

Poster Programme

Poster Session 1

Tuesday, 28 November 2017 18:00-19:30

All posters with an odd number will be presented from 18:00-18:45, Tuesday 28 November e.g. P1.001, P1.003 etc.
All posters with an even number will be presented from 18:45-19:30, Tuesday 28 November e.g. P1.002, P1.004 etc.

- [P1.001] **Phylodynamics of enterovirus 71 in Vietnam, Malaysia and China**
C.M. Donato*¹, D. Vijaykrishna^{1,2}, ¹Monash University, Australia, ²Duke-NUS Medical School, Singapore
- [P1.002] **Assessing the transmission dynamics of measles in Japan, 2016**
H. Nishiura*, K. Mizumoto, Y. Asai, Hokkaido University, Japan
- [P1.003] **Quantifying the age-dependent susceptibility of measles in Japan**
R. Kinoshita*, H. Nishiura, Hokkaido University, Japan
- [P1.004] **Identifying the transmission route of influenza in 2009 in Japan by transportation network data and genome information**
Y. Asai*, H. Nishiura, Hokkaido University, Japan
- [P1.005] **An explicit quantification of the seasonal driver of the transmission dynamics of Lassa fever in Nigeria**
A. Akhmetzhanov, Y. Asai*, H. Nishiura, Hokkaido University, Japan
- [P1.006] **Mathematical modelling of vector-borne diseases**
D. Mathebula, University of Venda, South Africa
- [P1.007] **Will be presented as [P2.117]**
- [P1.008] **Differences in pathogenesis influence landscape epidemiology of two common pathogens in wild pigs in Florida, USA**
S.M. Wisely*¹, F.A. Hernandez¹, A.N. Carr¹, M.P. Milleson², H.R. Merrill¹, M.L. Avery², B.M. Parker¹, C.L. Pylant¹, J.D. Austin¹, ¹University of Florida, USA, ²United States Department of Agriculture, Animal Plant Health Inspection, USA
- [P1.009] **Time Series Analysis of monthly age- and geographical-specific numbers of newly registered cases of active tuberculosis in Japan**
A. Sumi*¹, Y. Kohei^{1,2}, N. Kobayashi¹, ¹Sapporo Medical University School of Medicine, Japan, ²Hokkaido Bunkyo University, Japan
- [P1.010] **Growing the use of optimisation technologies in epidemiology**
J.A. Enright*¹, C. Jefferson², C. McCreesh³, P. Prosser³, ¹University of Stirling, UK, ²University of St Andrews, UK, ³University of Glasgow, UK
- [P1.011] **Bushmeat hunting and zoonotic transmission of simian T-lymphotropic virus 1 in tropical West and Central Africa**
G. Schubert*¹, A. Mossoun², S. Calvignac-Spencer¹, C. Akoua-Koffi³, E. Couacy-Hymann⁴, J.J. Muyembe-Tamfum⁵, S. Karhemere⁵, R.M. Wittig⁶, F.H. Leendertz¹, ¹Robert Koch-Institute, Germany, ²Université Felix Houphouët Boigny, Cote D'Ivoire, ³Université Alassane Ouattara, Cote D'Ivoire, ⁴Laboratoire National d'appui au Développement Agricole, Cote D'Ivoire, ⁵Institut National de Recherche Bio-Médicale, Congo, ⁶Max-Planck-Institute for Evolutionary Anthropology, Germany
- [P1.012] **Years of life lost due to influenza-attributable mortality in the Netherlands in older adults: A competing risks approach**
S.A. McDonald, M. van Wijhe*, L. van Asten, W. van der Hoek, J. Wallinga, National Institute for Public Health and the Environment, The Netherlands
- [P1.013] **Modelling the global spread of diseases: A review of current practice and capability**
C.E. Walters*^{1,2}, M. Mesle^{1,3}, I.M. Hall¹, ¹Public Health England, UK, ²Imperial College London, UK, ³Liverpool University, UK
- [P1.014] **Mathematical estimation of Aedes albopictus establishment risk in Japan**

S. Tsuzuki*¹, T. Finnie², I. Hall², S. Leach², ¹Hokkaido University, Japan, ²Public Health England, UK

[P1.015] Exploring the impact of population migration on the estimate of dengue susceptibility and transmission

H.M. Lam*¹, N.H.T. Vy¹, H.T. Phuong¹, N.T.L. Thanh¹, M.F. Boni², H. Clapham^{1,3}, ¹Oxford University Clinical Research Unit, Viet Nam, ²Pennsylvania State University, USA, ³Oxford University, UK

[P1.016] Robust vs recurrent patterns of influenza spread in France

P. Coletti*², C. Turberlin¹, C. Poletti¹, T. Blanchon¹, V. Colizza^{1,2}, ¹Sorbonne Universités, UPMC Univ Paris 06, INSERM, Institut Pierre Louis d'Epidémiologie et de Santé Publique (IPLESP), France, ²ISI Foundation, Italy

[P1.017] Recurring infection with ecologically distinct human papillomavirus types explains high prevalence and diversity

S.L. Ranjeva*^{1,2}, S. Cobey¹, G. Dwyer¹, A.R. Giuliano³, ¹University of Chicago, USA, ²University of Chicago, USA, ³H. Lee Moffitt Cancer Center and Research Institute, USA

[P1.018] Surveillance of respiratory illness using pathogen specific diagnostic test utilization: an alternative to influenza-like illness

A. Faucett*¹, J. Nawrocki¹, A. Hoffee¹, B.M. Althouse^{2,3}, S.V. Scarpino⁴, M.A. Poritz⁵, L. Meyers¹, ¹BioFire Diagnostics, USA, ²University of Washington, USA, ³New Mexico State University, USA, ⁴Northeastern University, USA, ⁵BioFire Defense, USA

[P1.019] How much can HIV transmission be reduced in high-risk MSM by targeting testing to detect and treat primary HIV infection (PHI)? Analysis of a cohort study using an individual-based model

P.J. White*^{1,2}, J. Fox³, J. Weber¹, H. Ward¹, S. Fidler¹, ¹Imperial College London, UK, ²Public Health England, UK, ³Kings College London, UK

[P1.020] Epidemiology of influenza transmission in an urban cohort of households

C. Reed*¹, S. Shepard¹, C. Vargas², E. Larson², L. Saiman², P. LaRussa², J. Barnes¹, M. Stockwell², ¹Centers for Disease Control and Prevention, USA, ²Columbia University Medical Center, USA

[P1.021] Analysis of the dengue outbreak in Tokyo, Japan in 2014 based on a mathematical model

H. Ishikawa*¹, R. Shimogawara¹, K. Fueda², ¹Graduate School of Tokyo Medical and Dental University, Japan, ²Shiga University, Japan

[P1.022] Artemisinin-induced parasite growth retardation in blood-stage Plasmodium falciparum: A potential contributor to drug-resistance

J.M. McCaw*¹, P. Cao¹, N. Klonis¹, S.G. Zaloumis¹, D. Khoury², D. Cromer², M. Davenport², L. Tilley¹, J.A. Simpson¹, ¹University of Melbourne, Australia, ²UNSW Australia, Australia

[P1.023] Introducing tools for assessing validity of time-place-type clusters: an application to mumps outbreaks in the Netherlands reported between 2009 and mid-2016

L.C. Soetens*^{1,2}, J.A. Backer¹, S.J.M. Hahné¹, R.S. van Binnendijk¹, S. Gouma³, J. Wallinga^{1,2}, ¹National Institute for Public Health and the Environment, The Netherlands, ²Leiden University Medical Centre, The Netherlands, ³University of Pennsylvania, USA

[P1.024] Genetic diversity of multiple respiratory viruses identified during a hospital disease surveillance in Vietnam using next generation sequencing

L. Lu*¹, A. Avens, M. Woolhouse, University of Edinburgh, UK

[P1.025] Evaluating vaccines demands for the elimination of yellow fever epidemics in Africa

K. Jean*^{1,2}, A. Hamlet², O. Ronveaux³, W. Perea³, K. Nishino³, J. Benzler³, L. Cibrelus³, S. Yactayo³, N.M. Ferguson², T. Garske¹, ¹Conservatoire National des Arts et Métiers, France, ²Imperial College, UK, ³WHO, Switzerland, ⁴AFRO, Burkina Faso

[P1.026] Vaccinating children against influenza virus increases variation in epidemic size

J.A. Backer*¹, M. Van Boven¹, W. Van der Hoek¹, J. Wallinga^{1,2}, ¹National Institute for Public Health and the Environment, The Netherlands, ²Leiden University, The Netherlands

[P1.027] The impact of case-area targeted interventions in response to cholera outbreaks: A modeling study

F. Finger*¹, E. Bertuzzo^{1,2}, F. Luquero^{3,4}, B. Toure⁴, K. Porten⁴, J. Lessler³, A. Rinaldo^{1,5}, A. Azman³, ¹École Polytechnique Fédérale de Lausanne, Switzerland, ²Università Ca'Foscari Venezia, Italy, ³Johns Hopkins Bloomberg School of Public Health, USA, ⁴Epicentre, France, ⁵Università di Padova, Italy

[P1.028] Deploying digital data to optimize influenza surveillance at national and local scales

E.C. Lee*¹, S. Bansal¹, ¹Georgetown University, USA, ²Fogarty International Center, USA

- [P1.029] Inter-individual proximity networks support the hospital transmission of ESBL-producing *K. pneumoniae* but not *E. coli***
A. Duval*¹, T. Obadia⁵, P.Y. Boëlle⁴, E. Fleury³, J.L. Herrmann⁶, D. Guillemot¹, L. Temime², L. Opatowski¹, ¹Institut Pasteur, France, ²Conservatoire National des arts et Métiers, France, ³ENS de Lyon, France, ⁴Institut Pierre Louis d'Epidémiologie et de Santé Publique, France, ⁵Institut Pasteur, France, ⁶UVSQ, Inserm, France
- [P1.030] Moved to poster session 2**
- [P1.031] Characterizing multinational patterns of seasonal asymmetry in human movement and its implications for infectious disease dynamics**
A. Wesolowski*¹, E. zu Erbach-Schoenberg³, B.T. Grenfell², A.J. Tatem³, C. Viboud⁴, V. Charu⁴, C.O. Buckee⁵, C.J.E. Metcalf², ¹Johns Hopkins Bloomberg School of Public Health, USA, ²Princeton University, USA, ³University of Southampton, UK, ⁴Fogarty International Center, USA, ⁵Harvard TH Chan School of Public Health, USA
- [P1.032] Dengue fever in Taiwan: A multidisciplinary approach to produce a decision support tool**
R.I. Hickson*¹, D-P. Liu², Y-L. Liu², ¹IBM Research, Australia, ²Taiwan Centers for Disease Control, Taiwan
- [P1.033] Changing patterns of liver fluke transmission in northeast Thailand: Integrating data in the context of Lawa model control efforts**
T.M. Leon*¹, R.C. Spear¹, K. Kuntiyawichai², V. Plermakamon², S. Kaewkes², W. Kaewkes², B. Sripa², ¹University of California, Berkeley, USA, ²Khon Kaen University, Thailand
- [P1.034] Inverse association between ambient ozone and influenza transmissibility in Hong Kong**
S.T. Ali*¹, L. Tian¹, P. Wu¹, S. Cauchemez², D. He³, V.J. Fang¹, B.J. Cowling¹, ¹University of Hong Kong, Hong Kong, ²Institut Pasteur, France, ³Hong Kong Polytechnic University, Hong Kong
- [P1.035] Epidemiological risks for Chikungunya, Dengue and Zika in temperate Europe and cost-effectiveness analysis of routine larviciding as a preventive measure**
G. Guzzetta*¹, P. Poletti¹, F. Trentini², A. Melegaro², F. Montarsi³, G. Capelli³, F.A. Baldacchino⁴, A. Rizzoli⁴, R. Rosa⁴, S. Merler¹, ¹Fondazione Bruno Kessler, Italy, ²Bocconi University, Italy, ³Istituto Zooprofilattico Sperimentale delle Venezie, Italy, ⁴Fondazione Edmund Mach, Italy
- [P1.036] The autocatalytic dynamics of horizontal gene transfer result in non-Darwinian selection of plasmid-mediated antibiotic resistance**
R.C. Jackson*¹, B.M. Adger², Y. Hu^{3,4}, A.R. Coates^{3,4}, ¹Pharmacometrics Ltd, UK, ²Sepagen Ltd, UK, ³Helperby Therapeutics Ltd, UK, ⁴Univ of London, UK
- [P1.037] Control of recurrent measles epidemics in Ethiopia: Evidences from the field and model-based evaluations**
P. Poletti*¹, S. Parlamento¹, T. Feyissa², R. Feyissa², M. Lusiani³, A. Tsegaye³, G. Segafredo⁴, G. Putoto⁴, F. Manenti⁴, S. Merler¹, ¹Fondazione Bruno Kessler, Italy, ²South West Shoa Zone Health Office, Ethiopia, ³Woliso Hospital, Ethiopia, ⁴Doctors with Africa Cuamm, Italy
- [P1.038] Seasonal influenza vaccines for the elderly population of England: The cost-effectiveness of the quadrivalent, high dose and adjuvant options**
D.L. Thorrington¹, E. van Leeuwen^{1,2}, M. Ramsay¹, R. Pebody¹, M. Baguelin*^{1,3}, ¹Public Health England, UK, ²Imperial College London, UK, ³London School of Hygiene and Tropical Medicine, UK
- [P1.039] Research on cross-species transmission potential of Influenza A virus using machine learning**
Y. Pei*¹, B. Xu, Tsinghua University, China
- [P1.040] Using large serological studies in livestock to reconstruct the history of the BTV-8 epidemic and the impact of successive vaccination campaigns in France**
N.C. Courtejoie*^{1,2}, H.S. Salje¹, B.D. Durand², G.Z. Zanella², S.C. Cauchemez¹, ¹Institut Pasteur, France, ²ANSES, France
- [P1.041] Serology as an immunity indicator: Improving seasonal influenza modelling across several seasons**
E. van Leeuwen*^{1,2}, K. Hoschler¹, R. Pebody¹, M. Zambon¹, S. Riley², M. Baguelin^{1,3}, ¹Public Health England, UK, ²Imperial College London, UK, ³London School of Hygiene and Tropical Medicine, UK

- [P1.042] Space-time analysis of pneumonia hospitalisations in the Netherlands**
E. Benincà*^{1,2}, M. van Boven¹, T. Hagenaars², W. van der Hoek¹, ¹National Institute for Public Health and the Environment, The Netherlands, ²Wageningen Bioveterinary Research, The Netherlands
- [P1.043] Estimating the malaria transmission process in near-elimination settings**
I. Routledge*¹, E. Chévez³, Z. Cucunubá¹, C. Guinovart², K. Schneider², P. Walker¹, A. Ghani¹, S. Bhatt¹, ¹Imperial College London, UK, ²PATH, USA, ³MINSAL, El Salvador
- [P1.044] Risk maps for the transmission of zoonotic pathogens: The impact of spatial clustering and disease dispersal**
E. Benincà*^{1,2}, T. Hagenaars², J. van de Kasstele¹, G.J. Boender², M. van Boven¹, ¹National Institute for Public Health and the Environment, The Netherlands, ²Wageningen Bioveterinary Research, The Netherlands
- [P1.045] First detection of human coronavirus OC43 in habituated great apes**
L.V. Patrono*¹, L. Nourifar¹, R. Wittig², S. Calvignac-Spencer¹, F.H. Leendertz¹, ¹Robert Koch Institute, Germany, ²Max Planck Institute for Evolutionary Anthropology, Germany
- [P1.046] Using participatory Web-based surveillance data to improve seasonal influenza forecasting in Italy**
D. Perrotta*, M. Tizzoni, D. Paolotti, Institute for Scientific Interchange Foundation, Italy
- [P1.047] Moved to Poster session 3**
- [P1.048] A meta-population model for the transmission of *peste des petits ruminants virus* in west Africa**
A. Apolloni*^{1,3}, G. Nicolas², C. Coste¹, B.O. El Mami⁴, P. Hammami¹, M. Ciss³, Y. Amevo³, I. Seck⁵, R. Lancelot¹, M. Gilbert², ¹CIRAD, France, ²Université Libre de Bruxelles, Belgium, ³ISRA, Senegal, ⁴CNERV, Mauritania, ⁵FAO, Senegal
- [P1.049] Ecology and virulence of sexually transmitted infections in stratified epithelia**
C-L. Murali*¹, N. Boulle², M. Segondy², S. Alizon¹, ¹CNRS, France, ²INSERM, France
- [P1.050] Patterns of assortative sexual preference among men who have sex with men in seven US cities**
N.N. Abuelezam^{1,2}, Y. Reshef³, Y.H. Grad^{2,4}, D.S. Novak⁵, G.R. Seage III², K. Mayer^{4,6}, M. Lipsitch*^{2,7}, ¹Boston College, USA, ²Harvard T.H. Chan School of Public Health, USA, ³Harvard University, USA, ⁴Harvard Medical School, USA, ⁵Online Buddies, Inc., USA, ⁶Fenway Health, USA, ⁷Center for Communicable Disease Dynamics, USA
- [P1.051] 'Keeping your kids at home' can limit the persistence of pathogens in social animals**
L. Marescot*, M. Franz, S. Benhaiem, M.L. East, H. Hofer, S. Kramer-Schadt, Leibniz Institute for Zoo and Wildlife Research, Germany
- [P1.052] Phylodynamics and predictive factors for foot-and-mouth disease spread in Africa**
F. Duchatel*, M. Bronvoort, S. Lycett, University of Edinburgh, UK
- [P1.053] Effect of artesunate on the within-host dynamics of *Plasmodium falciparum* parasitaemia in severe malaria patients**
S.G. Zaloumis*¹, R.N. Price^{2,3}, J.M. McCaw¹, P. Cao¹, J.A. Simpson¹, ¹University of Melbourne, Australia, ²Menzies School of Health Research, Australia, ³University of Oxford, UK
- [P1.054] Influence of inter-animal variability of HI titres on antigenic cartography in the study of avian influenza viruses**
I. Sitaras*^{1,2}, B. Peeters², M.C.M. de Jong¹, ¹Wageningen University and Research, The Netherlands, ²Wageningen Bioveterinary Research, The Netherlands
- [P1.055] Moved to poster session 2**
- [P1.056] A decade into the epidemic of social contact surveys relevant for the spread of close contact infections: A systematic review**
T. Hoang*¹, P. Coletti¹, A. Melegaro², J. Wallinga³, W.J. Edmunds⁴, P. Beutels⁵, N. Hens^{1,5}, ¹Hasselt University, Belgium, ²Bocconi University, Italy, ³Leiden University Medical Center, The Netherlands, ⁴London School of Hygiene and Tropical Medicine, UK, ⁵University of Antwerp, Belgium
- [P1.057] Back-calculation of the incidence of leprosy in Brazilian states accounting for inter-state migration**
R.E. Crump*¹, G.F. Medley¹, ¹The University of Warwick, UK, ²London School of Hygiene and

[P1.058] Will be presented as [P3.001]

[P1.059] **Biased inferences in phylodynamics arising from the violation of the homogeneous mixing assumption**

A. Hidano*¹, C. Gates¹, T. Vaughan², ¹Massey University, New Zealand, ²University of Auckland, New Zealand

[P1.060] **Predictive spatial modelling of Highly Pathogenic Avian Influenza subtype H5N8 in France, 2016-2017**

C. Guinat*^{1,2}, J. Artois³, A. Bronner⁴, J.L. Guérin^{1,2}, M. Gilbert^{3,5}, M.C. Paul^{1,2}, ¹École Nationale Vétérinaire de Toulouse, France, ²Institut National de la Recherche Agronomique, France, ³Université Libre de Bruxelles, Belgium, ⁴Direction Générale de l'Alimentation, France, ⁵Fonds National de la Recherche Scientifique, Belgium

[P1.061] **Unravelling drivers of spatial heterogeneity in the spread of Chikungunya virus in Bangladesh**

Q.A. ten Bosch*¹, H. Salje¹, K.K. Paul², A.M. Naser², M. Rahman³, S. Alam², H.M. Al-Amin², M.Z. Rahman², S. Afroj², D.A.T. Cummings⁴, ¹Institut Pasteur, France, ²International Centre for Diarrhoeal Diseases Research, Bangladesh, ³Institute for Epidemiology, Disease Control and Research, Bangladesh, ⁴University of Florida, USA, ⁵University of New South Wales, Australia, ⁶Stanford University, USA

[P1.062] **Control of high pathogenic avian influenza: Using modelling to resolve uncertainties in the 2004 H5N1 epidemics in Thailand**

R. Retkute*¹, C.P. Jewell², T. van Boeckel³, X. Xiao⁴, M. Gilbert⁵, M. Keeling¹, M.J. Tildesley¹, ¹University of Warwick, UK, ²Lancaster University, UK, ³ETC Zurich, Switzerland, ⁴University of Oklahoma, USA, ⁵Université Libre de Bruxelles, Belgium

[P1.063] **Modelling the role of carriers in endemic foot and mouth disease**

I. McLachlan*^{1,2}, T. Porphyre¹, G. Marion², I. McKendrick², I. Handel¹, M. Bronsvoort¹, ¹University of Edinburgh, UK, ²Biomathematics and Statistics Scotland, UK

[P1.064] **Efficient simulation of multi-locus genetic data from malaria transmission models: A coalescent approach**

R. Verity*¹, S. Meshnick², D. Conway³, D. Kwiatkowski⁴, A. Ghani¹, ¹Imperial College London, UK, ²University of North Carolina, USA, ³London School of Hygiene and Tropical Medicine, UK, ⁴Wellcome Trust Sanger Institute, UK

[P1.065] **Geographical clustering patterns of MRSA carriage in a livestock-dense region in the Netherlands**

V.H. Arntzen*¹, H. Korthals-Altes², S.G. Feenstra³, E. Benincà², M.H. Nabuurs-Franssen⁴, E.M. Mascini⁵, T.T.N. Le^{6,7}, J. Hopman¹, H. Wertheim¹, ¹Radboud university medical center, The Netherlands, ²National institute for public health and the environment (RIVM), The Netherlands, ³Public Health Service (GGD) Gelderland-Zuid, The Netherlands, ⁴Canisius Wilhelmina Hospital, The Netherlands, ⁵Rijnstate Ziekenhuis, The Netherlands, ⁶Gelderse Vallei Hospital, The Netherlands, ⁷Hospital Rivierenland, The Netherlands

[P1.066] **Heterogeneity in evolutionary rates may reflect ecological and biological differences between dengue genotypes**

S. Pollett^{1,2}, I.M. Berry*¹, M.C. Melendrez¹, S.G. Duchene³, R.G. Jarman¹, ¹Walter Reed Army Institute of Research, USA, ²University of Sydney, Australia, ³University of Melbourne, Australia

[P1.067] **Implications of defining proportional attributable fraction for infectious diseases**

L. Danon¹, E. Brooks-Pollock*², ¹University of Exeter, UK, ²University of Bristol, UK

[P1.068] **Moved to Poster session 3**

[P1.069] **Comparing the seasonality of influenza-like illnesses and invasive pneumococcal diseases using seasonal waveforms**

M.D. de Cellès¹, H. Arduin¹, E. Varon^{2,3}, C. Souty^{4,5}, P-Y. Boëlle^{4,5}, D. Lévy-Bruhl⁶, S. van der Werf^{7,8}, D. Guillemot¹, L. Watier¹, L. Opatowski*¹, ¹Institut Pasteur, France, ²AP-HP, Hôpital Européen Georges-Pompidou, France, ³Centre National de Référence des Pneumocoques, France, ⁴INSERM, France, ⁵Institut Pierre Louis d'Epidémiologie et de Santé Publique, France, ⁶Institut de Veille Sanitaire (InVS), France, ⁷Unité de Génétique Moléculaire des Virus à ARN, France, ⁸CNRS,

France, ⁹Université Paris Diderot, France, ¹⁰Open Rome (Organize and Promote Epidemiological Network), France

- [P1.070] **Estimating population-level HIV incidence by combining synthetic cohort and recency biomarker approaches: a demonstration using survey data from KwaZulu-Natal, South Africa**
E. Grebe*¹, A. Welte¹, L. Johnson^{2,3}, G. Van Cutsem³, A. Puren⁴, T. Ellman⁵, J.F. Etard^{5,6}, H. Huerga⁵, ¹DST-NRF Stellenbosch University, South Africa, ²University of Cape Town, South Africa, ³Médecins Sans Frontières, South Africa, ⁴National Institute for Communicable Diseases (NICD), South Africa, ⁵Epicentre, France, ⁶Institut de Recherche pour le Développement, Montpellier University, France
- [P1.071] **Spatial clustering of visceral leishmaniasis cases over the course of an epidemic in Fulbaria, Bangladesh 2002-10: Estimating how transmission risk decreases with distance**
T.M. Pollington*^{1,3}, L.A.C. Chapman^{1,3}, C. Bern^{2,3}, T.D. Hollingsworth^{1,3}, ¹University of Warwick, UK, ²UCSF, USA, ³NTD Modelling Consortium, UK
- [P1.072] **The impact of vaccination on inequalities in infectious disease**
J.D. Munday*¹, A.J. van Hoek¹, K.E. Atkins¹, ¹London School of Hygiene and Tropical Medicine, UK, ²The Dutch National Institute for Public Health and the Environment (RIVM), The Netherlands
- [P1.073] **Impact of migration on dynamics of avian influenza: A multi-site, multi-species transmission model along East Asian-Australian Flyway**
A. Endo*¹, H. Nishiura^{1,2}, ¹Hokkaido University, Japan, ²Japan Science and Technology Agency, Japan
- [P1.074] **Moved to poster session 2**
- [P1.075] **Role of haulage companies in the connectivity of pig farms in Great Britain: A network analysis**
T. Porphyre*¹, B.M. Bronsvort¹, G.J. Gunn², C. Correia-Gomes², ¹The Roslin Institute, UK, ²Scotland's Rural College, UK
- [P1.076] **Sample size consideration for influenza transmission experiments using ferret model**
R. Matsuyama*, Y. Asai, H. Nishiura, Hokkaido University, Japan
- [P1.077] **Strategies to improve rotavirus vaccine impact and effectiveness during the second year of life in Blantyre, Malawi: A mathematical modelling study**
V.E. Pitzer*¹, A. Bennett^{2,3}, N. Bar-Zeev^{2,3}, B.A. Lopman⁴, U.D. Parashar⁵, N.A. Cunliffe³, ¹Yale School of Public Health, USA, ²Malawi-Liverpool-Wellcome Trust Clinical Research Programme, Malawi, ³University of Liverpool, UK, ⁴Emory University, USA, ⁵Centers for Disease Control and Prevention, USA
- [P1.078] **Withdrawn**
- [P1.079] **A multi-scale, multi-paradigm epidemiological modelling language for investigating Q Fever regional infection dynamics**
S. Picault*^{1,2}, Y-L. Huang¹, V. Sicard¹, T. Hoch¹, E. Vergu¹, F. Beaudeau¹, P. Ezanno¹, ¹INRA, France, ²Univ. Lille, France
- [P1.080] **Rift valley fever dynamics at the human-wildlife interface in Botswana: The quandary of silent circulation in advancing predictive biology**
K.A. Alexander*^{1,2}, F. Jori^{3,4}, N. Moolland^{5,6}, C.E. Sanderson^{1,2}, J.T. Paweska^{5,6}, ¹Virginia Tech, USA, ²CARACAL, Botswana, ³CIRAD, France, ⁴Botswana College of Agriculture, Botswana, ⁵National Institute of Communicable Diseases of the National Health Laboratory Services, South Africa, ⁶University of Witwatersrand, South Africa
- [P1.081] **Measuring and modelling the effects of systematic non-adherence to mass drug administration**
L. Dyson*¹, W.A. Stolk², S.H. Farrell³, T.D. Hollingsworth¹, ¹University of Warwick, UK, ²Erasmus MC, The Netherlands, ³Imperial College London, UK
- [P1.082] **Targeted catch-up immunisation for measles can make a difference: An individual-based modelling study**
L. Willem*¹, F. Verelst¹, E. Kuylen¹, N. Hens^{1,2}, P. Beutels^{1,3}, ¹University of Antwerp, Belgium, ²UHasselt, Belgium, ³The University of New South Wales, Australia
- [P1.083] **Moved to poster session 2**

- [P1.084] Utility of a simple mean ensemble in forecasting infectious diseases**
C.J. McGowan, M. Biggerstaff*, M.A. Johansson, C. Reed, *Centers for Disease Control and Prevention, USA*
- [P1.085] The genetic and antigenic evolution of dengue viruses in Bangkok, Thailand (1995-2006) in relation to global antigenic diversity**
L. Katzelnick*^{1,2}, H. Salje^{4,5}, A. Coello-Escoto^{1,3}, C. Chavez^{1,3}, I.M. Berry⁶, I. Rodriguez-Barraquer², D. Smith⁷, R. Jarman⁶, S. Whitehead³, D. Cummings^{1,5}, ¹University of Florida, USA, ²University of California, USA, ³National Institutes of Health, USA, ⁴Institut Pasteur, France, ⁵Johns Hopkins Bloomberg School of Public Health, USA, ⁶Walter Reed Army Institute of Research, USA, ⁷University of Cambridge, UK
- [P1.086] Social mixing, animal contact and travel patterns in South East Asia**
J.M. Read*^{1,2}, W.J. Edmunds¹, ¹Lancaster University, UK, ²University of Liverpool, UK, ³LSHTM, UK
- [P1.087] Identifying the social network information associated with Influenza B infection among schoolchildren in Pittsburgh, Pennsylvania, USA**
J.M. Read*^{1,2}, C. Jewell¹, R. Lester¹, S. Zimmer^{3,4}, D.A.T. Cummings^{5,6}, ¹Lancaster University, UK, ²University of Liverpool, UK, ³University of Pittsburgh, USA, ⁴University of Colorado, USA, ⁵University of Florida, USA, ⁶Johns Hopkins Bloomberg School of Public Health, USA
- [P1.088] DTKDengue: Presentation, calibration, and application of a new agent-based model for dengue virus transmission**
Q.A.T. Bosch^{1,2}, K.J. Soda*¹, S.M. Moore¹, G. España¹, J. Bloedow³, B. Raybaud³, E. Wenger³, P. Eckhoff³, T.A. Perkins¹, ¹University of Notre Dame, USA, ²Institut Pasteur, France, ³Institute for Disease Modeling, USA
- [P1.089] Vaccine effectiveness estimation and real time influenza forecast**
M. Galanti*, J. Shaman, *Columbia University, USA*
- [P1.090] Are we on the right track? Stopping criteria for ending soil-transmitted helminths randomized clinical trials**
M. Werkman*^{1,2}, J.E. Truscott^{1,2}, J.E. Wright^{1,2}, J. Toor¹, K. Ásbjörnsdóttir^{2,3}, A.R. Means^{2,3}, S. Farrell¹, J. Watson^{2,3}, R.M. Anderson^{1,2}, ¹Imperial College London, UK, ²The DeWorm3 Project, UK, ³University of Washington, USA
- [P1.091] Approximating the probability of pathogen invasion for stochastic population models**
R.K. Borchering*¹, S.A. McKinley¹, ¹University of Florida, USA, ²Tulane University, USA
- [P1.092] Travelling waves of seasonal influenza across Russian cities**
M. Churakov*^{1,2}, V. Leonenko¹, ¹Institut Pasteur, France, ²CNRS, France, ³ITMO University, Russia
- [P1.093] Fine-scale models of human mobility in Africa**
C. Ciavarella*, A. Ghani, N.M. Ferguson, *Imperial College London, UK*
- [P1.094] Infection control of Vancomycin-Resistant Enterococci in hospitals: a cost-effectiveness modelling analysis of a French outbreak**
R. Assab*¹, R. Choukroun², D. Guillemot², L. Temime¹, F. Espinasse³, S. Bahrami^{3,4}, L. Opatowski², ¹Conservatoire National des Arts et Métiers/Institut Pasteur, France, ²Institut Pasteur/UVSQ/Inserm, France, ³Assistance Publique Hôpitaux de Paris, France, ⁴UVSQ, France
- [P1.095] Fine-scale spatial predictions of lymphatic filariasis elimination in Ethiopia – linking maps and models**
P. Touloupou*¹, J.M. Prada¹, S.E.F. Spencer¹, ¹University of Warwick, UK, ²Lancaster University, UK, ³University Medical Center Rotterdam, The Netherlands, ⁴University of Notre Dame, USA, ⁵London School of Hygiene and Tropical Medicine, UK, ⁶Ethiopia Public Health Institute, Ethiopia, ⁷Federal Ministry of Health, Ethiopia
- [P1.096] Inferring determinants of transmissibility from viral sequence data**
C.K. Lumby*, C.J.R. Illingworth, *University of Cambridge, UK*
- [P1.097] Projecting the public health impact of dengue vaccination in light of uncertainties associated with vaccine efficacy estimates from clinical trials**
G. Espana*¹, R.C. Reiner², Q.A.T. Bosch^{1,3}, A.C. Morrison⁴, T.W. Scott⁴, D.L. Smith², T.A. Perkins¹, ¹University of Notre Dame, USA, ²University of Washington, USA, ³Institut Pasteur, France, ⁴University of California, USA

- [P1.098] Phones and flu: An evaluation infection dynamics among social networks during the introduction of pandemic H1N1 into Iceland in 2009 using anonymized call records**
N. Kishore*¹, R. Mitchell¹, T.L. Lash¹, L. Danon³, G. Sigmundsdóttir¹, Y. Vigfusson^{1,4}, ¹Emory University, USA, ²Directorate of Health, Iceland, ³University of Exeter, UK, ⁴Reykjavik University, Iceland
- [P1.099] Influence of pigs turnover on the establishment of japanese encephalitis virus in pig farms in cambodia**
A.O. Diallo*^{1,2}, R. Duboz^{1,2}, V. Chevalier^{1,2}, J. Cappelle^{1,3}, D. Fontenille², B. Durand⁴, ¹CIRAD UMR ASTRE, France, ²Institut Pasteur du Cambodge, Cambodia, ³UMR EpiA, France, ⁴Agence Française de Sécurité Sanitaire des Aliments, France
- [P1.100] Quantifying potential oral cholera vaccine demand and impact at policy-relevant spatial levels**
S.M. Moore*¹, A.S. Azman², H.S. McKay², J. Lessler², ¹University of Notre Dame, USA, ²Johns Hopkins Bloomberg School of Public Health, USA
- [P1.101] Unravelling the dynamics of hepatitis-E infections in displaced populations: Implications for reactive vaccination campaigns**
A. Camacho*^{1,2}, E. Gignoux¹, A.S. Azman^{3,4}, ¹Epicentre, France, ²London School of Hygiene and Tropical Medicine, UK, ³Médecins sans Frontières, Switzerland, ⁴Johns Hopkins Bloomberg School of Public Health, USA
- [P1.102] Untargeted treatment of *Mycoplasma genitalium* accelerates the spread of antibiotic resistance**
D. Cadosch*, V. Garcia, C. Althaus, N. Low, University of Bern, Switzerland
- [P1.103] Estimating vaccine efficacy against acquisition of *Streptococcus pneumoniae* using serotype-specific antibody concentrations**
L.M. Li*¹, R. Dagan², M. Lipsitch¹, ¹Harvard T.H. Chan School of Public Health, USA, ²Ben-Gurion University of the Negev, Israel
- [P1.104] Creating a model world: Introducing dynamic modeling to infectious disease ecology and epidemiology students via an active-learning approach**
J.R.C. Pulliam*¹, S.E. Bellan², J. Dushoff³, A.G. Hitchcock¹, J. Hargrove¹, T.C. Porco⁴, J.C. Scott⁵, B.G. Williams¹, A. Welte¹, ¹South African DST-NRF Centre of Excellence in Epidemiological Modelling and Analysis (SACEMA), South Africa, ²University of Georgia, USA, ³McMaster University, Canada, ⁴University of California, USA, ⁵Colby College, USA
- [P1.105] An alternative global strategy for measles elimination: honeymoon eradication**
A.K. Winter*¹, J. Lessler², M.J. Ferrari³, B.T. Grenfell¹, C.J.E. Metcalf¹, ¹Princeton University, USA, ²Johns Hopkins Bloomberg School of Public Health, USA, ³The Pennsylvania State University, USA
- [P1.106] Cost-effectiveness analysis of typhoid conjugate vaccine in Gavi-eligible countries**
M. Antillon*^{1,2}, J. Bilcke^{1,2}, A.D. Paltiel¹, V.E. Pitzer¹, ¹Yale University, USA, ²University of Antwerp, Belgium
- [P1.107] Interplay between cooperative and competitive effects in multi-pathogen systems**
F. Pinotti*^{1,2}, F. Ghanbarnejad³, P. Hövel³, C. Poletto^{1,2}, ¹INSERM, France, ²UPMC, France, ³Institute of Theoretical Physics, Germany
- [P1.108] Competing effects of indirect protection and clustering on the power of a cluster-randomized controlled vaccine trial**
M.D.T. Hitchings*¹, M. Lipsitch¹, S.E. Bellan², ¹Harvard T.H. Chan School of Public Health, USA, ²College of Public Health, University of Georgia, USA
- [P1.109] Presence and ecological effect of a raccoon rabies expansion load**
O. Yvellez*¹, E. Zhao¹, R. Biek², H. Trewby², L. Real³, K. Koelle³, ¹Duke University, USA, ²University of Glasgow, UK, ³Emory University, USA
- [P1.110] Multivariate imputation of missing data to calibrate an agent-based model of HIV transmission**
T. Chibawara¹, J. Liesenborgs^{2,3}, F. Van Reeth^{2,3}, N. Hens^{2,4}, W. Delva*^{1,5}, ¹Stellenbosch University, South Africa, ²imec, Belgium, ³Hasselt University, Belgium, ⁴University of Antwerp, Belgium, ⁵Ghent University, Belgium, ⁶KU Leuven, Belgium
- [P1.111] Modelling the role of long lasting insecticide-treated bednets in the reduction of Lymphatic filariasis prevalence in The Gambia**
E.L. Davis*, M.J. Keeling, T.D. Hollingsworth, University of Warwick, UK

- [P1.112] **Evaluating the quality of surveillance systems and its consequences for immunization planning and elimination prospects of canine rabies: a case study of the Bicol Region, Philippines**
K. Rysava*¹, M. Tildesely¹, R.C. Abila³, M.J.N. Gordoncillo², T.R.M. Barroga³, ¹University of Warwick, UK, ²Food and Agriculture Organization of the United Nations, Thailand, ³World Organisation for Animal Health, Thailand
- [P1.113] **Spatial dynamics of *Plasmodium falciparum* malaria during an outbreak: A case of Northern Namibia**
S. Tessema*¹, M. Murphy¹, A. Bennett¹, H.J.W. Sturrock¹, J.L. Smith¹, R. Gosling¹, M.S. Hsiang¹, D. Mumbengegwi², B. Greenhouse¹, ¹University of California, USA, ²University of Namibia, Namibia
- [P1.114] **Hamiltonian analysis of subcritical stochastic epidemic dynamics**
L. Worden*¹, I.B. Schwartz², S. Bianco³, S.F. Ackley¹, T.M. Lietman¹, T.C. Porco¹, ¹UCSF, USA, ²US Naval Research Laboratory, USA, ³IBM Almaden Research Center, USA
- [P1.115] **Age trends in asymptomatic and symptomatic Leishmanial infection in the Indian subcontinent**
L.A.C. Chapman*¹, A.L.K. Morgan^{1,2}, E.R. Adams³, C. Bern⁴, T.D. Hollingsworth¹, ¹Warwick University, UK, ²LSHTM, UK, ³LSTM, UK, ⁴UCSF, USA
- [P1.117] **Seasonality of dengue fever in rural Ecuador: 2009-2016**
R. Sippy*¹, D. Gaus², D. Herrera², R. Gangnon¹, J. Osorio¹, J. Patz¹, ¹University of Wisconsin-Madison, USA, ²Saludesa, Ecuador
- [P1.118] **Concentrated distribution of vaccines and its effect on final size of Japanese rubella epidemic**
M.M. Saito*¹, R. Kinoshita², H. Nishiura², ¹The Institute of Statistical Mathematics, Japan, ²Hokkaido University, Japan
- [P1.119] **Health outcomes from multi-drug resistant *Salmonella* infections in high-income countries: A systematic review and meta-analysis**
A. Parisi*^{1,2}, J.A. Crump³, K. Glass¹, B.P. Howden⁴, L. Furuya-Kanamori⁵, D. Gray¹, S. Vilkins¹, M. Kirk¹, ¹Australian National University, Australia, ²Codaqua Foundation, Spain, ³University of Otago, New Zealand, ⁴University of Melbourne, Australia, ⁵Qatar University, Qatar
- [P1.120] **Sampling considerations to optimize viral genetic diversity capture in RSV surveillance**
N. Kibinge*¹, S. Brand², G. Githinji¹, C. Agoti¹, P. Munywoki¹, M. Kiti¹, M. Keeling¹, D.J. Nokes¹, ¹KEMRI-Wellcome Trust, Kenya, ²University of Warwick, UK
- [P1.121] **Direct and indirect effects of varicella and herpes zoster vaccination in Italy: A dynamic cost-effectiveness analysis in an aging population**
A. Melegaro*¹, E. Del Fava¹, V. Marziano², P. Poletti^{1,2}, M. Tirani³, S. Merler², ¹Bocconi University, Italy, ²Bruno Kessler Foundation, Italy, ³Università Vita e Salute San Raffaele, Italy
- [P1.122] **Prevalence, distribution and physiological effects of *Sarcocystis* on wild red deer in Italian central Alps**
S. Giacomelli*, A. Bianchi, I. Archetti, S. Rota Nodari, I. Bertoletti, Istituto Zooprofilattico Lombardia ed Emilia Romagna "Bruno Ubertini", Italy
- [P1.123] **Counterstrategy to cope with infectious disease in preparation for the exchange between South and North Korea and unification**
E.Y. Lee*¹, M.R. Ki¹, B.Y. Choi¹, ¹National Cancer Center, Graduate school of cancer science and policy, Republic of Korea, ²Hanyang University College of Medicine, Republic of Korea
- [P1.124] **Agent-based modelling to understand socio-epidemiological dynamics in livestock health management**
E.A.J. Fischer*¹, T.J. Hagenaars², J. Sok³, T. Verwaart⁴, ¹Utrecht University, The Netherlands, ²Wageningen Bioveterinary Research, The Netherlands, ³Wageningen University, The Netherlands, ⁴Wageningen Economic Research, The Netherlands
- [P1.125] **Optimizing spatial resolutions for modelling global disease transmission of multiple pathogens**
J.P. Glutting*, N. Dorratoltaj, T. Saksuriyongse, AIR Worldwide, USA
- [P1.126] **Spatial dynamics of disease spread in random spatial networks**
J.C. Miller*¹, J. Lang³, H. De Sterck¹, ¹Institute for Disease Modeling, USA, ²Monash University, Australia, ³UCLA, USA
- [P1.127] **Molecular epidemiological analysis of an outbreak of vancomycin-resistant *Enterococcus faecium* in a university hospital of Bogotá, 2016**
N.C. Corredor*^{1,2}, C. López^{1,3}, L.M. Prieto^{2,4}, G. Rodríguez-Leguizamón^{1,2}, J.M. Pardo^{1,2}, M.A. Patarroyo^{1,3}, ¹School of Medicine and Health Sciences, Universidad del Rosario, Colombia,

²Corporación Hospitalaria Juan Ciudad – Hospital Universitario Mayor (Méderi), Colombia,
³Molecular Biology and Immunology Department, Fundación Instituto de Inmunología de Colombia (FIDIC), Colombia, ⁴School of Medicine and Health Sciences, Universidad del Bosque, Colombia

[P1.128] **Withdrawn**

Poster Session 2

Wednesday, 29 November 2017 17:50-19:20

All posters with an odd number will be presented from 17:50-18:35, Wednesday 29 November e.g. P2.001, P2.003 etc.

All posters with an even number will be presented from 18:35-19:20, Wednesday 29 November e.g. P2.002, P2.004 etc.

[P2.001] Assessing the dynamics and control of droplet- and aerosol-transmitted influenza using an indoor positioning system

G.L. Lazzari^{*1}, T.S. Smieszek², M.S. Salathé¹, ¹Ecole Polytechnique Fédérale de Lausanne, Switzerland, ²Public Health England, UK

[P2.002] Agent-based models for influenza epidemic dynamics and its decision-making capability

V. Perminov, BioTeckFarm Ltd, Russia

[P2.003] The risk assessing of dengue infection among Japanese overseas travelers to endemic countries

B. Yuan*, H. Nishiura, Hokkaido University, Japan

[P2.004] Pig movements in France: Designing network models fitting the epidemiological context

M. Salines^{*1,2}, M. Andraud^{1,2}, N. Rose^{1,2}, ¹ANSES, Ploufragan/Plouzané Laboratory, France, ²Université Bretagne Loire, France

[P2.005] Fourfold rises in antibody titre to age-appropriate historical strains of influenza B suggest higher rates of infection than do homologous strains

K.O. Kwok^{*1}, H.Z. Zhu², J. Lessler³, J.M. Read^{4,5}, C.Q. Jiang⁶, D.A.T. Cummings⁷, Y. Guan², R. Steven⁸, ¹JC School of Public Health and Primary Care, CUHK, Hong Kong, ²WHO Collaborating Centre for Infectious Disease Epidemiology and Control, School of Public Health, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong, ³Johns Hopkins Bloomberg School of Public Health, USA, ⁴Lancaster University, UK, ⁵University of Liverpool, UK, ⁶Guangzhou People's Number 12 Hospital, China, ⁷University of Florida, USA, ⁸Imperial College London, UK

[P2.006] Sensitivity analysis for disease- and setting-specific social contact parameters in an agent-based influenza transmission model

H. Gao*, A. Uzicanin, Centers for Disease Control and Prevention, USA

[P2.007] A review of transmission models of methicillin-resistant staphylococcus aureus in non-hospital residential facilities

K.O. Kwok^{*1,2}, J.M. Read^{3,4}, A. Tang⁵, S. Riley⁶, K.M. Kam^{1,2}, ¹The Jockey Club School of Public Health and Primary Care, The Chinese University of Hong Kong, Hong Kong, ²Stanley Ho Centre for Emerging Infectious Diseases, The Chinese University of Hong Kong, Hong Kong, ³Institute of Infection and Global Health, The Farr Institute@HeRC, University of Liverpool, UK, ⁴Lancaster University, UK, ⁵Sungkyunkwan University, Republic of Korea, ⁶Imperial College London, UK

[P2.008] Partner age differences and associated sexual risk behaviours among adolescent girls and young women in a cash transfer programme for schooling in Malawi

R. Beauclair^{*1,2}, J. Dushoff³, W. Delva^{1,2}, ¹Ghent University, Belgium, ²Stellenbosch University, South Africa, ³McMaster University, Canada, ⁴Hasselt University, Belgium, ⁵KU Leuven, Belgium

[P2.009] SimpaCyan: A simulation engine for individual-based models in HIV epidemiology

J. Liesenborgs^{1,2}, D.M. Hendrickx^{*1}, F. Van Reeth^{1,2}, N. Hens^{1,3}, W. Delva^{1,4}, ¹Hasselt University, Belgium, ²imec, Belgium, ³University of Antwerp, Belgium, ⁴Stellenbosch University, South Africa,

- [P2.010] **A complex approach to estimate the true incidence and burden of foodborne diseases in Hungary**
A.G. Vajda*, Cs. Mohacsi-Farkas, Szent Istvan University, Hungary
- [P2.011] **Spatial patterns of multidrug resistant tuberculosis and relationships to socio-economic, demographic and household factors in northwest Ethiopia**
K.A. Alene*^{1,2}, K. Viney^{1,4}, E. McBryde³, A. Clements¹, ¹Australian National University, Australia, ²University of Gondar, Ethiopia, ³James Cook University, Australia, ⁴Karolinska Institutet, Sweden
- [P2.012] **Cost-effectiveness of latent tuberculosis infection case-finding and treatment among the London homeless population**
T. Mugwagwa*^{1,2}, C.C. Lehman³, A.C. Hayward⁴, P.J. White^{1,2}, ¹National Infection Service, Public Health England, UK, ²Imperial College London, UK, ³University of Minnesota, USA, ⁴University College London, UK
- [P2.013] **Mathematical modelling of tuberculosis spreading, prevention and treatment**
L. Goscé*¹, G.A. Jaoude¹, D.J. Kedziora², A. Hussain², S. Jarvis², C.J. Benedikt³, H. Haghparast-Bidgoli¹, H. Stagg¹, J. Skordis-Worrall¹, I. Abubakar¹, ¹University College London, UK, ²Burnet Institute, Australia, ³World Bank, USA
- [P2.014] **Characterising the epidemiology of influenza**
J.V. Ross*, A. Black, L. Bubb, M. Chilver, R. Cope, L. Mitchell, N. Stocks, The University of Adelaide, Australia
- [P2.015] **Update about typing of Brucella field strains isolated from livestock and wildlife populations in Italy, 2007-2015**
F. De Massis*, K. Zilli, M. Ancora, G. Di Donato, L. Sacchini, E. Di Giannatale, National Reference Centre and OIE Reference Laboratory for Brucellosis, Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise 'G. Caporale', Teramo, Italy, Italy
- [P2.016] **Predicting chronic Hepatitis C prevalence in Canada via MCMC backcalculation**
A. Hamadeh*¹, Z.Z. Feng², W.W.L. Wong¹, ¹University of Waterloo, Canada, ²University of Guelph, Canada
- [P2.017] **Modeling the hepatitis C virus epidemic in Pakistan: Past trajectory and future trend**
H.H. Ayoub*^{1,2}, L.J. Abu-Raddad¹, ¹Weill Cornell Medicine - Qatar, Cornell University, Qatar, ²Weill Cornell Medicine, Cornell University, USA
- [P2.018] **How should we monitor chlamydia control programme effectiveness? Comparing performance indicators using evidence synthesis to estimate local incidence and prevalence from surveillance data**
J. Lewis¹, P.J. White*¹, ¹Imperial College London, UK, ²Public Health England, UK
- [P2.019] **Adaptive management of epidemic disease outbreaks**
B. Atkins*, M. Tildesley, University of Warwick, UK
- [P2.020] **Individual versus superensemble forecasts of seasonal influenza outbreaks in the United States**
T.K. Yamana*, S. Kandula, J. Shaman, Columbia University, USA
- [P2.021] **Pathogen spillover at the core-matrix interface**
H.I. McCallum*¹, C.L. Faust², L.S.P. Bloomfield³, N.L. Gottdenker⁴, A.P. Dobson⁵, T.R. Gillespie⁶, R.K. Plowright⁷, ¹Griffith University, Australia, ²University of Glasgow, UK, ³Stanford University, USA, ⁴University of Georgia, USA, ⁵Princeton University, USA, ⁶Emory University, USA, ⁷Montana State University, USA
- [P2.022] **Correlations between stochastic epidemics in coupled populations**
S. Meakin*, M. Keeling, University of Warwick, UK
- [P2.023] **Population dynamics of CD4 T cell epitopes in the influenza A virus**
R.G. Woolthuis^{1,2}, M. van Boven*¹, R.J. de Boer², ¹National Institute for Public Health, The Netherlands, ²Utrecht University, The Netherlands
- [P2.024] **Spatial pattern and potential drivers of seasonal dengue in Brazil**
M. Churakov*^{1,2}, C.J. Villabona-Arenas^{3,4}, M.U.G. Kraemer^{5,6}, H. Salje^{1,2}, S. Cauchemez^{1,2},

¹Institut Pasteur, France, ²CNRS, France, ³IRD, France, ⁴Université de Montpellier, France, ⁵Harvard Medical School, USA, ⁶University of Oxford, UK

- [P2.025] **A temperature and mortality driven population dynamics of tsetse flies in endemic area: Insights from a mechanistic spatio-temporal model calibrated on observed data**
P. Ezanno*¹, H. Cécilia¹, A. Dicko², S. Arnoux¹, S. Picault^{1,3}, J. Bouyer², ¹INRA, Oniris, France, ²CIRAD, France, ³Univ. Lille, CNRS, Centrale Lille, France
- [P2.026] **Mapping influenza epidemics in France using Bayesian model-based geostatistics**
J. Paireau*¹, C. Pelat², Y. Le Strat², D. Lévy-Bruhl², S. Cauchemez¹, ¹Institut Pasteur, France, ²Santé publique France, France
- [P2.027] **A multi-scale stochastic model for the within-host infection dynamics of Francisella tularensis**
J. Carruthers¹, M. Lopez-Garcia*¹, J. Gillard², T. Laws², G. Lythe¹, C. Molina-Paris¹, ¹University of Leeds, UK, ²Defence Science and Technology Laboratory, UK
- [P2.028] **Phylogenetic analysis of a type-2 vaccine-derived poliovirus outbreak in Nigeria**
S. Radhakrishnan*¹, M. Pons-Salort¹, L.M. Li², N. Grassly¹, ¹Imperial College London, UK, ²Harvard University, USA
- [P2.029] **Model for assessing immunization strategies with second-generation live-attenuated dengue vaccines**
E.H. Elbasha*, M.A. Marks, J.R. Sachs, B-A. Coller, A. Sinha, Merck & Co., Inc., USA
- [P2.030] **Sexual network structure, HIV prevalence, and the evolution of set point viral load**
S. Goodreau*, S. Stansfield, J. Murphy, K. Peebles, G. Gottlieb, N. Abernethy, J. Herbeck, J. Mittler, University of Washington, USA
- [P2.031] **Genotype-specific measles transmissibility: A branching process analysis**
S.F. Ackley¹, J.K. Hacker⁴, W.T.A. Enanoria¹, L. Worden*¹, S. Blumberg^{1,5}, T.C. Porco¹, J. Zipprich¹, ¹University of California, USA, ²California Department of Public Health, USA, ³St. Mary's Medical Center, USA
- [P2.032] **Comparative modelling of zoonotic virus persistence in bat reservoirs**
E.E. Glennon*, O. Restif, University of Cambridge, UK
- [P2.033] **Inferring epidemiological dynamics of infectious diseases using Tajima's D statistic on nucleotide sequences of pathogens**
K. Ito*, K. Kim, R. Omori, Hokkaido University, Japan
- [P2.034] **Metapopulation Epidemic Model with the public transportation and mobile phone data**
W-S. Son, Korea Research Institute of Chemical Technology, Republic of Korea
- [P2.035] **Understanding measles outbreaks in vaccinated populations**
K.A. Broadfoot*, M.J. Keeling, University of Warwick, UK
- [P2.036] **What can we say from the death of layer chickens? Estimating within-flock HPAI (H5N2) dynamics using an approximate Bayesian computation framework**
T. Porphyre*¹, A. Delgado², M. Schoenbaum², M.K. Torchetti³, ¹The Roslin Institute, UK, ²Veterinary Services, USA, ³National Veterinary Services Laboratory, USA
- [P2.037] **Inference of interactions between pathogen types using patterns of co-occurrence in cross-sectional prevalence data: Relevance and pitfalls in predicting type replacement**
I. Man*^{1,2}, J. Wallinga^{1,2}, J.A. Bogaards^{1,3}, ¹National Institute for Public Health and the Environment, The Netherlands, ²Leiden University Medical Center, The Netherlands, ³VU University Medical Center, The Netherlands
- [P2.038] **Reconstructing 19th century Influenza transmission patterns with antigenic imprinting**
K.H. Grantz*^{1,2}, S. Cauchemez^{3,4}, D.A.T. Cummings^{1,5}, H. Salje^{3,4}, ¹University of Florida, USA, ²Epicentre, France, ³Institut Pasteur, France, ⁴Centre National de la Recherche Scientifique, France, ⁵Johns Hopkins Bloomberg School of Public Health, USA
- [P2.039] **Estimation of genetic effects on susceptibility and infectivity from data on Digital Dermatitis**
F. Biemans*, M.C.M. de Jong, P. Bijma, Wageningen University and Research, The Netherlands

- [P2.040] The importance of within-host dynamics for the population level evolution of Influenza**
V. Karamitsou*, L.S. Tiley, J.R. Gog, *University of Cambridge, UK*
- [P2.041] Overlapping epidemics: Epidemiologic characteristics and population-level impact of seasonal influenza viruses**
M.A. Rolfes*, S. Garg, D. Mustaqim, L. Brammer, S.J. Olsen, A.M. Fry, C. Reed, *Centers for Disease Control and Prevention, USA*
- [P2.042] Seasonality of vector-borne plague transmission in pre-industrial Europe: A modelling approach**
F. Krauer*, K.R. Dean, N.C. Stenseth, B.V. Schmid, *Centre for Ecological and Evolutionary Synthesis, University of Oslo, Norway*
- [P2.043] Similarities and differences of in-school simulated influenza transmission among 10 primary and secondary schools in Utah**
M. Leecaster*^{1,2}, D. Toth^{1,2}, W. Pettey², H. Gao³, J. Rainey³, A. Uzicanin³, M. Samore^{1,3}, ¹*University of Utah, USA*, ²*Veterans Affairs, USA*, ³*Centers for Disease Control and Prevention, USA*
- [P2.044] Region-specific risk of infection with chikungunya and dengue among travellers returning to the United Kingdom**
M.M.I. Mesle*^{1,2}, I.M. Hall^{1,3}, R.M. Christley^{1,2}, S. Leach^{1,3}, J. Freedman³, C. Jewell⁴, J.M. Read^{1,4}, ¹*NIHR Health Protection Research Unit in Emerging and Zoonotic Infections, UK*, ²*The University of Liverpool, UK*, ³*Public Health England, UK*, ⁴*Lancaster University, UK*
- [P2.045] Understanding the dynamics of West Nile virus in Emilia-Romagna, Italy**
M. Tosato¹, L. Bolzoni², G. Marini³, R. Rosà³, A. Pugliese*¹, ¹*University of Trento, Italy*, ²*Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Italy*, ³*San Michele all'Adige (TN), Italy*
- [P2.046] The impact of increased STI testing on the spread of HIV and gonorrhoea among men who have sex with men**
M.T. Reitsema*^{1,2}, J. Wallinga^{1,2}, B.H. van Benthem¹, A.I. van Sighem³, M.F.S. van der Loeff⁴, M. Xiridou¹, ¹*National Institute for Public Health and Environment, The Netherlands*, ²*Leiden University Medical Center, The Netherlands*, ³*Stichting HIV Monitoring, The Netherlands*, ⁴*Public Health Service Amsterdam, The Netherlands*
- [P2.047] Assessing the impact of imperfect adherence to artemether-lumefantrine on malaria treatment outcomes using within-host modelling**
J.D. Challenger*¹, K. Bruxvoort², A.C. Ghani¹, L.C. Okell¹, ¹*Imperial College London, UK*, ²*London School of Hygiene and Tropical Medicine, UK*
- [P2.048] Community transmission of tuberculosis in a household contact study**
A.I. McIntosh², C.R. Horsburgh¹, H.E. Jenkins¹, L.F. White*¹, ¹*Boston University, USA*, ²*Novartis, USA*
- [P2.049] Development of a mathematical model for natural history of Hepatitis B virus infection in Korean population**
K. Bae*¹, S. Choi^{1,2}, S. Lee¹, B. Kim¹, M. Ki¹, H. Cho¹, ¹*National Cancer Center Graduate school of Cancer Science and Policy, Republic of Korea*, ²*Hanyang University, Republic of Korea*
- [P2.050] Potential for Zika Virus to Establish a Sylvatic Transmission Cycle in the Americas**
B.M. Althouse*^{1,2}, N. Vasilakis³, A.A. Sall⁴, M. Diallo⁴, S.C. Weaver³, K. Hanley¹, ¹*Institute for Disease Modeling, USA*, ²*New Mexico State University, USA*, ³*University of Texas Medical Branch, USA*, ⁴*Institut Pasteur de Dakar, Senegal*
- [P2.051] A dynamic model for acquired immunity to Campylobacter and its applications to risk-assessment**
A.H. Havelaar², A.N. Swart*¹, ¹*RIVM, The Netherlands*, ²*University of Florida, USA*
- [P2.052] Economic and epidemiological incentives in responding to livestock disease threat: The case of avian influenza in Vietnam**
A. Delabougliuse*, M.F. Boni, *The Pennsylvania State University, USA*
- [P2.053] Investigating recent cases of parapoxvirus infection in canadian muskoxen**
C. Dalton*¹, S. Kutz¹, F. Careem¹, K. Ruckstuhl¹, M. Tomaselli¹, F. Mavrot¹, J. Di Francesco¹, L.

Leclerc², F. van der Meer¹, ¹University of Calgary, Canada, ²Government of Nunavut, Canada

[P2.054] How do we allocate finite resources to maximise impact of HIV interventions targeting female sex workers across different and multiply Avahan districts?

J. Panovska-Griffiths*^{1,2}, A. Lepine², H. Prudden², A. Vassall², P. Vickerman³, ¹University College London, UK, ²London School of Hygiene and Tropical Medicine, UK, ³University of Bristol, UK

[P2.055] A model for novel influenza surveillance using a respiratory panel cloud based epidemiological network

J. Jones*, J. Nawrocki, B. Galvin, A. Faucett, L. Meyers, *BioFire Diagnostics, LLC, USA*

[P2.056] Modelling vaccine trials in epidemics with asymptomatic infection

R. Kahn*, M. Hitchings, M. Lipsitch, *Harvard T.H. Chan School of Public Health, USA*

[P2.057] The interaction between AIDS and tuberculosis in Ho Chi Minh City from 1996 to 2015

D.N. Vinh*¹, D.T.M. Ha^{1,2}, G. Thwaites¹, M.F. Boni^{1,3}, H. Clapham¹, N.T.T. Thuong¹, ¹Oxford University Clinical Research Unit, Viet Nam, ²Pham Ngoc Thach Hospital, Viet Nam, ³The Pennsylvania State University, USA

[P2.058] Changes in the force of infection of dengue virus from 1994 to 2015 in a pediatric cohort study in Nicaragua

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[P2.059] Investigation into the effect of host migration on the transmission of *Onchocerca volvulus* using a patch model

K. McCulloch*¹, J. McCaw², J. McVernon³, S.M. Hedtke¹, M. Walker⁴, P. Milton⁵, M.G. Basáñez⁵, W. Grant¹, ¹La Trobe University, Australia, ²University of Melbourne, Australia, ³University of Melbourne & Royal Melbourne Hospital, Australia, ⁴Royal Veterinary College and London Centre for Neglected Tropical Disease Research, UK, ⁵Imperial College London and London Centre for Neglected Tropical Disease Research, UK

[P2.060] Clonal differences in *Staphylococcus aureus* bacteraemia-associated mortality

M. Recker*¹, M. Laabei², R. Massey^{2,3}, ¹University of Exeter, UK, ²University of Bath, UK, ³University of Bristol, UK

[P2.061] Influzanet: A European network of participatory systems for the monitoring of Influenza-Like illnesses

D. Paolotti¹, D. Perrotta*¹, V. Colizza^{2,1}, C. Guerrisi², C. Turbelin², J. Duggan³, W.J. Edmunds⁴, A. Flahault⁵, D. Dietrich⁵, O. Wolley-Meza⁶, ¹ISI Foundation, Italy, ²Sorbonne Universités, France, ³National University of Ireland, Ireland, ⁴London School of Hygiene and Tropical Medicine, UK, ⁵University of Geneva, Switzerland, ⁶ETH Zurich, Switzerland

[P2.062] Migrants and infection control at the backdoor to Europe

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[P2.063] Maximising the impact of global malaria funding using an optimal allocation framework

P. Winskill*¹, P.G.T. Walker¹, J.T. Griffin^{1,2}, E. Patouillard^{3,4}, A.C. Ghani¹, ¹Imperial College London, UK, ²Queen Mary University, UK, ³GMP, WHO, Switzerland, ⁴Swiss Tropical and Public Health Institute, Switzerland

[P2.064] Rapid re-emergence and geographic transmission dynamics of a recombinant GII.P16-GII.2 norovirus in the winter of 2016/17

K. Kwok*¹, N. Lee², E.A.S. Nelson¹, T.F. Leung¹, R.W.M. Lai¹, P.K.S. Chan¹, M.C.W. Chan¹, ¹The Chinese University, Hong Kong, ²University of Alberta, Canada

[P2.065] Assessing statistical and mathematical methods' ability to detect between-pathogen interactions in humans: An agent-based model simulation study

H. Arduin*, M.D. de Celles, D. Guillemot, L. Watier, L. Opatowski, *Institut Pasteur, France*

[P2.066] Seasonality of urinary tract infections in the United Kingdom in different age groups

A. Rosello*^{1,2}, K.B. Pouwels^{1,3}, M.D. de Cellès⁴, E. Van Kleef^{5,6}, A.C. Hayward¹, S. Hopkins^{1,7}, J.V. Robotham¹, T. Smieszek^{1,3}, L. Opatowski⁴, S.R. Deeny⁸, ¹Public Health England, UK, ²UCL, UK,

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- [P2.067] **Within herd bovine tuberculosis transmission and detection in Michigan livestock**
A. Minter*¹, T. Lindström², C. Webb³, M. Tildesley¹, ¹University of Warwick, UK, ²Linköping University, Sweden, ³Colorado State University, USA
- [P2.068] **Quantifying the value of perfect information in emergency vaccination campaigns**
N.V. Bradbury*^{1,2}, W.J.M. Probert^{1,2}, K. Shea³, M.C. Runge⁴, C.J. Fonnesebeck⁵, M.J. Keeling¹, M.J. Tildesley¹, ¹University of Warwick, UK, ²University of Nottingham, UK, ³The Pennsylvania State University, USA, ⁴US Geological Survey, USA, ⁵Vanderbilt University, USA
- [P2.069] **Modelling target product profiles for the RTS,S/AS01 malaria vaccine**
A.B. Hogan*, R. Verity, P. Winskill, A.C. Ghani, Imperial College London, UK
- [P2.070] **Estimating the impact of a maternal RSV vaccine using a mathematical modelling approach**
A.B. Hogan*¹, P.T. Campbell², C.C. Blyth³, F.J. Lim³, P. Fathima³, S. Davis⁴, H.C. Moore³, K. Glass⁴, ¹Imperial College London, UK, ²University of Melbourne, Australia, ³University of Western Australia, Australia, ⁴Australian National University, Australia
- [P2.071] **Defining the Spatio-Temporal scale of Foot-And-Mouth disease virus lineages emergence in the Middle East region**
A. di Nardo*, L. Ferretti, J. Wadsworth, K. Bachanek-Bankowska, D.P. King, N.J. Knowles, The Pirbright Institute, UK
- [P2.072] **Early warning and detection of outbreaks on bovine transport networks: the role of markets**
F. Schirdewahn*², B. Vidondo¹, A. Kocher², H.H.K. Lentz³, V. Colizza⁴, P. Hövel², ¹University of Bern, Switzerland, ²Technische Universität Berlin, Germany, ³Friedrich-Loeffler-Institut, Germany, ⁴Sorbonne Universités, INSERM, France
- [P2.073] **Are associations between HIV and HPV transmission due to behavioural confounding factors or biological effects?**
C. van Schalkwyk*¹, J.R. Moodley², A. Welte¹, L.F. Johnson², ¹University of Stellenbosch, South Africa, ²University of Cape Town, South Africa
- [P2.074] **Risk of male to female sexual transmission of Zika virus**
M.J. Counotte, N. Low, C.L. Althaus*, University of Bern, Switzerland
- [P2.075] **Prospects of toxoplasmosis control by cat vaccination**
A.A. Bonacic*, M. Opsteegh, J.W.B. van der Giessen, RIVM, The Netherlands
- [P2.076] **Latent TB screening of recent immigrants in England: A cost-effectiveness analysis**
N. Green*¹, R. Aldridge², L. Gosce², I. Abubakar², P. White^{1,3}, ¹Imperial College London, UK, ²University College London, UK, ³Public Health England, UK
- [P2.077] **All for one, one for all: Across border lymphatic filariasis transmission can potentially compromise national elimination programs**
J.M. Prada*¹, L.J. Reimer², T.D. Hollingsworth¹, ¹University of Warwick, UK, ²Liverpool School of Tropical Medicine, UK
- [P2.078] **H1N1 pdm09 influenza viral kinetics in vaccinated pigs**
L. Canini*¹, M. Aramouni², S. Brookes², B. Charleston³, M.E.J. Woolhouse¹, ¹University of Edinburgh, UK, ²Animal and Plant Health Agency, UK, ³Weybridge, UK
- [P2.079] **The utility of serological and antibody data for end game surveillance: an example from *Chlamydia trachomatis***
A. Pinsent*¹, S. Migchelsen², A. Solomon², R. Bailey², R. Butcher², D. Mabey², C. Roberts², M.T. White³, ¹Monash University, Australia, ²London School of Tropical Medicine and Hygiene, UK, ³Institut Pasteur, France
- [P2.080] **Assessing Zika virus transmission within households and the proportion of asymptomatic infections during an outbreak in Martinique, 2015-2016**
A. Cousien*^{1,2}, S. Abel³, A. Monthieux³, F. Najjioullah³, I. Calmont⁴, M. Pircher³, S. Pierre-François³, R. Césaire³, A. Cabié^{3,5}, S. Cauchemez^{1,2}, ¹Institut Pasteur, France, ²Centre National de la

Recherche Scientifique, France, ³Centre Hospitalo-Universitaire de Fort-de-France, France, ⁴INSERM, France, ⁵Université des Antilles, France

- [P2.081] **The importance of life history traits in infectious disease outbreaks in marine mammals**
C.E. Sanderson*^{1,2}, K.A. Alexander^{1,2}, ¹Virginia Tech, USA, ²CARACAL, Botswana
- [P2.082] **In silico comparison of several test-and-slaughter protocols to control bovine tuberculosis in France**
H. Ladreyt², M. Saccareau*^{1,2}, S. Cauchemez¹, B. Durand², A. Courcoul², ¹Institut Pasteur, France, ²French Agency for Food, Environmental and Occupational Health & Safety, France
- [P2.083] **See and sequence: The use of whole genome sequencing for surveillance of antimicrobial resistance in the philippines**
S. Argimon^{1,2}, J. Gayeta³, M.A. Masim³, V. Cohen¹, M. Lagrada³, A. Olorosa³, B. Jeffries¹, S. David¹, C. Carlos³, D.M. Aanensen*^{1,2}, ¹Centre for Genomic Pathogen Surveillance, UK, ²Imperial College London, UK, ³Research Institute for Tropical Medicine, The Philippines
- [P2.084] **Risk of anthelmintic resistance in the era of mass drug administration against human helminth infections**
L.E. Coffeng*, W.A. Stolk, S.J. de Vlas, *University Medical Center Rotterdam, The Netherlands*
- [P2.085] **Effect of mass paediatric influenza vaccination on existing influenza vaccination programmes in England and Wales**
D. Hodgson¹, M. Baguelin^{2,3}, E. van Leeuwen², J. Panovska-Griffiths¹, M. Ramsay², R. Pebody², K.E. Atkins*³, ¹University College London, UK, ²Public Health England, UK, ³London School of Hygiene and Tropical Medicine, UK
- [P2.086] **Resistance gene selection in the human gut microbiome**
R. Niehus*^{1,2}, E. van Kleef^{1,2}, B. Cooper^{1,2}, ¹University of Oxford, UK, ²Mahidol University, Thailand
- [P2.087] **Asymptomatic shedding of respiratory virus among an ambulatory population**
R.B. Birger*¹, I. Filip¹, M. Galanti¹, D. Comito¹, B. Lane¹, C. Ligon¹, H. Morita¹, D. Rosenbloom¹, A. Shittu¹, M. Ud-Dean¹, ¹Columbia University, USA, ²American Museum of Natural History, USA, ³University of Pennsylvania, USA
- [P2.088] **Application of mathematical modelling for decision-making in pandemic influenza and infectious disease planning**
K.C. Allen*, J.A. Steele, *US European Command Headquarters, Germany*
- [P2.089] **Comparative analysis of mammalian viruses found in human and animal samples from Vietnam**
C. Bogaard†*, A.C. Ivens, A. Rambaut, M.E.J. Woolhouse, *University of Edinburgh, UK*
- [P2.090] **Guillain-Barré syndrome risk among individuals infected with Zika virus**
L. Mier-y-Teran-Romero*¹, M.J. Delorey¹, J.J. Sejvar¹, M.A. Johansson^{1,2}, ¹Centers for Disease Control and Prevention, USA, ²Harvard University, USA
- [P2.091] **Longitudinal mechanistic models to infer the breadth and duration of protection following influenza infection**
R. Subramanian*¹, S.L. Ranjeva¹, B.J. Cowling², S.E. Cobey¹, ¹University of Chicago, USA, ²The University of Hong Kong, Hong Kong
- [P2.092] **Modeling local and regional dynamics of chikungunya virus transmission in Colombia highlights the importance of spatial heterogeneity for disease forecasting**
S.M. Moore*¹, Q.A. ten Bosch², A.S. Siraj¹, K.J. Soda¹, B. Raybaud³, E. Wenger³, P. Eckhoff³, T.A. Perkins¹, ¹University of Notre Dame, USA, ²Institut Pasteur, France, ³Institute for Disease Modeling, USA
- [P2.093] **Modeling the evolution in time of CPE episodes in France**
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- [P2.094] Vaccination of health care workers to control Ebola virus disease**
A. Robert*¹, A. Camacho², W.J. Edmunds¹, M. Baguelin^{1,3}, J.J. Muyembe-Tanfum⁴, A. Rosello^{3,5}, S. Keïta⁶, R. Eggo¹, ¹London School of Hygiene & Tropical Medicine, UK, ²Epicentre Paris, France, ³Public Health England, UK, ⁴Institut National de Recherche Biomédicale, Congo, ⁵University College London, UK, ⁶Ministry of Health, Guinea
- [P2.095] Diversity and circulation of dengue virus serotypes 1-4 among subdistricts in Kamphaeng Phet, Thailand from 2010 – 2012: Implications for surveillance and control**
R.G. Jarman*¹, M.C. Melendrez¹, I.M. Berry¹, S. Pollett¹, C. Klungthong², A. Nisalak², B. Thaisomboonsuk², T. Li¹, T. Vallard¹, L. Macareo², ¹Walter Reed Army Institute of Research, USA, ²Armed Forces Research Institute of Medical Sciences, Thailand, ³University of Rhode Island, USA, ⁴International Vaccine Institute, Republic of Korea, ⁵Upstate Medical University of New York, USA
- [P2.096] Predicting primate sources Zika virus spillover infection**
B.A. Han*¹, S. Majumdar², A. Mojsilovic³, K. Varshney³, ¹Cary Institute of Ecosystem Studies, USA, ²University of Minnesota, USA, ³IBM T.J. Watson Research Center, USA
- [P2.097] Potential impact of paediatric TB prevention**
C. Ciavarella*, N. Arinaminpathy, B. Kampmann, *Imperial College London, UK*
- [P2.098] SIR model with time dependent infectivity parameter: Approximating the epidemic attractor and the importance of the phase**
S. Boatto*^{1,3}, C. Bonnet^{2,3}, B. Cazelles^{4,5}, F. Mazenc^{2,3}, M. Paez¹, ¹Universidade Federal de Rio de Janeiro, Brazil, ²CNRS-INRIA-Saclay, France, ³CentraleSupélec, France, ⁴UPMC-IRD, France, ⁵ENS, France
- [P2.099] Vaccination and the evolution of seasonal influenza**
F. Wen*, A. Malani, S. Cobey, *The University of Chicago, USA*
- [P2.100] The effect of partial observation on inference of epidemiological parameters in low-transmission malaria settings**
K.K. Harrod*¹, B. Greenhouse², T.A. Perkins¹, ¹University of Notre Dame, USA, ²University of California, San Francisco, USA
- [P2.101] A multi-parameter analysis of genetic structure of intra-host HCV populations at early and late stages of infection**
P. Icer¹, A. Artyomenko¹, S. Ramachandran², A. Zelikovsky¹, Y. Khudyakov², P. Skums*^{1,2}, ¹Georgia State University, USA, ²Centers for Disease Control and Prevention, USA
- [P2.102] Modelling the impact of curtailing antibiotic usage in food animals on antibiotic resistance in humans: Don't leave it too late!**
B.A.D. van Bunnik*, M.E.J. Woolhouse, *University of Edinburgh, UK*
- [P2.103] Building on forecasting models to assess the impact of an intervention**
S.A. Lauer*¹, L.B. Balzer¹, E.L. Ray², S. Iamsirithaworn⁴, J. Lessler³, N.G. Reich¹, ¹University of Massachusetts, Amherst, USA, ²Mt. Holyoke College, USA, ³Johns Hopkins University, USA, ⁴Department for Disease Control, Thailand
- [P2.104] Modelling and inference of strain-specific meningococcal vaccine effectiveness**
L. Argante*¹, M. Tizzoni², R. Beltrami¹, S.R. Parikh³, S.N. Ladhani³, D. Medini¹, ¹GSK, Italy, ²ISI Foundation, Italy, ³Public Health England, UK
- [P2.105] Dynamic risk mapping of zoonotic spillover**
J.M. Drake*¹, J.P. Schmidt¹, A.W. Park¹, A.M. Kramer¹, B. Han², L. Alexander³, ¹University of Georgia, USA, ²Cary Institute of Ecosystem Studies, USA, ³University of California, USA
- [P2.106] Implications of spatial epidemiology and intervention intensity on implementation units for disease elimination programs**
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- [P2.107] A modelling based approach for inferring infrequent non-human influenza A infections using serological data**

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[P2.108] Estimating underlying patterns of dengue susceptibility in Thailand, using multi-scale data

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[P2.109] Optimizing early detection of emerging outbreaks

K. Liu*¹, R. Srinivasan¹, Z. Ertem¹, L.A. Meyers^{1,2}, ¹The University of Texas at Austin, USA, ²The Santa Fe Institute, USA

[P2.110] Wormy households: Modelling and inference of soil-transmitted helminthiasis transmission dynamics

A. Bishop*¹, C. Holland², T. House³, T.D. Hollingsworth¹, ¹University of Warwick, UK, ²Trinity College Dublin, Ireland, ³University of Manchester, UK

[P2.111] Dynamic response of airborne infections to climate change: Predictions for varicella

A.S. Mahmud*, R.E. Baker, C.J.E. Metcalf, Princeton University, USA

[P2.112] Downgrading local Zika risk estimates using terminal importations

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[P2.113] Drivers for Riff Valley fever emergence on the island of Mayotte

R. Metras*¹, G. Fournie², L. Dommergues³, A. Camacho^{1,4}, L. Cavalerie^{6,7}, P. Merot⁸, M.J. Keeling⁹, C. Cetre-Sossah⁵, E. Cardinale⁵, W.J. Edmunds¹, ¹LSHTM, UK, ²RVC, UK, ³GDS-CoopADEM Mayotte, France, ⁴Epicentre, France, ⁵CIRAD, France, ⁶Direction Generale de l'Alimentation, France, ⁷Université de La Réunion, France, ⁸Direction de l'Alimentation, de l'Agriculture et de la Forêt de Mayotte, France, ⁹Warwick University, UK

[P2.114] Effectiveness of indoor residual spraying on dengue transmission

T.J. Hladish*¹, D.P. Rojas¹, C.A.B. Pearson², H. Gomez-Dantes³, M.E. Halloran^{4,5}, G.M. Vazquez-Prokopec⁶, I.M. Longini¹, ¹University of Florida, USA, ²Very Good Research & Development, LLC, USA, ³National Institute of Public Health, Mexico, ⁴Fred Hutchinson Cancer Research Center, USA, ⁵University of Washington, USA, ⁶Emory University, USA

[P2.115] Effects of within and between country variability in age-mixing patterns on the epidemic spread

D. Mistry¹, A. Pastore y Piontti¹, M. Litvinova*¹, X. Xiong¹, K. Mu¹, Q.H. Lui¹, M.F.C. Gomes², E. Panagakou¹, S.A. Haque¹, L. Fumanelli³, ¹Northeastern University, USA, ²Oswaldo Cruz Foundation, Brazil, ³Bruno Kessler Foundation, Italy

[P2.116] Simulating worker absenteeism by economic sector during influenza pandemics and implications for economic impact

K. Miller*, M. Gahan, C. Lam, M. Gallivan, V. Serhiyenko, N. Stephenson, N. Madhav, Metabiota, Inc., USA

[P2.117] Surveillance of norovirus-like illness in Ontario: Using Telehealth Ontario data to detect the onset of community activity

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[P2.118] Interactions between dengue immunity and Zika virus infection

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[P2.119] Insights on paratuberculosis in cattle from a metapopulation model and inference via a composite-likelihood approximation

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- [P2.120] **Population level mathematical modelling of antimicrobial resistance: A systematic review**
A.M. Niewiadomska¹, A.A. Livinski², B. Jayabalasingham^{1,3}, J.C. Seidman¹, D. Spiro¹, C. Viboud*¹, ¹Fogarty International Center, National Institutes of Health, USA, ²National Institutes of Health, USA, ³Elsevier, USA
- [P2.121] **Population-level antibiotic treatment policies in the setting of antibiotic resistance: A mathematical model of mass treatment of *Helicobacter pylori* in Mexico**
F. Alarid-Escudero*¹, E.A. Enns¹, J. Parsonnet², J. Torres³, R.F. Maclehose¹, K.M. Kuntz¹, ¹University of Minnesota, USA, ²Stanford University, USA, ³Mexican Social Security Institute, Mexico
- [P2.122] **Social contact dispersal and its relevance for the construction of epidemic models**
K. Van Kerckhove¹, L. Willem², C. Faes¹, P. Beutels^{2,3}, N. Hens*^{1,2}, ¹Hasselt University, Belgium, ²University of Antwerp, Belgium, ³The University of New South Wales, Australia
- [P2.123] **Analysis of *Escherichia coli* populations from ruminants that may be potential threats to human health in Mauritius**
S.I.L. Thierry*¹, Y. Jaufeerally-Fakim¹, J.E. Gannon², S.J. Santchurn¹, ¹University of Mauritius, Mauritius, ²American University of Sharjah, United Arab Emirates
- [P2.124] **Improving estimation of odds ratios in logistic regression when using data from imperfect tests**
G.T. Innocent*, I.J. McKendrick, *Biomathematics and Statistics Scotland (BioSS)*, UK
- [P2.125] **Can logistic models be applied to respondent-driven samples?**
S. Sperandei*^{1,2}, L.S. Bastos², M. Ribeiro-Alves³, F.I. Bastos¹, ¹ICICT - Oswaldo Cruz Foundation (FIOCRUZ), Brazil, ²PROCC - Oswaldo Cruz Foundation (FIOCRUZ), Brazil, ³INI - Oswaldo Cruz Foundation (FIOCRUZ), Brazil
- [P2.126] ***Mycobacterium tuberculosis* transmission across networks: Implications for disease control and prevention**
P.M. Miller*^{1,2}, J.M. Drake^{1,2}, C. Whalen³, ¹Odum School of Ecology, University of Georgia, USA, ²Center for the Ecology of Infectious Disease, University of Georgia, USA, ³College of Public Health, University of Georgia, USA
- [P2.127] **Decision tree learning for severe hand food mouth disease cases in Beijing from 2009-2014**
Z. Wong*¹, H. Qian¹, ¹St. Luke's International University, Japan, ²Beijing Center for Disease Prevention and Control, China
- [P2.128] **Tackling *Plasmodium knowlesi* malaria: Landscape of current research in *Plasmodium knowlesi***
M. Tusell*, K. Whitfield, *ISGlobal*, Spain
- [P2.129] **Unraveling the disease consequences and mechanisms of modular animal social organization**
P. Sah, S. Bansal*, *Georgetown University*, USA
- [P2.130] **Epidemics on networks: A Python package for studying disease spread in networks**
J.C. Miller, *Institute for Disease Modeling*, USA
- [P2.131] **Trend analysis between vancomycin consumption and incidence of vancomycin-resistant *Enterococcus faecium* between a local hospital and Colombian data, from 2013 to 2016**
N.C. Corredor*^{1,2}, L.M. Prieto^{1,3}, G. Rodriguez-Leguizamón^{1,2}, J.M. Pardo^{1,2}, ¹Corporación Hospitalaria Juan Ciudad – Hospital Universitario Mayor (Méderi), Colombia, ²School of Medicine and Health Sciences, Universidad del Rosario, Colombia, ³School of Medicine and Health Sciences, Universidad del Bosque, Colombia
- [P2.132] **Measuring hydrology in urban settings and its implications for waterborne diseases**
G. Pedra*¹, J. Lea², P. Diggle³, M. Begon¹, ¹University of Liverpool, UK, ²University of Liverpool, UK, ³Lancaster University, UK
- [P2.133] **Genetic diversity helps detect recent tuberculosis transmission**
D. Ayabina*¹, V. Eldholm², C. Colijn¹, ¹Imperial College London, UK, ²Norwegian Institute of Public Health, Norway
- [P1.030] **A general stochastic modelling framework for the spread of hospital-acquired infections until detection**
M. Lopez-Garcia, *University of Leeds*, UK

- [P1.074] A vaccine for norovirus: Potential impacts and target populations**
K. Gaythorpe*, C. Trotter, A. Conlan, University of Cambridge, UK
- [P1.055] Benefits and challenges of Sobol global sensitivity analysis for epidemiological simulation models - the example of a rabies model in northern Australia**
S. Dürr*¹, V. Brookes², M.P. Ward², B. Vidondo¹, ¹University of Bern, Switzerland, ²The University of Sydney, Australia
- [P1.083] The role of individual mechanistic movement as driver of disease dynamics in spatially structured landscapes**
C. Scherer¹, M. Franz¹, V. Radchuk¹, M. Lange², V. Grimm², H-H. Thulke², S. Kramer-Schadt*¹, ¹Leibniz Institute for Zoo and Wildlife Research, Germany, ²Helmholtz Centre for Environmental Research, Germany

Poster Session 3
Thursday, 30 November 2017 17:40-19:10

All posters with an odd number will be presented from 17:40-18:25, Thursday 30 November e.g. P3.001, P3.003 etc.
All posters with an even number will be presented from 18:25-19:10, Thursday 30 November e.g. P3.002, P3.004 etc.

- [P3.001] High resistance but slow recovery: Demographic responses of a free-ranging population of spotted hyenas to a virulent disease epidemic**
S. Benhaïem*¹, L. Marescot¹, M.L. East¹, S. Kramer-Schadt¹, O. Gimenez², J.D. Lebreton², H. Hofer¹, ¹Leibniz Institute for Zoo and Wildlife Research, Germany, ²Université de Montpellier, France
- [P3.002] A comparative analysis of Chikungunya and Zika transmission**
J. Riou*, C. Poletto, P-Y. Boëlle, Sorbonne Universités, France
- [P3.003] Reconstruction and analysis of Ebola virus disease outbreaks in Nigeria and Sierra Leone with missing data**
Y.H. Chan*, H. Nishiura, Hokkaido University, Japan
- [P3.004] Estimating and modelling the transmissibility of middle east respiratory syndrome corona virus during the 2015 outbreak in the republic of Korea**
X-S. zhang*^{1,2}, R. Pebody¹, A. Charlett¹, D. De Angelis^{1,3}, P. Birrell^{1,3}, H. Kang⁴, M. Baguelin¹, Y. Choi^{1,2}, ¹Public Health England, UK, ²Imperial College, UK, ³University of Cambridge, UK, ⁴Sungkyunkwan University, Republic of Korea
- [P3.005] Modelling the risk of Chagas disease in South Texas**
T. Oraby*, T.F. Arroyo, University of Texas Rio Grande Valley, USA
- [P3.006] Viral gastroenteritis and prevalence of norovirus and norovirus-like illness in Ontario, Canada -- 2009-2014**
S.L. Hughes*¹, A.L. Greer¹, A.J. Elliot², S.A. McEwen¹, I. Young³, A. Papadopoulos¹, ¹University of Guelph, Canada, ²Public Health England, UK, ³Ryerson University, Canada
- [P3.007] Withdrawn**
- [P3.008] Fitting stochastic epidemic to partially observed incidence via the linear noise approximation**
J. Fintzi*¹, J. Wakefield¹, V.N. Minin², ¹University of Washington, USA, ²University of California, USA
- [P3.009] Temporal dynamics of the resistance of *Escherichia coli* isolated from food-producing animals in France: A 14-year period time-series study**
C. Boireau*^{1,2}, E. Morignat¹, G. Cazeau¹, N. Jarrige¹, E. Jouy³, M. Haenni¹, J-Y. Madec¹, A. Leblond², E. Gay¹, ¹ANSES - University of Lyon, France, ²INRA - University of Lyon VetAgro Sup, France, ³ANSES - Université Bretagne Loire, France
- [P3.010] Modelling the first outbreak of Zika virus in continental USA**
G. Marini*¹, G. Guzzetta², R. Rosà¹, S. Merler², ¹Fondazione Edmund Mach, Italy, ²Fondazione Bruno Kessler, Italy

- [P3.011] “HIND-cite”: Data origins of tuberculosis mathematical models**
S. Ricks*, N. Arinaminpathy, *Imperial College London, UK*
- [P3.012] Geographically-dependent individual level models of disease spread**
R. Deardon, M. Mahsin*, *University of Calgary, Canada*
- [P3.013] El Niño and dengue epidemic prediction in Ecuador**
R. Lowe*^{1,2}, A.M. Stewart-Ibarra³, D. Petrova², M. García-Díez⁴, M.J. Borbor-Cordova⁵, R. Mejía⁶, M. Regato⁷, X. Rodó^{2,8}, ¹*London School of Hygiene & Tropical Medicine, UK*, ²*Barcelona Institute for Global Health (ISGLOBAL), Spain*, ³*State University of New York Upstate Medical University, USA*, ⁴*Predictia Intelligent Data Solutions, Spain*, ⁵*Escuela Superior Politecnica del Litoral (ESPOL), Ecuador*, ⁶*National Institute of Meteorology and Hydrology (INAMHI), Ecuador*, ⁷*National Institute of Public Health Research (INSPI), Ecuador*, ⁸*Institució Catalana de Recerca i Estudis Avançats (ICREA), Spain*
- [P3.014] Vaccine preventable diseases in the 20th century: The impact of long-standing mass vaccination programs on notified cases in the Netherlands**
M. van Wijhe*^{1,2}, A. Tulen¹, H. Korthals Altes¹, S. McDonald¹, H. de Melker¹, M. Postma^{2,3}, J. Wallinga^{1,4}, ¹*National Institute for Public Health and the Environment, The Netherlands*, ²*University of Groningen, The Netherlands*, ³*University Medical Center Groningen, The Netherlands*, ⁴*Leiden University Medical Center, The Netherlands*
- [P3.015] Mathematical models used to inform study design or surveillance systems in infectious diseases: a systematic review**
S. Blaizot*¹, S.A. Herzog², N. Hens^{1,3}, ¹*University of Antwerp, Belgium*, ²*Medical University of Graz, Austria*, ³*Hasselt University, Belgium*
- [P3.016] Dominance dynamics of novel influenza A/H3N2 antigenic types**
L.A. Castro*¹, L.A. Meyers^{1,2}, ¹*University of Texas at Austin, USA*, ²*The Santa Fe Institute, USA*
- [P3.017] Can we eliminate hepatitis C virus incidence in Egypt by 2030?**
H.H. Ayoub^{1,2}, L.J. Raddad*^{1,2}, ¹*Weill Cornell Medicine-Qatar, Cornell University, Qatar*, ²*Weill Cornell Medicine, Cornell University, USA*
- [P3.018] Theoretical analysis on the effect of air flow rate on airborne viral infection**
S.M.M. UD-Dean*, J.L. Shaman, *Columbia University, USA*
- [P3.019] Modelling the interactions between macrophages and bacteria in *Mycobacterium tuberculosis* infections**
C. Lack*¹, M. Keeling¹, I. Hall², C. Toniolo³, ¹*University of Warwick, UK*, ²*Public Health England, UK*, ³*Swiss Federal Institute of Technology, Switzerland*
- [P3.020] The public health impact of pyrethroid resistance on malaria transmission**
E. Sherrard-Smith*¹, P. Winskill¹, J. Griffin^{1,2}, T.S. Churcher¹, ¹*Imperial College London, UK*, ²*Queen Mary University of London, UK*
- [P3.021] The other side of the coin: Creating the optimum epidemic to control carp in south-east Australia using cyprinid herpes virus 3**
S.A. Davis*¹, A. Arakala¹, K. McColl², K. Graham², P. Durr², ¹*RMIT University, Australia*, ²*CSIRO - Australian Animal Health Laboratory, Australia*
- [P3.022] Modelling village-scale elimination of sleeping sickness**
C.N. Davis*, M.J. Keeling, *University of Warwick, UK*
- [P3.023] Real-time assessment of healthcare requirements during the Zika virus epidemic in Martinique**
A. Andronico*¹, F. Dorléans², J.L. Fergé³, H. Salje^{1,4}, F. Ghawché⁵, A. Signate³, E. Daudens-Vaysse², L. Baudouin⁵, T. Dub¹, M. Aubry⁶, ¹*Institut Pasteur, France*, ²*Santé Publique France, France*, ³*CHU de Martinique, France*, ⁴*Johns Hopkins Bloomberg School of Public Health, USA*, ⁵*Centre Hospitalier de Polynésie Française, French Polynesia*, ⁶*Institut Louis Malardé, French Polynesia*, ⁷*Bureau de Veille Sanitaire, French Polynesia*
- [P3.024] Drivers of measles transmission in the United States during the post-elimination era**
P.A. Gastanaduy*¹, B.A. Lopman², M. Gambhir³, P. Paul¹, ¹*Centers for Disease Control and Prevention, USA*, ²*Rollins School of Public Health Emory University, USA*, ³*Monash University,*

- [P3.025] Effect of aging population on the programme effectiveness of vaccinating against seasonal influenza**
J.A. Backer*¹, J. Wallinga^{1,2}, A. Meijer¹, W. Van der Hoek¹, M. Van Boven¹, ¹National Institute for Public Health and the Environment, The Netherlands, ²Leiden University, The Netherlands
- [P3.026] Sickness-induced lethargy can increase host contact rates and pathogen spread in water-limited environments**
M. Franz*, S. Kramer-Schadt, A.D. Greenwood, A. Courtiol, *Institute for Zoo and Wildlife Research, Germany*
- [P3.027] Improving early forecasts of arboviral emerging outbreaks using historical data**
J. Riou*, C. Poletto, P-Y. Boëlle, *Sorbonne Universités, France*
- [P3.028] Role of genetic heterogeneity in determining the epidemiological severity of H1N1 influenza**
N. Sambaturu¹, S. Mukherjee¹, M. Lopez-Garcia*², C. Molina-Paris², G.I. Menon^{3,4}, N. Chandra¹, ¹Indian Institute of Science, India, ²University of Leeds, UK, ³The Institute of Mathematical Sciences, India, ⁴Homi Bhabha National Institute, India
- [P3.029] Lessons learned about school closure policies for mitigating influenza spread**
M. Ajelli*^{1,2}, L. Fumanelli², C. Ciavarella³, M. Litvinova¹, S. Merler², C. Cattuto⁴, S. Cauchemez⁵, N.M. Ferguson³, ¹Northeastern University, USA, ²Bruno Kessler Foundation, Italy, ³Imperial College London, UK, ⁴ISI Foundation, Italy, ⁵Institut Pasteur, France
- [P3.030] Targeting HIV pre-exposure prophylaxis to adolescent sexual minority males in higher prevalence areas of the United States: A modeling study**
D. Hamilton¹, S. Goodreau*¹, S. Jenness², P. Sullivan², R. Valencia², L. Wang³, R. Dunville³, L. Barrios³, E. Rosenberg², ¹University of Washington, USA, ²Emory University, USA, ³Centers for Disease Control and Prevention, USA
- [P3.031] Inferring who-infected-whom-and-where for the 2016 zika outbreak in Singapore-a spatial-temporal model**
K. Prem*, A.R. Cook, *National University of Singapore, Singapore*
- [P3.032] Sexual network drivers of HIV and Herpes simplex virus type 2 transmission**
R. Omori*¹, L. Abu-Raddad¹, ¹Hokkaido University, Japan, ²Weill Cornell Medicine - Qatar, Qatar
- [P3.033] Role of absolute humidity in shaping influenza transmission and seasonality in a subtropical city, Hong Kong**
S.T. Ali*¹, P. Wu¹, V.J. Fang¹, D. He², S. Cauchemez³, B.J. Cowling¹, ¹University of Hong Kong, Hong Kong, ²Hong Kong Polytechnic University, Hong Kong, ³Institut Pasteur, France
- [P3.034] Within-host infection dynamic of Ebola virus and its implications on vaccination strategies**
V.K. Nguyen*, E.A. Hernandez-Vargas, *Frankfurt Institute for Advanced Studies, Germany*
- [P3.035] Assessing intervention responses against H5N1 avian influenza outbreaks in Bangladesh**
E.M. Hill*¹, T. House², M.S. Dhingra^{3,4}, M.G. Osmani⁵, X. Xiao⁶, M. Gilbert³, M.J. Tildesley¹, ¹University of Warwick, UK, ²The University of Manchester, UK, ³Université Libre de Bruxelles, Belgium, ⁴Department of Animal Husbandry and Dairying, India, ⁵Department of Livestock Services, Bangladesh, ⁶University of Oklahoma, USA
- [P3.036] Outbreaker2: Inferring transmission trees from temporal, genomic and contact data**
F. Campbell*, A. Cori, N. Ferguson, T. Jombart, *Imperial College London, UK*
- [P3.037] The transmissibility of *P. aeruginosa* in ICUs using mathematical models**
T.M. Pham*¹, M.E.E. Kretzschmar^{1,2}, M.C.J. Bootsma^{1,3}, ¹University Medical Center Utrecht, The Netherlands, ²National Institute of Public Health and the Environment (RIVM), The Netherlands, ³Utrecht University, The Netherlands
- [P3.038] Explaining spatial variation in human papillomavirus vaccination uptake in Switzerland**
M. Riesen*^{1,2}, G. Konstantinoudis¹, P. Lang³, N. Low¹, C. Hatz³, M. Mäusezahl⁴, A. Spaar⁴, B. Spycher¹, C.L. Althaus¹, ¹Institute of Social and Preventive Medicine (ISPM), University of Bern, Switzerland, ²Graduate School for Cellular and Biomedical Sciences, University of Bern, Switzerland, ³Epidemiology, Biostatistics and Prevention Institute, University of Zurich,

- [P3.039] Indigenous Australian household structure: A simple data collection tool and implications for close contact transmission of communicable diseases**
T. Vino*¹, G. Singh^{2,3}, B. Davison², P.T. Campbell^{4,6}, M. Lydeamore^{1,4}, A. Robinson^{1,5}, J. McVernon⁶, S.Y.C. Tong^{2,7}, N. Geard¹, ¹The University of Melbourne, Australia, ²Charles Darwin University, Australia, ³NT medical Program of Flinders and James Cook Universities, Australia, ⁴The Royal Children's Hospital, Australia, ⁵Centre of Excellence for Biosecurity Risk Analysis, Australia, ⁶The Royal Melbourne Hospital and The University of Melbourne, Australia, ⁷The Royal Melbourne Hospital, and The University of Melbourne, Australia
- [P3.040] An infectious way to teach students about outbreaks**
I. Cremin, O.J. Watson*, Imperial College London, UK
- [P3.041] Prioritization of infectious diseases: First test of the WHO R&D Blueprint**
M. Si Mehand*, P. Millett, B. Murgue, World Health Organization, Switzerland
- [P3.042] The value of crowdsourced surveillance systems in supplementing sentinel influenza networks: the case of France**
C. Guerrisi*¹, C. Turbelin¹, C. Souty¹, C. Poletto¹, T. Blanchon¹, T. Hanslik^{1,2}, I. Bonmarin⁴, D. Levy-Bruhl⁴, V. Colizza^{1,5}, ¹Institut Pierre Louis d'épidémiologie et de Santé Publique, France, ²Université Versailles-Saint-Quentin-en-Yvelines, France, ³AP-HP, France, ⁴Public Health France, France, ⁵ISI Foundation, Italy
- [P3.043] Methods to account for infections arising from external populations in HIV transmission models**
M. King*¹, M. Lurie¹, S. Galea², S.R. Friedman³, B.D.L. Marshall¹, ¹Brown University, USA, ²Boston University School of Public Health, USA, ³National Development and Research Institutes, USA
- [P3.044] Productive compartments and their role in the spread of Bovine viral diarrhoea on a cattle trade network**
B. Iotti*¹, E. Valdano², M. Giacobini¹, L. Candeloro³, L. Savini³, A. Giovannini³, S. Rosati¹, V. Colizza^{4,5}, ¹University of Turin, Italy, ²Universitat Rovira i Virgili, Spain, ³Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise G. Caporale, Italy, ⁴Institut Pierre Louis d'Epidemiologie et de la Santé Publique, France, ⁵ISI Foundation, Italy
- [P3.045] Geographic variation in dengue seroprevalence and force of infection in Indonesia**
C.C. Tam*^{1,2}, M. O'Driscoll³, A-F. Taurel⁴, J. Nealon⁴, S.R. Hadinegoro⁵, ¹National University of Singapore, Singapore, ²London School of Hygiene & Tropical Medicine, UK, ³Imperial College London, UK, ⁴Sanofi Pasteur, Singapore, ⁵University of Indonesia, Indonesia
- [P3.046] Spatiotemporal disparities of sporadic Legionnaires' disease cases in France: What part does climate play?**
C. Pelat*, C. Campese, D. Lévy-Bruhl, D. Che, French national public health agency, France
- [P3.047] Sexual role and HIV set point viral load among men who have sex with men**
S. Stansfield, J. Murphy, G. Gottlieb, D. Hamilton, J. Mittler, J. Herbeck, S. Goodreau*, University of Washington, USA
- [P3.048] Estimating the critical community size of Streptococcus pneumoniae transmission in multiple settings**
B.M. Althouse*^{1,2}, B. Wagner¹, H. Hu¹, ¹Institute for Disease Modeling, USA, ²University of Washington, USA, ³New Mexico State University, USA
- [P3.049] Principled stochastic network modelling for epidemics**
M. Morris*¹, S.M. Goodreau¹, S.M. Jenness², ¹University of Washington, USA, ²Emory University, USA
- [P3.050] An agent-based model of Zika virus to evaluate vaccination strategies in Colombia**
H. Diaz*¹, G. España², N. Castañeda¹, ¹Universidad Nacional de Colombia, Colombia, ²University of Notre Dame, USA
- [P3.051] Using a gene-level mutation model in BEAST to characterise transmission of Neisseria meningitidis (serogroup W: clonal complex 11) between countries**
D. Klinkenberg*¹, S.J. Hahné¹, A. Van der Ende², J.A. Backer¹, L.C. Soetens¹, M.J. Knol¹, ¹National Institute for Public Health and the Environment, The Netherlands, ²Academic Medical Centre,

- [P3.052] **A comparison of methods for forecasting flu via respiratory pathogen interactions using a cloud based epidemiological network**
J. Nawrocki¹, B. Galvin¹, A. Faucett¹, J. Jones¹, B.M. Althouse^{2,3}, L. Meyers¹, ¹BioFire Diagnostics, USA, ²University of Washington, USA, ³New Mexico State University, USA
- [P3.053] **Measles: Synchronization, local periodicities and human mobility**
A. Parisi, Lancaster University, UK
- [P3.054] **Forecasting influenza using primary care surveillance data**
R.C. Cope*, J.V. Ross, M. Chilver, N.P. Stocks, L. Mitchell, The University of Adelaide, Australia
- [P3.055] **Immunity against reinfection and increased testing of uninfected individuals limited the impact of screening on reducing chlamydia transmission in England**
J.H. Smid*, C.L. Althaus, N. Low, Institute of Social and Preventive Medicine, Switzerland
- [P3.056] **American foulbrood in honey bees - the difficult relationship between clinical symptoms of a colony and spore counts from individual bees**
J.G. Stephan*, E. Forsgren, Swedish University of Agricultural Sciences, Sweden
- [P3.057] **Behavioral change models for infectious disease transmission: A systematic review (2010-2015)**
F. Verelst¹, L. Willem¹, P. Beutels^{1,2}, ¹University of Antwerp, Belgium, ²The University of New South Wales, Australia
- [P3.058] **Extracting the incentives: vaccination behavior as a multi-criteria decision**
F. Verelst¹, L. Willem¹, R. Kessels^{1,3}, P. Beutels^{1,2}, ¹University of Antwerp, Belgium, ²The University of New South Wales, Australia, ³University of Amsterdam, The Netherlands
- [P3.059] **Evaluating the association between use of different antibiotics and trimethoprim resistance using elastic net regularization and generalized boosted regression models**
K.B. Pouwels^{1,2}, R. Freeman¹, B. Muller-Pebody¹, G. Rooney¹, K.L. Henderson¹, J.V. Robotham¹, T. Smieszek¹, ¹Public Health England, UK, ²University of Groningen, The Netherlands, ³Imperial College London, UK
- [P3.060] **Yellow fever transmission in South America and the potential for expansion of the endemic zone**
A. Hamlet*, N. Ferguson, T. Garske, Imperial College London, UK
- [P3.061] **The importance of US foreign aid for global malaria control and elimination**
P. Winskill*, H.C. Slater¹, J.T. Griffin², A.C. Ghani¹, P.G.T. Walker¹, ¹Imperial College London, UK, ²Queen Mary University, UK
- [P3.062] **What data should be collected to inform monitoring and evaluation for schistosomiasis?**
J. Toor¹, R. Alsallaq², J.E. Truscott^{1,3}, M. Werkman^{1,3}, H.C. Turner^{4,5}, D. Gurarie², C.H. King², R.M. Anderson^{1,3}, ¹Imperial College London, UK, ²Case Western Reserve University, USA, ³The DeWorm3 Project, UK, ⁴Oxford University Clinical Research Unit, Viet Nam, ⁵University of Oxford, UK
- [P3.063] **The effect of school closure against flu based on an individually based stochastic model**
M. Kakehashi¹, S. Kawano², M. Tsunematsu¹, ¹Hiroshima University, Japan, ²Kurume University, Japan
- [P3.064] **Assessing the use of a flavivirus protein microarray for inferring past dengue transmission in Vietnam**
T.N.T. Thao¹, N.H.T. Vy¹, T.H. Phuong¹, N.T. Le Thanh¹, H-J. van den Ham², M. Koopmans², E. Bruin², M. Boni³, H.E. Clapham^{1,4}, ¹Oxford University Clinical Research Unit, Viet Nam, ²Erasmus Medical Centre, The Netherlands, ³Penn State University, USA, ⁴University of Oxford, UK
- [P3.065] **Estimating Influenza-Associated deaths in Japan**
K. Mizumoto*, H. Nishiura, Georgia State University, USA
- [P3.066] **Modeling the dynamics of antibiotic resistance in gonorrhoea to determine fitness benefits and costs**
L.K. Whittles¹, P.J. White^{1,2}, X. Didelot¹, ¹Imperial College London, UK, ²Public Health England, UK

- [P3.067] Comparing bayesian decision networks and multilevel logistic regression models to predict spatial prevalence of malaria in papua new guinea**
E. Cleary*¹, M. Hetzel², C. Lau¹, A. Clements¹, ¹The Australian National University, Australia, ²Swiss Tropical and Public Health Institute, Switzerland
- [P3.068] Towards developing an age-structured version of the EPICYST model for taeniasis/cysticercosis epidemiology and control**
M.A. Dixon*¹, P. Winskill², M. Walker³, W.E. Harrison⁴, M-G. Basáñez¹, ¹Imperial College London and London Centre for Neglected Tropical Disease Research, UK, ²Imperial College London and MRC Centre for Outbreak Analysis and Modelling, UK, ³Royal Veterinary College and London Centre for Neglected Tropical Disease Research, UK, ⁴Schistosomiasis Control Initiative, UK
- [P3.069] Effects of community connectivity and environmental heterogeneities on the spread and persistence of dengue virus**
W. Tennant*, M. Recker, University of Exeter, UK
- [P3.070] The containment of potential outbreaks triggered by imported Chikungunya cases in Italy: A cost utility epidemiological assessment of vector control measures**
F. Trentini*¹, P. Poletti², S. Merler², A. Melegaro¹, ¹Bocconi University, Italy, ²Bruno Kessler Foundation, Italy
- [P3.071] fluEvidenceSynthesis: An R package for evidence synthesis based analysis of epidemiological outbreaks**
E. van Leeuwen*^{1,2}, P. Klepac^{1,2}, D. Thorrington¹, R. Pebody¹, M. Baguelin^{1,3}, ¹Public Health England, UK, ²Imperial College London, UK, ³London School of Hygiene and Tropical Medicine, UK
- [P3.072] Protection against campylobacter illness: A multi-strain cross-immunity model**
A.A. Bonacic*, P.F.M. Teunis, A.N. Swart, RIVM, The Netherlands
- [P3.073] Cross-sectional serology as an epidemiologic tool for measuring the impact of cholera control programs**
A.S. Azman*¹, F.J. Luquero^{2,1}, J. Lessler¹, A.I. Khan³, T.R. Bhuiyan³, F. Chowdhury³, S.B. Calderwood⁴, E.T. Ryan^{4,5}, F. Qadri³, D. Leung¹, ¹Johns Hopkins Bloomberg School of Public Health, USA, ²Epicentre, France, ³ICDDR, Bangladesh, ⁴Massachusetts General Hospital, USA, ⁵Harvard Medical School, USA, ⁶University of Utah, USA
- [P3.074] Age-mixing among HIV positive and negative men and women: Population and individual-level comparisons from a Cape Town sexual behaviour survey**
R. Beauclair*^{1,2}, N. Hens^{3,4}, W. Delva^{1,2}, ¹Ghent University, Belgium, ²Centre of Excellence in Epidemiological Modelling and Analysis (SACEMA), South Africa, ³Hasselt University, Belgium, ⁴University of Antwerp, Belgium, ⁵KU Leuven, Belgium
- [P3.075] Estimating the direct and indirect effects of the 2005 BCG vaccination policy change in England combining statistical approaches and dynamic modelling**
S. Abbott*, H. Christensen, E. Brooks-Pollock, University of Bristol, UK
- [P3.076] Understanding the relationship between egg and antigen based diagnostics of schistosomiasis infection pre- and post-treatment**
J.M. Prada*¹, P. Touloupou¹, M. Adriko², E.M. Tukahebwa², P.H.L. Lamberton³, T.D. Hollingsworth¹, ¹University of Warwick, UK, ²Ministry of Health, Uganda, ³University of Glasgow, UK
- [P3.077] pomp-astic inference for epidemic models: simple vs. complex**
T. Stocks*, T. Britton, M. Höhle, Stockholm University, Sweden
- [P3.078] DNA sequencing complements variable number of tandem repeats typing methods for Mycobacterium tuberculosis Bayesian phylogeny inference**
A. Dhawan¹, H.K. Altes*¹, D. van Soolingen^{1,3}, M. Bootsma², D. Klinkenberg¹, ¹National Institute for Public Health and the Environment, The Netherlands, ²Utrecht University, The Netherlands, ³Radboud University Nijmegen Medical Center, The Netherlands
- [P3.079] Investigating seasonal factors in Ascaris lumbricoides transmission and control using a novel compartmental model with temporal forcing**

E.L. Davis^{*1}, L. Danon², T.D. Hollingsworth¹, ¹University of Warwick, UK, ²University of Bristol, UK

- [P3.080] **Household modelling of Yaws data indicates that targeting treatment using case finding and contact tracing may be unsuccessful at eradicating the disease**
L. Dyson^{*1}, M. Marks², O.M. Crooks¹, O. Sokana³, A.W. Solomon³, A. Bishop¹, D.C.W. Mabey², T.D. Hollingsworth¹, ¹University of Warwick, UK, ²London School of Hygiene & Tropical Medicine, UK, ³Solomon Islands Ministry of Health and Medical Services, Solomon Islands
- [P3.081] **Lessons from a systematic review on individual-based models for infectious disease transmission (2006-2015)**
L. Willem^{*1}, F. Verelst¹, J. Bilcke¹, N. Hens^{1,2}, P. Beutels^{1,3}, ¹University of Antwerp, Belgium, ²UHasselt, Belgium, ³The University of New South Wales, Australia
- [P3.082] **Impact of RSV maternal immunization on RSV burden in the United States between 2008 and 2015**
N. Voirin^{*1}, V. Virlogeux², A. Kieffer³, ¹EPIMOD Epidemiology and Modelling in Infectious Diseases, France, ²Hospices Civils de Lyon, France, ³Sanofi Pasteur, France
- [P3.083] **The role of benzathine penicillin G in predicting and preventing all-cause acute respiratory disease in military recruits, 1991 - 2017**
J.D. Ball^{*1,2}, A. Brown², M.A. Prosperi¹, D.A.T. Cummings^{1,3}, C. Rivers^{2,3}, ¹University of Florida, USA, ²Army Public Health Center, USA, ³Johns Hopkins University, USA
- [P3.084] **The use of ante-natal care data to monitor malaria control in humanitarian settings**
J. Hellewell^{*1}, P. Walker¹, A. Ghani¹, B. Rao², T. Churcher¹, ¹Imperial College London, UK, ²Médecins Sans Frontières, Switzerland
- [P3.085] **Examining the impact of spatial scale on modelling of sleeping sickness dynamics**
K.S. Rock^{*}, M.J. Keeling, *The University of Warwick, UK*
- [P3.086] **Recasting agent-based model calibration as a missing data problem**
W. Delva^{*1,4}, J. Dushoff¹, ¹Stellenbosch University, South Africa, ²Ghent University, Belgium, ³KU Leuven, Belgium, ⁴Hasselt University, Belgium, ⁵McMaster University, Canada
- [P3.087] **Co-existence of multiple SIS processes on temporal networks: Implications for control of bacterial infections in hospitals**
F. Pinotti^{*1,2}, E. Fleury^{3,4}, D. Guillemot^{1,5}, P.Y. Boelle^{1,2}, C. Poletto^{1,2}, ¹INSERM, France, ²UPMC, France, ³ENS de Lyon, France, ⁴INRIA, France, ⁵Univ. Versailles St Quentin, France
- [P3.088] **Implementation of highly sensitive serological tests for zoonotic infections in Singapore**
A. Uehara^{*}, S. Mani, D.E. Anderson, L-F. Wang, *Duke-NUS Medical School, Singapore*
- [P3.089] **Risk ratios under epidemic assumptions**
O. Morozova^{*}, T. Cohen, F.W. Crawford, *Yale University, USA*
- [P3.090] **Phylogeography of rubella virus in Asia, 2000-2016**
B.A. Bozick^{*}, B.T. Grenfell, C.J. Metcalf, *Princeton University, USA*
- [P3.091] **Epidemiological modelling and bayesian inference with PhyDyn**
I. Siveroni^{*}, E.M. Volz, *Imperial College London, UK*
- [P3.092] **Comparing signatures predictive of malaria protection from protein microarray antibody data**
J.J. Valletta^{*1}, J. Skinner², E. Liu², P. Crompton², M. Recker¹, ¹University of Exeter, UK, ²National Institutes of Health, USA
- [P3.093] **Assessing the trade-offs between cost and sensitivity of active case-finding strategies for tuberculosis**
L. Cilloni^{*}, N. Arinaminpathy, *Imperial College London, UK*
- [P3.094] **Typhoid fever transmission dynamics in Fiji: Findings from sero-surveillance and age-ethnic mixing**
C.H. Watson^{*}, A.J. Kucharski, W.J. Edmunds, *London School of Hygiene & Tropical Medicine, UK*
- [P3.095] **How unfit is drug-resistant *Mycobacterium tuberculosis*?**
G.M. Knight^{*1}, M. Zimic³, S. Funk², J.S. Friedland¹, L. Grandjean¹, ¹Imperial College London, UK, ²London School of Hygiene and Tropical Medicine, UK, ³Universidad Peruana Cayetano, Peru

- [P3.096] Epidemic dynamics of enteroviruses associated with hand, foot, and mouth disease in Japan**
S. Takahashi^{*1}, C.J.E. Metcalf¹, B.T. Grenfell^{1,2}, ¹Princeton University, USA, ²National Institutes of Health, USA
- [P3.097] Assessing the impact of climate change on risk of infection with Fasciolosis using a new mechanistic hydro-epidemiological model**
L. Beltrame^{*}, T. Dunne, H. Rose, J. Walker, E. Morgan, P. Vickerman, T. Wagener, University of Bristol, UK
- [P3.098] Characterizing the impact of dynamic vector abundance on individual malaria prevalence in a high transmission area of northern Zambia**
M. Hast^{*1}, J. Stevenson^{1,2}, M. Muleba³, M. Chaponda³, J.B. Kabuya³, M. Mulenga³, J. Lessler¹, T. Shields¹, W. Moss¹, D. Norris¹, ¹Johns Hopkins Bloomberg School of Public Health, USA, ²Macha Research Trust, Zambia, ³Tropical Diseases Research Centre, Zambia
- [P3.099] Transmission and control of multi-drug resistant organisms in and between healthcare facilities: Nuanced roles of heterogeneous susceptibility and length of stay**
D.J.A. Toth^{*1,2}, K. Khader^{1,2}, M.H. Samore^{1,2}, ¹University of Utah, USA, ²Veterans Affairs Salt Lake City Healthcare System, USA
- [P3.100] Estimating the risk of Measles importation into the United States**
S.A. Truelove^{*1}, L. Mier-y-Teran-Romero², A.T. Walker¹, P.A. Gastanaduy², J. Lessler¹, M.A. Johansson^{2,3}, ¹Johns Hopkins Bloomberg School of Public Health, USA, ²Centers for Disease Control and Prevention, USA, ³Harvard TH Chan School of Public Health, USA
- [P3.101] Ecological dynamics of the emergence of Lumpy Skin Disease virus in Eurasia (2014-2016)**
G. Machado², F. Korennoy^{*1}, J. Alvarez², C. Picasso², A. Perez², K. VanderWaal², ¹Federal Center for Animal Health (FGBI ARRIAH), Russia, ²University of Minnesota, USA
- [P3.102] Competition between two Klebsiella pneumoniae epidemic clones during a hospital outbreak**
F. Comandatore^{*1}, M. Corbella², C. Ferrari³, P. Marone², S. Pongolini⁴, E. Scaltriti⁴, C.M. Bandi¹, D. Sasser³, ¹Università degli Studi di Milano, Italy, ²IRCCS Policlinico San Matteo, Italy, ³University of Pavia, Italy, ⁴Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Italy
- [P3.103] Value of information: Correctly parameterizing vaccine performance in model-based cost-effectiveness assessments of varicella vaccination**
L.J. Wolfson^{*1}, V.J. Daniels¹, J. Kyle¹, C.R. Burgess², ¹Merck & Co., Inc., USA, ²MathEcology, LLC, USA
- [P3.104] Stochastic effects on silent circulation of wild poliovirus during the eradication endgame**
C.J. Henry^{*}, M.A.L. Hayashi, M.C. Eisenberg, J.S. Koopman, University of Michigan, USA
- [P3.105] Participatory modeling and simulation: A case study on Japanese encephalitis and nipah in Cambodia**
R. Duboz^{*1,2}, P. Promburom⁴, J. Cappelle^{1,2}, A. Diallo^{1,2}, V. Chevalier¹, A. Binot¹, ¹CIRAD, France, ²Institut Pasteur du Cambodge, Cambodia, ³Kasetsart University, Thailand, ⁴Chiang Mai University, Thailand
- [P3.106] The use and reporting of airline passenger data for infectious disease modelling: A systematic review**
M.M.I. Mesle^{*1}, I.M. Hall^{1,2}, R.M. Christley¹, S. Leach^{1,2}, J.M. Read^{1,3}, ¹University of Liverpool, UK, ²Public Health England, UK, ³Lancaster University, UK
- [P3.107] Generation intervals in space: Understanding the effects of spatial and network structure on links between generation interval and growth rate**
J. Dushoff^{*2}, S.W. Park¹, D. Champredon¹, ¹McMaster University, Canada, ²York University, Canada
- [P3.108] Comparison of full age-infection profiles for schistosomiasis and soil-transmitted helminth infection from a recent three-year study in Uganda**
A.K. Deol^{*1,2}, M.D. French³, E. Tukahebwa⁴, ¹Imperial College London, UK, ²Schistosomiasis Control Initiative, UK, ³RTI International, USA, ⁴Ministry of Health Uganda, Uganda

- [P3.109] What is the most effective way to promote HIV self-tests for men who have sex with men?**
S. Cassels*¹, W. Luo¹, S.M. Goodreau², D.T. Hamilton², D.A. Katz², J. McKenney⁴, J.D. Stekler², E.S. Rosenberg³, P.S. Sullivan⁴, ¹University of California Santa Barbara, USA, ²University of Washington, USA, ³SUNY University at Albany School of Public Health, USA, ⁴Emory University Rollins School of Public Health, USA
- [P3.110] Inferring waning vaccine effectiveness under the test-negative design**
J.A. Lewnard, *Harvard TH Chan School of Public Health, USA*
- [P3.111] Building capacity in meaningful modeling of infectious disease dynamics: Insights from a decade of international, interdisciplinary training**
S.E. Bellan¹, J. Dushoff², J.W. Hargrove³, A.G. Hitchcock³, T.C. Porco⁴, J.C. Scott⁵, A. Welte³, B.G. Williams³, J.R.C. Pulliam*³, ¹University of Georgia, USA, ²McMaster University, Canada, ³South African DST-NRF Centre of Excellence in Epidemiological Modelling and Analysis (SACEMA), South Africa, ⁴University of California, USA, ⁵Colby College, USA
- [P3.112] Modeling the impact of immune responses on viral diversity and viral load dynamics in a monkey model for congenital cytomegalovirus infection**
D. Vera Cruz*^{1,4}, C.S. Nelson¹, K.M. Kialas¹, D. Tran², P.A. Barry³, A. Kaur², K. Koelle⁴, S.R. Permar¹, ¹Duke University, USA, ²Tulane University, USA, ³University of California, Davis, USA, ⁴Emory University, USA
- [P3.113] Does identifying high-risk individuals and giving them pre-exposure prophylaxis enhance the population-level benefits of “test and treat” for HIV-infection?**
S.B. Asimwe^{1,2}, F. Rerolle*¹, A. Amir², M. Roh¹, S. Ackley¹, J. Hahn¹, L. Worden¹, J. Martin¹, B. Williams¹, T. Porco¹, ¹University of California San Francisco, USA, ²Mbarara Regional Referral Hospital, Uganda, ³African Institute for Mathematical Sciences, South Africa
- [P3.114] Risk management and preparedness: Use of stochastic modeling and risk analytics to estimate frequency and severity of pandemics**
N. Stephenson*, K. Miller, M. Gahan, M. Gallivan, V. Serhiyenko, C. Lam, N. Madhav, *Metabiota, Inc., USA*
- [P3.115] Spatial analysis of visceral leishmaniasis transmission in the Indian subcontinent**
L.A.C. Chapman*¹, C.P. Jewell², S.E.F. Spencer¹, C. Bern³, G.F. Medley⁴, T.D. Hollingsworth¹, ¹Warwick University, UK, ²Lancaster University, UK, ³UCSF, USA, ⁴LSHTM, UK
- [P3.116] Modelling the impact of trachoma MDA on GU chlamydia**
S.R. Wannier*¹, L. Worden², T. Lietman^{1,2}, T.C. Porco¹, ¹University of California San Francisco, USA, ²Francis Eye Proctor Foundation, USA
- [P3.117] Identifying spatiotemporal dynamics of the Ebola outbreak in Sierra Leone from virus genomes**
J. Proctor*, K. Gustafson, *Institute for Disease Modelling, USA*
- [P3.118] Seasonality of dengue in Ecuador and vaccination timing**
R. Sippy*¹, D. Gaus², D. Herrera², J. Osorio¹, ¹University of Wisconsin-Madison, USA, ²Saludesa, Ecuador
- [P3.119] A history-based multi-outbreak influenza model**
R.I. Hickson*, A.J. Swan, *IBM Research, Australia*
- [P3.120] Withdrawn**
- [P3.121] A resource allocation model for large scale biosecurity events**
L.M. Gardner*, D. Rey, A. Zlojutro, *UNSW Sydney, Australia*
- [P3.122] Individual mixing patterns relevant for infectious diseases transmission in different social contexts in Sub-Saharan Africa**
A. Melegaro*¹, E. Del Fava¹, P. Poletti^{1,2}, I. Adema⁵, M. Kiti⁵, C. Nyamukapa⁴, J. Williams⁴, P. Manfredi³, S. Gregson⁴, J. Nokes⁵, ¹Bocconi University, Italy, ²Bruno Kessler Foundation, Italy, ³Pisa University, Italy, ⁴Imperial College, UK, ⁵KEMRI, Kenya
- [P3.123] Mapping encounter occurrence and SIVgor transmission in wild western lowland gorillas from southwest Cameroon**

C.J. Villabona-Arenas^{*1}, A. Ayouba¹, A. Esteban¹, H. de Nys¹, M. D'arc¹, E.M. Ngole^{1,2}, M. Peeters¹, ¹*Institut de Recherche pour le Développement, France*, ²*Centre de recherche sur les maladies émergentes et réémergentes, Cameroon*

[P3.124] Risk assessment from small scale and early phase epidemics

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[P3.125] Mapping epidemic data with bipartite networks

M. Neuman^{*}, D. Edler, M. Holmberg, M. Rosvall, *Umeå university, Sweden*

[P3.126] Controlling Aedes Aegypti populations by Wolbachia-based strategies

M. Rafikov^{*}, M.E.M. Meza, D.P.F. Correa, *Centro de Engenharia, Modelagem e Ciências Sociais Aplicadas (CECS), Brazil*

[P3.127] A stochastic model of canine rabies

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[P3.128] Optimizing distribution of pandemic influenza antivirals

B.S. Singh^{*1}, N.H. Huang¹, G.J. Johnson¹, L.M. Meyers¹, D.M. Morton², A.G. Gutfraind³, A.G. Galvani⁴, B.C. Clements⁵, ¹*The University of Texas at Austin, USA*, ²*Northwestern University, USA*, ³*University of Illinois at Chicago, USA*, ⁴*Yale University, USA*, ⁵*Texas Department of State Health Services, USA*

[P3.129] Epidemiological and economic effects of priming with the whole-cell *Bordetella pertussis* vaccine

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[P1.068] Dynamic network measures reveal the impact of cattle markets and alpine summering on the risk for epidemic outbreaks in the Swiss cattle population

B. Vidondo^{*}, B. Voelkl, *University of Bern, Switzerland*

[P1.047] Modelling African swine fever emergence and spread in France and evaluation of detection and control potential

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[P3.130] Control Fast or Control Smart: When should invading pathogens be controlled?

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