

Oral Program

Tuesday, 1 December 2015

11:00-13:00	Short Course Registration <i>Grand Ballroom Foyer</i>
13:00-17:30	Short Course <i>Salon G</i>
17:00-19:00	Registration <i>Grand Ballroom Foyer</i>
19:00-20:30	Welcome Reception & Poster Viewing <i>Salons A-D, Grand Ballroom Foyer, Citrus and Mangrove</i>
Room	Salons EFG Session Chair: Ira Longini
20:30-21:10	[PLN01] Malaria per se and malaria suppression v. malaria modeling B. Singer, <i>University of Florida, USA</i>

Wednesday, 2 December 2015

07:30-08:30	Registration <i>Grand Ballroom Foyer</i>		
Room	Salons EFG Session Chair: Hans Heesterbeek		
08:30-08:40	Welcome & Opening Remarks by Conference Chairs		
08:40-09:10	[PLN02] Interim results from the Guinea ring vaccination cluster-randomised trial A.M. Henao-Restrepo ^{*1} , I. Longini ² , M. Egger ³ , N.E. Dean ² , ¹ <i>World Health Organization, Switzerland</i> , ² <i>University of Florida, USA</i> , ³ <i>University of Bern, Switzerland</i>		
09:10-09:50	[PLN03] The state of the world's antibiotics R. Laxminarayan, <i>Center for Disease Dynamics, USA</i>		
09:50-10:30	[PLN04] Big Data in infectious disease dynamics M.A. Suchard, <i>University of California, Los Angeles, USA</i>		
10:30-11:10	[PLN05] Analysis of influenza a epidemiology through community-based studies B Cowling, <i>The University of Hong Kong, Hong Kong</i>		
11:10-11:40	Refreshment Break <i>Salons A-D, Grand Ballroom Foyer</i>		
Rooms	Salon E	Salon F	Salon G
11:40-13:00	Session 1: Influenza 1 <i>Session Chair: Cécile Viboud</i>	Session 2: HIV <i>Session Chair: Sebastian Bonhoeffer</i>	Session 3: Modelling Tools 1 <i>Session Chair: Mick Roberts</i>
11:40-12:00	[O1.1] Deep sequencing of influenza A virus from a human challenge study yields insight into the size of influenza's transmission bottleneck and the tempo of within-host viral evolution A. Sobel*, M. McClain, C. Woods, K. Koelle, <i>Duke University, USA</i>	[O2.1] Increasing heritability of Set-Point Viral Load in the HIV epidemic in Europe F. Blanquart ^{*1} , C. Wymant ¹ , M. Cornelissen ² , A. Gall ³ , C. Fraser ¹ et al ¹ <i>Imperial College London, UK</i> , ² <i>University of Amsterdam, The Netherlands</i> , ³ <i>Wellcome Trust Genome Campus, UK</i>	[O3.1] On the extinction probability in models of within-host infection: The role of latency and immunity A.W.C. Yan ^{*1} , P. Cao ¹ , J.M. McCaw ^{1,2} , ¹ <i>The University of Melbourne, Australia</i> , ² <i>Murdoch Childrens Research Institute, Australia</i>
12:00-12:20	[O1.2] High global burden and frequency of influenza H3N2 intra-subtype reassortment: Attributes and implications of reassortant spread I. Maljkovic Berry ^{*1} , M.C. Melendrez ¹ , A.W. Hawksworth ² , G.T. Brice ² , P.J. Blair ² , E.S. Halsey ³ , M. Williams ³ , S. Fernandez ⁴ , I.K. Yoon ⁴ , L. Edwards ⁵ , R. Kuschner ¹ , X. Lin ¹ , S.J. Thomas ¹ , R.G. Jarman ¹ et al, ¹ <i>Walter Reed Army Institute of Research, USA</i> , ² <i>Naval Health Research Center, USA</i> , ³ <i>US Naval Medical Research Unit -6, Peru</i> , ⁴ <i>Armed Forces Research Institute of Medical Sciences, Thailand</i> , ⁵ <i>US Department of State, USA</i>	[O2.2] Decomposing HIV virulence: Heritability of setpoint virus load, CD4+ T cell decline and per-pathogen pathogenicity F. Bertels ¹ , A. Marzel ² , G. Leventhal ¹ , J. Fellay ³ , H. Guenthardt ² , V. Müller ⁴ , S. Bonhoeffer ¹ , R. Kouyos ² , R.R. Regoes ^{*1} , ¹ <i>ETH Zurich, Switzerland</i> , ² <i>University Hospital Zurich, Switzerland</i> , ³ <i>École Polytechnique Fédérale de Lausanne, Switzerland</i> , ⁴ <i>Eötvös Loránd University, Hungary</i>	[O3.2] Little r: An under-rated epidemiological parameter J. Dushoff ^{*1} , S. Bellan ² , ¹ <i>McMaster University, Canada</i> , ² <i>University of Texas, USA</i>

12:20-12:40	[O1.3] The Possible impact of vaccination for seasonal influenza on emergence of pandemic Influenza via reassortment X-S. Zhang* ^{1,2} , R. Pebody ¹ , D. De Angelis ^{1,3} , P.J. White ^{1,2} , A. Charlett ¹ , J.W. McCauley ⁴ , ¹ Public Health England, UK, ² Imperial College, UK, ³ MRC Biostatistics Unit, Cambridge, UK, ⁴ MRC National Institute for Medical Research, Mill Hill, UK	[O2.3] Effect of the latent reservoir on the evolution of HIV at the within- and between-host levels H.M. Doekes ¹ , C. Fraser ² , K.A. Lythgoe* ^{2,3} , ¹ Utrecht University, The Netherlands, ² Imperial College London, UK, ³ University of Oxford, UK	[O3.3] Estimating finite-population reproductive numbers in heterogeneous populations L.T. Keegan*, J. Dushoff, McMaster University, Canada
12:40-13:00	[O1.4] The roles of innate and adaptive immunity in controlling influenza infection J.M. McCaw* ¹ , P. Cao ¹ , A.W.C. Yan ¹ , K. Laurie ² , ¹ University of Melbourne, Australia, ² WHO Collaborating Centre for Reference and Research on Influenza at the Peter Doherty Centre, Australia	[O2.4] Genetic diversity of HIV reveals the epidemiological role of high risk groups in Nigeria E.M. Volz* ¹ , R. Nowak ² , N. Ndembu ³ , G. Kijak ⁴ , S. Baral ⁵ , W. Blattner ² , M. Charurat ² , ¹ Imperial College London, UK, ² University of Maryland School of Medicine, USA, ³ Institute of Human Virology Nigeria, Nigeria, ⁴ U.S. Military HIV Research Program and Henry M. Jackson Foundation, USA, ⁵ Johns Hopkins University Bloomberg School of Public Health, USA	[O3.4] Estimating the effective reproductive number for a novel viral pathogen using a stochastic compartmental model C. Zimmer* ¹ , R. Yaesoubi ² , T. Cohen ² , ¹ Brigham and Women's Hospital, USA, ² Yale School of Public Health, USA
13:00-14:00	Lunch I Salons A-D, Grand Ballroom Foyer		
13:00-14:00	Author Workshop I Salon G		
Rooms	Salon E	Salon F	Salon G
14:00-15:40	Session 4: Influenza 2 Session Chair: Joseph Wu	Session 5: Malaria Session Chair: Azra Ghani	Session 6: Modelling Tools 2 Session Chair: Don Klinkenberg
14:00-14:20	[O4.1] Inference of seasonal and pandemic influenza transmission dynamics W. Yang* ¹ , M. Lipsitch ² , J. Shaman ¹ ¹ Columbia University, USA, ² Harvard School of Public Health, USA	[O5.1] Variation in relapse frequency and the transmission potential of <i>Plasmodium vivax</i> malaria M. White* ¹ , G. Shirreff ¹ , S. Karl ^{2,3} , A. Ghani ¹ , I. Mueller ^{2,3} , ¹ Imperial College London, UK, ² Walter and Eliza Hall Institute, Australia, ³ University of Melbourne, Australia	[O6.1] Beyond endemicity: Taxonomizing the epidemic dynamics of cholera and measles J. Lessler*, S.M. Moore, M. Graham, A.S. Azman, H.S. McKay, Johns Hopkins Bloomberg School of Public Health, USA
14:20-14:40	[O4.2] Influenza spatial diffusion varies with age patterns of infection and antigenic novelty V. Charu ^{1,2} , S. Zeger ² , J. Gog ^{3,1} , O. Bjornstad ^{4,1} , S. Kissler ³ , F. Khan ⁵ , L. Simonsen ^{6,1} , B. Grenfell ^{7,1} , C. Viboud* ¹ , ¹ Fogarty International Center, NIH, USA, ² Johns Hopkins University, USA, ³ University of Cambridge, UK, ⁴ Pennsylvania State University, USA, ⁵ IMS Health, USA, ⁶ George Washington University, USA, ⁷ Princeton University, USA	[O5.2] Understanding the historical spread of antimalarial resistance in Africa L.C. Okell* ¹ , J.T. Griffin ¹ , H. Slater ¹ , A.C. Ghani ¹ , C. Roper ² , ¹ Imperial College London, UK, ² London School of Hygiene & Tropical Medicine, UK	[O6.2] The influence of seasonal drivers on the predictability of measles dynamics Q. Caudron* ¹ , J.C.E. Metcalf ¹ , M. Gottfredsson ² , B.T. Grenfell ¹ , ¹ Princeton University, USA, ² University of Iceland, Iceland

14:40-15:00	<p>[O4.3] Spatiotemporal patterns in age structure in the 2009 influenza pandemic in the US S.M. Kissler*¹, J.R. Gog^{1,3}, C. Viboud³, V. Charu^{3,4}, O. Bjornstad⁵, L. Simonsen^{3,6}, B.T. Grenfell^{2,3}, ¹University of Cambridge, UK, ²Princeton University, USA, ³National Institutes of Health, USA, ⁴Johns Hopkins Bloomberg School of Public Health, USA, ⁵Pennsylvania State University, USA, ⁶George Washington University, USA</p>	<p>[O5.3] Synergistic and antagonistic interactions between bed-nets and vaccines in the control of malaria Y. Artzy-Radrup*^{1,2}, A. Dobson^{3,4}, M. Pascual^{1,4}, ¹University of Michigan, USA, ²University of Amsterdam, The Netherlands, ³Princeton University, USA, ⁴Santa Fe Institute, USA, ⁵University of Chicago, USA</p>	<p>[O6.3] Assessing the promise of tolerance-based therapy N. Hoze*, S. Bonhoeffer, R.R. Regoes, <i>ETH Zurich, Switzerland</i></p>
15:00-15:20	<p>[O4.4] Heterogeneous shedding of influenza by human subjects and its implications for control L. Canini*¹, M.E.J. Woolhouse¹, T.R. Maines², F. Carrat^{3,4}, ¹University of Edinburgh, UK, ²Centers for Disease Control and Prevention, USA, ³INSERM, France, ⁴UPMC University Paris 06, France</p>	<p>[O5.4] Modeling the dynamics of immunological memory to malaria L.M. Childs*, C.O. Buckee, <i>Harvard T. H. Chan School of Public Health, USA</i></p>	<p>[O6.4] Employing simple mathematical models of within-host viral dynamics to improve the design of clinical trials of novel immunotherapies against influenza A C. Hadjichrysanthou*, E. Cauet, C. Vegvari, E. Lawrence, F. de Wolf, R.M. Anderson, <i>Imperial College London, UK</i></p>
15:20-15:40	<p>[O4.5] Mitigating pandemic influenza: An assessment of England's National Pandemic Flu Service phone- & internet-based patient assessment and antiviral distribution system in the 2009 influenza A/H1N1 pandemic P.J. White*^{1,2}, P. Pelosse^{1,2}, A. Charlett¹, T. Nichols¹, R. Pebody¹, N.M. Ferguson², ¹Public Health England, UK, ²Imperial College London, UK</p>	<p>[O5.5] On the mechanisms of artemisinin action in plasmodium falciparum clearance P. Cao*¹, S. Zaloumis¹, J.A. Simpson¹, J.M. McCaw^{1,2}, ¹University of Melbourne, Australia, ²Murdoch Childrens Research Institute, Australia</p>	<p>[O6.5] The impact of dose-dependence on disease spread J.C. Miller*¹, Y. Grad², M. Lipsitch², ¹Monash University, Australia, ²Harvard School of Public Health, USA</p>
15:40-16:10	Refreshment Break I Salons A-D, Grand Ballroom Foyer		
Rooms	Salon E	Salon F	Salon G
16:10-17:50	<p>Session 7: Phylodynamics 1 <i>Session Chair: Thibaut Jombart</i></p>	<p>Session 8: Dengue <i>Session Chair: Katia Koelle</i></p>	<p>Session 9: Vaccination 1 <i>Session Chair: Elizabeth Halloran</i></p>
16:10-16:30	<p>[O7.1] Real-time evolutionary forecasting for influenza vaccine strain selection T. Bedford*¹, R.A. Neher¹, ¹Fred Hutchinson Cancer Research Center, USA, ²Max Planck Institute for Developmental Biology, Germany</p>	<p>[O8.1] Assessing the dynamics of within-host interactions between dengue serotypes using individual-level longitudinal serological data R.C. Reiner*^{1,2}, S.T. Stoodard^{1,3}, B.M. Forshey⁴, C. Guevara⁵, R. Hontz⁵, E.S. Halsey⁵, A. Morrison³, T.J. Koche⁵, T.W. Scott^{1,3}, ¹Fogarty International Center, USA, ²Indiana University School of Public Health, USA, ³University of California, USA, ⁴US Department of Defense, USA, ⁵US Naval Medical Research Unit No. 6, Peru</p>	<p>[O9.1] Can measles elimination be maintained? Inferring impact of measles vaccination campaigns with realistic demographic and epidemiological settings J. Prada*¹, C.J.E. Metcalf¹, S. Takahashi¹, J. Lessler³, A. Tatem⁴, M. Ferrari², ¹Princeton University, USA, ²Pennsylvania State University, USA, ³Johns Hopkins, USA, ⁴University of Southampton, UK</p>

16:30-16:50	[O7.2] Phylogenetic modelling of temporal heterogeneity in the circulation of human influenza lineages N. Sequeira Trovão* ¹ , G. Baele ¹ , F. Bielejec ¹ , M.A. Suchard ² , P. Lemey ¹ ¹ KU Leuven, Belgium, ² University of California, USA	[O8.2] Statistical fits to within-host dengue models provide insight into processes driving variation in viral load patterns R. Ben-Shachar*, K. Koelle, <i>Duke University, USA</i>	[O9.2] Did large-scale vaccination drive changes in the circulating rotavirus population in Belgium? V.E. Pitzer* ^{1,2} , J. Bilcke ³ , E. Heylen ⁴ , F.W. Crawford ¹ , M. Callens ⁵ , F. De Smet ^{4,5} , M. Van Ranst ⁴ , M. Zeller ⁴ , J. Matthijssens ⁴ , ¹ Yale School of Public Health, USA, ² Fogarty International Center, National Institutes of Health, USA, ³ University of Antwerp, Belgium, ⁴ KU Leuven - University of Leuven, Belgium, ⁵ National Alliance of Christian Sickness Funds, Belgium
16:50-17:10	[O7.3] Ecological factors shaping the phylogeography of influenza F. Wen* ¹ , T. Bedford ² , S. Cobey ¹ , ¹ University of Chicago, USA, ² Fred Hutchinson Cancer Research Center, USA	[O8.3] Forecasting for decision-making: The Dengue Forecasting Project experience M.A. Johansson* ^{1,2} , J.P. Chretien ³ , D.B. George ⁴ , ¹ Centers for Disease Control and Prevention, USA, ² Harvard TH Chan School of Public Health, USA, ³ Armed Forces Health Surveillance Center, USA, ⁴ White House Office of Science and Technology Policy, USA	[O9.3] The impact of vaccination programmes on mortality burden among children and young adults in the Netherlands over the 20th century M. van Wijhe* ^{1,2} , S. McDonald ¹ , H. de Melker ¹ , M.J. Postma ² , J. Wallinga ¹ , ¹ National Institute for Public Health and the Environment, The Netherlands, ² University of Groningen, The Netherlands
17:10-17:30	[O7.4] Algorithms linking phylogenetic and transmission trees for molecular infectious disease epidemiology E. Kenah* ¹ , T. Britton ² , M.E. Halloran ^{3,4} , I.M. Longini ¹ , ¹ University of Florida, USA, ² Stockholm University, Sweden, ³ Fred Hutchinson Cancer Research Center, USA, ⁴ University of Washington, USA	[O8.4] Dengue dynamics in rural Cambodia: Comparing hypothesis through epidemiologic mechanistic model selection C. Champagne ¹ , D.G. Salthouse ¹ , S. Ly ² , V. Duong ² , P. Buchy ² , A. Tarantola ² , B. Cazelles* ^{1,3} , ¹ IBENS, France, ² Institut Pasteur du Cambodge, Cambodia, ³ UMMISCO, France	[O9.4] Accounting for response timing in the deployment of reactive oral cholera vaccines C.M. Peak* ¹ , A. Hill ² , L. Ganda ³ , D. Legros ² , C.O. Buckee ¹ , ¹ Harvard T.H. Chan School of Public Health, USA, ² World Health Organization, Switzerland, ³ World Health Organization, Sierra Leone
17:30-17:50	[O7.5] Quantifying the effect of public health interventions on the spread of ebola virus disease using phylodynamic methods L. du Plessis*, T. Stadler, <i>ETH Zürich, Switzerland</i>	[O8.5] Evidence for transmission enhancement in incidence patterns of dengue in Thailand H.E. Clapham* ¹ , N. Reich ² , K. Sakrejda ² , I. Yoon ³ , L. Macareo ³ , A. Nisalak ³ , J. Lessler ¹ , D.A.T. Cummings ¹ , ¹ Johns Hopkins School of Public Health, USA, ² University of Massachusetts, USA, ³ AFRIMS, Thailand	[O9.5] Stopping silent polio circulation before stopping oral polio vaccine use J.S. Koopman*, M.C. Eisenberg, C.J. Henry, J.H. Park, D.W. Hutton, J.N. Eisenberg, E.L. Ionides, <i>University of Michigan, USA</i>
17:50-19:30	Poster Session 1 Salons A-D, Grand Ballroom Foyer, Citrus and Mangrove		
Thursday, 3 December 2015			
Room	Salons EFG Session Chair: Neil Ferguson		
08:30-09:10	[PLN06] Evaluating interventions to reduce malaria transmission: The role of mathematical modelling to guide policy A. Ghani, <i>Imperial College London, UK</i>		
09:10-09:50	[PLN07] Achieving the 2020 goals for neglected tropical diseases D. Hollingsworth, <i>University of Warwick, UK</i>		
09:50-10:30	[PLN08] What multi-level selection (and microcosm man) might tell us about the evolution of pathogens P.B. Rainey ¹ , ¹ Massey University, New Zealand, ² Max Planck Institute for Evolutionary Biology, Germany		
10:30-11:00	Refreshment Break I Salons A-D, Grand Ballroom Foyer		

Rooms	Salon E	Salon F	Salon G
11:40-12:40	Session 10: Ebola 1 <i>Session Chair: Ira Longini</i>	Session 11: Phylodynamics 2 <i>Session Chair: Trevor Bedford</i>	Session 12: Transm. Dynamics <i>Session Chair: Justin Lessler</i>
11:00-11:20	[O10.1] Heterogeneities in CFR in the Ebola outbreak in West Africa T. Garske* ¹ , WHO Ebola Response Team ² , ¹ Imperial College London, UK, ² World Health Organization, Switzerland This is the first of a connected series of three talks	[O11.1] Phylodynamic inference of sexual contact network structure D.A. Rasmussen*, T. Stadler, <i>ETH Zurich, Switzerland</i>	[O12.1] Evaluating spatial interaction models to regional mobility for directly transmitted and vector-borne disease dynamics A. Wesolowski* ¹ , W. Prudhomme O'Meara ² , N. Eagle ¹ , A.J. Tatem ³ , C.O. Buckee ¹ ¹ Harvard School of Public Health, USA, ² Duke University, USA, ³ University of Southampton, UK
11:20-11:40	[O10.2] The role of rapid diagnostics in managing Ebola epidemics P. Nouvellet* ¹ , T. Garske ¹ , H. Mills ¹ , G. Nedjati-Gilani ¹ , W. Hinsley ¹ , I.M. Blake ¹ , M.D. Van Kerkhove ^{1,2} , A. Cori ¹ , I. Dorigatti ¹ , T. Jombart ¹ et al ¹ Imperial College London, UK, ² Institute Pasteur, France This is the second of a connected series of three talks	[O11.2] Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant <i>Staphylococcus aureus</i> H-H. Chang* ¹ , J. Dordel ^{2,3} , T. Donker ⁴ , C. Worby ¹ , W.P. Hanage ¹ , S.D. Bentley ² , S.S. Huang ⁵ , M. Lipsitch ¹ , ¹ Harvard T.H. Chan School of Public Health, USA, ² The Wellcome Trust Sanger Institute, UK, ³ Drexel University, USA, ⁴ University of Groningen, The Netherlands, ⁵ University of California Irvine School of Medicine, USA	[O12.2] Chance and transmission in vector-borne diseases S.P.C. Brand*, K.S. Rock, M.J. Keeling, <i>University of Warwick, UK</i>
11:40-12:00	[O10.3] Contact patterns driving Ebola transmission in West Africa I.M. Blake ¹ , A. Cori* ¹ , H.L. Mills ¹ , W.H.O. Ebola response team ² , ¹ Imperial College London, UK, ² World Health Organization, Switzerland This is the third of a connected series of three talks	[O11.3] Testing degree distributions in HIV phylogenetic clusters B.L. Dearlove*, F. Xiang, S.D.W. Frost, <i>University of Cambridge, UK</i>	[O12.3] Estimating the number of dengue transmission chains circulating in Bangkok using spatial and genetic data H. Salje* ^{1,2} , R. Jarman ⁴ , J. Lessler ¹ , M. Melendrez ⁴ , I. Maljkovic ⁴ , A. Nisalak ³ , L. Macareo ³ , I-K. Yoon ³ , D.A.T. Cummings ⁵ , ¹ Johns Hopkins University, USA, ² Institut Pasteur, France, ³ AFRIMS, Thailand, ⁴ Walter Reed Army Institute of Research, USA, ⁵ University of Florida, USA
12:00-12:20	[O10.4] Characterizing epidemic growth patterns during the Ebola epidemic in West Africa G. Chowell* ^{1,2} , C. Viboud ² , J.M. Hyman ³ , L. Simonsen ⁴ , ¹ Georgia State University, USA, ² National Institutes of Health, USA, ³ Tulane University, USA, ⁴ George Washington University, USA	[O11.4] Statistical inference of <i>Plasmodium falciparum</i> malaria transmission networks based jointly on epidemiological and genetic data A. Perkins* ¹ , R. Nielsen ² , D. Smith ^{3,4} , B. Greenhouse ⁵ , ¹ University of Notre Dame, USA, ² University of California, Berkeley, USA, ³ University of Oxford, UK, ⁴ Sanaria Institute for Global Health and Tropical Medicine, USA, ⁵ University of California, San Francisco, USA	[O12.4] The role of demography in shaping inter-country differences in epidemiological patterns of measles F. Trentini* ¹ , P. Poletti ^{1,2} , A. Melegaro ¹ , ¹ Bocconi University, Italy, ² Bruno Kessler Foundation, Italy

12:20-12:40	[O10.5] Impact of spatial dispersion, evolution, and selection on Ebola Zaire Virus epidemic waves T. Azarian ¹ , A. Lo Presti ² , M. Giovanetti ² , E. Cella ^{1,2} , B. Rife ¹ , A. Lai ³ , G. Zehender ³ , M. Ciccozzi ^{2,4} , M. Salemi* ¹ , ¹ University of Florida, Gainesville, USA, ² Istituto Superiore di Sanità, Rome, Italy, ³ University of Milan, Milan, Italy, ⁴ University Hospital Campus Bio-Medico, Italy	[O11.5] Livestock disease transmission pattern inference using integrated phylodynamics S. Lycett* ¹ , G. Russell ² , R. Zadoks ^{2,3} , R. Kao ³ , ¹ University of Edinburgh, UK, ² Moredun Research Institute, UK, ³ University of Glasgow, UK	[O12.5] Opportunities for managing risks in the polio eradication endgame K.M. Thompson*, R.J. Duintjer Tebbens, <i>Kid Risk, Inc., USA</i>
12:40-14:00	Lunch I Salons A-D, Grand Ballroom Foyer		
Rooms	Salon E	Salon F	Salon G
14:00-16:00	Session 13: Ebola 2 Session Chair: Anne Cori	Session 14: Social structure Session Chair: Shweta Bansal	Session 15: Zoonoses & Vet. Session Chair: Simon Gubbins
14:00-14:20	[O13.1] Analysis of an Ebola vaccine trial using a ring vaccination design in Guinea, West Africa N.E. Dean*, I.M. Longini, <i>University of Florida, USA</i>	[O14.1] Accurate epidemic predictions: how much social structure do we need? L. Pellis* ¹ , S. Cauchemez ² , N.M. Ferguson ³ , C. Fraser ³ , ¹ University of Warwick, UK, ² Institute Pasteur, France, ³ Imperial College London, UK	[O15.1] Pigs and pandemics: the evolutionary dynamics of influenza A viruses in swine M.I. Nelson* ¹ , C. Viboud ¹ , P. Lemey ² , A.L. Vincent ³ , ¹ National Institutes of Health, USA, ² KU-Leuven University, Belgium, ³ United States Department of Health, USA
14:20-14:40	[O13.2] Measuring the impact of Ebola control measures in Sierra Leone A.J. Kucharski*, A. Camacho, S. Flasche, R. Glover, W.J. Edmunds, S. Funk, <i>London School of Hygiene & Tropical Medicine, UK</i>	[O14.2] Forecasting seasonal influenza with dynamic models assimilating digital social data Q. Zhang* ¹ , N. Perra ¹ , A. Vespignani ^{1,2} , ¹ Northeastern University, USA, ² ISI Foundation, Italy	[O15.2] A comparative and computational study of population structure and pathogen richness in bats T.C.D. Lucas*, H.M. Wilkinson-Herbots, K.E. Jones, <i>University College London, UK</i>
14:40-15:00	[O13.3] Spatiotemporal spread of the 2014 Ebola epidemic in Liberia and the effectiveness of non-pharmaceutical interventions S. Merler ¹ , M. Ajelli ¹ , L. Fumanelli ¹ , M.F.C. Gomes ² , A. Pastore y Piontti* ² , L. Rossi ³ , D.L. Chao ⁴ , I.M. Longini ⁵ , M.E. Halloran ^{4,6} , A. Vespignani ^{2,7} , ¹ Bruno Kessler Foundation, Italy, ² Northeastern University, USA, ³ Scientific Interchange Foundation, Italy, ⁴ Fred Hutchinson Cancer Research Center, USA, ⁵ University of Florida, USA, ⁶ University of Washington, USA, ⁷ Harvard University, USA	[O14.3] Estimating the contribution of asymptomatic infection using social contact data E. Santermans* ¹ , K. Van Kerckhove ¹ , A. Azmon ² , K.T.D. Eames ³ , P. Beutels ⁴ , W.J. Edmunds ³ , N. Hens ^{1,4} , ¹ Hasselt University, Belgium, ² Novartis Pharma AG, Switzerland, ³ London School of Hygiene & Tropical Medicine, UK, ⁴ University of Antwerp, Belgium	[O15.3] The multi-strain dynamics of avian influenza in live bird markets A. Pinsent* ¹ , K.M. Pepin ² , M.T. White ¹ , H. Zhu ^{3,4} , Y. Guan ^{3,4} , S. Riley ¹ , ¹ Imperial College London, UK, ² National Wildlife Research Center, USA, ³ Shantou University Medical College, China, ⁴ The University of Hong Kong, Hong Kong
15:00-15:20	[O13.4] Spatial analysis of Ebola virus outbreak in West Africa: Transmission patterns within and between countries J.A. Backer*, J. Wallinga, <i>RIVM, The Netherlands</i>	[O14.4] Estimating seasonal influenza dynamics with 2.7 billion geo-tagged tweets T.J. Bodnar ¹ , M. Salathe* ^{1,2} , ¹ Penn State University, USA, ² EPFL, Switzerland	[O15.4] Host phylogenetic distance and viral host breadth predict zoonotic viral spillover from mammals K.J. Olival*, P.R. Hosseini, T.L. Bogich et al, <i>EcoHealth Alliance, USA</i>

15:20-15:40	<p>[O13.5] Evaluating classic epidemiological methods, mathematical modeling and phylodynamic analyses to infer the transmission dynamics of Ebola virus disease C.L. Althaus*¹, R.R. Regoes², T. Stadler², ¹University of Bern, Switzerland, ²ETH Zurich, Switzerland</p>	<p>[O14.5] Tracking social contact networks with online respondent-driven detection M.L. Stein*^{1,2}, P.G.M. van der Heijden^{3,4}, V. Buskens³, J.E. van Steenberghe^{2,5}, L. Bengtsson^{6,7}, C.E. Koppeschaar⁸, A. Thorson⁶, M.E.E. Kretzschmar^{1,2}, ¹University Medical Center Utrecht, The Netherlands, ²National Institute for Public Health and the Environment, The Netherlands, ³University Utrecht, The Netherlands, ⁴University of Southampton, UK, ⁵Leiden University Medical Centre, The Netherlands, ⁶Karolinska Institutet, Sweden, ⁷Flowminder Foundation, Sweden, ⁸Science in Action BV, The Netherlands</p>	<p>[O15.5] Spread and control of enzootic cattle diseases: A data-driven multiscale modelling framework to prioritize complex regional strategies P. Ezanno*¹, G. Beaunée^{1,2}, B.L. Dutta^{1,2}, P. Pandit¹, T. Hoch¹, F. Beaudeau¹, E. Vergu², ¹LUNAM Université, France, ²INRA, France</p>
15:40-16:00	<p>[O13.6] Detecting changes in community transmission of Ebola in Lofa County, Liberia S. Funk*¹, B. Reeder², A. Camacho¹, R.M. Eggo¹, A.J. Kucharski¹, W.J. Edmunds¹, ¹London School of Hygiene & Tropical Medicine, UK, ²University of Saskatchewan, Canada</p>	<p>[O14.6] Socio-spatial human behaviour and the transmission of respiratory infections J.M. Read*^{1,2}, H.L. Mills³, J. Lessler¹, L.J. Tan⁵, K.O. Kwok⁶, Y. Guan^{6,7}, C.Q. Jiang⁵, S. Riley³, ¹University of Liverpool, UK, ²University of Lancaster, UK, ³Imperial College, UK, ⁴Johns Hopkins Bloomberg School of Public Health, USA, ⁵Guangzhou Hospital Number 12, China, ⁶Hong Kong University, Hong Kong, ⁷Shantou University, China</p>	<p>[O15.6] Supershedders not so super? Linking supershedding to transmission for Escherichia coli O157:H7 in feedlot cattle S.E.F. Spencer*¹, T.E. Besser², R. Cobbold³, N.P. French⁴, ¹University of Warwick, UK, ²Washington State University, USA, ³University of Queensland, Australia, ⁴Massey University, New Zealand</p>
16:00-16:20	Refreshment Break I Salons A-D, Grand Ballroom Foyer		
Rooms	Salon E	Salon F	Salon G
16:20-17:40	<p>Session 16: Ebola 3 Session Chair: Sebastian Funk</p>	<p>Session 17: Statistical Methods 1 Session Chair: Simon Cauchemez</p>	<p>Session 18: Vaccination 2 Session Chair: Michiel van Boven</p>
16:20-16:40	<p>[O16.1] The 2014 EVD outbreak in Pujehun, Sierra Leone: Insights for epidemic containment at the source S. Parlamento¹, M. Ajelli*¹, D. Bome², A. Kebbi², E. Pisani³, C. Frasson³, G. Putoto³, D. Carraro³, S. Merler¹, ¹Bruno Kessler Foundation, Italy, ²Pujehun Hospital, Sierra Leone, ³Doctors with Africa - CUAMM, Italy</p>	<p>[O17.1] A systematic Bayesian integration of epidemiological and genetic data M.S.Y. Lau*¹, G.J. Gibson², G. Marion³, G. Streftaris², ¹Princeton University, USA, ²Heriot-Watt University, UK, ³BioSS, UK</p>	<p>[O18.1] Ethical tradeoffs between alternative vaccine trial designs during acute emerging epidemics: A quantitative simulation-based framework S.E. Bellan*¹, J.R.C. Pulliam², R. van der Graaf³, J. Dushoff⁴, L.A. Meyers^{1,5}, ¹The University of Texas at Austin, USA, ²University of Florida, Gainesville, USA, ³University Medical Center, Utrecht, The Netherlands, ⁴McMaster University, Canada, ⁵The Santa Fe Institute, USA</p>

16:40-17:00	<p>[O16.2] Estimating, evaluating, and visualizing uncertainty in the cost-effectiveness of quarantine policies for Ebola N.G. Reich*¹, S. Cauchemez², J. Lessler³, ¹University of Massachusetts Amherst, USA, ²Institut Pasteur, France, ³Johns Hopkins Bloomberg School of Public Health, USA</p>	<p>[O17.2] Causal inference in infectious disease ecology S. Cobey*, E. Baskerville, <i>University of Chicago, USA</i></p>	<p>[O18.2] The public health impact and cost-effectiveness of malaria vaccine candidate RTS,S/AS01: A systematic comparison of predictions from four mathematical models M.A. Penny^{1,2}, R. Verity*³, C. Bever⁴, C. Sauboin⁵, K. Galactionova^{1,2}, S. Flasche⁶, M.T. White³, E.A. Wenger⁴, N. Van de Velde⁵, P. Pemberton-Ross^{1,2} et al, ¹Swiss Tropical and Public Health Institute, Switzerland, ²University of Basel, Switzerland, ³Imperial College London, UK, ⁴Institute for Disease Modelling, USA, ⁵GSK Vaccines, Belgium, ⁶London School of Hygiene and Tropical Medicine, UK, ⁷PATH, USA, ⁸Public Health England, UK, ⁹WHO, Switzerland</p>
17:00-17:20	<p>[O16.3] Can we predict without explaining? Real-time modelling and forecasting of the Ebola outbreak in West Africa A. Camacho*, A.J. Kucharski, R.M. Eggo, S. Funk, W.J. Edmunds, <i>London School of Hygiene & Tropical Medicine, UK</i></p>	<p>[O17.3] Bayesian model selection for evaluation of epidemiological hypotheses: The epidemiology of <i>Escherichia coli</i> O157:H7 in feedlot cattle P. Touloupou*, S.E.F. Spencer, B. Finkenstädt, <i>University of Warwick, UK</i></p>	<p>[O18.3] Yellow fever vaccine impact in Africa: Accounting for human herd immunity in the face of zoonotic transmission K. Jean*¹, N.M. Ferguson¹, M.D. Van Kerkhove², S. Yactayo³, W. Perea³, J. Biey⁴, M.E. Shibeshi⁵, T. Garske¹, ¹Imperial College London, UK, ²Institut Pasteur, France, ³WHO, Switzerland, ⁴AFRO West Africa Inter-country Support Team, Burkina Faso, ⁵AFRO Eastern and Southern Africa Inter-country Support Team, Zimbabwe</p>
17:20-17:40	<p>[O16.4] International spreading risk associated with the 2014 West African Ebola outbreak M.F.C. Gomes¹, A. Pastore y Piontti¹, L. Rossi², D.L. Chao³, M.E. Halloran³, I.M. Longini⁴, A. Vespignani*¹, ¹Northeastern University, USA, ²Institute for Scientific Interchange, Italy, ³Fred Hutchinson Cancer Research Center, USA, ⁴University of Florida, USA</p>	<p>[O17.4] Integrating multi-scale data into spatial and spatiotemporal models of disease incidence and risk S.M. Moore*, A.S. Azman, J. Lessler <i>Johns Hopkins Bloomberg School of Public Health, USA</i></p>	<p>[O18.4] Estimating dengue vaccine efficacy in the presence of missing data in both outcome and covariates Y. Meng*^{1,2}, Y. Yang^{1,2}, I. Longini^{1,2}, ¹University of Florida, USA, ²CSQUID, USA</p>
17:40-19:20	Poster Session 2 Salons A-D, Grand Ballroom Foyer, Citrus and Mangrove		
19:30-22:00	Conference Dinner – Ticket holders only <i>Location: Sandpiper/Blue Heron Deck</i>		
Friday, 4 December 2015			
Room	Salons EFG Session Chair: Alessandro Vespignani		
08:30-09:10	[PLN09] Niche partitioning in epidemiology: extensions of strain theory and empirical evidence M. Pascual ^{1,2} , ¹ University of Chicago, USA, ² The Santa Fe Institute, USA		
09:10-09:50	[PLN10] The hidden geometry of complex, network-driven contagion phenomena D. Brockmann, <i>Robert Koch-Institute, Germany</i>		
09:50-10:20	Refreshment Break I Salons A-D, Grand Ballroom Foyer		

Rooms	Salon E	Salon F	Salon G
10:20-12:00	Session 19: Statistical Methods 2 <i>Session Chair: Marcel Salathé</i>	Session 20: Vector Borne <i>Session Chair: Juliet Pulliam</i>	Session 21: Emerging Infections <i>Session Chair: Sarah Cobey</i>
10:20-10:40	[O19.1] Estimating the severe outcome burden associated with influenza and the respiratory syncytial virus E. Goldstein ^{*1} , C. Viboud ² , W.P. Hanage ¹ , M. Lipsitch ¹ , ¹ Harvard TH Chan School of Public Health, USA, ² National Institutes of Health, USA,	[O20.1] Effective control of dengue in Mexico by combining vaccines with vector reduction T.J. Hladish ^{*1} , C.A.B. Pearson ¹ , D.L. Chao ² , D.P. Rojas ¹ , G.L. Recchia ³ , H. Gomez Dantes ⁴ , M.E. Halloran ² , J.R.C. Pulliam ¹ , I.M. Longini ^{1,2} , ¹ University of Florida, USA, ² University of Washington, USA, ³ University of Cambridge, UK, ⁴ National Institute of Public Health, Mexico	[O21.1] Unravelling the key drivers of MERS-CoV transmission S. Cauchemez ^{*1} , P. Nouvellet ² , A. Cori ² , T. Jombart ² , T. Garske ² , H. Clapham ³ , S. Moore ³ , H. Mills ² , H. Salje ^{1,3} , C. Collins ² et al, ¹ Institut Pasteur, France, ² Imperial College, UK, ³ Johns Hopkins, USA, ⁴ Ministry of Health, Saudi Arabia
10:40-11:00	[O19.2] Transmission patterns of human cytomegalovirus uncovered by analysis of cross-sectional serological data M. van Boven [*] , M.J. Korndewal, H.E. de Melker, J. van de Kasstele <i>National Institute for Public Health, The Netherlands</i>	[O20.2] How hot is malaria? - open challenges in evaluating the impact of climate on the transmission of vector-borne disease L.R. Johnson ^{*1} , T. Ben-Horin ² , K.D. Lafferty ^{3,4} , A. McNally ⁴ , E. Mordecai ⁵ , K.P. Paaijmans ⁶ , S. Pawar ⁷ , S.J. Ryan ⁸ , ¹ University of South Florida, USA, ² Rutgers University, USA, ³ U.S. Geological Survey, USA, ⁴ Univeristy of California Santa Barbara, USA, ⁵ Stanford University, USA, ⁶ Universitat de Barcelona, Spain, ⁷ Imperial College London, UK, ⁸ University of Florida, USA	[O21.2] Transmission characteristics of MERS and SARS in the healthcare setting: a comparative study G. Chowell ^{1,2} , F. Abdirizak ¹ , S. Lee ³ , J. Lee ⁴ , E. Jung ⁴ , H. Nishiura ^{*5,6} , C. Viboud ² , ¹ Georgia State University, USA, ² National Institutes of Health, USA, ³ Kyung Hee University, Republic of Korea, ⁴ Konkuk University, Republic of Korea, ⁵ The University of Tokyo, Japan, ⁶ Japan Science and Technology Agency, Japan
11:00-11:20	[O19.3] Characterizing pandemic severity and transmissibility from FF100 data A.J. Black ¹ , N. Geard ² , J.M. McCaw ² , J. McVernon ² , J.V. Ross ^{*1} ¹ The University of Adelaide, Australia, ² The University of Melbourne, Australia	[O20.3] The performance of Wolbachia in Aedes aegypti in reducing human dengue cases: A two serotype model M.Z. Ndi ¹ , D. Allingham ¹ , R.I. Hickson ^{*2} , K. Glass ³ , ¹ University of Newcastle, Australia, ² IBM Research--Australia, Australia, ³ Australian National University, Australia	[O21.3] Quantifying spatiotemporal heterogeneity of MERS-CoV transmission in the Middle East region: A combined modeling approach C. Poletto ^{*1} , V. Colizza ^{1,2} , P.Y. Boëlle ¹ , ¹ INSERM & UPMC, France, ² ISI Foundation, Italy
11:20-11:40	[O19.4] Inference of reporting rate and variance of the offspring distribution from epidemiological and genetic data L.M. Li [*] , N.C. Grassly, C. Fraser, <i>Imperial College London, UK</i>	[O20.4] Density-dependent population dynamics in Aedes aegypti mosquitoes alter the invasion dynamics of Wolbachia bacteria: Implications for Wolbachia release strategies for dengue control P.A. Hancock ^{*1} , V.L. White ² , A.G. Callahan ² , H.C.J. Godfray ¹ , A.A. Hoffmann ² , S.A. Ritchie ³ , ¹ University of Oxford, UK, ² University of Melbourne, Australia, ³ James Cook University, Australia	[O21.4] A multi-pathogen hierarchical Bayesian spatio-temporal model for transmission of hand, foot, and mouth disease in China X. Tang [*] , Y. Yang, N. Bliznyuk, I. Longini, <i>University of Florida, USA</i>

11:40-12:00	<p>[O19.5] Assessing the role of different age groups, and of vaccination, during disease outbreaks using case reporting data C.J. Worby^{*1}, C. Kenyon², R. Lynfield², S.S. Chaves³, L. Finelli³, J. Wallinga⁴, M. Lipsitch¹, E. Goldstein¹, ¹<i>Harvard TH Chan School of Public Health, USA</i>, ²<i>Minnesota Department of Health, USA</i>, ³<i>Centers for Disease Control and Prevention, USA</i>, ⁴<i>National Institute of Public Health and the Environment, The Netherlands</i></p>	<p>[O20.5] Modelling the role of host heterogeneity in Gambian human African trypanosomiasis K.S. Rock^{*1}, S.J. Torr², M.J. Keeling¹ ¹<i>Warwick University, UK</i>, ²<i>Liverpool School of Tropical Medicine, UK</i></p>	<p>[O21.5] Early-warning signals for emerging and re-emerging disease outbreaks T.S. Brett^{*1,2}, P. Rohani¹, ¹<i>University of Michigan, USA</i>, ²<i>University of Georgia, USA</i></p>
12:00:12:20	Refreshment Break I <i>Salons A-D, Grand Ballroom Foyer</i>		
Room	Salons EFG Session Chair: Ira Longini		
12:20-13:00	<p>[PLN11] Epidemiology, ecology and rational risk assessment for pathogen emergence J.O. Lloyd-Smith¹, ¹<i>University of California, Los Angeles, USA</i>, ²<i>Fogarty International Center, National Institutes of Health, USA</i></p>		
13:00-13:20	Conference Closing		