Poster Program

Poster Session 1 – Tuesday 3 December - 17:30-19:00
Poster Session 2 – Wednesday 4 December - 17:50-19:20
Poster Session 3 – Thursday 5 December - 17:30-19:00
Room - Ballroom AB

Poster Session 1 Tuesday 3 December 17:00-19:00	
[P1.001]	**When Sexual Selection Benefits Parasite Transmission** P. Aavani*, S. Rice, *Texas Tech University, USA*
[P1.002]	**Knowledge, attitudes and practices (KAPs) and risk factors of brucellosis at the human-animal interface in Egypt** E.W. Abd El-Wahab*[1], Y. Hegazy[2], W.F. El-Tras[2], A.I. Mikeal[4], A.F. Kapaby[5], M. Abdelfatah[2], M. Bruce[7], M. Eltholth[2,8], [1]*Alexandria University, Egypt,* [2]*Kafrelsheikh University, Egypt,* [3]*Damanhour Fever Hospital, Egypt,* [4]*Alexandria Fever Hospital, Egypt,* [5]*Murdoch University, Australia,* [6]*University of Stirling, UK*
[P1.003]	**The Cascade Analysis Tool: software to improve technical and allocative efficiencies along the continuum of care** R.G. Abeysuriya*[1], D.J. Kedziora[1], V.S. Harbuz[2], C.C. Kerr[3], G.L. Chadderdon[1], R.M. Stuart[4], [1]*Burnet Institute, Australia,* [2]*The World Bank Group, USA,* [3]*University of Sydney, Australia,* [4]*University of Copenhagen, Denmark*
[P1.004]	**Determinants of *S. aureus* carriage in the developing infant nasal microbiome** E. Accorsi*[1], E.A. Franzosa[1,2], T. Hsu[1,2], R. Cordy[3], A. Maayan-Metzger[4,5], H. Jaber[5], A. Reiss-Mandel[5], M. Lipsitch[1], G. Regev-Yochay[4,5], C. Huttenhower[1,2], [1]*Harvard University, USA,* [2]*Broad Institute, USA,* [3]*Wake Forest University, USA,* [4]*Sackler School of Medicine, Israel,* [5]*Sheba Medical Center, Israel*
[P1.005]	**Phylodynamic analysis of influenza A/H1N1pdm09 in India from 2009 to 2017** D.C. Adam*[1], M. Scotch[2], C.R. MacIntyre[1], [1]*University of New South Wales, Australia,* [2]*Arizona State University, USA*
[P1.006]	**Quantifying the roles of vomiting, diarrhea, and residents vs. staff in norovirus transmission in U.S. nursing home outbreaks** C. Adams*[1], D. Young[2], P.A. Gastanaduy[3], P. Paul[3], Z. Marsh[3], A.J. Hall[3], B.A. Lopman[1], [1]*Emory University Rollins School of Public Health, USA,* [2]*South Carolina Department of Health and Environmental Control, USA,* [3]*Centers for Disease Control and Prevention, USA*
[P1.007]	**HIV/AIDS epidemiology in africa: past, present and future perspective** M.O. Adegboyega*[1], V.A.N. Nicholas-Okpara[2], C.A. Okeke[3], [1]*UNIVERSITY OF BENIN, Nigeria,* [2]*federal Institute of Industrial Research Oshodi Lagos, Nigeria,* [3]*srivanthi And East Energy Ltd, Nigeria*
[P1.008]	**Modelling the Contribution of Relapse versus Re-infection to the Burden of TB** A. Adekunle*[1], J. Trauer[2], E. McBryde[1], [1]*James Cook University, Townsville, Australia,* [2]*Monash University, Australia*
[P1.009]	**The long-term impact of bedaquiline-containing regimens on cost burden to the healthcare system and families of patients with drug-resistant tuberculosis in China** A.M. Agnarson*[1], W. XiaoChun[2], R. Potluri[3], H. Bhandari[4], A. Dhir[4], C. Kambili[1], L. Metz[1], [1]*Johnson & Johnson, USA,* [2]*Xian Janssen Pharmaceutical Ltd, China,* [3]*SmartAnalyst Inc., USA,* [4]*SmartAnalyst India Pvt Ltd, India*
[P1.010]	**Model-based comparison of annual and biannual childhood influenza vaccination strategies** K.E.C. Ainslie*, S. Riley, *Imperial College London, UK*
[P1.011]	**Temporal shifts in the predominant carbapenemase gene types among carbapanemase-producing *Klebsiella pneumoniae* isolated in Bangkok, Thailand, during 2013-2016** Y. Akeda*[1], W. Laolerd[2], Y. Sugawara[1], N. Sakamoto[1], D. Motooka[1], N. Yamamoto[1], D. Takeuchi[1], R.K. Shanmugakani[1], I. Nishi[1], M. Suzuki[3], [1]*Osaka University, Japan,* [2]*Mahidol University, Thailand,* [3]*National Institute of Infectious Diseases, Japan*

[P1.012]	Will be presented in P3.115
[P1.013]	**Dynamical Analysis of a Disease Transmission Model Coupled with Two Pre-emptive Provisions and Quarantine-Isolation Policy- An Approach Based on Evolutionary Game Theory** M. Alam*[1,2], J. Tanimoto[1], [1]*Kyushu University, Japan,* [2]*University of Dhaka, Bangladesh*
[P1.014]	**Network structure and eco-evolutionary dynamics of CRISPR-induced immune diversification** S. Alcala-Corona*[1], S. Pilosof[1], T. Wang[2], S. Maslov[2], R. Whitaker[2], M. Pascual[1], [1]*The University of Chicago, USA,* [2]*University of Illinois at Urbana Champaign, USA*
[P1.015]	**CEDAR-MC: Clinical and environmental dynamics of antibiotic resistance within microbial communities** G. Hanna[1,3], B. Hamidi[1], S. Curry[1], M. Johnson[1,2], C. Carmack[3], A.V. Alekseyenko*[1], [1]*Medical University of South Carolina, USA,* [2]*South Carolina State University, USA,* [3]*Charleston Waterkeeper, USA*
[P1.016]	**Role of meteorological factors in respiratory syncytial virus transmission in Singapore** S.T. Ali*[1], C.C. Tam[2], B.J. Cowling[1], C.F. Yung[3], [1]*The University of Hong Kong, Hong Kong,* [2]*National University of Singapore and National University Health System, Singapore,* [3]*KK Women's and Children's Hospital, Singapore*
[P1.017]	**The role of asymptomatic infections in sleeping sickness control and elimination** M. Aliee*, K. Rock, M. Keeling, *University of Warwick, UK*
[P1.018]	**Hidden dynamics of respiratory pathogen transmission in the US** B.M. Althouse*[1,2], S.V. Scarpino[3,4], B. Galvin[1], J. Nawrocki[5], K. Olin[5], J.D. Jones[5], L. Meyers[5], [1]*University of Washington, USA,* [2]*New Mexico State University, USA,* [3]*Northeastern University, USA,* [4]*ISI Foundation, Italy,* [5]*BioFire Diagnostics, USA*
[P1.019]	**Google searches accurately forecast RSV hospitalizations** B.M. Althouse*[1,2], D.M. Weinberger[3], S.V. Scarpino[4,5], V.E. Pitzer[3], J.W. Ayers[6], E. Wenger[1], I.C.H. Fung[7], M. Dredze[8], H. Hu[1], [1]*Institute for Disease Modeling, USA,* [2]*University of Washington, USA,* [3]*Yale School of Public Health, USA,* [4]*Northeastern University, USA,* [5]*ISI Foundation, Italy,* [6]*University of California San Diego, USA,* [7]*Jiann-Ping Hsu College of Public Health, Georgia Southern University, USA,* [8]*Johns Hopkins University, USA*
[P1.020]	**Potential impacts of a prenatal maternal RSV vaccine on under 5 hospitalizations in Washington State** B.M. Althouse*[1,2], S.V. Scarpino[3,4], [1]*Institute for Disease Modeling, USA,* [2]*University of Washington, USA,* [3]*Northeastern University, USA,* [4]*ISI Foundation, Italy*
[P1.021]	**A two-species model to study the transmission and persistence of MERS-COV** M. Althubyani*[1,2], J. Heffernan[1], [1]*York University, Canada,* [2]*AlBaha University, Saudi Arabia*
[P1.022]	**Evaluating serology-based rapid diagnostic tests as a tool to improve *Plasmodium falciparum* surveillance in low-transmission settings** M.R. Ambrose*[1], V.M. Hunt[2], C.M. Bachman[2], D. Cate[2], B.H. Weigl[2], C. Drakeley[3], D. Bell[4], I. Rodriguez-Barraquer[5], B. Greenhouse[5], C. Bever[1], [1]*Institute for Disease Modeling, USA,* [2]*Intellectual Ventures, USA,* [3]*London School of Hygiene and Tropical Medicine, UK,* [4]*DB Global Health, USA,* [5]*University of California, USA,* [6]*Northwestern University, USA*
[P1.023]	**Mapping for malaria control in Grand'Anse, Haiti using a multi-metric Bayesian approach.** P. Amratia*[1], E. Cameron[1], A. Young[2], K. Twohig[1], A. Python[1], D. Bhavani[2], E. Pothin[2,3], A. Le Menach[2], J.M. Cohen[2], S. Marseille[4], [1]*University of Oxford, UK,* [2]*Clinton Health Access Initiative, USA,* [3]*Swiss Tropical and Public Health Institute, Switzerland,* [4]*Programme National de Contrôle de la Malaria/MSPP, Haiti*
[P1.024]	**Temporal and geographic changes of reporting rates and case fatality for measles in Denmark 1870-1960** V. Andreasen*, M. van Wijhe, M. Mølbak Ingholt, M. Linnet Perner, L. Simonsen, *Roskilde University, Denmark*
[P1.025]	**Highly pathogenic avian influenza H5N8 in south-west France 2016-2017: A modeling study of control strategies** A. Andronico*[1], A. Courcoul[2], A. Bronner[3], A. Scoizec[2], S. Lebouquin-Leneveu[2], C. Guinat[4], M. Paul[4], B. Durand[2], S. Cauchemez[1], [1]*Institut Pasteur, France,* [2]*Environment and Occupational Health and Safety (ANSES) Maisons-Alfort, France,* [3]*Direction générale de l'Alimentation, France,* [4]*Université de Toulouse, France*

[P1.026]	**Modeling and forecasting dengue virus transmission in Réunion island** A. Andronico*[1], L. Menudier[2], J. Paireau[1], H. de Valk[2], M-C. Paty[2], P. Gallian[3,4], X. de Lamballerie[4], B. Pastorino[4], H. Salje[1], P. Vilain[2], *[1]Institut Pasteur, France, [2]French Public Health Agency (Santé publique France), France, [3]Etablissement Français du Sang Provence Alpes Côte d'Azur et Corse, France, [4]UVE Aix-Marseille, France*
[P1.027]	**Learning from the past: Improving mechanistic models to forecast seasonal influenza in France** A. Andronico*[1], J. Paireau[1], C. Campese[2], S. Cauchemez[1], *[1]Institut Pasteur, France, [2]French Public Health Agency (Santé publique France), France*
[P1.028]	**Estimating antigenic distances for influenza vaccines and patient viruses in the United States** L.S. Arakaki*[1], S.E. Hawes[1], M.L. Jackson[2], B. Flannery[3], X. Xu[3], *[1]University of Washington, USA, [2]Kaiser Permanente Washington Health Research Institute, USA, [3]Centers for Disease Control and Prevention, USA*
[P1.029]	**Earliest infections predict the age distribution of seasonal influenza A cases** P. Arevalo*[1], H.Q. McLean[2], E.A. Belongia[2], S. Cobey[1], *[1]University of Chicago, USA, [2]Marshfield Clinic Research Institute, USA*
[P1.030]	**Gone to the dogs: Modeling Guinea worm disease transmission dynamics in humans, copepods, and dogs** A. Avitto*, G. Smith, *University of Pennsylvania, USA*
[P1.031]	**Vaccine delivery strategies for improving measles outbreak response in hard-to-reach populations** J.M. Azam*[1], M.J. Ferrari[2], J.R.C. Pulliam[1], *[1]DST-NRF Centre of Excellence in Epidemiological Modelling and Analysis, South Africa, [2]The Pennsylvania State University, USA*
[P1.032]	**Vaccinating children against influenza: The costs, effects, and the unexpected potential for undesirable outcomes** P.T. De Boer[1], J.A. Backer*[1], A.J. Van Hoek[1,2], J. Wallinga[1,3], *[1]National Institute for Public Health and the Environment, The Netherlands, [2]London School of Hygiene & Tropical Medicine, UK, [3]Leiden University Medical Center, The Netherlands*
[P1.033]	**Contemporary statistical inference for infectious disease models using Stan** A. Chatzilena[1], E. van Leeuwen[2], O. Ratmann[3], M. Baguelin*[3,4], N. Demiris[1], *[1]Athens University of Economics and Business, Greece, [2]Public Health England, UK, [3]Imperial College London, UK, [4]London School of Hygiene and Tropical Medicine, UK*
[P1.034]	**Impact of aerosol on Nm A** A. bah*[1], M. lam[1], A. bah[1], S. bowong[2], *[1]University Cheikh Anta Diop, Senegal, [2]University of Douala, Cameroon*
[P1.035]	**Spatio-temporal Aedes aegypti density modeling with meteorological and remote sensing data, French Guiana** S. Bailly*[1], V. Machaults[2], S. Beneteau[1], P. Palany[3], J-P. Lacaux[3], P. Quenel[4], C. Flamand[1], *[1]Institut Pasteur in French Guiana, French Guiana, [2]Toulouse university, French Guiana, [3]Meteo France Antilles-Guyane, France, [4]School of Public Health, France*
[P1.036]	**Machine learning identifies key predictors of pathogen strain type from multilocus sequence typing databases** K. Eckstrom[1], S. Scarpino[2], J. Barlow*[1], *[1]University of Vermont, USA, [2]Northeastern University, USA*
[P1.037]	**Predicting the spatial invasion of Ebola: Towards an R package implementing gravity models with Bayesian inference** R.C. Barnard*, P. Nouvellet, *University of Sussex, UK*
[P1.038]	**Updated estimation of the burden of rabies in Cambodia using spatial Bayesian regression modelling** J. Baron*[1], V. Chevalier[3,2], S. Ly[2], P. Dussart[2], D. Fontenille[2], B. Martinez-Lopez[1], *[1]University of California Davis, USA, [2]Institut Pasteur du Cambodge, Cambodia, [3]Centre de Coopération Internationale en Recherche Agronomique pour le Développement, France*
[P1.039]	**Analysis of heterogeneous genomic samples using sequence image normalization and machine learning** S. Basodi*[1], P. Icer Baykal[1], A. Zelikovsky[1,2], Y. Khudyakov[3], P. Skums[1], Y. Pan[1], *[1]Georgia State University, USA, [2]I.M. Sechenov First Moscow State Medical University, Russia, [3]Centers for Disease Control and Prevention, USA*

[P1.040]	**Temporal relationship between antimicrobial use and resistance in livestock: Bayesian analysis of a longitudinal study in French calves farms** J. Bastard*[1,2], E. Gay[3], J.Y. Madec[3], M. Haenni[3], L. Temime[2], L. Opatowski[1], *[1]Institut Pasteur, France, [2]Conservatoire National des Arts et Métiers, France, [3]Lyon laboratory, France*
[P1.041]	**A modelling study of Livestock-Associated Methicillin Resistant Staphylococcus aureus in French pig farms** J. Bastard*[1,2], M. Andraud[4,5], C. Chauvin[4,5], P. Glaser[3], L. Opatowski[1], L. Temime[2], *[1]Institut Pasteur, France, [2]Conservatoire National des Arts et Métiers, France, [3]University Paris-Sud, France, [4]French Agency for Food, Environmental and Occupational Health & Safety, France, [5]University Bretagne Loire, France*
[P1.042]	**An Epidemiological Tool for Warfighter Readiness** S. Batni, *Defense Threat Reduction Agency, USA*
[P1.043]	**Drivers of disease transmission in spatially structured populations** E. Benincà*[1], T. Hagenaars[2], G. Boender[2], J. van de Kassteele[1], M. van Boven[1], *[1]National Institute for Public Health and the Environment, The Netherlands, [2]Wageningen Bioveterinary Research, The Netherlands*
[P1.044]	**A dose response model for campylobacteriosis severity of illness** E. Benincà*[1], A.A. Bonacic Marinovic[1], D.R. Tribble[2], C.K. Porter[3], A. Swart[1], *[1]National Institute for Public Health and the Environment, The Netherlands, [2]Uniformed Services University of the Health Sciences, USA, [3]Naval Medical Research Center, USA*
[P1.045]	**Models and data on human mobility in the African continent – A Review** S. Bhatia*[1], M. Kraemer[2], P. Nouvellet[3], A. Cori[1], *[1]Imperial College Lodnon, UK, [2]University of Oxford, UK, [3]University of Sussex, UK*
[P1.046]	**The creation and validation of a sub-national, global index measuring vulnerability to infectious disease outbreaks** D. Bhatia*[1], J. Johns[1], R. Moineddin[1,2], A. Watts[1], K. Khan[1], *[1]BlueDot Inc., Canada, [2]University of Toronto, Canada, [3]St. Michael's Hospital, Canada*
[P1.047]	**Impact of background exposure dose on direct and indirect effect of killed oral cholera vaccines** Q. Bi*, A. Azman, J. Lessler, *Johns Hopkins Bloomberg School of Public Health, USA*
[P1.048]	**Network structure and the hiv/syphilis syndemic: Evaluation of hiv and syphilis network interconnectivity through community detection** R. Billock*[1], P. Mucha[1], E. Samoff[2], A. Dennis[1], K. Powers[1], *[1]University of North Carolina at Chapel Hill, USA, [2]North Carolina Department of Health and Human Services, USA*
[P1.049]	**Towards a nuanced view of diagnostic test properties: an application to blood safety** J. Bingham*[1,2], E. Grebe[3], A. Welte[1,2], *[1]SACEMA, South Africa, [2]Stellenbosch University, South Africa, [3]Vitalant Research Institute, South Africa*
[P1.050]	**Decoding the ecological and immunological dynamics of typhoid and paratyphoid in preparation for Typhoid Conjugate Vaccine roll-out** R. Birger*[1], N.J. Saad[1], A. Karkey[2], B. Basnyat[2,3], S. Baker[4,5], V.E. Pitzer[1], *[1]Yale School of Public Health, USA, [2]Oxford University Clinical Research Unit, Patan Academy of Health Sciences, Nepal, [3]Oxford University, UK, [4]Oxford University Clinical Research Unit, Hospital for Tropical Diseases, Viet Nam, [5]University of Cambridge, UK*
[P1.051]	**Interactions between vaccine and non-vaccine human papillomavirus genotypes in a partnership network: an individual-based model** M. Bonneault*[1], C. Poletto[2], M. Flauder[1], M. Pons-Salort[3], D. Guillemot[1], E. Delarocque-Astagneau[1], A. thiébaut[1], L. Opatowski[1], *[1]Institut Pasteur Paris, France, [2]Sorbonne Université, France, [3]Imperial College London, UK*
[P1.052]	**Social contact and the risk of influenza B infection amongst students in a K-12 cohort in Pittsburgh, PA** B.A. Borgert*, M.D.T. Hitchings, D.A.T. Cummings, *University of Florida, USA*
[P1.053]	**Mathematical models of viral infection within mosquitoes** P. Bosetti*, S. Cauchemez, *Institut Pasteur, France*
[P1.054]	**Identification of yellow fever vaccine deserts in the United States** S.E. Bowden*[1,2], S. Morrison[1,2], E. McIntyre[1,3], A. Grills[1], *[1]Centers for Disease Control and Prevention, USA, [2]Eagle Medical Services, USA, [3]Perspecta, USA*

[P1.055]	**The impact of vaccination efforts on the dynamics of the 2016-19 hepatitis A outbreak in Michigan** A.F. Brouwer*[1], M.C. Eisenberg[1], J.L. Zelner[1], M. Ladisky[2], J. Collins[2], J.N.S. Eisenberg[1], *[1]University of Michigan, USA, [2]Michigan Department of Health and Human Services, USA*
[P1.056]	**Determining the household-level impact of antenatal vaccination for respiratory syncytial virus in a high-income setting** P. Campbell*[1,3], A. Hogan[2], N. Geard[1], *[1]The University of Melbourne, Australia, [2]Imperial College London, UK, [3]Murdoch Children's Research Institute, Australia*
[P1.057]	**The role of seasonality and climatic factors in the spatiotemporal transmission dynamics of dengue in Brazil** L. Castro*, C. Manore, S. Del Valle, *Los Alamos National Laboratory, USA*
[P1.058]	**Within-host HIV-1 evolutionary dynamics reflected in deconstructed ancestral recombination graphs** L. Castro*[1,3], E. Romero-Severson[3], L. Ancel Meyers[1,2], T. Leitner[3], *[1]The University of Texas at Austin, USA, [2]Santa Fe Institute, USA, [3]Los Alamos National Laboratory, USA*
[P1.059]	**Optimizing the deployment of ultra-low volume insecticide spraying to reduce arboviral disease incidence** S.M. Cavany*[1], G. Camargo España[1], A. Lloyd[2], L. Waller[3], U. Kitron[3], G.M. Vazquez-Prokopec[3], W.H. Elson[5], H. Astete[4], T.W. Scott[5], A.C. Morrison[4,5], *[1]University of Notre Dame, USA, [2]North Carolina State University, USA, [3]Emory University, USA, [4]Naval Medical Research Unit No. 6, Peru, [5]University of California, USA, [6]University of Washington, USA*
[P1.060]	**Accounting for non-stationarity in epidemiology using stochastic models with time-varying parameters** B. Cazelles*, C. Champagne, *Ecole Normale Superieure, France*
[P1.061]	**Diagnosing infectious disease models as a part of bayesian mcmc** B. Nguyen-Van-Yen[1,2], B. Cazelles*[2], R. Paul[1], *[1]Institut Pasteur, France, [2]Ecole Normale Superieure, France*
[P1.062]	**Bayesian inference for spatiotemporal transmission of visceral leishmaniasis: quantifying the role of post-kala-azar dermal leishmaniasis in transmission** L.A.C. Chapman*[1,2], S.E.F. Spencer[2], T.M. Pollington[2], C.P. Jewell[3], T.D. Hollingsworth[4], C. Bern[5], G.F. Medley[1], *[1]London School of Hygiene and Tropical Medicine, UK, [2]University of Warwick, UK, [3]Lancaster University, UK, [4]University of Oxford, UK, [5]University of California San Francisco, USA*
[P1.063]	**Spatial and temporal spread of Zika and chikungunya viruses in Colombia, a gravity-model based approach** K.A. Charniga*[1], Z.M. Cucunubá[1], M. Mercado[2], F. Prieto[2], M. Ospina[2], P. Nouvelle[3], C.A. Donnelly[1,4], *[1]Imperial College London, UK, [2]Instituto Nacional de Salud, Colombia, [3]University of Sussex, UK, [4]University of Oxford, UK*
[P1.064]	**Examining strain diversity and evolutionary history of human respiratory syncytial virus** J. Chen*, J. Bahl, *University of Georgia, USA*
[P1.065]	**Epidemiological consequences of enduring strain-specific immunity to Group A *Streptococcus* requiring repeated episodes of infection** R.H. Chisholm*[1], N. Sonenberg[1], J.A. Lacey[2], M.I. McDonald[3], M. Pandey[4], M.R. Davies[2], S.Y.C. Tong[2,5], J. McVernon[1,2], N. Geard[1,2], *[1]The University of Melbourne, Australia, [2]The Peter Doherty Institute for Infection and Immunity, Australia, [3]James Cook University, Australia, [4]Griffith University, Australia, [5]The Royal Melbourne Hospital, Australia, [6]Menzies School of Health Research, Australia, [7]Murdoch Childrens Research Institute, Australia*
[P1.066]	**Assessing the potential impact of vector-borne disease transmission following heavy rainfall events using Big Data and dynamic modeling** G. Chowell*[1], K. Mizumoto[1], J. Banda[2], S. Poccia[3], C. Perrings[1], *[1]Georgia State University, USA, [2]University of Torino, Italy, [3]Arizona State University, USA*
[P1.067]	**Vaccination strategies to control Ebola epidemics in the context of variable household inaccessibility levels-->** G. Chowell*[1,2], A. Tariq[1], M. Kiskowski[3], *[1]Georgia State University, USA, [2]Fogarty International Center, USA, [3]University South Alabama, USA*

[P1.068]	**Systematic literature review of local human movement data sources, methodologies, and possible applications in public health** M. Chuttani*[1,2], A. Thomas-Bachli[3], K. Petrasek[3], S. Morrison[1,4], [1]*Centers for Disease Control and Prevention, USA,* [2]*Oak Ridge Institute for Science and Education, USA,* [3]*BlueDot, Canada,* [4]*Eagle Medical Services, LLC, USA*
[P1.069]	**Antimicrobial resistance in E. coli: Which mechanisms lead to additional infections and which to replacement of infections with susceptible strains** N.G. Godijk*[1], M.C.J. Bootsma[1], C.H. van Werkhoven[1], V.A. Schweitzer[1], A.F. Schoffelen[2], S. de Greeff[2], M.J.M. Bonten[1], [1]*Julius Center for Health Sciences and Primary Care, UMC Utrecht, University of Utrecht, The Netherlands,* [2]*National Institute for Public Health and the Environment (RIVM), The Netherlands*
[P1.070]	**Spatially refined estimates of the global burden of Japanese Encephalitis using machine learning method** D. Nguyen[1], Q. Tran[2], H. Clapham*[1,3], [1]*Oxford University Clinical Research Unit, Viet Nam,* [2]*University of Notre Dame, USA,* [3]*University of Oxford, UK*
[P1.071]	**Inferring population susceptibility to dengue and dengue transmission intensity, implications for disease prediction and vaccination policy in Vietnam** H.M. Lam[1], H.T. Phuong[1], N.T.L. Thanh[1], N.H.T. Vy[1], H. Clapham*[1,2], [1]*Oxford University Clinical Research Unit, Viet Nam,* [2]*University of Oxford, UK*
[P1.072]	**Serostatus testing & dengue vaccine cost-benefit analysis** C.A.B. Pearson[1,2], K.M. Abbas[1], S. Clifford*[1], S. Flasche[1], T.J. Hladish[3], [1]*London School of Hygiene and Tropical Medicine, UK,* [2]*Stellenbosch University, South Africa,* [3]*University of Florida, USA*
[P1.073]	**The impact of regular school closure on seasonal influenza epidemics** P. Coletti*[1], V. Colizza[2], N. Hens[1,3], [1]*Hasselt University, Belgium,* [2]*Sorbonne Universités, France,* [3]*University of Antwerp, Belgium*
[P1.074]	**Joint inference of severity and transmission of influenza from multiple dependent data sources** A. Corbella*[1,2], A. Presanis[2], P. Birrell[2,3], D. De Angelis[2,3], [1]*University of Warwick, UK,* [2]*University of Cambridge, UK,* [3]*Public Health England, UK*
[P1.075]	**Modelling the epidemiology of residual *Plasmodium vivax* malaria in a heterogeneous host population: A case study in the Amazon Basin** R.M. Corder*[1], M.U. Ferreira[1], G.M. Gomes[2,3], [1]*University of São Paulo, Brazil,* [2]*Liverpool School of Tropical Medicine, UK,* [3]*Universidade do Porto, Portugal*
[P1.076]	**B cell dynamics shape population-level impacts of broadly protective influenza immunity** K.M. Gostic*[1], C. Viboud[4], M. Worobey[3], J.O. Lloyd-Smith[2,4], [1]*University of Chicago, USA,* [2]*University of California Los Angeles, USA,* [3]*University of Arizona, USA,* [4]*Fogarty International Center, USA*
[P1.077]	**Characterizing the dynamics of cholera in the democratic republic of the Congo** A. Costello*[1], J. Lessler[2], E.C. Lee[2], A.S. Azman[2], B.F. Zaitchik[3], D. Bompangue[4,5], S.M. Moore[1], [1]*University of Notre Dame, USA,* [2]*Johns Hopkins School of Public Health, USA,* [3]*Johns Hopkins University, USA,* [4]*Ministère de la Santé, Democratic Republic of the Congo,* [5]*Université de Kinshasa, Democratic Republic of the Congo*
[P1.078]	**Quantifying the threat of animal reservoirs to elimination of sleeping sickness across DRC** R.E. Crump*[1], C. Huang[1], E. Knock[1], E. Mwamba Miaka[2], S.E.F. Spencer[1], M.J. Keeling[1], K.S. Rock[1], [1]*University of Warwick, UK,* [2]*Programme National de Lutte Contre la Trypanosomiase Humaine Africaine, Democratic Republic of the Congo*
[P1.079]	**Genetic diversity of malaria according to surveillance strategy and study design** C. Dailey*, J. Bahl, *University of Georgia, USA*
[P1.080]	**Genomic analyses of differential substitution rates in avian influenza viruses between wild birds and domestic poultry** L. Damodaran*, J. Bahl, *University of Georgia, USA*
[P1.081]	**Branching process approximation for a simple stochastic SIR epidemic model** E.A. Dankwa, *University of Oxford, UK*

[P1.082]	**HIV Phylogeography in Pakistan suggests multiple introductions in the country** A. de Bernardi Schneider*[1], F. Cholette[2], L.H. Thompson[3], J.F. Blanchard[3], F. Emmanuel[3], T. Reza[4], N. Ikram[5], J.B. Joy[6], P. Sandstrom[2], J.O. Wertheim[1], [1]*University of California San Diego, USA,* [2]*JC Wilt Infectious Disease Research Centre, Canada,* [3]*University of Manitoba, Canada,* [4]*National AIDS Control Program, Pakistan,* [5]*National Referral Laboratory, Pakistan,* [6]*BC Centre for Excellence in HIV/AIDS, Canada*
[P1.083]	**Compute bounds for transmission parameters of multi-host infections from endemic prevalences** M.C.M. de Jong, *Wageningen University, The Netherlands*
[P1.084]	**Machine learning methods for fast, approximate inference for spatial epidemic models** R. Deardon*[1], C. Augusta[2], G. Taylor[2], [1]*University of Calgary, Canada,* [2]*University of Guelph, Canada*
[P1.085]	**Spatial scale of an ensemble forecast model of West Nile virus** N. DeFelice*[1], J. Shaman[1], [1]*Icahn School of Medicine at Mount Sinai, USA,* [2]*Columbia University, USA*
[P1.086]	**The effect of salting on *Toxoplasma gondii* viability evaluated and implemented in a quantitative risk assessment of meat-borne human infection** H. Deng*, A. Swart, A.A.B. Marinovic, J.W.B. van der Giessen, *National Institute for Public Health and the Environment, The Netherlands*
[P1.087]	**Quantifying the transmission dynamics of MRSA in the community and healthcare settings in a low-prevalence country: A modelling study** F. Di Ruscio*[1,2], G. Guzzetta[3], J.V. Bjørnholt[2,4], T.M. Leegaard[2,5], A.E.F. Moen[2,5], S. Merler[3], B.F. de Blasio[1,2], [1]*Norwegian Institute of Public Health, Norway,* [2]*University of Oslo, Norway,* [3]*Bruno Kessler Foundation, Italy,* [4]*Oslo University Hospital, Norway,* [5]*Akershus University Hospital, Norway*
[P1.088]	**A quantitative framework to define the end of an outbreak** B.A. Djaafara*[1,2], N. Imai[1], E. Hamblion[3], B. Impouma[3], C.A. Donnelly[1,4], A. Cori[1], [1]*Imperial College London, UK,* [2]*Eijkman-Oxford Clinical Research Unit, Indonesia,* [3]*WHO Regional Office for Africa, Congo,* [4]*University of Oxford, UK*
[P1.089]	**Age-mixing patterns and associations between partner age differences and relationship characteristics that affect HIV transmission risk in Eswatini** E.M. Dominic*[1], R. Beauclair[1,2], Z. Mnisi[3], J. Dushoff[4], W. Delva[1,5], [1]*South African Centre for Epidemiological Modelling and Analysis, Stellenbosch University, South Africa,* [2]*Data Yarn, South Africa,* [3]*Swaziland National AIDS Program, Swaziland,* [4]*McMaster University, Canada,* [5]*Ghent University, Belgium*
[P1.090]	**Dynamics of epidemic transitions** J. Drake, *University of Georgia, USA*
[P1.091]	**Evolution-informed ahead-of-season influenza incidence forecasting for the US** X. Du, *Sun Yat-sen University, China*
[P1.092]	**Impact of social network structure on effectiveness of ring vaccination for Ebola virus disease** C.A.B. Pearson[1], T.J. Hladish[2], W.J. Edmunds[1], R.M. Eggo*[1], [1]*London School of Hygiene & Tropical Medicine, UK,* [2]*University of Florida, USA*
[P1.093]	**Mapping the spread of vaccine misinformation on Twitter** C. Eisenhauer*[1,2], H. Salje[1,3], S. Cauchemez[1], [1]*Institut Pasteur, France,* [2]*Université de Paris, France,* [3]*Johns Hopkins School of Public Health, USA*
[P1.094]	**Using age-disaggregated data to estimate changes in annual risk of infection of drug-resistant tuberculosis** C.F. McQuaid[1], T. Cohen[2], A.S. Dean[3], R.M.G.J. Houben[1], G.M. Knight[1], M. Zignol[3], R.G. White[1], J. Emery*[1], [1]*London School of Hygiene and Tropical Medicine, UK,* [2]*Yale School of Public Health, USA,* [3]*World Health Organization, Switzerland*
[P1.095]	**Self-cure of latent tuberculosis infection: implications for population at-risk and lifetime risk of reactivation disease** J.C. Emery*[1], A.S. Richards[1], K.D. Dale[2,3], C.F. McQuaid[1], R.G. White[1], J.T. Denholm[2], R.M.G.J. Houben[1], [1]*London School of Hygiene & Tropical Medicine, UK,* [2]*Melbourne Health, Australia,* [3]*The University of Melbourne, Australia*

[P1.096]	**Estimating the contribution of subclinical tuberculosis to transmission - A modelling approach** J. Emery*, T. Sumner, A.S. Richards, R.G. White, R.M.G.J. Houben, *London School of Hygiene & Tropical Medicine, UK*
[P1.097]	**Firefighter games as a measure of network defensibility** J. Enright, *University of Glasgow, UK*
[P1.098]	**Generating synthetic populations to enable realistic simulations of dengue vaccine trials using an agent-based model** G. España*, T.A. Perkins, *University of Notre Dame, USA*
[P1.099]	**Accounting for space and uncertainty in real-time-location-system-derived contact networks** T. Farthing*[1], D. Dawson[1], M. Sanderson[2], C. Lanzas[1], [1]*North Carolina State University, USA,* [2]*Kansas State University, USA*
[P1.100]	**A preliminary agent-based model to explore the coupled natural human system of human-tick interactions.** M.P. Fernandez*, M.A. Diuk-Wasser, *Columbia University, USA*
[P1.101]	**Within-host HIV evolution and its impact on viral transmission** L. Ferretti*, C. Wymant, M. Hall, L. Zhao, C. Fraser, *University of Oxford, UK*
[P1.102]	**Age-stratified serological study identifies different modes of transmission for Q fever in French Guiana** C. Flamand*[1], N. Hozé[2], S. Bailly[1], A. Zhu-Soubise[1], A. Mbouangoro[1], F. Djossou[1], D. Rousset[1], S. Bisser[1], S. Cauchemez[1], [1]*Institut Pasteur in French Guiana, French Guiana,* [2]*Institut Pasteur, France,* [3]*Cntre Hospitalier de Cayenne, French Guiana*
[P1.103]	**Developing intervention strategies for measles control and elimination in an environment of persistent importation** K. Frey*, N. Thakkar, K.A. McCarthy, *Institute for Disease Modeling, USA*
[P1.104]	**Assessing the genomic relatedness and evolutionary rates of verotoxogenic escherichia coli in cattle** L-Y. Wang[1], C. Laing[2], R. Johnson[1], K. Ziebell[1], V. Gannon*[1], [1]*Public Health Agency of Canada, Canada,* [2]*Canadian Food Inspection Agency, Canada*
[P1.105]	**Inferring the generalized-growth model via maximum likelihood estimation: a reflection on the impact of overdispersion** T. Ganyani*[1], C. Faes[1], N. Hens[1,2], [1]*Hasselt University, Belgium,* [2]*Antwerp University, Belgium*
[P1.106]	Will be presented in P3.117
[P1.107]	Will be presented in P3.116
[P1.108]	**Eco-epidemiological consequences of breastfeeding and vaccination disparities in the United States** R. Garnier*, S. Bansal, *Georgetown University, USA*
[P1.109]	**Modelling vaccine stockpiles for emerging viral pathogens in an interconnected world** R. Garnier*, S. Bansal, *Georgetown University, USA*
[P1.110]	**Timeliness and impact of public health responses to measles in the United States 2001-2017** D. Mahood[1], B. Lopman[1], P. Gastanaduy*[1], [1]*Centers for Disease Control and Prevention, USA,* [2]*Emory University Rollins School of Public Health, USA*
[P1.111]	**Yellow fever in a changing climate: the effect on burden in Africa** K.A.M. Gaythorpe*[1], A. Hamlet[1], L. Cibrelus[2], T. Garske[1], N.M. Ferguson[1], [1]*Imperial College London, UK,* [2]*World Health Organisation, Switzerland*
[P1.112]	**Contact and Mobility Patterns in a Remote Aboriginal Community (CAMP-remote): A pilot study to capture dynamic household structure and mobility within and between remote Aboriginal communities** K.B. Gibney*[1], S.Y.C. Tong[1,2], M. McKinnon[2], R.G. Dhurrkay[2], G.G. Gurruwiwi[2], N. Geard[1], J. McVernon[1], [1]*University of Melbourne, Australia,* [2]*Menzies School of Health Research, Australia*

[P1.113]	**The duration of travel impacts the spatial dynamics of infectious diseases** J.R. Giles*[1], E. Erbach-Schoenberg[2], A.J. Tatem[2,3], K. Grantz[1], L. Gardner[4], C.J.E. Metcalf[5], [1]*Johns Hopkins University Bloomberg School of Public Health, Baltimore, MD, USA,* [2]*University of Southampton, Southampton, UK,* [3]*Fogarty International Center, National Institute of Health, Bethesda, MD, USA,* [4]*Johns Hopkins University, Baltimore, MD, USA,* [5]*Princeton University, Princeton, NJ, USA*
[P1.114]	**Computational Modelling of Emerging Vector-borne Diseases** J-P. Glutting*, T. Saksuriyongse, N. Dorratoltaj, *AIR Worldwide, USA*
[P1.115]	**Intensive localized culling as a management tool for chronic wasting disease in white-tailed deer** S. Berg*[1], D. Weber[1], M. Craft[2], J. Forester[2], [1]*University of St. Thomas, USA,* [2]*University of Minnesota, USA*
[P1.116]	**Heterogeneity in the longevity of immunological memory in humans** R. Antia, *Emory University, Georgia*
	Poster Session 2 **Wednesday 4 December** **17:50-19:20**
[P2.001]	**Towards elimination of hepatitis C virus infection: Treatment-as-prevention among people who inject drugs in Baltimore, USA** K.H. Grantz*[1], L. Mier-y-Teran-Romero[2], D.L. Thomas[1,3], D.A.T. Cummings[1,4], S.H. Mehta[1], [1]*Johns Hopkins Bloomberg School of Public Health, USA,* [2]*Naval Research Laboratory, USA,* [3]*Johns Hopkins School of Medicine, USA,* [4]*University of Florida, USA*
[P2.002]	**Identifying opportunities for improved biosecurity at a Standardbred training facility in order to reduce the transmission of infectious respiratory disease** T.M. Rossi[1], R.M. Milwid[1], A. Moore[2], T.L. O'Sullivan[1], A.L. Greer*[1], [1]*University of Guelph, Canada,* [2]*Ontario Ministry of Agriculture, Food, and Rural Affairs, Canada*
[P2.003]	**Investigating the efficacy of vaccine strategies against foot-and-mouth disease in the Republic of Turkey using a mathematical epidemiological model** G. Guyver-Fletcher*, E. Gorsich, M.J. Tildesley, *University of Warwick, UK*
[P2.004]	***Could awareness-induced changes in personal risk behaviour explain the dynamics of the Ebola virus epidemic in west Africa 2014-2016?*** G. Halvorsen*[1], L. Simonsen[2], K. Sneppen[1], [1]*University of Copenhagen, Denmark,* [2]*Roskilde University, Denmark*
[P2.005]	**Exploring the impact of variation in spatial patterns of community contact on the effectiveness of household- vs. community-based screening interventions for Tuberculosis** J. Havumaki*[1], T. Cohen[1], J. Zelner[2], [1]*Yale School of Public Health, USA,* [2]*University of Michigan School of Public Health, USA*
[P2.006]	**Short-sighted evolution of influenza cellular receptor binding in human populations** J.A. Hay*[1], S. Riley[1], H.Y. Yuan[2], [1]*Imperial College London, UK,* [2]*City University of Hong Kong, Hong Kong*
[P2.007]	**Decision for dengue vaccination: Transmissibility, age at vaccination and vaccination coverage** K. Hayashi*, H. Nishiura, *Hokkaido University, Japan*
[P2.008]	**Calibration of individual-based models to epidemiological data:a systematic review** C.M. Hazelbag*[1], J. Dushoff[2], E. Dominic[1], Z. Mthombothi[1], W. Delva[1], [1]*Stellenbosch university, South Africa,* [2]*McMaster University, Canada*
[P2.009]	**Cross protection between serotypes and introduction of an inactivated EV71 vaccine explain changing serotype dynamics of hand, foot, and mouth disease in a major transmission center in China** J. Head*[1], P. Collender[1], J. Lewnard[1], [1]*University of California Berkeley, USA,* [2]*Emory University, USA,* [3]*Sichuan Center for Disease Control and Prevention, China,* [4]*University of Florida, USA*
[P2.010]	**Ensemble Forecast and Parameter Inference of Childhood Diarrhea in Chobe District, Botswana** A. Heaney*[1], K. Alexander[3,4], J. Shaman[2], [1]*University of California Berkeley, USA,* [2]*Columbia University, USA,* [3]*Virginia Tech, USA,* [4]*Chobe Research Institute, Botswana*

[P2.011]	**The Geographic Distribution of Cholera in Bangladesh** S. Hegde*[1], A.I. Khan[2], F. Chowdhury[2], M.T. Islam[2], J. Kaminsky[1], E.S. Gurley[1], J. Lessler[1], F. Qadri[2], A. Azman[1], [1]*Johns Hopkins University, USA,* [2]*icddr,b (International Centre for Diarrhoeal Disease Research, Bangladesh), Bangladesh*
[P2.012]	**Heterogeneities that contribute to increased *Peste des petits ruminants* virus seroprevalence in a multi-host system of sheep, goats, and cattle in northern Tanzania** C.M. Herzog*[1], W. de Glanville[2], B.J. Willett[3], T. Kibona[4], I.M. Cattadori[1], V. Kapur[1], P.J. Hudson[1], J. Buza[4], S. Cleaveland[2], O.N. Bjørnstad[1], [1]*Pennsylvania State University, USA,* [2]*Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow, UK,* [3]*MRC-University of Glasgow Centre for Virus Research, UK,* [4]*Nelson Mandela African Institute of Science and Technology, Tanzania*
[P2.013]	**Spatio-temporal modelling of *Leishmania infantum* infection among domestic dogs: A simulation study and sensitivity analysis applied to rural Brazil** E.M. Hill*[1], E. Buckingham-Jeffery[2], S. Datta[3], E. Dilger[1], O. Courtenay[1], [1]*University of Warwick, UK,* [2]*The University of Manchester, UK,* [3]*National Institute of Water and Atmospheric Research, New Zealand*
[P2.014]	**Seasonal influenza in England: Modelling approaches to capture immunity propagation** E.M. Hill*[1], S. Petrou[1], S. de Lusignan[2,3], I. Yonova[2,3], M.J. Keeling[1], [1]*University of Warwick, UK,* [2]*University of Surrey, UK,* [3]*Royal College of General Practitioners, UK*
[P2.015]	**Bistability, resurgenceand intermittency in SEIR models withreinfection and migration (A new breakthrough submitted for oral presentation)** D. Hincapie*[1], J. Ospina[1], [1]*Universidad de Antioquia, Colombia,* [2]*EAFIT University, Colombia*
[P2.016]	**Modelling the potential impact of maternal immunization and intensified surveillance on the effective reproductive number** D. Hincapie-Palacio*[1], J. Ospina[1], [1]*University of Antioquia, Colombia,* [2]*Eafit University, Colombia*
[P2.017]	**Association between maternal antibodies, response to vaccination, and rotavirus infection: Secondary analysis of a rotavirus vaccine trial in children in Niger** M.D.T. Hitchings*[1], S. Isanaka[2,3], R.F. Grais[3], D.A.T. Cummings[1], [1]*University of Florida, USA,* [2]*Harvard T.H. Chan School of Public Health, USA,* [3]*Epicentre, France*
[P2.018]	**Cities as drivers for pandemic influenza transmission in Sweden** M. Holmberg*, D. Edler, M. Neuman, A. Bóta, M. Rosvall, *Umeå university, Sweden*
[P2.019]	**Where and what kind of intensified interventions are needed to achieve the elimination of sleeping sickness across DRC?** C. Huang*[1], R.E. Crump[1], E. Mwamba Miaka[2], M.J. Keeling[1], K.S. Rock[1], [1]*University of Warwick, UK,* [2]*Programme National de Lutte contre le Trypanosomiase Humaine Africaine (PNLTHA), Democratic Republic of the Congo*
[P2.020]	**Determinants of neutralization titers of global reference antisera against dengue viruses in Thailand, 1994-2014** A. Huang*[1,4], H. Salje[2], A. Coello Escoto[1], N. Chowdhury[1], C. Chávez[1], B. Garcia-Carreras[1], W. Rutvisuttinunt[3], I. Maljkovic Berry[3], C. Klungthong[4], B. Thaisomboonsuk[4], [1]*University of Florida, USA,* [2]*Institut Pasteur, France,* [3]*Walter Reed Army Institute of Research, USA,* [4]*Armed Forces Research Institute of Medical Sciences, Thailand,* [5]*University of California, San Francisco, USA,* [6]*State University of New York Upstate Medical University, USA,* [7]*University of Cambridge, UK,* [8]*National Institute of Health, USA,* [9]*University of California, Berkeley, USA*
[P2.021]	**Estimating population mobility in and around the Ebola-affected area, North Kivu Ebola outbreak, Democratic Republic of Congo, 2018-2019** C. Huber*[1], A. Watts[1], A. Thomas[1], E. McIntyre[2], A. Tuite[1], K. Khan[1,3], R. Merrill[2], [1]*BlueDot, Canada,* [2]*Centers for Disease Control and Prevention, USA,* [3]*St. Michael's Hospital, Canada,* [4]*University of Toronto, Canada*
[P2.022]	**Tackling malaria in Venezuela: short-term impacts are within reach, but long-term solutions will require sustained effort** J. Huber*[1], L. Chaves[2], A. Siraj[1], J. Moreno[3], M. Villegas[4], L. Pocaterra[5], L. Villegas[4,6], T.A. Perkins[1], [1]*University of Notre Dame, USA,* [2]*INCIENSA, Costa Rica,* [3]*Centro de Investigación de Campo Francesco Vitanza, Venezuela,* [4]*Global Development One, USA,* [5]*Universidad Central de Venezuela, Venezuela,* [6]*Asociación Civil Impacto Social (ASOCIS), Venezuela*

[P2.023]	**Comparing the results of a *de novo* model of dengue transmission to the existing models** A. Tytula[1], S. Aballéa[2], E. Kharitonova[3], C. Kelly[4], N.V. Hung*[5], [1]*Creativ-Ceutical, Poland,* [2]*Creativ-Ceutical, The Netherlands,* [3]*Creativ-Ceutical, France,* [4]*Takeda Vaccines Inc., USA,* [5]*VHN consulting, Canada*
[P2.024]	**Challenges of Avian Influenza outbreak control in Nigeria: a qualitative study** S. Ijoma*, V-I. Ifende, H. Osemeke, R-E. Agusi, A. Akpa, M-B. Bolajoko, C-A. Meseko, *National Veterinary Research Institute, Nigeria*
[P2.025]	**Predicting health-related workplace absenteeism for pandemic influenza preparedness and planning** A. Jackson*, H. Gao, M. Groenewold, F. Ahmed, *Centers for Disease Control and Prevention, USA*
[P2.026]	**Lower within-host basic reproductive ratios in men-who-have-sex-with-men than in heterosexual populations suggests decreasing HIV fitness with time** A. James*, N. Dixit, *Indian Institute of Science, India*
[P2.027]	**Modelling within-host antibiotic treatment effects for *Neisseria gonorrhoeae*** P. Jayasundara*, D.G. Regan, J.G. Wood, *UNSW Sydney, Australia*
[P2.028]	**Successive waves of cholera in South Sudan** F.K. Jones*[1], J.F. Wamala[3], F.J. Luquero[1,2], S. Wohl[1], A.S. Azman[1], [1]*Johns Hopkins Bloomberg School of Public Health, USA,* [2]*Epicentre, France,* [3]*World Health Organization, Switzerland*
[P2.029]	**Childhood vaccines with multiple doses complicate immunization programs and catch-up campaigns** F.K. Jones*[1], K. Mensah[2], J.M. Heraud[3], F.M. Randriatsarafara[4], C.J.E. Metcalf[2], A. Wesolowski[1], [1]*Johns Hopkins Bloomberg School of Public Health, USA,* [2]*Princeton University, USA,* [3]*Institut Pasteur, Madagascar,* [4]*Département de Santé Publique Faculté de Médecine d'Antananarivo, Madagascar*
[P2.030]	**Using measles IgG antibody levels to distinguish immunity due to vaccination and natural infection** K. Joshi*, J. Lessler, *Johns Hopkins Bloomberg School of Public Health, USA*
[P2.031]	**Impact of climatological factors on influenza seasonality in Japan** S. Jung*, A.R. Akhmetzhanov, H. Nishiura, *Hokkaido University, Japan*
[P2.032]	**Superspreader and keystone species for multi-host parasites: community network properties matter as much as species properties** S. Kada*[1], K. McCoy[2,4], T. Boulinier[3,4], B. Roche[2,4], [1]*CDC - Dengue Branch, Puerto Rico,* [2]*MIVEGEC - IRD, France,* [3]*CEFE, France,* [4]*Universite de Montpellier, France*
[P2.033]	**Leveraging pathogen sequence data to enhance vaccine trials in emerging epidemics** R. Kahn*, M. Lipsitch, *Harvard T.H. Chan School of Public Health, USA*
[P2.034]	**The Influence of the Absence of Human Papilloma Virus Vaccination in the Population under Mass Screening of Cervical Cancer** M. Kakehashi*, M. Tsunematsu, R. Matsuyama, *Hiroshima University, Japan*
[P2.035]	**Incorporating a dose-response relationship into models of typhoid fever transmission** Y. Kao*[1], M. Antillón[2], V. Pitzer[1], [1]*Yale School of Public Health, USA,* [2]*Swiss Tropical and Public Health Institute, Switzerland*
[P2.036]	**Simultaneous inference of patient and environment transmission trees in healthcare facilities** L.T. Keegan*[1], M. Leecaster[1,2], K. Khader[1,2], W. Tanner[1], D. Toth[1], M. Samore[1,2], M. Rubin[1,2], [1]*Department of Internal Medicine, Division of Epidemiology, University of Utah, Salt Lake City, Utah, USA,* [2]*Veterans Affairs Salt Lake City Health Care System, Salt Lake City, Utah, USA*
[P2.037]	**Clinical and Epidemiological Aspects of Diphtheria: A Systematic Review and Pooled Analysis** L.T. Keegan*[1], S. Truelove[1], W.J. Moss[1,2], L.H. Chaisson[1], E. Macher[3], A.S. Azman[1,3], J. Lessler[1], [1]*Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA,* [2]*2 International Vaccine Access Center, Department of International Health, Johns Hopkins Bloomberg School of Public Health, USA,* [3]*Médecins Sans Frontières, Geneva, Switzerland*
[P2.038]	**Mathematical Model and Intervention Strategies for a New Emerging Influenza: Based on A(H1N1)pdm09 in the Republic of Korea** S. Kim*, E. Jung, *Konkuk University, Republic of Korea*

[P2.039]	**Impact of Strategies for Use of Future MERS-CoV Vaccines During An Emergency Response: Modeling the 2015 South Korean Outbreak** J.H. Kim*[1], K.S. Lee[1], Y. Chon[1], H.W. Seo[1], S. Cauchemez[2], M. Jit[3], I.K. Yoon[1], [1]*International Vaccine Institute, Republic of Korea,* [2]*Institut Pasteur, France,* [3]*London School of Hygiene and Tropical Medicine, UK*
[P2.040]	**Epidemic dynamics of measles in Japan, 1949-1984** R. Kinoshita*[1], S. Takahashi[2,3], C.J.E. Metcalf[2], H. Nishiura[1], B.T. Grenfell[2], [1]*Hokkaido University, Japan,* [2]*Princeton University, USA,* [3]*University of California, San Francisco, USA*
[P2.041]	**A Generalised linear model for dependent binary outcomes in population sub-units** T. Kinyanjui*, T. House, *University of Manchester, UK*
[P2.042]	**Assessing the impact of a community intervention targeting HIV transmission among PWID in multiple sites in India: insights from transmission models.** A. Kirpich*[1], S.S. Solomon[2], S.H. Mehta[2], D.A.T. Cummings[1], [1]*University of Florida, USA,* [2]*Johns Hopkins University, USA*
[P2.043]	**The decrease in outpatient antibiotic prescribing observed in Massachusetts from 2011-2015 is explained primarily by a reduction in observed disease and secondarily by improved stewardship** S. Kissler*, M. Barnett, Y. Grad, *Harvard T.H. Chan School of Public Health, USA*
[P2.044]	**Measuring herd protection of unvaccinated children: measles-mumps-rubella vaccination coverage in schools in the Netherlands** D. Klinkenberg*, A.J. van Hoek, I. Veldhuijzen, S. Hahné, J. Wallinga, *National Institute for Public Health and the Environment, The Netherlands*
[P2.045]	**Bayesian analysis of spatial and age-group dynamics in the spread of the 2009 influenza pandemic in England** E. Knock*, M. Baguelin, *Imperial College London, UK*
[P2.046]	**A Systematic Bayesian Integration of Epidemiological, Genetic and Movement Data** S.K. Kodikara*[1], M.S.Y. Lau[2], M. van Andel[3], M.A. Stevenson[4], B.T. Grenfell[5], N. French[6], L. Stone[1,7], H. Demirhan[1], S.M. Firestone[4], [1]*Royal Melbourne Institute of Technology, Australia,* [2]*Emory University, USA,* [3]*Ministry of Primary Industries, New Zealand,* [4]*The University of Melbourne, Australia,* [5]*Princeton, USA,* [6]*Massey University, New Zealand,* [7]*Tel-Aviv University, Israel*
[P2.047]	**Molecular evolutionary analysis of dengue virus 2 strains isolated from Koreans traveling abroad** E.H. Hwang, G. Kim, H.S. Oh, J.J. Hong, B.S. Koo*, *Korea Research Institute of Bioscience and Biotechnology, Republic of Korea*
[P2.048]	**Latent tuberculosis screening and treatment impact on tuberculosis elimination in a low-prevalence country: a mathematical modelling approach** H. Korthals Altes*[3], D. Klinkenberg[3], I. Spruijt[1], C. Erkens[1], D. van Soolingen[3], F. Cobelens[2], S. van den Hof[3], [1]*KNCV Tuberculosis Foundation, The Netherlands,* [2]*Amsterdam University Medical Center, The Netherlands,* [3]*National Institute for Public Health and the Environment, The Netherlands*
[P2.049]	**Catastrophic consequences of in utero mother-child transmission: Mechanistic modeling of Zika and other viral pathogens** A.N.M. Kraay*, A.F. Brouwer, M.C. Eisenberg, *University of Michigan, USA*
[P2.050]	**Interacting dynamics of health-risk related opinions and infectious disease** A. Teslya[1], E. Alsina[1], M.E. Kretzschmar*[1,2], [1]*Utrecht University, The Netherlands,* [2]*National Institute of Public Health and the Environment (RIVM), The Netherlands*
[P2.051]	**Systematic review of epidemic models of contact tracing for severe acute respiratory syndrome and middle east respiratory syndrome** K.O. Kwok*[1,2], A. Tang[3], W.I. Wei[1], H.P. Woo[3], E.K. Yeoh[1], S. Riley[4], [1]*The Chinese University of Hong Kong, Hong Kong,* [2]*Sungkyunkwan University, Republic of Korea,* [3]*MRC Centre for Outbreak Analysis and Modelling, UK*
[P2.052]	**Lineage-specific dynamics of antibody responses to influenza B virus infections** Y.C. Lau*[1], R.A.P.M. Perera[1], V.J. Fang[1], L.H. Luk[1], D.K.W. Chu[1], P. Wu[1], I.G. Barr[2,3], J.S.M. Peiris[1], B.J. Cowling[1], [1]*The University of Hong Kong, Hong Kong,* [2]*World Health Organization Collaborating Centre for Reference and Research, Australia,* [3]*University of Melbourne, Australia*

[P2.053]	**Modelling the transmission dynamics of influenza B virus by lineage** Y.C. Lau*, S.T. Ali, B.J. Cowling, E.H.Y. Lau, P. Wu, *The University of Hong Kong, Hong Kong*
[P2.054]	**A systematic review on dog rabies dynamics: towards the integration of modelling and phylogeography analyses** M. Layan*[1,2], H. Bourhy[2], H. Salje[2], S. Cauchemez[2], [1]*Pasteur-CNAM School of Public Health, France,* [2]*Institut Pasteur, France*
[P2.055]	**Mathematical modelling to study the horizontal transfer of antimicrobial resistance genes in bacteria: current state of the field and recommendations** Q. Leclerc*[1], J. Lindsay[2], G. Knight[1], [1]*London School of Hygiene & Tropical Medicine, UK,* [2]*St George's University of London, UK*
[P2.056]	**Chagas Disease Force of Infection and disease burden estimation at the departmental level in Colombia** J. Ledien*[1], Z.M. Cucunubá[2], E. Rodriguez-Monguí[3], G.J. Parra-Henao[4], M-G. Basanez[2], P. Nouvellet[1], [1]*University of Sussex, UK,* [2]*Imperial College London, UK,* [3]*PAHO, Colombia,* [4]*Universidad Cooperativa de Colombia, Colombia*
[P2.057]	**Assessing the potential impact of vaccination on ebola virus disease epidemic** H. Lee*, H. Nishiura, *Hokkaido University, Japan*
[P2.058]	**Differences in contact patterns between mild and severe illness in Bangladesh: Nipah virus as a case study** K. Lee*[1], B. Nikolay[2], H.M.S. Sazzad[3], M.J. Hossain[3], M. Rahman[3], S. Luby[4], H. Salje[2], E. Gurley[1], [1]*Johns Hopkins Bloomberg School of Public Health, USA,* [2]*Institut Pasteur, France,* [3]*icddr,b, Bangladesh,* [4]*Stanford, USA*
[P2.059]	**Spatial heterogeneity and control measures during avian influenza epidemic 2016-2017 in South Korea** J. Lee*[1], Y. Ko[2], E. Jung[2], [1]*National Institute for Mathematical Sciences, Republic of Korea,* [2]*Konkuk University, Republic of Korea*
[P2.060]	**Molecular surveillance reveals spatio-temporal trends of malaria transmission in Thiès Senegal** A. Lee*[1], S.F. Schaffner[2], R.F. Daniels[3], Y.D. Ndiaye[4], A.B. Deme[4], A.S. Badiane[5], B. MacInnis[2], S.K. Volkman[3], D.F. Wirth[3], D. Ndiaye[5], [1]*Institute for Diseaes Modeling, USA,* [2]*Broad Institute, USA,* [3]*Harvard T.H. Chan School of Public Health, USA,* [4]*Dantec Teaching and Research Hospital, Senegal,* [5]*Cheikh Anta Diop University, Senegal,* [6]*Harvard University, USA*
[P2.061]	**Social contact networks and implications for influenza transmission in 11 schools** M. Leecaster*[1], K. Khader[1,2], M. Samore[1,2], [1]*University of Utah, USA,* [2]*Veterans Affairs, USA*
[P2.062]	**Patterns of healthcare provider visits to patient rooms in two intensive care units** M. Leecaster*[1,2], K. Khader[1,2], M. Rubin[1,2], [1]*University of Utah, USA,* [2]*Veterans Affairs, USA*
[P2.063]	**Understanding whopping cough maintenance and spread across spatial scales using genetic data** N. Lefrancq*, V. Bouchez, J. Toubiana, S. Guillot, S. Cauchemez, H. Salje, S. Brisse, *Institut Pasteur, Paris, France*
[P2.064]	**Incorporating environmental variables into mosquito gene drive modelling: fine-scale dispersal, temperature, and landscape-dependent connectivity** T.M. León*[1], J.B. Bennett[1], A.J. Cornel[2], J.M. Marshall[1], [1]*University of California, Berkeley, USA,* [2]*University of California, Davis, USA*
[P2.065]	**Habitat sharing, interactions and viral populations at the interface between bats and pigs in italian intensive farms** S. Leopardi*[1], P. Priori[2], L. Cavicchio[1], G. Zamperin[1], M.S. Beato[1], P. De Benedictis[1], [1]*istituto zooprofilattico sperimentale delle venezie, Italy,* [2]*S.T.E.R.N.A., Italy*
[P2.066]	**Modelling of the impact of environmental transmission on the long term prevalence of antimicrobial resistance in humans** H.C. Lepper*, M.E.J. Woolhouse, B.A.D. van Bunnik, *University of Edinburgh, UK*
[P2.067]	**Identifying the community and household transmission of tuberculosis via random graphs: findings based on a Brazilian household contact study** T. Li*, L. White, *Boston University, USA*
[P2.068]	**Intrinsic and extrinsic drivers of transmission dynamics of hemorrhagic fever with renal syndrome caused by Seoul hantavirus** Y. Li*[1], B. Cazelles[2], G. Yang[3], M. Laine[4], Z. Huang[5], J. Cai[6], H. Tan[7], N.C. Stenseth[8], H. Tian[1], [1]*Beijing Normal University, China,* [2]*IBENS, UMR 8197 CNRS-ENS Ecole Normale Supérieure,*

	France, [3]Huludao Municipal Center for Disease Control and Prevention, China, [4]Finnish Meteorological Institute, Finland, [5]Nanjing Normal University, China, [6]Tsinghua University, China, [7]University of Texas Health Science Center, USA, [8]University of Oslo, Norway
[P2.069]	**Mathematical model of meropenem against Mycobacterium tuberculosis** J. Liang*[1], M.P. Arenaz-Callao[2], S. Ramón-García[2], P. Abel zur Wiesch[1,3], *[1]University of Tromsø, Norway, [2]Research & Development Agency of Aragon (ARAID) Foundation, Spain, [3]Pennsylvania State University, USA, [4]Nordic EMBL Partnership, Norway*
[P2.070]	**Impact of mass vaccination campaigns on measles transmission during a nationwide outbreak in Guinea, 2017** N. Linton*[2,1], M. Keita[3], M. Moitinho de Almeida[1], J. Gil Cuesta[4], D. Guha Sapir[1], H. Nishiura[2], J. van Loenhout[1], *[1]UCLouvain, Belgium, [2]Hokkaido University, Japan, [3]World Health Organization Country Office, Guinea, [4]Médecins Sans Frontières, Luxembourg*
[P2.071]	**Impact of treatment thresholds and co-operation on the evolution of treatment resistance in sea lice** D. Lipschutz-Powell*[1], A. O'Hare[2], A. Sturm[2], A.G. Murray[3], J. Enright[1], *[1]University of Edinburgh, UK, [2]University of Stirling, UK, [3]Marine Scotland, UK*
[P2.072]	**Correcting prevalence estimates in a digital health surveillance system by estimating user behaviours** D. Liu*[1], L. Mitchell[1,2], R.C. Cope[1], S.J. Carlson[3], J.V. Ross[1], *[1]The University of Adelaide, Australia, [2]Data to Decisions CRC, Australia, [3]Hunter New England Population Health, Australia*
[P2.073]	**A Bayesian approach for predicting pneumococcal serotype-specific invasiveness in children and adults in global settings** A. Løchen*, J. Truscott, N. Croucher, *Imperial College London, UK*
[P2.074]	**Emergent intensive care unit population structure drives differential methicillin-resistant *Staphylococcus aureus* colonization dynamics** M. Mietchen[1], C. Short[1], M. Samore[2], E. Lofgren*[1], *[1]Washington State University, USA, [2]University of Utah, USA*
[P2.075]	**Retrospective analysis of mosquito abundance and infection with West Nile in Sardinia, Italy** F. Loi*[1,2], C. Foxi[1], G. Satta[1], A. Coccollone[1,2], S. Rolesu[1,2], S. Cappai[1,2], *[1]Istituto Zooprofilattico Sperimentale della Sardegna, Italy, [2]Osservatorio Epidemiologico Veterinario Regionale della Sardegna, Italy*
[P2.076]	**Modelling the health benefits of a rapid intervention in an influenza pandemic with a partially matched pre-pandemic vaccine** S. Lovick*[1], V.H. Nguyen[2], M. Mazur[3], *[1]Sam Lovick Consulting, Australia, [2]VHN consulting, Canada, [3]Seqirus, United States Minor Outlying Islands*
[P2.077]	**Obesity and influenza A transmission in households in Managua, Nicaragua** H.E. Maier*[1], G. Kuan[2,3], L. Gresh[2], R. Lopez[2,3], N. Sanchez[2], A. Schiller[1], S. Ojeda[2], A. Balmaseda[1], A. Gordon[1], *[1]University of Michigan, USA, [2]Sustainable Sciences Institute, Nicaragua, [3]Ministry of Health, Nicaragua*
[P2.078]	**Basic reproduction number of the inter-farm spread of porcine epidemic diarrhea during the initial phase of the epidemic in Japan in 2013-2014** K. Makita*[1], T. Yamamoto[1], *[1]Rakuno Gakuen University, Japan, [2]National Institute of Animal Health, Japan*
[P2.079]	**Potential strategic plan for diagnosis of drug resistance tuberculosis in India: A model based analysis** S. Mandal*[1], V. Bhatia[2], N. Arinaminpathy[3], *[1]Public Health Foundation of India, India, [2]World Health Organization, India, [3]Imperial College, UK*
[P2.080]	**The dynamics of influenza A(H3N2) defective viral genomes from a human challenge study** M.A. Martin*[1], C.W. Woods[2], K. Koelle[1], *[1]Emory University, USA, [2]Duke University, USA*
[P2.081]	**Cost-effectiveness of post-treatment follow-up and secondary prevention of tuberculosis in a high-incidence setting – a model-based analysis** F.M. Marx*[1,2], T. Cohen[3], N.A. Menzies[4], J.A. Salomon[5], R. Yaesoubi[3], *[1]DST-NRF South African Centre of Excellence in Epidemiological Modelling and Analysis, South Africa, [2]Stellenbosch University, South Africa, [3]Yale School of Public Health, USA, [4]Harvard T H Chan School of Public Health, USA, [5]Stanford University School of Medicine, USA*

[P2.082]	**Measles vaccination of parents to hasten the progress towards measles elimination in Italy** V. Marziano*[1], P. Poletti[1], F. Trentini[1], A. Melegaro[2], M. Ajelli[1,3], S. Merler[1], [1]*Fondazione Bruno Kessler, Italy,* [2]*Bocconi University, Italy,* [3]*Northeastern University, USA*
[P2.083]	**Modelling the environmental transmission of norovirus within a hierarchical population structure: A re-analysis of an outbreak event during a jamboree in the Netherlands in 2004** R. Matsuyama*[1], M.C.M. de Jong[1], [1]*Hiroshima University, Japan,* [2]*Wageningen University & Research, The Netherlands*
[P2.084]	**Linking real-time evidence and pandemic plans: what do we do next?** F.M. Shearer, R. Moss, J.M. McCaw*, *The University of Melbourne, Australia*
[P2.085]	**What constitutes 'best' use of limited vaccine supplies in early pandemic response?** R. Moss[1], A. Dawson[2], J. Fielding[1], P. Massey[3,4], S.G. Sullivan[1], J. Williams[2], J.M. McCaw[1], J. McVernon*[1], [1]*The University of Melbourne, Australia,* [2]*The University of Sydney, Australia,* [3]*Hunter New England Population Health, Australia,* [4]*James Cook University, Australia,* [5]*Murdoch Childrens Research Institute, Australia*
[P2.086]	**Measuring *Plasmodium falciparum*relatedness and population connectivity in high transmission settings** S. Mehra*[1,2], G.L. Harrison[1], M. Hetzel[3,4], P. Siba[3], I. Mueller[1,5], M. Bahlo[1,2], A.E. Barry[1,2], [1]*Walter and Eliza Hall Institute of Medical Research, Australia,* [2]*University of Melbourne, Australia,* [3]*Papua New Guinea Institute of Medical Research, Papua New Guinea,* [4]*Swiss Tropical and Public Health Institute, Switzerland,* [5]*Institut Pasteur Paris, France*
[P2.087]	**Capturing heterogeneous infectiousness in transmission dynamic models of tuberculosis: A compartmental modelling approach** Y. Melsew*[1,2], R. Ragonnet[1], A. Cheng[1], E. McBryde[3], J. Trauer[1], [1]*Monash University, Australia,* [2]*University of Gondar, Ethiopia,* [3]*James Cook University, Australia*
[P2.088]	**Multi-pathogen forecasting via state space approaches and filtering methods** X. Meng*, N. Reich, *University of Massachusetts Amherst, USA*
[P2.089]	**2018 Enterovirus D68 outbreak detection through a syndromic disease epidemiology network** L. Meyers*[1], B. Galvin[1], J. Nawrocki[1], K. Olin[1], A. Leber[2], [1]*BioFire Diagnostics, USA,* [2]*nationwide Children's Hospital, USA*
[P2.090]	**Tuberculosis transmission and social network structure: Simulations on structured networks and a case study in Kampala, Uganda** P.B. Miller*[1,2], J.M. Drake[1,2], N. Kiwanuka[3], C.C. Whalen[1], [1]*University of Georgia, USA,* [2]*Center for the Ecology of Infectious Diseases, USA,* [3]*Makerere University, Uganda*
[P2.091]	**Quantifying the improvement of targeted screening for sleeping sickness using a novel age-structured model** B. Miller*, K.S. Rock, M.J. Keeling, *University of Warwick, UK*
[P2.092]	**Quantifying antibody dynamics following influenza virus infection using high-resolution diagnostic and serological data from the PHIRST study in South Africa** A. Minter*, A. Kucharski, *London School of Hygiene and Tropical Medicine, UK*
[P2.093]	**The longstanding effects of disease awareness and social memory on infectious disease transmission in multi-generational networks** D. Mistry*[1], L. Hébert-Dufresne[2], B.M. Althouse[1,3], [1]*Institute for Disease Modeling, USA,* [2]*University of Vermont, USA,* [3]*University of Washington, USA,* [4]*New Mexico State University, Las Cruces, USA*
[P2.094]	**How to use human challenge studies to predict the effect of variable susceptibility on infection dynamics and the impact of vaccination: an application for norovirus** F. Miura*[1,2], D. Klinkenberg[2], J. Wallinga[2,3], [1]*The university of Tokyo, Japan,* [2]*National institute for public health and the environment, The Netherlands,* [3]*Leiden university medical center, The Netherlands*
[P2.095]	**Estimating human-to-human transmission potential of avian influenza H5N1 in Egypt: Analysis using genetic sequence data** W. Mohamed*, R. Omori, K. Ito, *Hokkaido University, Japan*
[P2.096]	**Modelling the effect of livestock antibiotic usage on human food-borne disease** A.L.K. Morgan*, M.E.J. Woolhouse, B.A.D. van Bunnik, *University of Edinburgh, UK*
[P2.097]	**Direct intervention effects in randomized and observational studies of infectious diseases** O. Morozova*, D.J. Eck, F.W. Crawford, *Yale University, USA*

[P2.098]	**An epidemic modelling framework for implementation science and local public health policy support** M. Morris*, J.K. Birnbaum, D.T. Hamilton, *University of Washington, USA*
[P2.099]	**A network-based mathematical model to evaluate the impact of pre-exposure prophylaxis on HIV incidence among men who have sex with men (MSM) in Washington State: context matters** D.W. Rao[1], S. Goodreau[1], M.R. Golden[1,2], M. Morris*[1], [1]*University of Washington, USA,* [2]*Public Health--Seattle & King County, USA*
[P2.100]	**Estimating the burden of antimalarial treatment failure in Africa: Evidence from household surveys** A. Mousa*, J.D. Challenger, A.C. Ghani, L.C. Okell, *Imperial College London, UK*
[P2.101]	**Building local capacity in use of mathematical models in public health in Kenya** Z.E. Mthombothi*[1], E.D. Dominic[1], I. Kombe[2,3], J. Dawa[4,5], S.M. Thumbi[4,5], J.R.C. Pulliam[1], [1]*Stellenbosch University, South Africa,* [2]*Kenya Medical Research Institute Center for Geographical Medicine Research, Kenya,* [3]*London School of Hygiene & Tropical Medicine, UK,* [4]*University of Nairobi Institute of Tropical and Infectious Diseases, Kenya,* [5]*Washington State University, USA,* [6]*Center for Global Health Research, Kenya*
[P2.102]	**TB diagnostic testing using GeneXpert and whole-genome sequencing in England: A cost-effectiveness analysis using transmission-dynamic modelling** T. Mugwagwa*[1,2], I. Abubakar[1,3], P.J. White[1,2], [1]*Public Health England, UK,* [2]*Imperial College London, UK,* [3]*University College London, UK*
[P2.103]	**Descriptive analysis of contact network structure among tuberculosis cases and their contacts, Birmingham, United Kingdom** M. Munang*[1,2], M. Dedicoat[2], G. Medley[3], D. Hollingsworth[4], [1]*University of Warwick, UK,* [2]*Heart of England NHS Foundation Trust, UK,* [3]*London School of Hygiene and Tropical Medicine, UK,* [4]*University of Oxford, UK*
[P2.104]	**What happens to tuberculosis contacts? Competing risks application to estimate risks of infection with single versus repeat exposures** M. Munang*[1,2], M. Dedicoat[2], D. Hollingsworth[1,3], G. Medley[4], [1]*University of Warwick, UK,* [2]*Heart of England NHS Foundation Trust, UK,* [3]*University of Oxford, UK,* [4]*London School of Hygiene and Tropical Medicine, UK*
[P2.105]	**Assessing outbreak risk using a national social network of school children: A case study of measles in the Netherlands** J.D. Munday*[1], D. Klinkenberg[2], M. Meurs[3], E. Fleur[3], S. Hahné[2], J. Wallinga[2], K.E. Atkins[1,4], A.J. van Hoek[1,2], [1]*London School of Hygiene and Tropical Medicine, UK,* [2]*National Institute for Public Health and the Environment (RIVM), The Netherlands,* [3]*The Education Executive Agency of the Dutch Ministry of Education, The Netherlands,* [4]*The University of Edinburgh, UK*
[P2.106]	**Analysis of a pathogen driven model for Influenza-Like-Illness forecasting in the US 2018-2019 season** J. Nawrocki*, K. Olin, B. Galvin, J. Jones, L. Meyers, *BioFire Diagnostics, LLC, USA*
[P2.107]	**Platform diagnostic technology could reduce epidemic size in outbreaks of previously unknown infectious diseases** C. Nelson*, R. Thompson, M. Bonsall, *University of Oxford, UK*
[P2.108]	**Attributing diarrheal disease to norovirus across epidemiologic contexts** K.N. Nelson*, B.A. Lopman, *Emory University, USA*
[P2.109]	Will be presented in Poster session 3
[P2.110]	**Modeling the spatiotemporal dynamics of dengue epidemic in French Polynesia** T. Nemoto*[1,2], H. Salje[1], M. Aubry[3], Y. Teissier[3,4], R. Paul[1,5], V.M. Cao-Lormeau[3], S. Cauchemez[1], [1]*Institut pasteur, France,* [2]*École Normale Supérieure, France,* [3]*Institut Louis Malardé, French Polynesia,* [4]*Ministry of Health, French Polynesia,* [5]*Pasteur Kyoto International Joint Research Unit for Integrative Vaccinomics, Japan*
[P2.111]	**The epidemiological and economic impact of a cell-based quadrivalent influenza vaccine in adult population in the United States: A dynamic modelling approach** V.H. Nguyen*[1], Y. Hilsky[2], J. Mould-Quevedo[2], [1]*VHN Consulting, Canada,* [2]*Seqirus Vaccines Ltd., USA*

[P2.112]	**Quantifying effects of antibiotics and probiotics on the microbiomes of neonates in an intensive care unit** R. Niehus*[1], S. Gweon[2], P. Turner[3], M. Lipsitch[1], [1]*Harvard T.H. Chan School of Public Health, USA,* [2]*University of Reading, UK,* [3]*University of Oxford, UK*
[P2.113]	**A framework to monitor changes in transmission and epidemiology of emerging pathogens: Lessons from Nipah virus** B. Nikolay*[1], H. Salje[1], A.K.M. Khan[2], H.M.S. Sazzad[2], S.M. Satter[2], M. Rahman[2], S. Doan[3], B. Knust[3], M.S. Flora[4], S.P. Luby[5], [1]*Institut Pasteur, France,* [2]*icddr,b, Bangladesh,* [3]*Centers for Disease Control and Prevention, USA,* [4]*Institute of Epidemiology Disease Control and Research, Bangladesh,* [5]*Stanford University, USA,* [6]*Johns Hopkins Bloomberg School of Public Health, USA*
[P2.114]	**Nipah vaccine trials- assessing the feasibility based on previous outbreaks in Bangladesh** B. Nikolay*[1], H. Salje[1], M. Lipsitch[2], S.P. Luby[3], E.S. Gurley[4,5], S. Cauchemez[1], [1]*Institut Pasteur, France,* [2]*Harvard T.H. Chan School of Public Health, USA,* [3]*Stanford University, USA,* [4]*icddr,b, Bangladesh,* [5]*Johns Hopkins Bloomberg School of Public Health, USA*
[P2.115]	**Measles in the context of an international migration crisis at the Brazil - Venezuela border** Z.M. Cucunubá[1], A. Freitas[2], M.C. Castro[3], A. Cuspoca[4], M. Pons-Salort[1], I. Rodriguez-Barraquer[5], N. Ferguson[1], A. Cori*[1], [1]*MRC Centre for Global Infectious Disease Analysis, Imperial College London, UK,* [2]*São Leopoldo Mandic Medical School, Brazil,* [3]*Harvard T.H. Chan School of Public Health, USA,* [4]*Universidad Pedagógica y Tecnológica de Colombia, Colombia,* [5]*University of California, USA*
	Poster Session 3 **Thursday 5 December** **17:00-19:00**
[P3.001]	**Estimating the impact of vaccination for disease eradication strategies** D. Olivera*, P. Winskill, K. Hauck, A. Ghani, *Imperial College London, UK*
[P3.002]	**Associations between different sexually transmitted infections propagating on sexual networks of men who have sex with men** R. Omori*[1], L. Abu-Raddad[1], [1]*Hokkaido University, Japan,* [2]*Weill Cornell Medical College – Qatar, Qatar*
[P3.003]	**Stochastic simulation of disease spread and parental vaccine acceptance diffusion using random network models** T. Oraby*, C. Stuart, A. Balogh, *The University oF Texas Rio Grande Valley, USA*
[P3.004]	**Epidemiological characteristic of social contact structure in Biliran Island, Philippines** H. Otomaru*[1], T. Kamigaki[1], J. Sornillo[2], H. Oshitani[1], [1]*Tohoku University, Japan,* [2]*Research Institute for Tropical Medicine, The Philippines*
[P3.005]	**Long term immunity against hepatitis B in Mongolia** S. Oyu-Erdene*, M. Yerkebulan, H. Ser-Od, E. Uranbaigali, N. Bira, R. Otgonbayar, D. Davaalkham, *MNUMS, Mongolia*
[P3.006]	**Insights from a mathematical model of gonorrhoea transmission which includes female sex worker and client interactions** T.N. Padeniya*[1], J.G. Wood[2], B.B. Hui[1], D.G. Regan[1], [1]*Kirby Institute, Australia,* [2]*School of Public Health and Community Medicine,, Australia*
[P3.007]	**Measles susceptibility in France: Assessing age profile, temporal trends and spatial heterogeneities** J. Paireau*[1], D. Antona[2], L. Fonteneau[2], F. Belghiti[2], D. Che[2], D. Lévy-Bruhl[2], B. Grenfell[3], S. Cauchemez[1], [1]*Institut Pasteur, France,* [2]*Santé publique France, France,* [3]*Princeton University, USA*
[P3.008]	**Using serological data to evaluate the performance of the surveillance system for arboviral infections in French Guiana** J. Paireau*[1], L. Carvalho[2], D. Rousset[3], N. Hozé[1], A. Andrieu[2], C. Rousseau[2], B. Nikolay[1], C. Flamand[3], S. Cauchemez[1], [1]*Institut Pasteur, France,* [2]*CIRE Guyane, French Guiana,* [3]*Institut Pasteur de la Guyane, French Guiana*
[P3.009]	**Ensemble predictions of seasonal influenza epidemics in real-time in France** J. Paireau*[1], A. Andronico[1], S. Bernard-Stoecklin[2], A. Fouillet[2], Y. Le Strat[2], D. Lévy-Bruhl[2], B. Coignard[2], S. Cauchemez[1], [1]*Institut Pasteur, France,* [2]*Santé publique France, France*

[P3.010]	**Genomic epidemiology of toxigenic *Vibrio cholerae* in Haiti: a switch in serotype** T.K. Paisie*, C. Mavian, M. Cash, M.T. Alam, A. Ali, J.G. Morris Jr., M. Salemi, *University of Florida, USA*
[P3.011]	**Estimates of the basic reproduction number for rubella and indicators for the epidemiology of rubella** T. Papadopoulos*[1], E. Vynnycky[1,2], [1]*Public Health England, UK,* [2]*London School of Hygiene & Tropical Medicine, UK*
[P3.012]	**Temporal dynamics of co-circulating lineages of porcine reproductive and respiratory syndrome virus in U.S. swine populations** I. Paploski*[1], C. Corzo[1], A. Rovira[1], M. Murtaugh[1], J. Sanhueza[1], C. Vilalta[1], D. Schroeder[1,2], K. VanderWaal[1], [1]*University of Minnesota, USA,* [2]*University of Reading, UK*
[P3.013]	**Impact of MDR-TB treatment history on pyrazinamide resistance transmission fitness** J. Pecerska*[1,2], S.M. Gygli[3,4], D. Kuhnert[5], C.J. Meehan[6], M. Coscolla[7], B.C. de Jong[8], S. Gagneux[3,4], T. Stadler[1,2], [1]*ETHZ, Switzerland,* [2]*SIB, Switzerland,* [3]*Swiss TPH, Switzerland,* [4]*University of Basel, Switzerland,* [5]*Max Planck Institute for the Science of Human History, Germany,* [6]*University of Bradford, UK,* [7]*University of Valencia-CSIC, Spain,* [8]*Institute of Tropical Medicine, Belgium*
[P3.014]	**Forecasting influenza-like-illness by aggregating predictions for multiple respiratory pathogens** S. Pei*, S. Kandula, J. Shaman, *Columbia University, USA*
[P3.015]	**The hidden burden of measles in Ethiopia: how distance to hospital shapes the disease mortality rate** P. Poletti*[1], S. Parlamento[1], T. Fayyisaa[2], R. Feyyiss[2], M. Lusiani[3], A. Tsegaye[3], G. Segafredo[4], G. Putoto[4], F. Manenti[4], S. Merler[1], [1]*Bruno Kessler Foundation, Italy,* [2]*South West Shoa Zone Health Office, Ethiopia,* [3]*Doctors with Africa CUAMM, Ethiopia,* [4]*Doctors with Africa CUAMM, Italy*
[P3.016]	**Measuring spatiotemporal dependence of disease using the tau and phi statistics: a literature review, normative commentary and new avenues** T.M. Pollington, *University of Warwick, UK*
[P3.017]	**Representing the changing distribution of relationship duration over the lifecourse: Insights and implications for the dynamic network modeling of epidemics** E. Pollock*, S. Goodreau, M. Morris, *University of Washington, USA*
[P3.018]	**Modelling measles importation into the United States using international measles incidence and air passenger travel data** M. Poterek*[1], M. Kraemer[2], A. Watts[3], K. Khan[3], T.A. Perkins[1], [1]*University of Notre Dame, USA,* [2]*Harvard Medical School, USA,* [3]*University of Toronto, Canada*
[P3.019]	**Neighbour effects for achieving Lymphatic Filariasis elimination targets and resurgence** J.M. Prada*[1], L. Reimer[2], T.D. Hollingsworth[3], [1]*University of Surrey, UK,* [2]*Liverpool School of Tropical Medicine, UK,* [3]*University of Oxford, UK*
[P3.020]	**Evaluating the impact of meningococcal vaccines with synthetic controls** O. Prunas*[1,3], M. Tizzoni[2], L. Argante[3], D. Medini[3], [1]*Università degli Studi di Torino, Italy,* [2]*ISI Foundation, Italy,* [3]*GSK Vaccines, Italy*
[P3.021]	**Projecting the impact of a product recall on the South African Listeriosis outbreak** J.R.C. Pulliam*[1], A. Welte[1], K. McCarthy[2], [1]*SACEMA, Stellenbosch University, South Africa,* [2]*National Institute for Communicable Diseases, South Africa*
[P3.022]	**Estimated impact of human papillomavirus vaccines on infection burden: The effect of structural assumptions** C. van Schalkwyk[1], J. Moodley[2], A. Welte[1], J. Pulliam*[1], L. Johnson[2], [1]*University of Stellenbosch, South Africa,* [2]*University of Cape Town, South Africa*
[P3.023]	**Structurally informed evolutionary models improve phylogenetic reconstruction for emerging, seasonal, and pandemic influenza viruses** X. Qiu*[1], J. Bahl[1], [1]*University of Georgia, USA,* [2]*Duke-National University of Singapore Graduate Medical School, Singapore*

[P3.024]	**Dengue epidemic synchrony in the Americas** T.M. Quandelacy*[1], I. Rodriguez-Barraquer[2], R. Lowe[3], A. Stewart[4], M. Vincenti-Gonzalez[5], E. Ortiz-Prado[6], C. Munayco[7], M. Borbor-Cordova[8], D.A.T. Cummings[13], M. Johansson[1], [1]*Centers for Disease Control and Prevention, USA,* [2]*University of California San Francisco, USA,* [3]*London School of Hygiene and Tropical Medicine, UK,* [4]*State University of New York, USA,* [5]*University of Groningen, The Netherlands,* [6]*Universidad de las Americas, Ecuador,* [7]*Ministerio de Salud, Peru,* [8]*Escuela Superior Politecnica del Litoral, Ecuador,* [9]*Ministry of Health and Welness, Barbados,* [10]*Ministerio de Salud y Asistencia Social, Guatemala,* [11]*Ministerio de Salud, El Salvador,* [12]*Universidad Central de Venezuela, Venezuela,* [13]*University of Florida, USA*
[P3.025]	**Who determines the outcome of infection: Comparing *Leptospira* infection in two species of rodents?** S. Rajeev*[1], K. Shiokawa[2], A. Llanes[4], M. Rajeev[3], C. Restrepo[4], [1]*University Of Florida, USA,* [2]*Ross University, Saint Kitts and Nevis,* [3]*Princeton University, USA,* [4]*INDICASAT, Panama*
[P3.026]	**Spatio-temporal dynamics of pertussis and its association with socio-demographic factors within King County, Washington** M. Rane*[1], E. Halloran[1,2], J. Wakefield[1], [1]*University of Washington, USA,* [2]*Fred Hutchinson Cancer Research Center, USA*
[P3.027]	**Highly-targeted spatiotemporal interventions against cholera epidemics, 2000-2018** R. Ratnayake*, F. Finger, W.J. Edmunds, F. Checchi, *London School of Hygiene and Tropical Medicine, UK*
[P3.028]	**Risk factors for respiratory viral illness among healthcare personnel in the United States, 2011-2015: The ResPECT study** T.M. Perl[1,2], S.M. Rattigan*[3], D.A.T. Cummings[2,3], J. Lykken[1], L.J. Radonovich[1], [1]*University of Texas Southwestern, USA,* [2]*Johns Hopkins Bloomberg School of Public Health, USA,* [3]*University of Florida, USA,* [4]*Michael E DeBakey Veterans Affairs Medical Center, USA,* [5]*Baylor College of Medicine, USA,* [6]*Veterans Affairs New York Harbor Healthcare System, USA,* [7]*Veterans Affairs Eastern Colorado Healthcare System, USA,* [8]*University of Colorado - Denver School of Medicine, USA,* [9]*Veterans Affairs Medical Center DC, USA,* [10]*George Washington University School of Medical and Health Sciences, USA,* [11]*Children's Hospital Colorado, USA,* [12]*Denver Health, USA,* [13]*University of Massachusetts Amherst, USA,* [14]*Johns Hopkins School of Medicine, USA,* [15]*Veterans Affairs St Louis Healthcare System, USA,* [16]*Saint Louis University School of Medicine, USA,* [17]*Centers for Disease Control and Prevention, USA*
[P3.029]	**Toward more refined influenza forecasts: Using virologic testing data sources to inform pathogen-specific model structure** E.L. Ray*[1], I. Beaudry[2], G.C. Gibson[3], N.G. Reich[3], [1]*Mount Holyoke College, USA,* [2]*Pontificia Universidad Catolica de Chile, Chile,* [3]*University of Massachusetts Amherst, USA*
[P3.030]	**Evolution of higher HIV virulence in response to a theoretical disease-modifying vaccine: A modeling study** M. Reid*, J. Murphy, K. Peebles, S. Stansfield, S. Goodreau, N. Abernethy, G. Gottlieb, J. Mittler, J. Herbeck, *University of Washington, USA*
[P3.031]	**Contagion and homophily of mental health status in a social network of university students** A. Renson*[1], A. Ye[1], P. Zivich III[1], A. Volfovsky[2], A. Aiello[1], [1]*University of North Carolina-Chapel Hill, USA,* [2]*Duke University, USA*
[P3.032]	**Assessment of public health interventions impact, focus on Dengue in Rio de Janeiro** G. Ribeiro dos Santos*, S. Cauchemez, H. Salje, *Institut Pasteur, France*
[P3.033]	**How landscape connectivity modulates the spatial-temporal dynamics of wild yellow fever virus?** P. Ribeiro Prist*[1], L. Reverberi Tambosi[2], J. R. Rhodes[5], A. Pinter[3], L.F. Mucci[3], R. Pereira de Souza[4], J.P. Metzger[1], [1]*University of Sao Paulo, Brazil,* [2]*Universidade Federal do ABC, Brazil,* [3]*Endemics Control Superintendence, Brazil,* [4]*Adolfo Lutz Institute, Brazil,* [5]*The University of Queensland, Australia*
[P3.034]	**The potential impact of new, urine-based tests for TB: A modelling study** S. Ricks*[1], C. Denkinger[2], S. Schumacher[2], N. Arinaminpathy[1], [1]*Imperial College London, UK,* [2]*FIND, Switzerland*

[P3.035]	**The EPIFORGE initiative: Development of an epidemic forecasting reporting guideline to standardize forecasting reporting, reproducibility and transparency** S. Pollett[1,2], M. Johansson[3], D. Brett-Major[2], N. Reich[4], A. Deshpande[6], A. Stewart-Ibarra[7], R. Sippy[7], I. Maljkovic Berry[1], C. Viboud[9], C. Rivers*[10], [1]*Walter Reed Army Institute of Research, USA,* [2]*USUHS, USA,* [3]*Centers for Disease Control and Prevention, USA,* [4]*University of Massachusetts Amherst, USA,* [5]*National Academies of Sciences, Engineering, and Medicine, USA,* [6]*Los Alamos National Laboratory, USA,* [7]*SUNY, USA,* [8]*Armed Forces Health Surveillance Branch, USA,* [9]*National Institutes of Health, USA,* [10]*Johns Hopkins Center for Health Security, USA*
[P3.036]	**Challenges and opportunities in using modelling to support public health decision making** C. Rivers*, D. Meyer, M. Snyder, *Johns Hopkins, USA*
[P3.037]	**Human density: A neglected yet fundamental axis for mosquito-borne models in urban landscapes** V. Romeo-Aznar*[1,2], M. Pascual[1,3], [1]*University of Chicago, USA,* [2]*Mansueto institute, USA,* [3]*Santa Fe Institute, USA*
[P3.038]	**Assessment of parameter identifibility in the presence of overdispersion: comparison of estimation methods** K. Roosa*[1], R. Luo[1], G. Chowell[1,2], [1]*Georgia State University, USA,* [2]*National Institute of Health, USA*
[P3.039]	**Modelling West Nile virus transmission in Emilia-Romagna region (Italy): 2018 vs. previous seasons** G. Marini[1], M. Calzolari[2], I. Dorigatti[3], B. Nikolay[4], A. Pugliese[5], M. Tamba[2], R. Rosa'*[5,1], [1]*San Michele all'Adige (Trento), Italy,* [2]*Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Italy,* [3]*Imperial College London, UK,* [4]*Institut Pasteur, France,* [5]*University of Trento, Italy*
[P3.040]	**Is vaccination of patients and visitors in healthcare centres an effective strategy in controlling an outbreak of Ebola Virus Disease?** A. Rosello*[1], A. Kucharski[1], A. Camacho[2], W.J. Edmunds[1], [1]*London School of Hygiene & Tropical Medicine, UK,* [2]*MSF, France*
[P3.041]	**Mathematically modeling spillover dynamics of emerging infectious zoonoses with intermediate hosts** K. Royce*, F. Fu, *Dartmouth College, USA*
[P3.042]	**A data-driven analysis of the impact of vaccination against cytomegalovirus** G. Rozhnova*[1,2], M. Kretzschmar[1,2], F. van der Klis[2], D. van Baarle[1,2], M. Korndewal[2], M. van Boven[2], [1]*University Medical Center Utrecht, The Netherlands,* [2]*National Institute of Public Health and the Environment, The Netherlands*
[P3.043]	**Early warning of hand, foot, and mouth disease in Hunan Province, China** J. Rui*[1], K. Luo[2], Q. Chen[3], [1]*Xiamen University, China,* [2]*Hunan Provincial Center for Disease Control and Prevention, China,* [3]*Xiang'an Hospital of Xiamen University, China*
[P3.044]	**Beware of using homogeneous models to describe epidemics in heterogeneous populations** R. Sachak-Patwa*, H.M. Byrne, R.N. Thompson, *University of Oxford, UK*
[P3.045]	**Investigating the risk for importation of Zika virus into Canada under current and future climate** T. Sadeghieh*[1,2], J. Sargeant[1], A. Greer[1], O. Berke[1], V. Ng[2], [1]*University of Guelph, Canada,* [2]*Public Health Agency of Canada, Canada*
[P3.046]	**Drivers of resistance in Uganda and Malawi (DRUM)** M. Sammarro*[1,2], C. Jewell[1], L. Sedda[1], N. Feasey[2,3], [1]*Lancaster University, UK,* [2]*Liverpool School of Tropical Medicine, UK,* [3]*Malawi-Liverpool-Wellcome Trust Clinical Research Programme, Malawi*
[P3.047]	**Understanding circulation of Ebolaviruses in nature: What can we learn from serological surveillance?** S.N. Seifert*[1], T. Bushmaker[1], E. Kuisma[2], [1]*National Institutes of Health, USA,* [2]*Wildlife Conservation Society, Congo,* [3]*Wildlife Conservation Society, USA,* [4]*Uniformed Services University, USA,* [5]*Service d'Epidémiologie Moléculaire, Laboratoire National de Santé Publique, Congo*

[P3.048]	**Agricultural land-uses consistently exacerbate infectious disease risks in Southeast Asia: A systematic review and meta-analysis** H. Shah*[1], P. Huxley[1], J. Elmes[2,1], K. Murray[1], [1]*Imperial College London, UK,* [2]*London School of Hygiene and Tropical Medicine, UK*
[P3.049]	**Changes in malaria hotspots during a mass test and treat trial in western Kenya, 2013-2015** M.P. Shah*[1,2], L.A. Waller[1], W. Odongo[3], S. Kariuki[3], A.M. Samuels[2], M. Desai[2], M.R. Kramer[1], [1]*Emory Universit, USA,* [2]*Centers for Disease Control and Prevention, USA,* [3]*Kenya Medical Research Institute, Kenya*
[P3.050]	**Impact and effectiveness of state-level tuberculosis interventions in California, Florida, New York and Texas: A model-based analysis** S. Shrestha*[1], S. Cherng[1], A.N. Hill[2], S. Reynolds[2], J. Flood[3], P.M. Barry[3], A. Readhead[3], A. Oxtoby[4], M. Lauzardo[5], T. Privett[6], [1]*Johns Hopkins Bloomberg School of Public Health, USA,* [2]*Centers for Disease Control and Prevention, USA,* [3]*California Department of Public Health, USA,* [4]*New York State Department of Health, USA,* [5]*University of Florida, USA,* [6]*Florida Department of Health, USA*
[P3.051]	**Foodborne outbreak calendar synchronization: A time series analysis application** R.B. Simpson*[1], B. Zhou[1], S. Babool[2], E.N. Naumova[1], [1]*Tufts University Friedman School of Nutrition Science and Policy, USA,* [2]*University of Texas at Dallas, USA*
[P3.052]	**Structural network characteristics and vulnerability to rapid HIV transmission among people who inject drugs in a rural county in the United States: a modelling study** A.L. Singleton*[1], B.D.L. Marshall[1], M.T. Harrison[1], S.M. Goodreau[2], W.C. Goedel[1], [1]*Brown University, USA,* [2]*University of Washington, USA*
[P3.053]	**Interplay between geography and HIV transmission clusters in Los Angeles County** B. Skaathun*[1], M. Ragonnet-Cronin[1,2], Z. Sheng[3], K. Poortinga[3], Y.W. Hu[3], J.O. Wertheim[1], [1]*University of California, USA,* [2]*Imperial College London, UK,* [3]*Division of HIV and STD Programs, USA*
[P3.054]	**A spatial analysis of global health system performance and emerging infectious disease risk** J.E. Skarp*, K. Hauck, A. Cori, *Imperial College London, UK*
[P3.055]	**Interspecies interactions as drivers of antimicrobial resistance dynamics: A mathematical modelling study** D.R.M. Smith*[1,2], L. Temime[2], L. Opatowski[1], [1]*Institut Pasteur, France,* [2]*Conservatoire national des Arts et Métiers, France*
[P3.056]	**Validation and simulation of SABBIDiM-E: A Spatial, Agent-Based, Bayesian Infectious Disease Model of Ebola** N.R. Smith*, J. Keith, *Monash University, Australia*
[P3.057]	**Mitigation strategies for pandemic and seasonal influenza of South Korea** W-S. Son, *National Institute for Mathematical Sciences, Republic of Korea*
[P3.058]	**Multi-scale superinfection models in evolutionary epidemiology** H. Stage*[1], L. Pellis[1,2], [1]*The University of Manchester, UK,* [2]*The University of Warwick, UK*
[P3.059]	**Increasing PrEP coverage may select for less virulent HIV: a modeling study** S.E. Stansfield*, J.T. Herbeck, G.S. Gottlieb, N.F. Abernethy, J.T. Murphy, J.E. Mittler, S.M. Goodreau, *University of Washington, USA*
[P3.060]	**The H5 highly pathogenic avian influenza: understanding the patterns of virus spreading to/from Africa** A. Fusaro[1], B. Zecchin[1], B. Vrancken[2], C. Abolnik[3], R. Ademun[4], A. Alassane[5], A. Arafa[6], J. Awuni[7], E. Couacy-Hymann[8], M. Coulibaly[9], L. Stefania*[1], [1]*Istituto Zooprofilattico Sperimentale delle Venezie, Italy,* [2]*Rega Institute, Belgium,* [3]*University of Pretoria, South Africa,* [4]*National Animal Disease Diagnostics and Epidemiology Center, Uganda,* [5]*Laboratoire Central de l'Elevage, Niger,* [6]*National Laboratory for Veterinary Quality Control on Poultry Production, Egypt,* [7]*Accra Veterinary Laboratory, Ghana,* [8]*Laboratoire Central de Pathologie Animale, Cote D'Ivoire,* [9]*Laboratoire National D'Appui au Développement Agricole, Cote D'Ivoire,* [10]*CIRAD, France,* [11]*Laboratoire Central Vétérinaire de Lomé, Togo,* [12]*National Veterinary Research Institute, Nigeria,* [13]*Laboratoire National Vétérinaire, Cameroon*
[P3.061]	**Susceptible-Infected-Recovered-model (SIR) with movement-a new model for diesease outbreaks-** T. Stegmaier*, B. Schmidtmann, *University of Hamburg, Germany*

[P3.062]	**Back so soon: estimating re-emergence probabilities of dengue in Rio de Janeiro, Brazil** R. Subramanian*[1], V.R. Aznar[1], C. Codeço[2], M. Pascual[1], [1]*University of Chicago, USA,* [2]*Oswaldo Cruz Foundation: Rio de Janeiro, Brazil*
[P3.063]	**Spread of carbapenemase-producing *Enterobacteriaceae* in clinical and environmental settings in Yangon, Myanmar** Y. Sugawara*, Y. Akeda, S. Hamada, *Osaka University, Japan*
[P3.064]	**Identifying regions at high risk of potential Zika outbreaks in the contiguous US during the 2015-2016 Zika epidemic** K. Sun*[1], Q. Zhang[1], A. Pastore-Piontti[1], M. Chinazzi[1], N.E. Dean[2], D.P. Rojas[2], S. Merler[3], D. Mistry[1], P. Poletti[4], L. Rossi[5], [1]*Northeastern University, USA,* [2]*University of Florida, USA,* [3]*Bruno Kessler Foundation, Italy,* [4]*Bocconi University, Italy,* [5]*Institute for Scientific Interchange Foundation, Italy,* [6]*Fred Hutchinson Cancer Research Center, USA,* [7]*University of Washington, USA*
[P3.065]	**Interaction among influenza viruses A/H1N1, A/H3N2 and B in Japan** A. Suzuki*, H. Nishiura, *Hokkaido University, Japan*
[P3.066]	**Intra-hospital patient movement network and its role in pathogen spread – A modeling study** H. Tahir*[1], R. Mikolajczyk[2], M. Kretzschmar[1,3], [1]*Utrecht University, The Netherlands,* [2]*University Halle-Wittenberg, Germany,* [3]*National Institute of Public Health and the Environment, The Netherlands*
[P3.067]	**A high prevalence of *Bartonella* spp. infection in temple dogs in Chiang Mai, Thailand** S. Tangtrongsup*[1], C. Tosakulsak[1], N. Tasena[1], S. Singhanetr[1], S. Pichetworakoon[1], D. Pangjai[2], A. Sirimalaisuwan[1], M. Kosoy[3], [1]*Chiang Mai University, Thailand,* [2]*Ministry of Public Health, Thailand,* [3]*KB One Health, USA*
[P3.068]	**Effects of different contact patterns on measles dynamics in low- and middle-income countries** H. Tanvir*, K. Prem, P. Klepac, M. Jit, *London School of Hygiene and Tropical Medicine, UK*
[P3.069]	**Who infected whom? Creating a database of transmission trees for comparative outbreak analysis** J.C. Taube*[1], P.B. Miller[2], J.M. Drake[2], [1]*Bowdoin College, USA,* [2]*University of Georgia, USA*
[P3.070]	**Potential impact of outpatient stewardship interventions on antibiotic exposures of bacterial pathogens** C. Tedijanto*[1], Y. Grad[1,2], M. Lipsitch[1], [1]*Harvard T.H. Chan School of Public Health, USA,* [2]*Brigham and Women's Hospital, USA*
[P3.071]	**A framework to assess and optimize the use of diagnostics during epidemics: Application to the 2017 plague outbreak in Madagascar** Q. ten Bosch*[1,2], V. Andrianaivoarimanana[3], B. Ramasindrazana[3], G. Mikaty[1], R. Rakotonanahary[3], B. Nikolay[1], S. Rahajandraibe[3], M. Feher[1], Q. Grassin[1], J. Paireau[1], [1]*Institut Pasteur, France,* [2]*Wageningen University and Research, The Netherlands,* [3]*Institut Pasteur de Madagascar, Madagascar,* [4]*World Health Organization, Switzerland,* [5]*Ministry of Health, Madagascar*
[P3.072]	**Modelling the effect of mass dog vaccination delivery options on time to rabies elimination in rural Kenya** S.M. Thumbi*[1,2], F. Marx[4], E. Are[4], Z. Suboi[4], L. Babu[3], M. Nsuami[5], J.R.C. Pulliam[4], [1]*University of Nairobi, Kenya,* [2]*Kenya Medical Research Institute, Kenya,* [3]*Washington State University, USA,* [4]*South African Center for Epidemiological and Modeling Analysis, South Africa,* [5]*University of Western Cape, South Africa*
[P3.073]	**"No jab, no school" policy and the enhancement of routine vaccination uptake: The perspective of measles elimination in high-income countries** F. Trentini*[1], P. Poletti[1], A. Melegaro[2], S. Merler[1], [1]*Bruno Kessler Foundation, Italy,* [2]*Carlo F. Dondena Centre for Research on Social Dynamics and Public Policies and Department of Social and Political Sciences, Bocconi University, Italy*

[P3.074]	**The evolutionary dynamics of influenza A viruses circulating in mallards in duck hunting preserves in Maryland, USA** N.S. Trovao*[1,2], J.M. Nolting[3], R.D. Slemons[3], M.I. Nelson[1], [1]*National Institutes of Health, USA,* [2]*Icahn School of Medicine at Mount Sinai, USA,* [3]*The Ohio State University, USA*
[P3.075]	**Evaluating virus interference in a trial of influenza vaccination** T. Tsang*[1], V. Fang[1], K. Chan[1], D. Ip[1], E. Lau[1], G. Leung[1], J. Peiris[1], S. Cauchemez[2], B. Cowling[1], [1]*The University of Hong Kong, Hong Kong,* [2]*Institut Pasteur, France*
[P3.076]	**Who to focus on in the general practice to reduce bystander selection of asymptomatic carried bacteria, such as streptococcus pneumoniae?** A.J. van Hoek*[1,2], E. van Kleef[1], J. Wallinga[1,3], [1]*National Institute for Public Health and the Environment, The Netherlands,* [2]*London School of Hygiene & Tropical Medicine, UK,* [3]*Leiden University Medical Center, The Netherlands*
[P3.077]	**Cross-immunity and immune imprinting in the age distributions of influenza B lineages** M. Vieira*[1], C. Donato[2], P. Arevalo[1], V. Dhanasekaran[2], K. Koelle[3], S. Cobey[1], [1]*University of Chicago, USA,* [2]*Monash University, Australia,* [3]*Emory University, USA*
[P3.078]	**Mathematical modelling as a tool to optimise experimental design in within-host bacterial population studies using isogenic tagged strains** M. Vlazaki*, O. Restif, *University of Cambridge, UK*
[P3.079]	**Model for comparing the transmissibility of influenza using data from ferret experiments** C.E. Walters*, R. Frise, W.S. Barclay, S. Riley, *Imperial College London, UK*
[P3.080]	**Forecasting influenza incidence as an ordinal variable using machine learning method: Booted Regression Tree** H. Wang*, S. Riley, *Imperial College London, UK*
[P3.081]	**Interactions between RSV and influenza: Can competition be inferred from surveillance data?** N. Waterlow*, S. Flasche, R. Eggo, *London School of Hygiene and Tropical Medicine, UK*
[P3.082]	**Reducing overprescription of antimalarials to treat non-malarial fevers as a method to improve cycling of first line therapies compared to multiple first line therapies** O.J. Watson*, R. Verity, A.C. Ghani, L. Okell, *Imperial College London, UK*
[P3.083]	**Predicting migration out of Venezuela using socioeconomic gravity models and parameter-free approaches for improved understanding of infectious disease risks in surrounding countries.** A. Thomas-Bachli[1], A. Tuite[1], A. Watts*[1], C. Huber[1], K. Khan[1,2], [1]*BlueDot, Canada,* [2]*St. Michael's Hospital, Canada,* [3]*Li Ka Shing Knowledge Institute, Canada*
[P3.084]	**The implications of social network structures of urban and non-urban PWID on HIV and HCV transmission** A. Wesolowski*, S. Mehta, G. Kirk, B. Genberg, *Johns Hopkins Bloomberg School of Public Health, USA*
[P3.085]	**Understanding relationships between chlamydia infection, symptoms and testing behaviour: An analysis of data from the 3rd National Survey of Sexual Attitudes and Lifestyles** J. Lewis[1], P.J. White*[1,2], [1]*Imperial College London, UK,* [2]*Public Health England, UK*
[P3.086]	**Estimating population burden of pelvic inflammatory disease due to *Mycoplasma genitalium* in England: an evidence synthesis** J. Lewis[1], P.J. Horner[2], P.J. White*[1,3], [1]*Imperial College London, UK,* [2]*University of Bristol, UK,* [3]*Public Health England, UK*
[P3.087]	**Testing and treatment strategies for limiting drug resistance in *Mycoplasma genitalium*** R. Birger[1], P.J. White*[2], [1]*Yale University, USA,* [2]*Imperial College London, UK,* [3]*Public Health England, UK*
[P3.088]	**Estimation of the serial interval of tuberculosis using cure models** Y. Ma[1], H.E. Jenkins[1], P. Sebastiani[1], J.J. Ellner[3], R. Dietze[2], C.R. Horsburgh[1], L.F. White*[1], [1]*Boston University, USA,* [2]*Universidade Federal do Espírito Santo, Brazil,* [3]*Rutgers Medical School, USA*
[P3.089]	**Effectiveness of vaccination strategies against antibiotic resistant gonorrhoea: A modelling analysis considering men who have sex with men in England** L.K. Whittles*[1], P.J. White[1,2], X. Didelot[3], [1]*Imperial College London, UK,* [2]*Public Health England, UK,* [3]*University of Warwick, UK*

[P3.090]	**Measurement of entomological parameters during an intervention trial leads to better estimates of epidemiological impact** A. Wieler*, N. Achee, J. Greico, S. Moore, A. Perkins, *University of Notre Dame, USA*
[P3.091]	**Land-use Impacts the Flow of Antibiotic Resistance Genes in Recreational Surface Waters** C. Wiesner*[1], R. Beattie[2], K. Hristova[2], J. Stewart[1], M. Serre[1], *[1]University of North Carolina-Chapel Hill, USA, [2]Marquette University, USA*
[P3.092]	**Modelling the heterogeneity of dengue transmission in Sri Lanka from age-specific case surveillance data** N. Wijayanandana*[1], N. Imai[2], F. Finger[1], H. Tissera[3], N. Ferguson[2], N. Alexander[1], *[1]London School of Hygiene and Tropical Medicine, UK, [2]Imperial College London, UK, [3]Ministry of Health, Sri Lanka*
[P3.093]	**Understanding the rebound in syphilis notifications in the early 21st century, in Victoria** K.E. Wilkins*[1], J.V. Ross[1], R.C. Cope[1], R. Sacks-Davis[2,3], *[1]The University of Adelaide, Australia, [2]Burnet Institute, Australia, [3]Monash University, Australia*
[P3.094]	**Lessons learned from a multi-country model application for RSV among children under 5 years in Gavi-eligible countries** L. Willem*[1], X. Li[1], M. Antillon[1,2], J. Bilcke[1], M. Jit[3], P. Beutels[1,4], *[1]University of Antwerp, Belgium, [2]Swiss Tropical and Public Health Institute, Switzerland, [3]London school of Hygiene and Tropical Medicine, UK, [4]The University of New South Wales, Australia*
[P3.095]	**Cost-benefit analysis of employer-funded quadrivalent influenza vaccination** F. Verelst[1], L. Willem*[1], N. Hens[1,2], P. Beutels[1,3], *[1]University of Antwerp, Belgium, [2]Hasselt University, Belgium, [3]The University of New South Wales, Australia*
[P3.096]	**The lack of proper respiratory hygiene behaviors and hand hygiene in public settings** R. Wolff, *South University, USA*
[P3.097]	**Inferring HIV incidence trends and transmission dynamics with a spatio-temporal HIV epidemic model** T.M. Wolock*, S.R. Flaxman, J.W. Eaton, *Imperial College London, UK*
[P3.098]	**Developing a complex agent-based network model to project HBV incidence and prevalence in Ontario, Canada** F. Tian, W.W.L. Wong*, *University of Waterloo, Canada*
[P3.099]	**Assessing the role of viral interference in the relationship between influenza and ARI in Nicaraguan children** S. Wraith*[1], A. Balmaseda[2,3], N. Sanchez[2,3], R. Lopez[2,3], S. Ojeda[2,3], G. Kuan[2,3], A. Gordon[1], *[1]University of Michigan, USA, [2]Ministry of Health, Nicaragua, [3]Sustainable Sciences Institute, Nicaragua*
[P3.100]	**A within-host compartmental model of influenza A (H9N2) virus infection dynamics and immune response in chickens** X.T. Xie*, S.U. Khan, A. Yitbarek, Z. Poljak, S. Sharif, A. Greer, *University of Guelph, Canada*
[P3.101]	**Calibration of a dynamic microsimulation model of a disease history model for Zika virus (ZIKV) infection** R. Ximenes*[1], D. Naimark[2], W. Wong3[3], B. Sander[1,4], *[1]University Health Network, Canada, [2]University of Toronto, Canada, [3]University of Waterloo, Canada, [4]Institute of Health Policy, Management and Evaluation, Canada*
[P3.102]	**Characteristics of Measles Epidemics in China (1951-2004) and Implications for Elimination: A Case Study of Three Key Locations** W. Yang*[1], J. Li[2], J. Shaman[1], *[1]Columbia University, USA, [2]Beijing Center for Disease Control and Prevention, China*
[P3.103]	**Pervasive exposure to influenza shapes human antibody profiles and future responses** B. Yang*[1], J. Lessler[2], H. Zhu[3,4], C.Q. Jiang[5], J. Read[6], R. Shen[5], K.O. Kwok[7,8], Y. Guan[3,4], S. Riley[9], D.A.T. Cummings[1], *[1]University of Florida, USA, [2]Johns Hopkins University, USA, [3]The University of Hong Kong, Hong Kong, [4]Shantou University, China, [5]Guangzhou No.12 Hospital, China, [6]Lancaster University, UK, [7]The Chinese University of Hong Kong, Hong Kong, [8]Shenzhen Research Institute of The Chinese University of Hong Kong, China, [9]Imperial College London, UK*
[P3.104]	**Assessing dengue control in Tokyo, 2014** B. Yuan*, H. Lee, H. Nishiura, *Hokkaido University, Japan*

[P3.105]	**Positively interacting strains that co-circulate within a network structured population induce cycling epidemics of *Mycoplasma pneumoniae*** X-S. Zhang*[1,2], H. Zhao[1], E. Vynnycky[1,3], V. Chalker[1], [1]*Centre for Infectious Disease Surveillance and Control, UK,* [2]*Imperial College School of Public Health, UK,* [3]*London School of Hygiene and Tropical Medicine, UK*
[P3.106]	**Global discovery of human-infective RNA viruses: a modelling analysis** F.F. Zhang*[1], M. Chase-Topping[1], C.G. Guo[2], B. van Bunnik[1], L. Brierley[3], M. Woolhouse[1], [1]*University of Edinburgh, UK,* [2]*University of Hong Kong, Hong Kong,* [3]*Coventry University, UK*
[P3.107]	**Age-specific transmissibility of shigellosis: a modelling Study in Hubei Province, China** Z. Zhao*[1], Q. Chen[2], B. Zhao[3], [1]*Xiamen University, China,* [2]*Hubei Provincial Center for Disease Control and Prevention, China,* [3]*Xiang'an Hospital of Xiamen University, China*
[P3.108]	**Use of daily internet search query data improves real-time influenza projections** C. Zimmer*[1,2], R. Yaesoubi[1], T. Cohen[1], [1]*Yale School of Public Health, USA,* [2]*Bosch Center for Artificial Intelligence, Germany*
[P3.109]	**Working while sick: the role of sickness behaviors and health disparities on influenza dynamics in the US** C. Zipfel*, S. Bansal, *Georgetown University, USA*
[P3.110]	**Disentangling the interaction between vaccination behavior and outbreaks for childhood infections** C. Zipfel*, S. Bansal, *Georgetown University, USA*
[P3.111]	**Representing TB transmission with complex contagion: An agent-based simulation modeling approach** E. Zwick*, C. Pepperell, O. Alagoz, *UW-Madison, USA*
[P3.112]	**Viziflu: An open-source tool for visualizing seasonal influenza forecasting results and uncertainties** A. Brennen*[1], D. George[1], G. Sieniawski[1], C. Reed[2], C. Lutz[2], F. Dahlgren[2], M. Biggerstaff[2], [1]*In-Q-Tel, USA,* [2]*Centers of Disease Control and Prevention, USA*
[P3.113]	**Elucidating the heterogeneous diagnosed proportions of people living with HIV/AIDS in Japan** H. Nishiura, *Hokkaido University, Japan*
[P3.114]	**Indicators of stability in SIR models with multiple observables** E. O'Dea*[1], A. Ghadami[2], B. Epureanu[2], J. Drake[1], [1]*University of Georgia, USA,* [2]*University of Michigan, USA*
[P3.115]	**Characterization of the spread of African swine fever in East and Southeast Asia during 2018–19** A.R. Akhmetzhanov*, S. Jung, H. Lee, N. Linton, Y. Yang, B. Yuan, H. Nishiura, *Hokkaido University, Japan*
[P3.116]	**Incorporating real-time climate forecasts into dengue outbreak prediction models** Y. Zhang[1], E. Dong[1], S. Siddiqui[1], A. Wesolowski[4], H. de Silva[2], L. Fernando[3], L. Gardner*[1], [1]*Johns Hopkins University, USA,* [2]*University of Colombo, Sri Lanka,* [3]*Centre for Clinical Management of Dengue and Dengue Haemorrhagic Fever, Sri Lanka,* [4]*Johns Hopkins School of Public Health, USA*
[P3.117]	**Incorporating international travel and vaccine resistance into measles outbreak risk assessment and control** L. Gardner*[1], E. Dong[1], K. Khan[3,4], S. Sarkar[1], [1]*Johns Hopkins University, USA,* [2]*University of Texas at Austin, USA,* [3]*University of Toronto, Canada,* [4]*St. Michaels Hospital, Canada*
[P2.109]	**Modeling missing cases and transmission links in networks of extensively drug-resistant tuberculosis in KwaZulu-Natal, South Africa** K.N. Nelson*[1], N.R. Gandhi[1], B. Mathema[1], B.A. Lopman[1], J.C.M. Brust[4], S.C. Auld[1], T.S. Brown[5], K. Mlisana[6,7], N.S. Shah[3], S.M. Jenness[1], [1]*Emory University, USA,* [2]*Columbia University, USA,* [3]*Centers for Disease Control and Prevention, USA,* [4]*Albert Einstein College of Medicine, USA,* [5]*Massachusetts General Hospital, USA,* [6]*University of KwaZulu-Natal, South Africa,* [7]*National Health Laboratory Service, South Africa*