session | **Session 38: Dynamics of Covid 3** Oral Session | **Session 39: Within-host 2** Katia Koelle Oral Session |

Session 37: Dengue 2
Derek Cummings
Oral Session

17:50-18:05 [O37.1]
Modelling the geographic spread of dengue in Brazil and Mexico
Vinyas Harish[1], Oliver Brady[2]
[1]*University of Toronto, Canada.* [2]*London School of Hygiene and Tropical Medicine, UK*

18:05-18:20 [O37.2]
Antigenic evolution of dengue viruses over multiple decades
Leah Katzelnick[1], Ana Coello Escoto[1], Angkana Huang[2], Bernardo Garcia-Carreras[2], Nayeem Chowdhury[2], Irina Maljkovic Berry[3], Richard Jarman[3], Stephen Whitehead[1], Henrik Salje[4], Derek Cummings[2]
[1]*National Institutes of Health, USA.* [2]*University of Florida, USA.* [3]*Walter Reed Army Institute of Research, USA.* [4]*University of Cambridge, UK*

18:20-18:35 [O37.3]
Diversity of dengue lineages in Bangkok, Thailand, 1973—2014
Rachel Sippy[1], Lin Wang[1], Richard Jarman[2], Irina Maljkovic Berry[2], Stefan Fernandez[3], Derek Cummings[4,5], Henrik Salje[1,5]
[1]*University of Cambridge, UK.* [2]*Walter Reed Army Institute of Research, USA.* [3]*Armed Forces Research Institute of Medical Sciences, Thailand.* [4]*University of Florida, USA.* [5]*Johns Hopkins Bloomberg School of Public Health, USA*

18:35-18:50
Q&A Panel discussion

Session 38: Dynamics of Covid 3
Oral Session

17:50-18:05 [O38.1]
A Cluster-based model for COVID-19 transmission dynamics
B Shayak[1], Mohit Manoj Sharma[2]
[1]*Cornell University, USA.* [2]*Weill Cornell Medicine, USA*

18:05-18:20 [O38.2]
Tracking epidemiological characteristics of SARS-CoV-2 over time: analysis of half a million transmission pairs since February 2020 in the Netherlands
Jantien Backer[1], Don Klinkenberg[1], Jacco Wallinga[1,2]
[1]*National Institute for Public Health and the Environment, The Netherlands.* [2]*Leiden University Medical Center, The Netherlands*

18:20-18:35 [O38.3]
Changes in the SARS-CoV-2 generation time during the COVID-19 pandemic
WS Hart[1], S Abbott[2], A Endo[2], J Hellewell[2], E Miller[2,3], N Andrews[3], S Funk[2], PK Maini[1], RN Thompson[4]
[1]*University of Oxford, UK.* [2]*London School of Hygiene and Tropical Medicine, UK.* [3]*Public Health England, UK.* [4]*University of Warwick, UK*

18:35-18:50
Q&A Panel discussion

Session 39: Within-host 2
Katia Koelle
Oral Session

17:50-18:05 [O39.1]
Viral trajectory inference using densely sampled longitudinal RT-qPCR
Stephen Kissler[1], Joseph Fauver[2], Christina Mack[3], Jay Wohlgemuth[4], James Weisberger[5], John DiFiori[6], Deverick Anderson[7], David Ho[8], Nathan Grubaugh[2], Yonatan Grad[1]
[1]*Harvard T.H. Chan School of Public Health, USA.* [2]*Yale School of Public Health, USA.* [3]*IQVIA, USA.* [4]*Quest Diagnostics, USA.* [5]*Bioreference Laboratories, USA.* [6]*Hospital for Special Surgery, and the National Basketball Association, USA.* [7]*Duke Center for Antimicrobial Stewardship and Infection Prevention, USA.* [8]*Columbia University Aaron Diamond AIDS Research Center, USA*

18:05-18:20 [O39.2]
SARS-CoV-2 serology across scales: implications of heterogeneity in antibody responses on population seroprevalence estimates
Saki Takahashi, Michael Peluso, Jill Hakim, Keirstinne Turcios, Owen Jansen, Isobel Routledge, Jeffrey Martin, Steven Deeks, Timothy Henrich, Bryan Greenhouse
University of California, San Francisco, USA

18:20-18:35 [O39.3]
Investigating model alternatives for acute HIV infection
Ellie Mainou
The Pennsylvania State University, University Park, PA, USA

18:35-18:50
Q&A Panel discussion

18:50-19:10	**Break** Break and Social Events		

| 19:10-20:10 | **Session 40: Policy** Rebecca Kahn Oral Session | **Session 41: Vaccination Covid 2** Laura White Oral Session | **Session 42: Vector-borne infections** Adam Kucharski Oral Session |

Session 40: Policy
Rebecca Kahn
Oral Session

19:10-19:25 [O40.1]
Disease transmission and control modelling at the science-policy interface
Ruth McCabe[1,2], Christl Donnelly[1,2,3]
[1]*University of Oxford, UK.* [2]*NIHR Health Research Protection Unit in Emerging and Zoonotic Diseases, UK.* [3]*Imperial College London, UK*

19:25-19:40 [O40.2]
Behind the curtain: lessons learned from the johns hopkins university csse covid-19 dashboard
Jeremy Ratcliff[1,2], Ensheng Dong[2], Aaron Katz[2], Tamara Goyea[2], Timothy Ng[2], Ryan Lau[2], Sean Breyer[3], Paul Dodd[2], Reina Murray[2], Lauren Gardner[2]
[1]*University of Oxford, UK.* [2]*Johns Hopkins University, USA.* [3]*Esri Inc., USA*

Session 41: Vaccination Covid 2
Laura White
Oral Session

19:10-19:25 [O41.1]
Vaccination with BNT162b2 reduces transmission of SARS-CoV-2 to household contacts in Israel
Ottavia Prunas[1], Joshua L. Warren[2], Forrest W. Crawford[2], Sivan Gazit[3], Tal Patalon[3], Daniel M. Weinberger[2], Virginia E. Pitzer[2]
[1]*Yale University, New Haven, CT, USA.* [2]*Yale University, USA.* [3]*Maccabi Institute for Research & Innovation, Maccabi Healthcare Services, Israel*

19:25-19:40 [O41.2]
Optimizing vaccine allocation for COVID-19 vaccines shows the potential role of single-dose vaccination
Laura Matrajt[1], Julia Eaton[2], Tiffany Leung[1], Dobromir Dimitrov[1], Joshua Schiffer[1], David Swan[1], Holly Janes[1]

Session 42: Vector-borne infections
Adam Kucharski
Oral Session

19:10-19:25 [O42.1]
Assessing arbovirus circulation in a context of serological cross-reactivity: the case of Chikungunya and O'nyong-nyong viruses in Mali
Nathanael Hoze[1], Issa Diarra[2], Abdoul Karim Sangaré[3], Boris Pastorino[2], Laura Pezzi[2], Bourema Kouriba[3], Issaka Sagara[3], Abdoulaye Dabo[3], Abdoulaye Djimde[4], Mahamadou Ali Thera[3]
[1]*Institut Pasteur, France.* [2]*Aix Marseille Universite, France.* [3]*Malaria Research and Training Center, Mali.* [4]*Aix Marseille Universite, Mali*

19:25-19:40 [O42.2]
Seasonal herd movements and rift valley fever in the sahel: insights from a metapopulation model
Hélène Cecilia[1], Sandie Arnoux[1], Benoit Durand[2], Raphaëlle Métras[3], Renaud Lancelot[4], Véronique Chevalier[5,6,7], Pauline Ezanno[1]

19:40-19:55 [O40.3]
Challenges on the interaction of models and policy for pandemic control
<u>Liza Hadley</u>[1], Peter Challenor[2], Chris Dent[3,4], Valerie Isham[5], Denis Mollison[6], Duncan Robertson[7,8], Ben Swallow[9], Cerian Webb[1]
[1]*University of Cambridge, UK.* [2]*University of Exeter, UK.* [3]*University of Edinburgh, UK.* [4]*Alan Turing Institute, UK.* [5]*University College London, UK.* [6]*Heriott-Watt University, UK.* [7]*Loughborough University, UK.* [8]*University of Oxford, UK.* [9]*University of Glasgow, UK*
19:55-20:10
Q&A Panel discussion

[1]*Fred Hutchinson Cancer Research Center, Seattle, WA, USA.* [2]*University of Washington Tacoma, Tacoma, WA, USA*

19:40-19:55 [O41.3]
Immunological heterogeneity informs estimation of the durability of COVID-19 vaccine protection
<u>Matthieu Domenech de Cellès</u>[1], Anabelle Wong[1], Laura Barrero Guevara[1], Pejman Rohani[2]
[1]*Max Planck Institute for Infection Biology, Germany.* [2]*University of Georgia, USA*
19:55-20:10
Q&A Panel discussion

[1]*INRAE, ONIRIS, France.* [2]*French Agency for Food, Environmental and Occupational Health and Safety (ANSES), University Paris-Est, France.* [3]*INSERM, Sorbonne Université, Institut Pierre Louis d'Épidémiologie et de Santé Publique, France.* [4]*CIRAD, INRAE, Montpellier University, France.* [5]*CIRAD, France.* [6]*CIRAD, Cambodia.* [7]*Institut Pasteur du Cambodge, Cambodia*

19:40-19:55 [O42.3]
A novel dynamic model of yellow fever incorporating sylvatic reservoir spillover and urban outbreaks
<u>Keith Fraser</u>[1], Arran Hamlet[1], Jean Kévin[2,1], Katy Gaythorpe[1]
[1]*Imperial College London, UK.* [2]*Laboratoire MESuRS, Conservatoire national des Arts et Métiers, Paris, France*
19:55-20:10
Q&A Panel discussion

20:10-20:20	**Break** Break and Social Events

20:20-21:10	**Closing plenary lecture 9 - Maria Van Kerkhove, WHO, Switzerland & Closing of the conference by chairs/Epidemics Editors-in-chief** Anne Cori Plenary Session Overview of the global COVID-19 situation **20:20-21:00 [PLN.09]** **Overview of the global COVID-19 situation** <u>Maria Van Kerkhove</u> *World Health Organization, Genève, Switzerland*