

Oral Programme

Tuesday 3 rd December 2019			
15:30-17:30	Registration Ballroom Foyer B		
17:30-19:00	Welcome reception and poster session 1 Ballroom AB		
Wednesday 4 th December 2019			
Ballroom C			
08:30-08:40	Welcome and opening remarks by session chair		
08:40-09:10	[INV01] Changing Dynamics of the US Drug Overdose Epidemic Donald (Don) S. Burke, <i>University of Pittsburgh, USA</i>		
09:10-09:50	[INV02] From dependent happenings to causal inference with interference Betz Halloran, <i>University of Washington, USA and Fred Hutchinson Cancer Research Center, USA</i>		
09:50-10:30	[INV03] How to get a good travel history from a malaria parasite Bryan Greenhouse, <i>University of California San Francisco, USA</i>		
10:30-11:00	Refreshment break		
11:00-12:40	Session 1 Vaccination 1	Session 2 Dynamics	Session 3 Phylodynamics 1
	Ballroom C	Meeting Room 6&7	Meeting Room 8&9
11:00-11:20	[O1.1] Successes and failures of the live-attenuated influenza vaccine: can we do better? L. Matrajt ^{*1} , E. Halloran ^{1,2} , R. Antia ³ , <i>¹Fred Hutchinson Cancer Research Center, USA, ²University of Washington, USA, ³Emory University, USA</i>	[O2.1] The influence of birth rate and meteorological indices on the temporal patterns of rotavirus infection in Dhaka, Bangladesh E.O. Asare ^{*1} , M.A. Al-Mamun ¹ , M. Sarmin ² , A.S.G. Faruque ² , T. Ahmed ² , V.E. Pitzer ¹ , <i>¹Yale School of Public Health, USA, ²International Centre for Diarrhoeal Disease Research, Bangladesh (ICDDR, B), Bangladesh</i>	[O3.1] Intra-host phylodynamics: Quantifying selection in viral populations using high-throughput sequencing data. V. Tsyvina, P. Skums [*] <i>Georgia State University, USA</i>
11:20-11:40	[O1.2] Direct and indirect effects of immunising school-age children against influenza: Evidence from a three-year pilot programme in England E. van Leeuwen ^{*1} , R.G. Pebody ¹ , P. Klepac ³ , S. Riley ² , M. Baguelin ² , <i>¹Public Health England, UK, ²Imperial College London, UK, ³London School for Hygiene & Tropical Medicine, UK</i>	[O2.2] Environmental and Demographic Drivers of Respiratory Syncytial Virus (RSV) Transmission in the US K. Sun ^{*1} , C. Viboud ¹ , Z. Karaca ² , <i>¹Fogarty International Center, National Institutes of Health, Bethesda, MD, USA, ²Agency for Healthcare Research and Quality, Rockville, MD, USA</i>	[O3.2] Deep learning from phylogenies to understand the dynamics of epidemics J. Voznica ^{*1,2} , A. Zhukova ¹ , T. Dot ¹ , K. Ocaña ¹ , F. Lemoine ¹ , M. Moslonka-Lefebvre ¹ , O. Gascuel ¹ <i>¹Institut Pasteur, France, ²Université Sorbonne Paris Cité, France</i>
11:40-12:00	[O1.3] Potential public health benefits from reduced delay in the production of pandemic influenza vaccine K. Ainslie [*] , D. Haw, J. Hay, C. Walters, A. Yan, S. Riley, <i>Imperial College, UK</i>	[O2.3] Evidence synthesis revealing the transmission dynamics of Respiratory Syncytial Virus (RSV) and impact of vaccination M. van Boven ^{*1} , A. Teirlinck ¹ , R. Reeves ² , M. Hooiveld ¹ , A. Meijer ¹ , W. van der Hoek ¹ , <i>¹National Institute for Public Health, The Netherlands, ²University of Edinburgh, UK</i>	

12:00-12:20	<p>[O1.4] Drivers of uneven gene-specific evolutionary rates shaping microbial genomes in highly vaccinated populations A. Bento*^{1,2}, A. King³, R. Taulajale², T. Bosch⁴, C. Schot⁴, P. Rohani², ¹Indiana University, USA, ²University of Georgia, USA, ³University of Michigan, USA, ⁴RIVM, The Netherlands</p>	<p>[O2.4] Dynamics of cholera outbreaks in sub-Saharan Africa Q. Zheng*, J. Kaminsky, H. McKay, A. Azman, J. Lessler, Johns Hopkins Bloomberg School of Public Health, Baltimore, USA</p>	<p>[O3.4] High-resolution mapping of respiratory pathogens in the Seattle Metro area M. Famulare*¹, T. Bedford², M. Boeckh², H.Y. Chu³, J.A. Englund⁴, B.R. Lutz³, D.A. Nickerson³, M. Rieder³, L.M. Starita³, M. Thompson³, ¹Institute for Disease Modeling, USA, ²University of Washington, USA, ³Fred Hutchinson Cancer Research Center, USA, ⁴Seattle Children's Hospital, USA, ⁵Blaze Clinical, USA, ⁶Microsoft, USA, ⁷Kaiser Permanente Research Institute, USA</p>
12:20-12:40	<p>[O1.5] Comparison of rubella models and results: The effects of small variations in methods, assumptions, and data S. Truelove¹, A.K. Winter*¹, T. Papadopolous², C.J.E. Metcalf^{3,4}, J. Lessler¹, E. Vynnycky^{2,5}, ¹Johns Hopkins University, USA, ²Public Health England, UK, ³Princeton University, USA, ⁴University of Oxford, UK, ⁵London School of Hygiene & Tropical Medicine, UK</p>	<p>[O2.5] Unraveling the seasonal epidemiology of pneumococcus M. Domenech de Celles^{1,2}, H. Arduin^{1,2}, D. Lévy-Bruhl⁴, S. Georges⁴, C. Souty^{3,5}, D. Guillemot^{1,2}, L. Watier^{1,3}, L. Opatowski*^{1,2}, ¹Université de Versailles Saint Quentin, France, ²Institut Pasteur, France, ³Inserm, France, ⁴Santé Publique France, France, ⁵Sorbonne Université, France</p>	<p>[O3.5] Estimating transmission bottleneck sizes from viral variants unique to recipient hosts J. Harris*¹, K. Johnson², K. Koelle¹, ¹Emory University, USA, ²New York University, USA</p>
12:40-13:40	Lunch Ballroom AB		
12:40-13:40	Author workshop Ballroom Foyer		
13:40-15:40	Session 4 Vaccination 2	Session 5 Forecasting	Session 6 HIV
	Ballroom C	Meeting Room 6&7	Meeting Room 8&9
13:40-14:00	<p>[O4.1] Estimating sample size for future chikungunya vaccine trials based on projections of epidemic size that account for pre-existing immunity Q. Tran*¹, J. Soda¹, A. Siraj¹, S. Moore¹, H. Clapham^{2,3}, A. Perkins¹, ¹University of Notre Dame, USA, ²Oxford University Clinical Research Unit, Vietnam, ³University of Oxford, UK</p>	<p>[O5.1] A novel sub-epidemic modeling framework for epidemic wave forecasting G. Chowell^{1,2}, A. Tariq*¹, J. Hyman³ ¹Georgia State University, USA, ²National Institutes of Health, USA, ³Tulane University, USA</p>	

14:00-14:20	<p>[O4.2] Evaluating prophylactic Ebola vaccination in the presence of reactive ring vaccination C.A.B. Pearson*¹, T.J. Hladish², W.J. Edmunds¹, R.M. Eggo¹, ¹London School of Hygiene & Tropical Medicine, UK, ²University of Florida, USA</p>	<p>[O5.2] Accuracy of multi-model ensemble influenza forecasts in the US: Results from the 2017/2018 and 2018/2019 seasons N.G. Reich*¹, C.J. McGowan², T.K. Yamana³, E.L. Ray⁴, D. Osthus⁵, S. Kandula³, L.C. Brooks⁶, G.C. Gibson¹, N. Wattanachit¹, M. Biggerstaff², ¹University of Massachusetts Amherst, USA, ²Centers for Disease Control and Prevention, USA, ³Columbia University, USA, ⁴Mount Holyoke College, USA, ⁵Los Alamos National Laboratory, USA, ⁶Carnegie Mellon University, USA</p>	<p>[O6.2] Natural selection favoring more transmissible HIV detected in U.S. molecular transmission network J.O. Wertheim*¹, A.M. Oster², W.M. Switzer², C. Zhang², N. Panneer², E. Campbell², N. Saduvala³, J.A. Johnson², W. Heneine², ¹University of California San Diego, USA, ²Centers for Disease Control and Prevention, USA, ³ICF International, USA</p>
14:20-14:40	<p>[O4.3] Predicting evolution using frequency-dependent selection in bacterial populations T. Azarian*^{1,2}, P.P. Martinez², L.R. Grant³, J. Corander^{4,5}, C. Fraser⁷, N.J. Croucher⁸, L.L. Hammitt³, K.L. O'Brien⁹, M. Lipsitch², W.P. Hanage², ¹University of Central Florida, USA, ²Harvard University, USA, ³Johns Hopkins Bloomberg School of Public Health, USA, ⁴University of Helsinki, Finland, ⁵University of Oslo, Norway, ⁶Wellcome Trust Genome Campus, UK, ⁷University of Oxford, UK, ⁸Imperial College London, UK, ⁹World Health Organization, Switzerland</p>	<p>[O5.3] Integrative forecasting of seasonal influenza A/H3N2 evolution by genotype and phenotype J. Huddleston*^{1,2}, R. Neher^{3,4}, T. Bedford¹, ¹Fred Hutchinson Cancer Research Center, USA, ²University of Washington, USA, ³University of Basel, Switzerland, ⁴SIB Swiss Institute of Bioinformatics, Switzerland</p>	<p>[O6.3] Using phylogenies to detect fitness differences and selection among HIV-1 strains of different viral load L. Zhao*, L. Ferretti, C. Fraser, University of Oxford, UK</p>
14:40-15:00	<p>[O4.4] How should the dynamics of EBV transmission inform a vaccine target product profile and future vaccination strategy? L. Goscé*¹, J.R. Winter^{1,2}, G.S. Taylor³, J.E.A. Lewis^{1,4}, H.R. Stagg^{1,5}, ¹University College London, UK, ²King's college London, UK, ³University of Birmingham, UK, ⁴Imperial College, UK, ⁵The University of Edinburgh, UK</p>	<p>[O5.4] Real-time forecasting of epidemic trajectories using computational dynamic ensembles G. Chowell*^{1,2}, R. Luo¹, K. Sun², K. Roosa¹, A. Tariq¹, C. Viboud², ¹Georgia State University School of Public Health, USA, ²National Institutes of Health, USA</p>	<p>[O6.4] Quantifying the contribution of different-aged men and women to onwards transmission of HIV-1 in generalised epidemics in sub-Saharan Africa: A modelling and phylogenetics approach from the HPTN071 (PopART) trial M. Hall*¹, W. Probert¹, X. Xi², R. Sauter¹, T. Golubchik¹, D. Bonsall¹, L. Abeler-Dörner¹, M. Pickles¹, A. Cori², J. Bwalya³, ¹University of Oxford, UK, ²Imperial College London, UK, ³Zambart, Zambia, ⁴London School of Hygiene and Tropical Medicine, UK, ⁵Stellenbosch University, South Africa, ⁶Fred Hutchinson Cancer Research Center, USA, ⁷Johns Hopkins University, USA, ⁸African Health Research Institute, South Africa</p>

15:00-15:20	<p>[O4.5] The impact of geographic targeting of oral cholera vaccination in sub-Saharan Africa: A modelling study E.C. Lee*¹, A.S. Azman¹, J. Kaminsky¹, S.M. Moore², H.S. McKay¹, J. Lessler¹, ¹Johns Hopkins Bloomberg School of Public Health, USA, ²University of Notre Dame, USA</p>	<p>[O5.5] A look into the future - using digital disease surveillance tools for near real-time epidemic forecasting S. Bhatia*¹, B. Lassmann², E. Cohn³, M. Kraemer⁴, M. Herringer⁵, J. Brownstein³, L. Madoff², A. Cori¹, P. Nouvellet⁶, ¹Imperial College London, UK, ²International Society for Infectious Diseases, USA, ³Boston Children's Hospital, USA, ⁴University of Oxford, UK, ⁵healthsites.io, UK, ⁶University of Sussex, UK</p>	<p>[O6.5] Linking phylogenetic topology with HIV transmission history C.J. Villabona-Arenas*¹, M. Hall², S.G. Gaffney³, K.A. Lythgoe², S. Hue¹, K.E. Atkins¹, ⁴London School of Hygiene & Tropical Medicine, UK, ²University of Oxford, UK, ³Yale University, USA, ⁴The University of Edinburgh, UK</p>
15:20-15:40	<p>[O4.6] Prediction of post-vaccine <i>Streptococcus pneumoniae</i> lineage frequencies based on potential accessory genes under selection P.P. Martinez*¹, S. Palace¹, T. Azarian^{1,2}, W. Hanage¹, M. Lipsitch¹, ¹Harvard, USA, ²University of Central Florida, USA</p>	<p>[O5.6] Adaptively stacked ensembles for influenza forecasting with incomplete data T. McAndrew*, N. Reich, University of Massachusetts Amherst, USA</p>	<p>[O6.6] Why does age at infection correlate with set point viral load among persons with HIV? S. Goodreau*, S. Stansfield, J. Murphy, N. Abernethy, G. Gottlieb, M. Reid, J. Mittler, J. Herbeck, University of Washington, USA</p>
15:40-16:10	Refreshment Break Ballroom Foyer		
16:10-17:50	Session 7 Machine learning	Session 8 Transmission	Session 9 Phylodynamics 2
	Ballroom C	Meeting Room 6&7	Meeting Room 8&9
16:10-16:30	<p>[O7.1] Estimating the relative probability of direct transmission between infectious disease patients S.V. Leavitt*¹, R.S. Lee², P. Sebastiani¹, C.R. Horsburgh Jr.¹, H.E. Jenkins¹, L.F. White¹, ¹Boston University, USA, ²Harvard T.H. Chan School of Public Health, USA</p>	<p>[O8.1] Modelling interhuman transmission dynamics during pneumonic plague outbreaks in Madagascar B. Nikolay*¹, V. Andrianaivoarimanana², H. Razafimandimby³, S. Rahelinirina², P. Piola², S. Andrianalimanana⁴, V. Richard², C. Rogier², M. Ratsitorahina², M. Rajerison², ¹Institut Pasteur, France, ²Institut Pasteur de Madagascar, Madagascar, ³Ministry of Public Health, Madagascar, ⁴Central Laboratory of Plague, Madagascar</p>	<p>[O9.1] Evidence of environmental persistence-driven evolution of <i>vibrio cholerae</i> in aquatic reservoirs C. Mavian*, T.K. Paisie, M.T. Alam, S. Nembrini, M.N. Cash, E. Nelson, A. Ali, J.G. Morris Jr, M. Salemi University of Florida, USA</p>
16:30-16:50	<p>[O7.2] Developing machine learning algorithms using natural language processing to extract infectious disease data from open-source data A. Verster¹, E.E. Rees², F. Liu³, J. Knox², G. Penn³, V. Ng*², ¹Health Canada, Canada, ²Public Health Agency of Canada, Canada, ³University of Toronto, Canada</p>	<p>[O8.2] Using cross-sectional serology to infer leptospirosis transmission dynamics in Fiji E. Rees*¹, C. Lau², E. Togami³, J. Edmunds¹, R. Lowe¹, A. Kucharski¹, ¹London School of Hygiene & Tropical Medicine, UK, ²University of Queensland, Australia, ³Yale School of Public Health, USA</p>	<p>[O9.2] Selective pressure of American mosquito vectors on <i>P. falciparum</i> genes M.S. Tagliamonte*, M. Salemi, J.B. Dame University of Florida, USA</p>
16:50-17:10	<p>[O7.3] Super-ensemble seasonal influenza forecasting with machine</p>	<p>[O8.3] Probabilistic reconstruction of measles transmission clusters in the</p>	<p>[O9.3] Phylodynamic approaches for investigating the dynamics of Ebola virus</p>

	<p>learning augmented mechanistic models X. Xiong*¹, Q. Zhang¹, F. Lu², M. Santillana^{2,3}, A. Vespignani^{1,4}, ¹Northeastern University, USA, ²Boston Children's Hospital, USA, ³Harvard Medical School, USA, ⁴ISI Foundation, Italy</p>	<p>United States from 2003-2017 using routine case reports. A. Robert*, A.J. Kucharski, S. Funk, London School of Hygiene and Tropical Medicine, UK</p>	<p>disease in Sierra Leone V. Hill*, A. Rambaut University of Edinburgh, UK</p>
17:10-17:30	<p>[O7.4] Feasibility of incorporating contextual data in reconstructing HIV transmission network: A machine learning approach S. Mazrouee*, S. Little, J. Wertheim, University of California - San Diego, USA</p>	<p>[O8.4] Global and country-specific rubella R₀ estimation using serology and Bayesian methods S. Truelove*¹, A.K. Winter¹, C.J.E. Metcalf^{2,3}, J. Lessler¹, ¹Johns Hopkins University, USA, ²Princeton University, USA, ³University of Oxford, UK</p>	<p>[O9.4] West Nile virus spread in North America: What can we learn from genomic data? S. Dellicour*^{1,2}, S. Lequime¹, B. Vrancken¹, M.S. Bastide¹, K. Gangavarapu³, M.I. Nelson⁴, N. Grubaugh^{5,3}, K.G. Andersen^{3,6}, O.G. Pybus⁷, P. Lemey¹ ¹University of Brussels (ULB), Belgium, ²KU Leuven - University of Leuven, Belgium, ³Scripps Research Institute, USA, ⁴National Institutes of Health, USA, ⁵Yale School of Public Health, USA, ⁶Scripps Research Translational Institute, USA, ⁷University of Oxford, UK</p>
17:30-17:50	<p>[O7.5] Machine learning for vector representation of GB farms within cattle movement network to predict future herd-level bTB and BVD breakdowns K. Stanski*, S. Lycett, T. Porphyre, B.M. Bronsvort, The University of Edinburgh, UK</p>	<p>[O8.5] Waning and boosting of immunity of pertussis under natural infection and vaccination L.M. Childs*¹, Z. Feng², J. Glasser³, J. Heffernan⁴, J. Li⁵, G. Rost⁶, ¹Virginia Tech, USA, ²Purdue University, USA, ³Centers for Disease Control and Prevention, USA, ⁴York University, Canada, ⁵California State University, USA, ⁶University of Szeged, Hungary</p>	<p>[O9.5] Long read sequencing of Vibrio cholerae reveals regional transmission dynamics in Malawi S. Wohl*¹, W. Kasambara², I. Chibwe², A. Debes¹, D. Mohr³, J. Lessler¹, A. Azman¹ ¹Johns Hopkins Bloomberg School of Public Health, USA, ²Public Health Institute of Malawi, Malawi, ³Johns Hopkins University School of Medicine, USA</p>
17:50-19:20	<p>Poster session 2 Ballroom AB</p>		
<p>Thursday 5th December 2019</p>			
<p>Ballroom C</p>			
08:30-09:10	<p>[INV04] Understanding cholera dynamics for public health Justin Lessler, Johns Hopkins University, USA</p>		
09:10-09:50	<p>[INV05] The new fight against an old foe: Making the case for typhoid conjugate vaccine introduction Virginia Pitzer, Yale School of Public Health, USA</p>		
09:50-10:30	<p>[INV06] Modeling and decision-making in crises: some lessons from recent case studies Rebecca Grais, Epicentre MSF, France</p>		
10:30-11:00	<p>Refreshment break Ballroom Foyer</p>		
11:00-12:40	<p>Session 10 Non-vacc. interv.</p>	<p>Session 11 Vector-borne infec.</p>	<p>Session 12 Interaction 1</p>
	<p>Ballroom C</p>	<p>Meeting Room 6&7</p>	<p>Meeting Room 8&9</p>
11:00-11:20	<p>[O10.1] The 'breakpoint' of soil-transmitted helminthiasis with infected human migration R.J. Hardwick*, C. Vegvari, J.E. Truscott, R.M. Anderson Imperial College London, UK</p>	<p>[O11.1] Focal transmission and the role of human mobility in the 2017 chikungunya outbreak in Lazio, Italy G. Guzzetta*¹, F. Vairo², A. Mammoni², S. Lanini², P.</p>	<p>[O12.1] Measurability of the epidemic reproduction number and generation time in data-driven contact networks M. Ajelli*^{1,2}, Q-H. Liu^{3,1}, A. Aleta⁴, S. Merler¹, Y. Moreno⁴</p>

		Poletti ¹ , M. Manica ⁴ , R. Rosa ^{1,3} , B. Caputo ⁵ , A. Solimini ⁵ , A. Della Torre ⁵ , P. Scognamiglio ¹ , A. Zumla ¹ , G. Ippolito ¹ , S. Merler ¹ , ¹ Fondazione Bruno Kessler, Italy, ² National Institute for Infectious Diseases Lazzaro Spallanzani, Italy, ³ University of Trento, Italy, ⁴ Fondazione Edmund Mach, Italy, ⁵ Sapienza University of Rome, Italy, ⁶ University College London, UK	.5, A. Vespignani ^{1,5} , ¹ Northeastern University, USA, ² Bruno Kessler Foundation, Italy, ³ University of Electronic Science and Technology of China, China, ⁴ University of Zaragoza, Spain, ⁵ ISI Foundation, Italy
11:20-11:40	[O10.2] Changes in historical typhoid transmission across 16 U.S. cities, 1889-1931: Quantifying the impact of investments in water and sewer infrastructures M.T. Phillips* ¹ , K.A. Owers ¹ , B.T. Grenfell ² , V.E. Pitzer ¹ ¹ Yale School of Public Health, USA, ² Princeton University, USA	[O11.2] Joint epidemic and geostatistical modelling approach for vector-borne disease outbreaks L. Koepfel*, C.P. Jewell, P.J. Neal, Lancaster University, UK	[O12.2] Model-based indicators of nodes criticality to design and assess targeted strategies for epidemic control on a cattle trade network P. Montagnon ^{1,2} , F. Deslandes ¹ , V. Bansaye ² , E. Vergu* ¹ , ¹ INRA, France, ² Ecole Polytechnique, France
11:40-12:00	[O10.3] Measuring the effect of reactive school closure in altering the network of social interactions and reducing the spread of influenza M. Litvinova* ^{1,2} , Q-H. Liu ^{3,1} , E.S. Kulikov ⁴ , M. Ajelli ^{1,5} ¹ Northeastern University, USA, ² ISI Foundation, Italy, ³ University of Electronic Science and Technology of China, China, ⁴ Siberian State Medical University, Russia, ⁵ Bruno Kessler Foundation, Ital	[O11.3] Burden is in the eye of the beholder: Yellow fever burden estimates are highly sensitive to choices about data interpretation T.A. Perkins*, J.H. Huber, Q. Tran, R.J. Oidtman, M.K. Walters, A.S. Siraj, S.M. Moore, University of Notre Dame, USA	[O12.3] Metapopulation models of infectious disease dynamics are sensitive to underlying host movement models D. Citron* ¹ , C. Guerra ² , J. Henry ¹ , S. Wu ³ , H. Sánchez ³ , D. Smith ¹ , ¹ University of Washington, USA, ² Medical Care Development International, USA, ³ University of California Berkeley, USA
12:00-12:20	[O10.4] Predicting the impact of public health interventions for preventing antibiotic-resistant infections N.G. Davies* ¹ , C. Chae ¹ , S. Flasche ¹ , M. Jit ^{1,2} , K.E. Atkins ^{1,3} ¹ London School of Hygiene and Tropical Medicine, UK, ² Public Health England, UK, ³ University of Edinburgh, UK	[O11.4] Leveraging multiple data types to estimate the true size of the Zika epidemic in the Americas S. Moore* ¹ , R. Oidtman ¹ , K.J. Soda ¹ , A. Siraj ¹ , R. Reiner ² , C. Barker ³ , T.A. Perkins ¹ , ¹ University of Notre Dame, USA, ² University of Washington, USA, ³ University of California, Davis, USA	[O12.4] Reorganization of nurse scheduling reduces the risk of healthcare associated infections E. Valdano ² , C. Poletto ¹ , P-Y. Boelle ¹ , V. Colizza* ¹ , ¹ Institut Pierre Louis d'Epidémiologie et de Santé Publique (IPLESP), France, ² University of California Los Angeles, USA
12:20-12:40	[O10.5] Optimization of the effects of school closures on mitigating influenza epidemics in Hong Kong S.T. Ali*, E.H.Y. Lau, V.J. Fang, G.M. Leung, B.J. Cowling The University of Hong Kong, Hong Kong	[O11.5] A chain-binomial model accounting for transmission risk factors with application to Zika and Chikungunya transmission in households in French Guiana A. Cousien* ¹ , D. Rousset ² , S. Cauchemez ¹ , C. Flamand ² , ¹ Institut Pasteur, France, ² Institut Pasteur, French Guiana	[O12.5] Host contact dynamics shapes richness and dominance of pathogen strains C. Poletto* ¹ , F. Pinotti ¹ , E. Fleury ² , D. Guillemot ³ , P-Y. Boëlle ¹ , ¹ INSERM, Sorbonne Université, France, ² INRIA, France, ³ INSERM, Institut Pasteur, Université Paris-Saclay, France
12:40-13:40	Lunch Ballroom AB		

13:40-15:40	Session 13 Statistics	Session 14 Malaria	Session 15 Interaction 2
	Ballroom C	Meeting Room 6&7	Meeting Room 8&9
13:40-14:00	<p>[O13.1] Serosolver: An open source tool to infer epidemiological and immunological dynamics from serological data J.A. Hay*¹, A. Minter², K. Ainslie¹, J. Lessler³, A. Kucharski², S. Riley¹, ¹Imperial College London, UK, ²London School of Hygiene and Tropical Medicine, UK, ³Johns Hopkins Bloomberg School of Public Health, USA</p>	<p>[O14.1] Parameterising individual-based malaria models to diverse data using gaussian process stacked generalization T. Reiker*^{1,2}, E. Cameron³, S. Filippi⁴, M. Penny^{1,2}, ¹Swiss Tropical and Public Health Institute, Switzerland, ²University of Basel, Switzerland, ³University of Oxford, UK, ⁴Imperial College, UK</p>	<p>[O15.1] On the generalisability of within household contact networks and impact on epidemic spread P.N. Krivitsky¹, P. Coletti*², N. Hens^{2,3}, ¹University of Wollongong, Australia, ²Hasselt University, Belgium, ³University of Antwerp, Belgium</p>
14:00-14:20	<p>[O13.2] Novel approaches for the reconstruction of epidemics history from serological surveys N. Hozé, H. Salje*, S. Cauchemez, <i>Institut Pasteur, France</i></p>	<p>[O14.2] Breaking highly endemic transmission in malaria: a novel epidemiological threshold related to parasite antigenic diversification Q. He*, M. Pascual, <i>University of Chicago, USA</i></p>	<p>[O15.2] Household contact studies for tuberculosis: potential for population inferences L.F. White*, T. Li, H.E. Jenkins, C.R. Horsburgh, <i>Boston University, USA</i></p>
14:20-14:40	<p>[O13.3] Feature selection for dynamic epidemiological models E. Glennon*¹, B. Han², O. Restif¹, ¹University of Cambridge, UK, ²Cary Institute of Ecosystem Studies, USA</p>	<p>[O14.3] Modelling the population dynamics of Plasmodium falciparum gametocytes in humans during malaria infection J.M. McCaw*^{1,2}, P. Cao¹, K.A. Collins³, S.G. Zaloumis¹, T. Wattanakul^{4,5}, J. Tarning^{4,5}, J.A. Simpson¹, J.S. McCarthy⁶, ¹The University of Melbourne, Australia, ²Peter Doherty Institute for Infection and Immunity, Australia, ³Radboud University Medical Center, The Netherlands, ⁴Mahidol University, Thailand, ⁵University of Oxford, UK, ⁶QIMR Berghofer Medical Research Institute, Australia</p>	<p>[O15.3] A household-structured approach to endemic infections J. Hilton*, M.J. Keeling, <i>University of Warwick, UK</i></p>
14:40-15:00	<p>[O13.4] Statistical methods for calibrating a dynamic transmission model to setting-specific historical malaria trends M. Winkel*^{1,2}, M. Runge^{1,2}, E. Pothin^{1,2}, T. Smith^{1,2}, ¹Swiss Tropical and Public Health Institute, Switzerland, ²University of Basel, Switzerland, ³Clinton Health Access Initiative, USA</p>	<p>[O14.4] Modelling the effect of hypothesised interactions between falciparum and vivax malaria on prevalence R.I. Hickson*¹, R. Aguas^{2,4}, A. Devine³, J.M. McCaw¹, P. Ngor^{4,5}, D.J. Price¹, L. White^{2,4}, ¹The University of Melbourne, Australia, ²Oxford University, UK, ³Menzies School of Health Research, Australia, ⁴Mahidol Oxford Tropical Medicine Research Unit, Thailand, ⁵National Center for Parasitology, Entomology and Malaria Control, Cambodia</p>	<p>[O15.4] Fine-scale family structure shapes influenza transmission risk in households: Insights from primary schools in Matsumoto city, 2014/15 A. Endo*¹, M. Uchida², A.J. Kucharski¹, S. Funk¹, ¹London School of Hygiene & Tropical Medicine, UK, ²Gunma University, Japan</p>
15:00-15:20	<p>[O13.5] Integrating geostatistical maps and transmission models using adaptive multiple importance sampling</p>	<p>Tracking progress towards malaria in elimination in [O14.5] China: estimates of malaria reproduction</p>	<p>[O15.4] Disentangling social contagion and media drivers in the emergence of health threats awareness</p>

	R. Retkute* ¹ , P. Touloupou ¹ , D. Hollingsworth ² , S.E.F. Spencer ¹ , ¹ University of Warwick, UK, ² University of Oxford, UK	numbers and their spatio-temporal variation I. Routledge* ¹ , S. Lai ² , K.E. Battle ³ , A.C. Ghani ¹ , M. Gomez Rodriguez ⁴ , K.B. Gustafson ⁵ , S. Mishra ¹ , J.L. Proctor ⁶ , Z. Li ⁷ , S. Bhatt ¹ , ¹ Imperial College London, UK, ² University of Southampton, UK, ³ University of Oxford, UK, ⁴ Max Planck Institute for Software Systems, Germany, ⁵ United States Department of the Navy, USA, ⁶ Institute of Disease Modelling, USA, ⁷ Chinese Centers for Disease Control and Prevention, China	P. Bosetti* ¹ , P. Poletti ² , C. Consonni ³ , B. Lepri ² , D. Lazer ⁴ , S. Merler ² , A. Vespignani ⁴ , ¹ Institut Pasteur, France, ² Fondazione Bruno Kessler, Italy, ³ University of Trento, Italy, ⁴ Northeastern University, USA
15:20-15:40	[O13.6] Paths to valid inferences through theory and data J. Koopman, University of Michigan, USA	[O14.6] Inference of Plasmodium falciparum transmission networks in the presence of superinfection by genetically distinct parasites A. Lerch* ¹ , M. Hsiang ² , J. Huber ¹ , R. Nielsen ³ , B. Greenhouse ⁴ , A. Perkins ¹ , ¹ University of Notre Dame, USA, ² University of Texas Southwestern Medical Center, USA, ³ University of California Berkeley, USA, ⁴ University of California San Francisco, USA	[O15.5] How contact patterns change in an ageing population J.A. Backer* ¹ , J. Van de Kasteleel ¹ , J. Wallinga ^{1,2} , ¹ National Institute for Public Health and the Environment, The Netherlands, ² Leiden University Medical Center, The Netherlands
15:40-16:10	Refreshment break Ballroom Foyer		
16:10-17:30	Session 16 Surveillance Ballroom C	Session 17 Within-host dyn. Meeting Room 6&7	Session 18 Phylodynamics 3 Meeting Room 8&9
16:10-16:30	[O16.1] Designing a typhoid environmental surveillance study: A simulation model for optimum sampling site allocation Y-K. Wang* ¹ , C.L. Moe ¹ , S. Dutta ² , A. Wadhwa ¹ , S. Kanungo ² , W. Mairinger ¹ , Y-C. Zhao ³ , Y. Jiang ³ , P.F.M. Teunis ¹ , ¹ Emory University, USA, ² National Institute of Cholera and Enteric Diseases, India, ³ Georgia State University, USA	[O17.1] A macroparasite within-host framework accommodating spatial structure can recapitulate key aspects of influenza A infection dynamics M. Gallagher* ¹ , R. Ke ² , C. Brooke ³ , K. Koelle ¹ , ¹ Emory University, USA, ² Los Alamos National Labs, USA, ³ University of Illinois Urbana-Champaign, USA	[O18.1] Relating whole genome sequencing of methicillin-resistant staphylococcus aureus isolates to transmission dynamics and efficacy of control interventions S. Blumberg* ^{1,2} , T. Porco ¹ , B. Shopsin ² , M. Phillips ² , ¹ University of California, USA, ² New York University, USA
16:30-16:50	[O16.2] The typo challenge: A citizen science approach to improve data quality during outbreaks using a Bayesian inferential framework A. Cori* ¹ , M. Baguelin ^{1,2} , ¹ Imperial College London, UK, ² London School of Hygiene and Tropical Medicine, UK	[O17.2] Modelling the impact of immunity on artemisinin sensitive and resistant Plasmodium falciparum infections S.G. Zaloumis* ¹ , I. Harris ¹ , P. Cao ¹ , S. Dini ¹ , J.M. McCaw ¹ , J. Tarning ^{2,3} , E.A. Ashley ^{2,3} , J-A. Chan ⁴ , K. O'Flaherty ⁴ , E. Takashima ⁵ , ¹ University of Melbourne, Australia, ² Mahidol University, Thailand, ³ University of Oxford, UK,	[O18.2] Bayesian reconstruction of nosocomial outbreaks using whole genome sequences and patient ward data F. Campbell* ¹ , A. Cori ¹ , N. Ferguson ¹ , T. Jombart ^{2,1} , ¹ Imperial College London, UK, ² London School of Hygiene and Tropical Medicine, UK

		<p>⁴Burnet Institute, Australia, ⁵Ehime University, Japan, ⁶University of Maryland School of Medicine, USA, ⁷National Institutes of Health, USA, ⁸National Center for Parasitology, Entomology and Malaria Control, Cambodia, ⁹Hospital for Tropical Diseases, Viet Nam, ¹⁰Department of Medical Research, Myanmar, ¹¹Mahosot Hospital, People's Democratic Republic of Lao, ¹²University of Health Sciences, People's Democratic Republic of Lao, ¹³Malaria Research Group and Dev Care Foundation, Bangladesh, ¹⁴Monash University, Australia</p>	
16:50-17:10	<p>[O16.3] Optimizing respiratory virus surveillance networks using uncertainty propagation S. Pei*¹, X. Teng², P. Lewis³, J. Shaman¹, ¹Columbia University, USA, ²University of Pittsburgh, USA, ³Armed Forces Health Surveillance Branch, USA</p>	<p>[O17.3] Ensemble modeling highlights importance of understanding parasite-host behavior in preclinical antimalarial drug development L. Burgert*^{1,2}, M. Rottmann^{1,2}, S. Wittlin^{1,2}, N. Gobeau^{1,3}, A. Krause^{1,4}, J. Dingemans^{1,4}, J.J. Möhrle^{1,3}, M.A. Penny^{1,2}, ¹Swiss Tropical and Public Health Institute, Switzerland, ²University of Basel, Switzerland, ³Medicines for Malaria Venture, Switzerland, ⁴Idorsia Pharmaceuticals Ltd, Switzerland</p>	<p>[O18.3] Inferring environmental transmission using phylodynamics: A case-study using simulated evolution of an enteric pathogen D. Dawson*, D. Rasmussen, X. Peng, C. Lanzas, North Carolina State University, USA</p>
17:10-17:30	<p>[O16.4] Reconstructing Mayaro virus circulation in French Guiana shows frequent spillovers N. Hozé*¹, H. Salje¹, D. Rousset², C. Fritzell², J. Vanhomwegen¹, S. Bailly², M. Najm¹, A. Enfissi², J-C. Manuguerra¹, C. Flamand², ¹Institut Pasteur, France, ²Institut Pasteur, French Guiana</p>	<p>[O17.4] Quantifying influenza viral dynamics in different cell types to understand how receptor binding switching facilitates human adaptation A.W.C. Yan*, J. Zhou, W.S. Barclay, S. Riley, Imperial College London, UK</p>	<p>[O18.4] Quantitative difference between intra-host HCV populations from persons with recently established and persistent infections P. Icer¹, J. Lara², A. Zelikovsky¹, Y. Khudyakov², P. Skums*¹, ¹Georgia State University, USA, ²Centers for Disease Control and Prevention, USA</p>
17:30-19:00	Poster session 3 Ballroom AB		
19:00-22:00	Conference dinner (ticket holders only)		
Friday 6th December 2019			
Ballroom C			
08:30-09:10	<p>[INV07] Geospatial data integration to map population distributions, demographics and dynamics for disease control Andy Tatem, University of Southampton, UK</p>		
09:10-09:50	<p>[INV08] Sex differences in immune function: probing ultimate drivers, and exploring consequences Jessica Metcalf, Princeton University, USA</p>		
09:50-10:20	Refreshment break Ballroom Foyer		
10:20-12:00	Session 19 Interaction 3	Session 20 Dengue	Session 21 Influenza evolution
	Ballroom C	Meeting Room 6&7	Meeting Room 8&9

10:20-10:40	<p>[O19.1] Characterizing human mobility patterns in low-income settings as a function of trip distance and urbanicity H. Meredith^{*1}, J. Guiles¹, C. Buckee², A. Tatem^{3,4}, J. Metcalf⁵, A. Wesolowski¹, ¹Johns Hopkins Bloomberg School of Public Health, USA, ²Harvard TH Chan School of Public Health, USA, ³University of Southampton, UK, ⁴Flowminder Foundation, Sweden, ⁵Princeton University, USA</p>	<p>[O20.1] Reconstructing four decades of Dengue transmission in Bangkok, Thailand L. Wang^{*1}, A. Huang^{2,4}, R. Jarman³, S. Fernandez⁴, S. Cauchemez¹, D. Cummings², H. Salje^{1,5}, ¹Institut Pasteur, France, ²University of Florida, USA, ³Walter Reed Army Institute of Research, USA, ⁴Armed Forces Research Institute of Medical Sciences, Thailand, ⁵Johns Hopkins Bloomberg School of Public Health, USA</p>	<p>[O21.1] Impact of influenza antigenic evolution on disease dynamics in the United States A. Perofsky^{*1}, J. Huddleston², N. Trovão¹, M. Nelson¹, T. Bedford², C. Viboud¹, ¹Fogarty International Center, National Institutes of Health, USA, ²Fred Hutchinson Cancer Research Center, USA</p>
10:40-11:00	<p>[O19.2] Measuring human interactions and determining optimal vaccination strategies using mobile phones and citizen science S. Kissler^{*1,2}, P. Klepac³, M. Tang¹, A. Conlan¹, J. Gog¹, ¹University of Cambridge, UK, ²Harvard T.H. Chan School of Public Health, USA, ³London School of Hygiene and Tropical Medicine, UK</p>	<p>[O20.2] Modeling the effects of vaccination on dengue virulence evolution E. Mainou^{*1,2}, K. Koelle¹, ¹Emory University, USA, ²Penn State University, USA</p>	<p>[O21.2] Evolutionary and epidemiological dynamics of influenza viruses in Hong Kong during 1998-2018 W. Yang^{*1}, E.H.Y. Lau², B.J. Cowling², ¹Columbia University, USA, ²The University of Hong Kong, Hong Kong</p>
11:00-11:20	<p>[O19.3] Mobile phone data, human mobility networks, and epidemic risk in megacities T.S. Brown^{*1,4}, K. Engø-Monsen², M. Kiang³, C. Buckee⁴, ¹Massachusetts General Hospital, USA, ²Telenor Group, Norway, ³Stanford University, USA, ⁴Harvard University, USA</p>	<p>[O20.3] Using longitudinal serology and surveillance data to quantify dengue transmission and control during two recent outbreaks in Fiji A. Henderson^{*1}, M. Kama², V-M. Cao-Lormeau³, M. Aubry³, C. Lau⁴, P. Matadigo², J. Edmunds¹, A. Kucharski¹, ¹London School of Hygiene & Tropical Medicine, UK, ²The Centre of Communicable Diseases, Fiji, ³Institut Louis Malardé, French Polynesia, ⁴Australian National University, Australia</p>	<p>[O21.3] High-resolution phylogenetic tracking of city-level spread of seasonal influenza T. Bedford^{*2}, H.Y. Chu¹, M. Boeckh², J.A. Englund³, M. Famulare⁴, B.R. Lutz¹, D.A. Nickerson¹, M. Rieder¹, L.M. Starita¹, M. Thompson¹, ¹University of Washington, USA, ²Fred Hutchinson Cancer Research Center, USA, ³Seattle Children's Hospital, USA, ⁴Institute for Disease Modeling, USA</p>
11:20-11:40	<p>[O19.4] Population movement patterns of importance to malaria control in Namibia C. Ciavarella^{*1}, H.C. Slater^{1,2}, N.W. Ruktanonchai³, N.M. Ferguson¹ ¹Imperial College London, UK, ²PATH, USA, ³University of Southampton, UK</p>	<p>[O20.4] Designing effective control of dengue with combined interventions T.J. Hladish^{*1}, C.A.B. Pearson^{2,3}, K.B. Toh¹, D.P. Rojas¹, P. Manrique-Saide⁴, G.M. Vazquez-Prokopec⁵, M.E. Halloran^{6,7}, I.M. Longini¹, ¹University of Florida, USA, ²London School of Hygiene & Tropical Medicine, UK, ³Stellenbosch University, South Africa, ⁴Universidad Autónoma de Yucatán, Mexico, ⁵Emory University, USA, ⁶Fred Hutchinson Cancer Research Center, USA, ⁷University of Washington, USA</p>	<p>[O21.4] Reconstructing the antigenic evolution of influenza A viruses in multiple hosts N.S. Trovao^{*1,2}, J. Cherry², S. Khan², T. Bedford⁴, P. Lemey⁵, M.I. Nelson², ¹Icahn School of Medicine at Mount Sinai, USA, ²National Institutes of Health, USA, ³Fred Hutchinson Cancer Research Center, USA, ⁴University of Leuven, Belgium</p>

11:40-12:00	<p>[O19.5] Social networks with strong spatial embedding generate non-standard epidemic dynamics driven by higher-order clustering D.J. Haw*, R. Pung, S. Riley, <i>Imperial College London, UK</i></p>	<p>[O20.5] Genomic tracing of dengue household spread in Kamphaeng Phet, Thailand: Implications for surveillance and control I. Maljkovic Berry*¹, M. Melendrez¹, S. Pollett¹, C. Klungthong², A. Nisalak², M. Panciera¹, B. Thaisomboonsuk², T. Li¹, S. Thomas³, T. Endy³, ¹Walter Reed Army Institute of Research, USA, ²Armed Forces Research Institute of Medical Sciences, Thailand, ³Upstate Medical University of New York, USA</p>	<p>[O21.5] Identifying age cohort effects in seasonal influenza D. Vera Cruz*¹, K. Koelle¹, ¹Duke University, USA, ²Emory University, USA</p>
12:00-12:40	<p>[INV09] Ecological and Analytical Approaches to Predicting and Preventing Viral Emergence Kevin Olival, <i>EcoHealth Alliance, USA</i></p>		
12:40-13:00	<p>Conference closing</p>		
13:00-13:30	<p>Refreshment Break Ballroom Foyer</p>		