# Oral Programme

| Tuesday 28th November 2017 | |
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| 12:30-13:00 | Pre Conference Workshop Registration I *Auditorium Hall* |
| 13:00-17:30 | **Pre Conference Workshop (Ticket holders only)** I *Mestral 1+2* |
| 17:00-19:00 | Registration I *Auditorium Hall* |
| 18:00-19:30 | **Welcome Reception & Poster Session 1** I *Hall Auditorium & Hall Tramuntana* |

| Wednesday 29th November 2017 | |
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| 07:30-08:30 | Registration I *Auditorium Hall* |
| **Room** | *Auditorium  \|  Session Chair:* Hans Heesterbeek |
| 08:30-08:40 | Welcome & Opening Remarks by Conference Chairs |
| 08:40-09:10 | **[PLN01] Progress in the study of the transmission dynamics of human helminth infections and control by mass drug administration**<br>Roy Anderson, *Imperial College London, UK* |
| 09:10-09:50 | **[PLN02] Liz Corbett,** *London School of Hygiene and Tropical Medicine, UK* |
| 09:50-10:30 | **[PLN03] Many Varieties of Error: Combining Spatial Models and Data for Malaria Elimination**<br>Caroline Buckee, *Harvard School of Public Health, USA* |
| 10:30-11:10 | **[PLN04] Antibiotic resistance: Tales of the unexpected**<br>Marc Bonten, *University Medical Center Utrecht, The Netherlands* |
| 11:10-11:40 | **Refreshment Break I** *Hall Auditorium & Hall Tramuntana* |

| Rooms | *Auditorium* | *Tramuntana 1* | *Tramuntana 2* |
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| 11:40-13:00 | **Session 1: AMR 1**<br>*Session Chair: Marc Bonten* | **Session 2: Contact**<br>*Session Chair: Martina Morris* | **Session 3: Evolution**<br>*Session Chair: Samuel Alizon* |
| 11:40-12:00 | **[O1.1] Why sensitive bacteria are resistant to hospital infection control**<br>E. van Kleef*[1,2], N. Luangasanatip[3], M.J.M. Bonten[1], B.S. Cooper[1,4], *[1]University Medical Center Utrecht, The Netherlands, [2]Mahidol-Oxford Tropical Medicine Research Unit, Thailand, [3]London School of Hygiene and Tropical Medicine, UK, [4]University of Oxford, UK* | **[O2.1] Impact of regular school closure on seasonal influenza epidemics**<br>G. De Luca[1], K. Van Kerckhove[2], P. Coletti[2], C. Poletto[1], N. Bossuyt[3], N. Hens[2,4], V. Colizza*[1,5], *[1]Inserm, France, [2]Hasselt University, Belgium, [3]Scientific Institute of Public Health, Belgium, [4]University of Antwerp, Belgium, [5]ISI Foundation, Italy* | **[O3.1] Diversity of multiple infection patterns and virulence evolution**<br>M.T. Sofonea*, S. Alizon, Y. Michalakis, *MIVEGEC, France* |
| 12:00-12:20 | **[O1.2] Ecological association between unequal antibiotic consumption and antibiotic resistance**<br>S.W. Olesen*[1], M.L. Barnett[1,2], D. MacFadden[1,3], M. Lipsitch[1], Y.H. Grad[1,2], *[1]Harvard T. H. Chan School of Public Health, USA, [2]Brigham and Women's Hospital, USA, [3]University of Toronto, Canada* | **[O2.2] Quantifying the effectiveness of contact tracing efforts using mathmatical modeling: The 2014 Ebola outbreak in Mali as a case study**<br>L.F. Moriarty*, G. Chowell, *Georgia State University, USA* | **[O3.2] Neutral mutations and selection drive pervasive loss of mutability in long-lived B cell lineages during chronic HIV infection**<br>M. Vieira*, D. Zinder, S. Cobey, *University of Chicago, USA* |
| 12:20-12:40 | **[O1.3] Elucidating plausible mechanisms of coexistence helps predict the impact of vaccination upon antibiotic resistance**<br>N.G. Davies*, S. Flasche, M. Jit, K.E. Atkins, *London School of Hygiene & Tropical* | **[O2.3] A nonparametric method for simulating sexual contact networks using limited data: Applications to the South African HIV epidemic**<br>K.A. Risher*[1,2], D.D. Celentano[2], S.H. Mehta[2], L. Simbayi[3], O. Shisana[4], T. Rehle[3,5], J. | **[O3.3] Real-time genomic surveillance of pathogen evolution and spread**<br>T. Bedford, *Fred Hutchinson Cancer Research Center, USA* |

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| | *Medicine, UK* | Lessler[2], *[1]London School of Hygiene and Tropical Medicine, UK, [2]Johns Hopkins Bloomberg School of Public Health, USA, [3]Human Sciences Research Council, South Africa, [4]Evidence Based Solutions, South Africa, [5]University of Cape Town, South Africa* | |
| 12:40-13:00 | **[O1.4] An evolutionary model to predict the frequency of antibiotic resistance under seasonal antibiotic use, and an application to** *Streptococcus pneumoniae* F. Blanquart*, S. Lehtinen, C. Fraser, *University of Oxford, UK* | **[O2.4] Participatory development of a contact diary tool to capture dynamic household structure and mobility within and between remote Aboriginal and Torres Strait Islander communities** J. McVernon*[1 ,2], K. Gibney[1], S. Hanieh[1], B. Biggs[1], J. Shield[1], B. Davison[3], G. Singh[3 ,4], T. Kearns[3], M. McKinnon[3], R.G. Dhurrkay[3], *[1]The Royal Melbourne Hospital and the University of Melbourne at the Peter Doherty Institute for Infection and Immunity, Australia, [2]The University of Melbourne, Australia, [3]Menzies School of Health Research, Australia, [4]Northern Territory Medical Program of Flinders and James Cook Universities, Australia,* | **[O3.4] Detecting signatures of transmission reduction on the road to eradication** G. Rydevik, S. Lycett*, *University of Edinburgh, UK* |
| 13:00-14:00 | Lunch  \| *Noray Restaurant* | | |
| 13:00-14:00 | **Author Workshop I** *Tramuntana 1* | | |
| **Rooms** | *Auditorium* | *Tramuntana 1* | *Tramuntana 2* |
| 14:00-15:40 | **Session 4: Influenza 1** *Session Chair:* Derek Cummings | **Session 5: Genetic diversity** *Session Chair:* Christophe Fraser | **Session 6:  Social & network** *Session Chair:* Shweta Bansal |
| 14:00-14:20 | **[O4.1] Collaborative efforts to routinely forecast seasonal influenza in the United States across four influenza seasons, 2013-14 to 2016-17** M. Biggerstaff*, C. McGowan, M. Johansson, C. Reed, *Centers for Disease Control and Prevention, USA* | 14:00-14:40 · **[O5.1] Phyloscanner: Analysing within- and between-host pathogen genetic diversity to identify transmission, multiple infection, recombination and contamination** C. Wymant*[1 ,2], M. Hall[1 ,2], O. Ratmann[2], D. Bonsall[1], T. Golubchik[1], M. de Cesare[1], A. Gall[3], M. Cornelissen[4], C. Fraser[1 ,2], *[1]University of Oxford, UK, [2]Imperial College London, UK, [3]University of Cambridge, UK, [4]University of Amsterdam, The Netherlands* **[O5.2] Resolving HIV-1 transmission between agrarian, trading and fisherfolk communities in Rakai, Uganda, with deep sequencing data** | **[O6.1] A data-driven social behavioural model for individual vaccination decisions** J.J. Hoogink*[1 ,2], D.W.F. van Krevelen[1], J. Wallinga[1 ,2], *[1]National Institute for Public Health and Environment, The Netherlands, [2]Leiden University Medical Center, The Netherlands* |

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| | | O. Ratmann*[1], M.K. Grabowski[2,3], M. Hall[4], T. Golubchik[4], C. Wymant[4], T. Quinn[5,3], M. Wawer[2,3], D. Serwadda[3,6], R. Gray[2,3], C. Fraser[4], *[1]Imperial College London, UK, [2]Johns Hopkins Bloomberg School of Public Health, USA, [3]Rakai Health Sciences Program, Uganda, [4]University of Oxford, UK, [5]National Institute of Allergy and Infectious Diseases, USA, [6]Makerere University School of Public Health, Uganda* | |
| 14:20-14:40 | **[O4.2] Forecasting the spatial transmission of influenza in the United States** S. Pei*, S. Kandula, W. Yang, J. Shaman, *Columbia University, USA* | **[O5.3] Using phyloscanner to identify HIV transmission clusters and epidemiological correlates of transmission** M.D. Hall*[1], C. Wymant[1], O. Ratmann[2], C. Fraser[1], *[1]University of Oxford, UK, [2]Imperial College London, UK* | **[O6.2] Statistical estimation of network models from egocentrically sampled network data** M. Morris*[1], P.N. Krivitsky[2], *[1]University of Washington, USA, [2]University of Wollongong, Australia* |
| 15:00-15:20 | **[O4.4] Immune history and forecasting the evolution of seasonal influenza virus** K. Kim*[1], S. Hensley[2], S. Cobey[1], *[1]The University of Chicago, USA, [2]The University of Pennsylvania, USA* | **[O5.5] The Virome of Manhattan: A testbed for radically advancing understanding and forecast of viral respiratory infections** J. Shaman*[1,2], P. Planet[2,3], R. Rabadan[1], W. Chung[1], S. Anthony[1], D. Hsu[1], G. Freyer[1], *[1]Columbia University, USA, [2]American Museum of Natural History, USA, [3]University of Pennsylvania, USA* | **[O6.4] Spread of hospital-acquired infections: A comparison of healthcare networks** N. Nekkab*[1,2], P. Astagneau[3,4], L. Temime[1,2], P. Crépey[3,6], *[1]Conservatoire National des Arts et Métiers, France, [2]Institut Pasteur, France, [3]Ecole des Hautes Etudes en Santé Publique, France, [4]Centre de Prévention des Infections Associées aux Soins, France, [5]Sorbonne Universités, France, [6]Faculté de Médecine-Timone, France, [7]Université de Rennes 1, France* |
| 15:20-15:40 | **[O4.5] Comparison of ensemble methods for forecasting influenza in the United States** N.G. Reich*, A. Tushar, G.C. Gibson, E.L. Ray, *University of Massachusetts Amerst, USA* | **[O5.6] What drives antigenic diversity in pathogenic bacteria? Insights from integrated genomic approaches** R.J. Mostowy, *Imperial College London, UK* | **[O6.5] A novel methodology to study the uncertainty in the structure of contact leading to transmission** M. Baguelin*[1,2], E. van Leeuwen[1,3], P. Klepac[1,3], N. Demiris[4], *[1]Public Health England, UK, [2]London School of Hygiene and Tropical Medicine, UK, [3]Imperial College London, UK, [4]Athens University of Economics and Business, Greece* |
| 15:40-16:10 | **Refreshment Break I** *Hall Auditorium & Hall Tramuntana* | | |

| Rooms | Auditorium | Tramuntana 1 | Tramuntana 2 |
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| 16:10-17:50 | **Session 7: Malaria VBD** *Session Chair:* Caroline Buckee | **Session 8: Forecasting** *Session Chair:* Tini Garske | **Session 9: Multiple path/host** *Session Chair:* Michiel van Boven |
| 16:10-16:30 | **[O7.1]** Estimating household mosquito biting propensities and identifying malaria hotspots for intervention S.Y. Kang*[1], D. Bisanzio[1], D.L. Smith[2], *[1]University of Oxford, UK, [2]University of Washington, UK* | **[O8.1]** Identifying novel zoonotic viruses from hospital patients with diseases of unknown origin using metagenomics and multivariate statistical techniques G.S. Robertson*, J.L. Ashworth, L. Lu, M.E.J. Woolhouse, *University of Edinburgh, UK* | **[O9.1]** Multiple infections: Taming combinatorial complexity provides insights into HPV epidemiology S. Alizon*[1,2], C.L. Murall[1,3], E. Saulnier[3,1], M. Sofonea[3,1], *[1]CNRS, France, [2]IRD, France, [3]Université de Montpellier, France* |
| 16:30-16:50 | **[O7.2]** Understanding the decline and rebound in immunity to symptomatic malaria due to intervention disruption in malaria transmission J.R. Russell*[1], J. Gerardin[1], A.L. Ouedraogo[1], D.L. Smith[2], I. Rodriguez-Barraquer[3], M. Kamya[4], J. Nankabirwa[4], G. Dorsey[3], B. Greenhouse[3], E.A. Wenger[1], *[1]Institute for Disease Modeling, USA, [2]University of Washington, USA, [3]University of California, USA, [4]Makerere University College of Health Sciences, Uganda* | **[O8.2]** Real-time West Nile virus forecasts for the 2017 season N. DeFelice*, J. Shaman, *Columbia University, USA* | **[O9.2]** Prior illness provides short-term protection against respiratory illness, but is a risk factor for gastroenteritis: Pathogen interference in a national survey K. Glass*, A. Lal, M. Kirk, *Australian National University, Australia* |
| 16:50-17:10 | **[O7.3]** A modified model for vector-borne transmission linking vector abundance to human density V.T.R. Aznar*, M. Pascual, *University of Chicago, USA* | **[O8.3]** Estimating recent tuberculosis transmission from cluster size distributions E. Brooks-Pollock*[1], H.K. Altes[2], L. Danon[3], A. Pollock[4], D. van Sooligen[2], J. Davidson[5], M. Lalor[5], *[1]University of Bristol, UK, [2]National Institute for Public Health and the Environment (RIVM), The Netherlands, [3]University of Exeter, UK, [4]University of Sheffield, UK, [5]Public Health England, UK* | **[O9.3]** Common respiratory viruses exhibit interlinked epidemiological dynamics S. Nickbakhsh*[1], C. Mair[1], L. Matthews[1], R. Reeve[1], F. Thorburn[2], B. Von Wissmann[2], A. Reynolds[3], J. McMenamin[3], R.N. Gunson[2], P.R. Murcia[1], *[1]University of Glasgow, UK, [2]NHS Greater Glasgow and Clyde, UK, [3]Health Protection Scotland, UK* |
| 17:10-17:30 | **[O7.4]** Connecting the dots of malaria transmission using genetic networks B. Greenhouse*[1], M. Hsiang[1], T.A. Perkins[2], S. Tessema[1], R. Nielsen[3], M. Makame[4], A. Schwartz[1], M. Murphy[1], J. Kemere[1], K. Baltzell[1], *[1]University of California San Francisco, USA, [2]University of Notre Dame, USA, [3]University of California Berkeley, USA, [4]Zanzibar Malaria Elimination Program, Tanzania, [5]Karolinska Institute, Sweden, [6]University of Namibia, Namibi* | **[O8.4]** Real-time decision-making during emergency disease outbreaks W.J.M. Probert*[1,8], C.P. Jewell[2], M. Werkman[3], C.J. Fonnesbeck[4], M.C. Runge[6], S. Sekiguchi[5], K. Shea[7], M.J. Keeling[1], M.J. Ferrari[7], M.J. Tildesley[1], *[1]University of Warwick, UK, [2]Lancaster University, UK, [3]Imperial College London, UK, [4]Vanderbilt University, USA, [5]University of Miyazaki, Japan, [6]US Geological Survey, USA, [7]The Pennsylvania State University, USA, [8]University of Oxford, UK* | **[O9.4]** Influenza vaccines alter within- and between-host bacterial pathogen dynamics via *generalized herd-effects* M.J. Mina*[1], J.A. McCullers[2], R. Antia[3], K.P. Klugman[3], *[1]Harvard Medical School, USA, [2]St. Jude Children's Research Hospital, USA, [3]Emory University, USA, [4]Emory University, USA* |
| 17:30-17:50 | **[O7.5]** Tracking malaria by its shadows: Using serology to reconstruct malaria transmission I. Rodriguez-Barraquer*[1], K. Tetteh[3], I. Ssewanyana[2], C. Drakeley[3], B. Greenhouse[1], *[1]University of* | **[O8.5]** Integrating multiple data streams for early outbreak detection: A graph approach A. Cori[1], P. Nouvellet*[1], T. Garske[1], H. Bourhy[2], E. Nakouné[3], T. Jombart[1], *[1]Imperial College London, UK, [2]Institut Pasteur,* | **[O9.5]** The role of host community composition in Chagas disease transmission cycles D. Erazo*[1], J. Cordovez[1], C. Cabrera[2], J. Calzada[3], A. Saldaña[3], N. |

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| | *California, USA, [2]Infectious Disease Research Collaboration, Uganda, [3]London School of Hygiene and Tropical Medicine, UK* | *France, [3]Institut Pasteur de Baugui, Central African Republic* | Gottdenker[2], *[1]BIOMAC, Universidad de los Andes, Colombia, [2]University of Georgia, USA, [3]Instituto Commemorativo Gorgas de Estudios de la Salud, Panama* |

| 17:50-19:20 | **Poster Session 2** I *Hall Auditorium & Hall Tramuntana* |
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## Thursday, 30th November 2017

| Room | *Auditorium* | *Session Chair:* Cecile Viboud |
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| 08:30-09:10 | **[PLN05] Friend or foe?: Protection and enhancement mediated by immune responses to Dengue and Zika viruses**<br>Eva Harris, *University of California Berkeley, USA* |
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| 09:10-09:50 | **[PLN06] Diversity of immune repertoires**<br>Aleksandra Walczak, *Ecole Normale Supérieure, France* |
| 09:50-10:30 | **[PLN07] Characterizing infectious disease transmission from detailed outbreak data**<br>Simon Cauchemez, *Institut Pasteur, France* |
| 10:30-11:00 | **Refreshment Break** I *Hall Auditorium & Hall Tramuntana* |

| Rooms | *Auditorium* | *Tramuntana 1* | *Tramuntana 2* |
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| 11:00-12:40 | **Session 10: Phylodynamics**<br>*Session Chair:* Katia Koelle | **Session 11: Zika**<br>*Session Chair:* Christian Althaus | **Session 12: Epidemics**<br>*Session Chair:* Ellen Brooks-Pollock |
| 11:00-11:20 | **[O10.1] Reconstruction of disease transmissions from viral quasispecies genomic data**<br>P. Skums*[1,2], A. Zelikovsky[1], R. Singh[2], Z. Dimitrova[2], S. Ramachandran[2], D. Campo[2], D. Jha[2], L. Bunimovich[3], E. Costenbader[4], C. Sexton[2], *[1]Georgia State University, USA, [2]Centers for Disease Control and Prevention, USA, [3]Georgia Institute of Technology, USA, [4]FHI 360, USA* | **[O11.1] Genomic epidemiology reveals epidemic dynamics of Zika virus in the Caribbean and U.S. Virgin Islands**<br>A. Black*[1,2], B. Potter[2], G. Dudas[2], L.R. Feldstein[2], M.E. Halloran[1,2], N.D. Grubaugh[3], K.G. Andersen[3], B.R. Ellis[4], E.M. Ellis[4], T. Bedford[2], *[1]University of Washington, USA, [2]Fred Hutchinson Cancer Research Center, USA, [3]The Scripps Research Institute, USA, [4]U.S. Virgin Islands Department of Health, U.S. Virgin Islands* | **[O12.1] Modelling arboviral disease epidemics in the Pacific islands**<br>C. Champagne*[1,2], B. Cazelles[1,3], *[1]Eco-evolutionary Mathematic, IBENS, France, [2]CREST, ENSAE, Université Paris Saclay, France, [3]UMMISCO, UPMC-IRD, France* |
| 11:20-11:40 | **[O10.2] Integrating viral sequence and epidemiological data to define transmission patterns for respiratory syncytial virus (RSV)**<br>I.K. Kombe*[1,2], G.F. Medley[2], M. Baguelin[2,3], J. Nokes[1,4], *[1]KEMRI-Wellcome Trust Research Programme, Kenya, [2]London School of Hygiene and Tropical Medicine, UK, [3]Public Health England, UK, [4]University of Warwick, UK* | **[O11.2] Using serological and surveillance data to infer the unobserved transmission dynamics of Zika virus in Fiji 2013-2017**<br>A. Henderson*[1], M. Kama[2], V.M. Cao-Lormeau[3], C. Lau[4], J. Edmunds[1], C. Watson[1], A. Kucharski[1], *[1]London School of Hygiene & Tropical Medicine, UK, [2]Ministry of Health, Fiji, [3]Institut Louis Malardé, French Polynesia, [4]University of Queensland, Australia* | **[O12.2] Explaining the transmission dynamics of enterovirus serotypes: From regular epidemics to infrequent outbreaks**<br>M. Pons-Salort*, N.C. Grassly, *Imperial College London, UK* |
| 11:40-12:00 | **[O10.3] Viral phylodynamics using regression-based approximate bayesian computation**<br>E. Saulnier*[1,2], O. Gascuel[2,3], S. Alizon[1], *[1]Laboratoire MIVEGEC (CNRS, IRD, UM), France, [2]IBC (LIRMM, CNRS, UM), France, [3]C3BI (CNRS, Institut Pasteur), France* | **[O11.3] Spread of Zika Virus in the Americas: A computational modelling approach**<br>A. Vespignani*[1], Q. Zhang[1], K. Sun[1], A. Pastore y Piontti[1], M. Chinazzi[1], N.E. Dean[2], S. Merler[3], L. Rossi[4], D.P. Rojas[2], D. Mistry[1], *[1]Northeastern University, USA, [2]University of Florida, USA, [3]Bruno Kessler Foundation, Italy, [4]Institute for Scientific Interchange Foundation, Italy, [5]Fred Hutchinson Cancer* | **[O12.3] Successive waves of human migrations shaped the global population structure of *Mycobacterium tuberculosis* in France**<br>M. Barbier[1,2], G. Lina[3,4], J-P. Flandrois[4], P. Supply[5], T. Wirth*[1,2], J-P. Rasigade[3,4], *[1]Université Pierre et Marie Curie, Sorbonne Universités, France, [2]PSL Research University, France, [3]CIRI, University of Lyon, France, [4]Hospices Civils* |

| | Auditorium | Tramuntana 1 | Tramuntana 2 |
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| | *Research Center, USA, [6]Bocconi University, Italy* | | *de Lyon, France, [5]Center for Infection and Immunity of Lille, France* |
| 12:00-12:20 | **[O10.4] Simulation and inference of phylodynamic individual level models**<br>J. Angevaare*[1], Z. Feng[1], R. Deardon[2], *[1]University of Guelph, Canada, [2]University of Calgary, Canada* | **[O11.4] Combining different data sources to understand Zika outbreaks**<br>S. Funk*, A.J. Kucharski, O.J. Brady, *London School of Hygiene & Tropical Medicine, UK* | **[O12.4] Cholera in 1853: Historic epidemics provide new clues in the fight against an old enemy**<br>M.D. Phelps*[1], M.L. Perner[1], V.E. Pitzer[2], P.K.M. Jensen[1], V. Andreasen[3], L. Simonsen[1], *[1]University of Copenhagen, Denmark, [2]Yale University, USA, [3]Roskilde University, Denmark* |
| 12:20-12:40 | **[O10.5] Phybreak: A method and R-package to reconstruct transmission trees with sequence data**<br>D. Klinkenberg*[1], C. Colijn[2], X. Didelot[2], J. Wallinga[1,3], *[1]National Institute for Public Health and the Environment, The Netherlands, [2]Imperial College London, UK, [3]Leiden University Medical Centre, The Netherlands* | **[O11.5] Inferring the risk factors behind the geographical spread and transmission of Zika in the Americas**<br>L.M. Gardner*[1], A. Bota[1], N.D. Grubaugh[2], K. Gangavarapu[2], M.U.G. Kraemer[3,4], *[1]UNSW Sydney, Australia, [2]Scripps Research Institute, USA, [3]University of Oxford, UK, [4]Boston Children's Hospital, USA, [5]Harvard Medical School, USA* | **[O12.5] Characterizing infectious diseases threats using epidemic doubling times**<br>G. Chowell*[1,2], L. DeCamp[1], C. Viboud[2], *[1]Georgia State University, USA, [2]National Institutes of Health, USA* |
| 12:40-14:00 | **Lunch I** *Noray Restaurant* | | |

| Rooms | Auditorium | Tramuntana 1 | Tramuntana 2 |
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| 14:00-16:00 | **Session 13: Dengue**<br>*Session Chair:* Christl Donnelly | **Session 14: Statistical methods**<br>*Session Chair:* Hiroshi Nishiura | **Session 15: Vaccination**<br>*Session Chair:* Virginia Pitzer |
| 14:00-14:20 | **[O13.1] Mapping global variation in dengue transmission intensity and assessing the impact of control strategies**<br>L. Cattarino*[1], I. Rodríguez-Barraquer[2], D.A.T. Cummings[3], N. Imai[1], N.M. Ferguson[1], *[1]Imperial College London, UK, [2]Johns Hopkins University, USA, [3]University of Florida, USA* | **[O14.1] Confronting uncertainty: Bayesian analytics and simulation to support the Zika epidemic response**<br>M.A. Johansson*[1,2], L. Mier-y-Teran[1], D.M. Rodriguez[1], J.M. Healy[1], B.R. Greening Jr.[1], S.P. Russell[1], T.M. Quandelacy[1,3], *[1]Center for Disease Control and Prevention, USA, [2]Harvard TH Chan School of Public Health, USA, [3]Johns Hopkins Bloomberg School of Public Health, USA* | **[O15.1] The polio 'end game' challenge – eradicating a vaccine: Spatial and temporal dynamics of type-2 vaccine poliovirus detection in stool and sewage following global withdrawal in April 2016**<br>I.M. Blake*, M. Pons-Salort, N. Molodecky, N.C. Grassly, *Imperial College London, UK* |
| 14:20-14:40 | **[O13.2] Antibody titer dynamics provide insight into dengue disease risk**<br>Antibody titer dynamics provide insight into dengue disease risk<br>H. Salje*[1,2], D.A.T. Cummings[3,2], I. Rodriguez-Barraquer[4], *[1]Institut Pasteur, France, [2]Johns Hopkins, USA, [3]University of Florida, USA, [4]UCSF, USA* | **[O14.2] A novel Bayesian geostatistical method for estimating tuberculosis incidence reveals many missed TB cases in Ethiopia**<br>D. Shaweno*[1,3], J.M. Trauer[1,2], J.T. Denholm[3,4], E.S. McBryde[1,5], *[1]University of Melbourne, Australia, [2]Monash University, Australia, [3]Victorian Tuberculosis Program at the Peter Doherty Institute for Infection and Immunity, Australia, [4]University of Melbourne, Australia, [5]James* | **[O15.2] Vaccination-induced immunity versus antigenic distance in the transmission dynamics of H5N1 influenza viruses**<br>I. Sitaras*[1,2], B. Peeters[2], M.C.M. de Jong[1], *[1]Wageningen University and Research, The Netherlands, [2]Wageningen Bioveterinary Research, The Netherlands* |

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| | | *Cook University, Australia* |
| 14:40-15:00 | **[O13.3] Characterizing the extent and impact of dengue antigenic diversity** S.M. Bell*[1],[2], T. Bedford[1], *[1]Fred Hutch Cancer Research Center, USA, [2]University of Washington, USA* | **[O14.3] The R Epidemics Consortium: Building the next generation of statistical tools for outbreak response using R** T. Jombart, *Imperial College London, UK* | **[O15.3] Model-based projections of Zika virus infections to inform vaccine trial site selection** T.A. Perkins*[1], A.S. Siraj[1], S.M. Moore[1], C.M. Barker[2], R.C. Reiner[3], *[1]University of Notre Dame, USA, [2]University of California, USA, [3]University of Washington, USA* |
| 15:00-15:20 | **[O13.4] Transmission-recovery trade-offs indicate that dengue virulence evolution depends on epidemiological context** R. Ben-Shachar*[1], K. Koelle[2], *[1]UC Berkeley, USA, [2]Emory University, USA, [3]Duke University, USA* | **[O14.4] Using ensemble models to predict outbreaks of vector-borne disease** A.L. Buczak*, B. Baugher, L. Moniz, S. Babin, *Johns Hopkins University APL, USA* | **[O15.4] A method to quantify the impact of changes to an immunisation programme: Illustrative application to the UK routine childhood vaccine schedule** J. Panovska-Griffiths*[1],[2], S. Crowe[1], C. Pagel[1], G. Walker[3], G. Wooton[3], P. Grove[3], M. Utley[1], *[1]University College London, UK, [2]London School of Hygiene and Tropical Medicine, UK, [3]Department of Health, UK* |
| 15:20-15:40 | **[O13.5] Disentangling the relative roles of environmental conditions and importation in driving interannual variation in dengue epidemics in Guangzhou, China** R.J. Oidtman*[1], Z. Huang[2], S. Lai[2],[3], Y. Li[2], R.C. Reiner[4], A.J. Tatem[3],[5], H. Yu[2], T.A. Perkins[1], *University of Notre Dame, USA, [2]Center for Disease Control and Prevention, China, [3]University of Southampton, UK, [4]University of Washington, USA, [5]Flowminder Foundation, Sweden* | **[O14.5] Modelling outbreaks with a sub-exponential branching process** A.E. Zarebski*[1], R. Moss[1], P. Dawson[3], J.M. McCaw[1],[2], *[1]The University of Melbourne, Australia, [2]Murdoch Childrens Research Institute, Australia, [3]Defence Science and Technology Group, Australia* | **[O15.5] Harnessing big data to quantify vaccine hesitancy and the erosion of herd immunity** S. Goldlust, S.Bansal*, *Georgetown University, USA* |
| 15:40-16:00 | **[O13.6] Refining the characterization of a live attenuated tetravalent dengue vaccine's efficacy profile using machine learning** I. Dorigatti*[1], C.A. Donnelly[1], D. Laydon[1], R. Small[2], N. Jackson[3], L. Coudeville[3], N.M. Ferguson[1], *[1]Imperial College London, UK, [2]Sanofi Pasteur, USA, [3]Sanofi Pasteur, France* | **[O14.6] Scalable inference for epidemic models with individual level data** S.E.F. Spencer*, P. Touloupou, B. Finkenstadt Rand, *University of Warwick, UK* | **[O15.6] Containing Ebola at the source with vaccination strategies** M. Ajelli*[1],[2], S. Merler[2], K. Sun[1], L. Fumanelli[2], S. Parlamento[2], A. Pastore y Piontti[1], M. Chinazzi[1], N.E. Dean[3], G. Putoto[4], D. Carraro[4], *[1]Northeastern University, USA, [2]Bruno Kessler Foundation, Italy, [3]University of Florida, USA, [4]Doctors with Africa – CUAMM, Italy* |
| 16:00-16:20 | **Refreshment Break I** *Hall Auditorium & Hall Tramuntana* | | |

| Rooms | Auditorium | Tramuntana 1 | Tramuntana 2 |
|---|---|---|---|
| 16:20-17:40 | **Session 16: AMR 2**<br>*Session Chair:* Egil Fisher | **Session 17: Influenza serology**<br>*Session Chair:* Steven Riley | **Session 18: Control**<br>*Session Chair:* Thibaut Jombart |
| 16:20-16:40 | **[O16.1] Using models to understand how molecular mechanisms of resistance affect the risk of acquired drug resistance during treatment**<br>F. Clarelli*[1], L. Chindelevitch[2], B. Singh[1], T. Cohen[3], S. Abel[1], P. Abel zur Wiesch[1], *[1]UiT Arctic University of Norway, Norway, [2]Simon Fraser University, Canada, [3]Yale School of Public Health, USA* | **[O17.1] Structure of general-population antibody titer distributions to influenza A virus**<br>N.T.D. Nguyen*[1,6], S. Todd[1,2], M.F. Boni[1,3], E. de Bruin[4,5], M. Koopmans[4,5], H.T.V. Nguyen[1], T.N.T. Tran[1], T.L.T. Nguyen[1], V.V.C. Nguyen[1], S. Baker[1,6], *[1]Oxford University Clinical Research Unit, Vietnam, [2]Liverpool School of Tropical Medicine, UK, [3]Pennsylvania State University, USA, [4]Erasmus Medical Centre, The Netherlands, [5]National Institute for Public Health and the Environment, The Netherlands, [6]University of Oxford, UK* | **[O18.1] Modelling the potential of ivermectin treated cattle as a novel malaria vector control tool: Implications of killing zoophilic mosquitoes**<br>A. Dighe*, A. Ghani, H. Slater, *Imperial College London, UK* |
| 16:40-17:00 | **[O16.2] Estimating the proportion of bystander selection for antibiotic resistance in the US**<br>C. Tedijanto*[1], S. Olesen[1], C. Huttenhower[1], Y. Grad[1,2], M. Lipsitch[1], *[1]Harvard T.H. Chan School of Public Health, USA, [2]Brigham and Women's Hospital, Harvard Medical School, USA* | **[O17.2] Uncovering the epidemiological and immunological dynamics of influenza from serological data**<br>A.J. Kucharski*[1], J. Lessler[2], D.A.T. Cummings[3], S. Riley[4], *[1]London School of Hygiene & Tropical Medicine, UK, [2]Johns Hopkins University, USA, [3]University of Florida, USA, [4]Imperial College London, UK* | **[O18.2] Achieving global goals for schistosomiasis: Rapidly reaching the 2020 and 2025 goals for control and elimination of morbidity**<br>A.K. Deol*[1,2], F. Fleming[1], B. Calvo-Urbano[1], *[1]Imperial College London, UK, [2]Schistosomiasis Control Initiative, UK,* |
| 17:00-17:20 | **[O16.3] How competition shapes the dynamics of antimicrobial resistance**<br>T.C.M. Dewé*[1], C. Fraser[2], N.J. Croucher[1], *[1]Imperial College London, UK, [2]University of Oxford, UK* | **[O17.3] Serological measures of influenza incidence in the presence of secular trends in exposure and immuno-modulation of response**<br>T.M. Quandelacy*[1], D.A.T. Cummings[1,2], C.Q. Jiang[3], K.O. Kwok[4], S. Ruiyin[3], J.M. Read[5], H. Zhu[6,7], Y. Guan[6,7], S. Riley[8], J. Lessler[1], *[1]Johns Hopkins Bloomberg School of Public Health, USA, [2]University of Florida, USA, [3]Guangzhou No. 12 Hospital, China, [4]Chinese University of Hong Kong, Hong Kong, [5]Lancaster Medical School, Lancaster University, UK, [6]University of Hong Kong School of Public Health, Hong Kong, [7]Shantou University Medical College, China, [8]Imperial College London, UK* | **[O18.3] Wormy households: Modelling and inference of soil-transmitted helminthiasis transmission dynamics**<br>A. Bishop*[1], C. Holland[2], T. House[3], T.D. Hollingsworth[1], *[1]University of Warwick, UK, [2]Trinity College, Ireland, [3]University of Manchester, UK* |
| 17:20-17:40 | **[O16.4] Mechanisms that maintain coexistence of antibiotic sensitivity and resistance also promote high frequencies of multi-drug resistance**<br>S. Lehtinen*[1], J. Lees[4], F. Blanquart[2], N. Croucher[2], S. Bentley[4], P. Turner[5], M. Lipsitch[2], C. Fraser[1], *[1]University of Oxford, UK, [2]Imperial College London, UK, [3]Harvard University, USA, [4]Wellcome Trust Genome* | **[O17.4] Forecasting future influenza seasons: The importance of serology**<br>E. van Leeuwen*[1,2], K. Hoschler[1], R. Pebody[1], M. Zambon[1], S. Riley[2], M. Baguelin[1,3], *[1]Public Health England, UK, [2]Imperial College London, UK, [3]London School of Hygiene and Tropical Medicine, UK* | **[O18.4] Characteristics of Ebola virus disease transmission in Guinea: Impact of the *Ebola ça Suffit* trial**<br>A. Robert[1], W.J. Edmunds[1], C.H. Watson[1], A.M. Henao-Restrepo[2], P.S. Gsell[2], I.M. Longini[2,3], A.J. Kucharski[1], R.M. Eggo*[1], *[1]London School of Hygiene & Tropical Medicine, UK, [2]WHO, Switzerland, [3]University of* |

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| | *Campus, UK, [5]Angkor Hospital for Children, Cambodia* | | *Florida, USA* |
| 17:40-19:10 | **Poster Session 3 I** *Hall Auditorium & Hall Tramuntana* | | |
| 19:30-22:00 | **Conference Dinner – Ticket holders only** <br> *Location: Finca Mas Solers* | | |

<table>
<tr><td colspan="4" align="center"><b>Friday, 1st December 2017</b></td></tr>
<tr><td><b>Room</b></td><td colspan="3"><b><i>Auditorium</i></b>| <i>Session Chair:</i> Neil Ferguson</td></tr>
<tr><td>08:30-09:10</td><td colspan="3"><b>[PLN08] Bovine TB control in the UK – where to now for evidence-based policy?</b><br>Christl Donnelly, <i>Imperial College London, UK</i></td></tr>
<tr><td>09:10-09:50</td><td colspan="3"><b>[PLN09] The RAPIDD Ebola forecasting challenge: Synthesis and lessons Learnt</b><br>Cecile Viboud, <i>Fogarty International Center, USA</i></td></tr>
<tr><td>09:50-10:20</td><td colspan="3"><b>Refreshment Break I</b> <i>Hall Auditorium & Hall Tramuntana</i></td></tr>
<tr><td><b>Rooms</b></td><td><b><i>Auditorium</i></b></td><td><b><i>Tramuntana 1</i></b></td><td><b><i>Tramuntana 2</i></b></td></tr>
<tr><td>10:20-12:00</td><td><b>Session 19: Spatial and related structure</b><br><i>Session Chair:</i> Sebastian Funk</td><td><b>Session 20: Within host</b><br><i>Session Chair:</i> Don Klinkenberg</td><td><b>Session 21: Influenza 2</b><br><i>Session Chair:</i> Tim Bedford TBC</td></tr>
<tr><td>10:20-10:40</td><td><b>[O19.1] Image-based, network models of pathogens' spatial spread</b><br>G.A. Almogy*, L.S. Stone, <i>RMIT University, Australia</i></td><td><b>[O20.1] Using sequential infection experiments to quantify innate and adaptive immunity during influenza infection</b><br>A.W.C. Yan*[1], S.G. Zaloumis[1], J.A. Simpson[1], J.M. McCaw[1,2], <i>[1]The University of Melbourne, Australia, [2]Murdoch Childrens Research Institute, Australia</i></td><td><b>[O21.1] Influenza A virus transmission bottleneck size estimation from viral deep-sequencing data</b><br>A.S. Leonard*[1,2], D. Weissman[3], B. Greenbaum[4], E. Ghedin[5], K. Koelle[1,3], <i>[1]Duke University, USA, [2]Duke University School of Medicine, USA, [3]Emory University, USA, [4]Icahn School of Medicine at Mount Sinai, USA, [5]New York University, USA</i></td></tr>
<tr><td>10:40-11:00</td><td><b>[O19.2] Unravelling the spatial pattern of the chikungunya virus emergence in the Martinique Island: Implications for the management of emerging arboviruses</b><br>T. Vergne*[1], B. Cazelles[2], M. Etienne[3], B. Roche[1], <i>[1]Institut de Recherche pour le Développement, France, [2]Ecole Normale Supérieure, France, [3]Collectivité Territoriale de Martinique, France</i></td><td><b>[O20.2] Using a mathematical model to optimally select a live attenuated influenza vaccine</b><br>L. Matrajt*[1], M.E. Halloran[1,2], R. Antia[3], <i>[1]Fred Hutchinson Cancer Research Center, USA, [2]University of Washington, USA, [3]Emory University, USA</i></td><td><b>[O21.2] Reconstructing the antigenic evolution of influenza A/H3 viruses in multiple hosts</b><br>N.S. Trovao*[1,2], M.I. Nelson[2], T. Bedford[3], P. Lemey[4], <i>[1]Icahn School of Medicine at Mount Sinai, USA, [2]Fogarty International Center, National Institutes of Health, USA, [3]Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Center, USA, [4]University of Leuven, Belgium</i></td></tr>
<tr><td>11:00-11:20</td><td><b>[O19.3] Geospatial Characteristics of Measles Transmission in China during 2005−2014</b><br>W. Yang*[1], L. Wen[2], S-L. Li[1], K. Chen[3], W-Y. Zhang[2], J. Shaman[1], <i>[1]Columbia University, USA, [2]Academy of Military Medical Sciences, China, [3]Nanjing University, China</i></td><td><b>[O20.3] Infectious reactivation of cytomegalovirus explaining age- and sex-specific patterns of seroprevalence</b><br>M. van Boven*[1], J. van de Kassteele[1], M.J. Korndewal[1,2], C.H. van Dorp[1,3], M. Kretzschmar[1], F. van der Klis[1], H.E. de Melker[1], A.C. Vossen[2], <i>[1]National Institute for Public Health, The Netherlands, [2]Leiden University Medical Center, The Netherlands, [3]Utrecht University, The Netherlands</i></td><td><b>[O21.3] Contrasting the geographic transmission of seasonal and pandemic influenza in the United States using a gravity-based model</b><br>S.M. Kissler*[1], C. Viboud[2], V. Charu[3], O.N. Bjørnstad[4], L. Simonsen[5], B.T. Grenfell[6], J.R. Gog[1], <i>[1]University of Cambridge, UK, [2]National Institutes of Health, USA, [3]Johns Hopkins Bloomberg School of Public Health, USA, [4]Pennsylvania State University, USA, [5]University of Copenhagen, Denmark, [6]Princeton University, USA</i></td></tr>
<tr><td>11:20-11:40</td><td><b>[O19.4] Extending household models to endemic settings</b><br>J.B. Hilton*, M.J.</td><td><b>[O20.4] Understanding the measles paradox: Modeling the impact of viral infection on the host immune</b></td><td><b>[O21.4] Minimum-path work-commute distance and the spatial spread of influenza</b></td></tr>
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| | Keeling, *University of Warwick, UK* | system<br>S.E. Morris[*1], A.N. Nelson[2], R.D. Kouyos[3], W-H. Lin[4], M.J. Mina[5], R.L. de Swart[6], A.J. Yates[7], D.E. Griffin[2], B.T. Grenfell[1], *[1]Princeton University, USA, [2]Johns Hopkins University, USA, [3]University Hospital Zurich, Switzerland, [4]Columbia University, USA, [5]Harvard Medical School, USA, [6]Erasmus Medical Center, The Netherlands, [7]University of Glasgow, UK* | V. Charu[1], S. Zeger[2], J. Gog[3 ,1], O. Bjornstad[4 ,1], S. Kissler[3], L. Simonsen[5 ,1], B. Grenfell[6 ,1], C. Viboud[*1], *[1]National Institutes of Health, USA, [2]Johns Hopkins University, USA, [3]University of Cambridge, UK, [4]Pennsylvania State University, USA, [5]Copenhagen University, Denmark, [6]Princeton University, USA* |
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| 11:40-12:00 | **[O19.5] The effects of metapopulation structure on fine-scale mosquito population dynamics and potential consequences for the transmission dynamics of dengue and malaria**<br>C. McCormack*, A.C. Ghani, N.M. Ferguson, *Imperial College London, UK* | **[O20.5] Capturing the roles of cellular coinfection and viral complementation in the within-host dynamics of influenza**<br>K. Koelle[*1], R. Ke[2], C. Brooke[3], *[1]Emory University, USA, [2]North Carolina State University, USA, [3]University of Illinois at Urbana-Champaign, USA* | **[O21.5] Integrating dynamical modelling and phylogeographic inference to uncover the drivers of global influenza circulation**<br>C. Poletto[*1], T. Bedford[2], M. Suchard[3], V. Colizza[1 ,4], P. Lemey[5], *[1]INSERM, France, [2]Fred Hutchinson Cancer Research Center, USA, [3]University of California, USA, [4]ISI Foundation, Italy, [5]University of Leuven, Belgium* |
| **Room** | *Auditorium* | *Session Chair:* Neil Ferguson | | |
| 12:00-12:10 | **Launch of WHO's modelling network for epidemic and pandemic preparedness and response**<br>Nahoko Shindo, *WHO* | | |
| 12:10-12:50 | **[PLN10] Co-infections of multiple antigenically distinct lineages of Influenza B**<br>Derek Cummings, *University of Florida, USA* | | |
| 12:50-13:00 | **Conference Closing** | | |