PRISM International Conference
20th-24th August 2018

Alamanda Palm Cove Boutique Hotel
1 Veivers Road
Palm Cove QLD 4879

Summary

This conference will bring together experts from various disciplines and backgrounds under the 4 PRISM themes: Immunisation, Respiratory Viruses, Emerging Infectious Diseases and New Methods for Simulation and Modelling. More information on our consortium, our staff and focus can be found on our website: http://prism.edu.au/theme/

The aim of our conference is to strengthen local and regional networks and provide a platform to share strengths and capabilities as well as explore new avenues to pursue in the context of Methods and Applied Mathematics. The Conference will take place over 4 days.

How to register

Registrations closed in mid April however there are still a few places left.

Should you wish to attend please contact prism-contact@unimelb.edu.au.

Invited Speakers PRISM International Conference

Marc Lipsitch
Harvard T.H. Chan School of Public Health.
Director Centre for Communicable Disease Dynamics.
NIH/NIGMS MIDAS Centre of Excellence.

Cécile Viboud,
Fogarty International Center, U.S National Institute of Health

	Katia Koelle Emory University		**Julia Gog** University of Cambridge
	Lisa White University of Oxford		**Niel Hens** Hasselt University. University of Antwerp
	Adam Kucharski London School of Hygiene & Tropical Medicine		

Invited Speaker Biographies

Marc Lipsitch

Marc Lipsitch is Professor of Epidemiology at the Harvard T.H. Chan School of Public Health and Director of the Center for Communicable Disease Dynamics (CCDD), an NIH/NIGMS MIDAS Center of Excellence. He is an author of more than 250 peer-reviewed publications on the impact of medical and public health interventions on the spread and evolution of infectious disease agents, and the consequences of these changes for human health. He has played a leading role in epidemiologic responses to infectious disease outbreaks, from SARS to pandemic influenza and Ebola. Ongoing studies of pandemic preparedness and response focus on preparedness for clinical trials in outbreaks. In addition, current research includes the application of population genomics to understand the spread of infections and the changes produced in bacterial population by human immunity, and modelling the effects of pneumococcal vaccination. He has contributed to our understanding of influenza seasonality, disease burden estimation, epidemiology of antimicrobial resistance, and novel methods for infectious disease epidemiology and modelling. Experimentally, his laboratory studies the immunity and antimicrobial resistance in Streptococcus pneumoniae, combining molecular biology and animal studies with population genomics, epidemiology and mathematical modelling.

Cecile Viboud

Cecile Viboud is a senior research scientist in the Division of International Epidemiology and Population Studies of the Fogarty International Center, National Institutes of Health, USA. Her research focuses on the epidemiology and transmission dynamics of acute viral infections, at the interface of public health and computational modelling. Her work has primarily concentrated on the epidemiology of respiratory viruses and pandemic influenza, but she has recently become interested in zoonotic infections, the potential of Big Data to strengthen infectious disease surveillance, and forecasting approaches.
A native of France, she received an engineer degree in biomedical technologies from the University of Lyon (1998), a Master of Public Health (1999) and a PhD in Biomathematics (2003) from Pierre and Marie Curie University, Paris, France.

Katia Koelle

Katia Koelle is an Associate Professor in the Department of Biology at Emory University. She has her PhD in Ecology and Evolutionary Biology from the University of Michigan (2005) and recently joined the Department of Biology at Emory after a decade on the faculty at Duke University. Her research interests include the

development of mathematical models to better understand patterns of viral evolution and disease dynamics between and within human hosts. She is further interested in the development and application of statistical approaches to characterize disease spread from viral sequence data. She works primarily on the 'phylodynamics' of RNA viruses, most notably influenza and dengue. Her research program currently spans primarily four topics of inquiry: (1) Understanding the interplay between viral evolution and the epidemiological spread of viral infectious diseases. (2) Understanding constraints on viral adaptation. (3) Understanding interindividual variation in within-host viral dynamics and evolution. (4) Understanding the impact of control measures of the epidemiological and evolutionary dynamics of viral infectious diseases.

Julia Gog

Julia Gog is the Professor of Mathematical Biology at the Department of Applied Mathematics and Theoretical Physics, University of Cambridge. She is also the David N. Moore Fellow at Queens' College, Cambridge. Julia's research interests are mainly in the dynamics and evolution of influenza. Part of her work is at the mathematical theory end, particularly in developing tractable approaches to modelling multiple strains and pathogen evolution, and also bioinformatic methods for application to viruses. Recent projects have also included large dataset analysis, including to understand the spatial patterns of influenza spread in the US. Julia and colleagues have also recently been busy with a big citizen science project, the "BBC pandemic", studying movement and contact patterns of many volunteers in the UK, partly for BBC documentary but also to generate a large dataset available to all scientists.

Lisa White

I am currently the head of an Oxford University mathematical and economic modelling (MAEMOD) group based in Thailand at the Mahidol-Oxford Tropical Medicine Research Unit whose research focus is on tropical infections and primarily malaria. MAEMOD coordinates an international network of infectious disease modellers and modelling research beneficiaries working in the Tropics (TDModNet). My work on malaria combines within and between host infection models with multi-strain/species modelling to consider the characterisation, emergence and spread of antimalarial drug resistance and its containment. I have strong collaborative links with the National Center of Malaria Control (CNM) in Cambodia and members of the WHO concerned with the containment of artemisinin resistance in its focus in Western Cambodia. I was also an active member of Malaria Eradication Research Agenda (malERA) an international consultative initiative aimed at identifying current knowledge gaps and new tools needed for malaria eradication. I am now developing mathematical models to be used as tools for national and international malaria elimination strategy design in the Asia Pacific Region. A large part of this approach will be to build capacity in the region for performing mathematical modelling research and for policymakers to access these new human resources effectively.

Niel Hens

Niel Hens is Professor at Hasselt University and the University of Antwerp where he is holder of the chair in evidence-based vaccinology. He has a background in mathematics and biostatistics and obtained a PhD in biostatistics in 2005 on the topic of 'Non- and Semi-parametric Techniques for Handling Missing Data'. During the completion of his PhD, he developed interest in modelling infectious diseases and participated in an EU FP6 project called POLYMOD on collecting social contact data relevant for the spread of infectious diseases in Europe. Using social contact data and serological data he has led the development of statistical methodology to estimate important infectious disease parameters. This has led to the publication of a successful monograph (Hens et al. Modelling Infectious Disease Parameters Based on Serological and Social Contact Data, Springer-Verlag, New York, 2012). In 2016, he was awarded an ERC consolidator grant for his work related to the aforementioned topic.

Adam Kucharski

Adam Kucharski is an Assistant Professor and Sir Henry Dale Fellow in the Department of Infectious Disease Epidemiology at the London School of Hygiene & Tropical Medicine. He is interested in how social behaviour and immunity shape disease transmission, and how knowledge of such processes can enhance surveillance and control measures. He worked on real-time modelling analysis during the 2013–16 Ebola epidemic in West Africa, and has also been involved in analysis of influenza, dengue fever and Zika outbreaks. From 2013–17 he held a Medical Research Council Career Development Award in Biostatistics, and prior to joining LSHTM he was a research associate at Imperial College London.

MONDAY 20TH AUGUST			
Arrivals			
TUESDAY 21st AUGUST			
9.45-10.15		Registrations-Morning tea	
10:15-10:30		**Introduction: What is PRISM? Why are we here?**	**Jodie McVernon**
10.30-12.30	**Workshop 1**	**Predictive modelling and policy** *Panel: Cecile Viboud, Adam Kucharski, Lisa White, James Wood, Rob Moss, Juan Pablo Villanueva Cabezas*	**Chair: James McCaw**
10:30-10:40	Rapid talk 1	Regional risk assessment in the face of health sector uncertainty	Nic Geard
10:40-10:50	Rapid talk 2	Risk modelling based on travel/mobility. Actionable time scale models for decision support.	Emma McBryde
10:50-11:00	Rapid talk 3	Informing elimination goals through predictive models	James Wood
11:00-11:10	Rapid talk 4	Cost-Effectiveness of Three Months of Weekly Rifapentine and Isoniazid Compared with Other Standard Treatment Regimens for Latent Tuberculosis Infection: A Decision Analysis Study	Tan Doan
11:10-11:20	Rapid talk 5	Who watches the watchmen? Surveillance data, prediction/forecasting, human behaviours	Rob Moss
11.20-11.30	Rapid talk 6	Development of a decision support system for pandemic influenza	Freya Shearer
11.30-12.30	Panel discussion	How do we make models fit for the purpose of policy decision support? Is elimination an appropriate goal for disease control programs?	
12:30-13.30		*LUNCH*	
Parallel sessions 13.30-15.30		**- Workshops for PhDs/ECRs:** *"How to manage yourself, your profile, and your projects, so that you can work more effectively"* **Part 1: Managing your CV/Professional profile** Trish Campbell will lead a session on managing all aspects of an academic profile. **Part 2: Managing your projects and reproducible research** Rob Moss will lead a session on how to manage and structure a project with a particular emphasis on reproducible research. **- Strategy meeting:** Future of PRISM discussions for CI's only.	**Trish Campbell + Rob Moss**
15.30-18.30		*Free time*	
18.30-21.30		CI + International speakers dinner	By invitation only

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WEDNESDAY 22nd AUGUST			
9.00-10.30	**Session 1**	**Regional issues in infectious disease control**	**Chair: Jodie McVernon**
9:00-9:30	Speaker 1	Malaria models and policy: Letters from Thailand	Lisa White
9.30-9.45	Short talk 1	Cost-effectiveness of interventions to improve hand hygiene in healthcare workers in middle-income hospital settings: a model-based analysis	Nantasit Luangasanatip
9:45-10:00	Short talk 2	Quantifying the blood-stage parasite kinetics in P. falciparum-infected humans based on controlled human malaria infection data	Pengxing Cao
10:00-10:15	Short talk 3	Modelling the dynamics of Wolbachia in Ae. aegypti population	Adeshina Adekunle
10:15-10:30	Short talk 4	From traditional to specialist modes of operation: village chicken production and implications for HPAI-H5N1 release in villages.	Juan Pablo Villanueva Cabezas
10:30-11:00		*Morning Tea*	
11.00-13.00	**Session 2**	**Heterogeneity in clinical trials and observational studies**	**Chair: Emma McBryde**
11.00-11.30	Speaker 1	Using simulation to enhance the design of vaccine clinical trials	Marc Lipsitch
11.30-11.45	Short talk 1	Modelling Thai population dynamics and seasonal movement to assess and predict the burden of melioidosis	Wiriya Mahikul
11.45-12.00	Short talk 2	Determining the household-level impact of a maternal vaccine for respiratory syncytial virus using an individual-based model	Trish Campbell
12.00-12.30	Speaker 2	Household members do not mix at random	Niel Hens
12.30-12.45	Short talk 3	The role of super-spreading events in Mycobacterium tuberculosis transmission: Evidence from contact tracing	Yayehirad Melsew
12.45-13.00	Short talk 4	Optimal design of group dose-response challenge experiments: a case-study in Campylobacter jejuni in chickens	David Price
13.00-14.00		*LUNCH*	
14.00-15.30		*Free time*	
15.30-17.30	**Session 3**	**Multi-strain and multi-scale modelling**	**Chair: James Wood**
15.30-16.00	Speaker 1	Using viral sequence data to infer transmission dynamics and bottlenecks	Katia Koelle
16.00-16.15	Short talk 1	Impact of B.pertussis pathogen evolution on pertussis epidemiology in NSW over the last decade (2008-2017) – A mathematical modelling study.	Duleepa Jayasundara
16.15-16.30	Short talk 2	Modelling the impact of viral biocontrol agents on Australia's exotic rabbit population	Thomas Prowse
16.30-16.45		*Afternoon Tea*	
16.45-17.15	Speaker 2	Modelling multiple co-circulating strains - making the mathematics work	Julia Gog
17.15-17.30	Short talk 3	Ecological and evolutionary dynamics of multi-strain, drug-resistant systems	Michael Meehan
17.30-17.45	Short talk 4	In-host dynamics of *N. gonorrhoeae* and resistance	Pavithra Jayasundara
18.00-20.00		**Substantive Canapes and Poster Session**	**At the Pavillion**

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THURSDAY 23rd AUGUST			
9.00-11.00	**Session 4**	**Transmission Dynamics**	**Chair: Josh Ross**
9:00-9:30	Speaker 1	Combining multiple data sources to understand the transmission and control of dengue and Zika	Adam Kucharski
9.30-9.45	Short talk 1	Propagation dynamics on multiplex (and duplex and simplex) networks	Michael Small
9:45-10.00	Short talk 2	Predicting spatial variation in the prevalence of hepatitis B in Australia	Karen McCulloch
10.00-10:30	Speaker 2	The spatial transmission dynamics of influenza	Cecile Viboud
10:30-10:45	Short talk 3	Bayesian log-Laplace quantile regression for spatiotemporal areal health data	Chawarat Rotejanaprasert
10.45-11.00	Short talk 4	A Spatially Explicit Agent-Based Modelling Framework for Long-term Transmission Dynamics of Lymphatic Filariasis in American Samoa	Sting Xu
11.00-11.30		*Morning Tea*	
11.30-13.00	**Workshop 2**	**Social networks and social contact patterns** ***Panel: Niel Hens, Julia Gog, Jodie McVernon, Sting Xu, Romain Ragonnet***	**Chair: Nic Geard**
11.30-11.40	Rapid Talk 1	Contagion - the BBC pandemic!	Julia Gog
11.40-11.50	Rapid Talk 2	Participatory development of a contact diary tool to capture dynamic household structure and mobility within and between remote Aboriginal and Torres Strait Islander communities	Jodie McVernon
11.50-12.00	Rapid Talk 3	Long term mobility patterns of Indigenous populations	Thiripura Vino
12.00-12.10	Rapid Talk 4	Simulating social mixing to profile tuberculosis transmission and burden in the Philippines	Romain Ragonnet
12.10-12.30	Panel Discussion	Discusson of challenges and next steps in social contact studies	
12.30-13.30	Workshop	Collating data collected in contact studies + Introduction to Social MixR package	Niel Hens
13.30-14.30		*LUNCH*	
14.30-16.00		Free time	
16.00-17.45	**Workshop 3**	**Modelling complex pathogen interactions** ***Panel: Marc Lipsitch, Katia Koelle, Nic Geard, Michael Meehan, Debebe Shaweno***	**Chair: Josh Ross**
16.00-16.10	Rapid Talk 1	How predictable is pneumococcal evolution in response to vaccines?	Marc Lipsitch
16.10-16.20	Rapid Talk 2	Modelling the diverse sources of C. difficile transmission within and outside hospitals	Angus Mclure
16.20-16.30	Rapid Talk 3	Unravelling the within-host dynamics of Group A *Streptococcus* from population-level observations of strain diversity and infection prevalence	Rebecca Chisholm
16.30-16.40	Rapid Talk 4	Coupled models of Group A Streptococcus and Scabies: How likely is eradication?	Michael Lydeamore
16.40-16.55		*Afternoon Tea*	
16.55-17.45	Panel Discussion	Modelling of multistrain systems. Incorporation of genomic data in multistrain models	
18.30-22.00		**Gala Dinner**	**Nu Nu Restaurant**

FRIDAY 24TH AUGUST			
9.00-10.30	**Workshop 4**	**Methods for estimation of infection and immunity from diverse data sources** *Panel: Adam Kucharski, Niel Hens, James McCaw, Trish Campbell, Michael Lydeamore*	**Chair: James Wood**
9:00-9:10	Rapid Talk 1	An ODE-based mixed modelling approach for B- and T-cell dynamics induced by Varicella-Zoster Virus vaccines in adults shows higher T-cell proliferation with Shingrix compared to Varilrix	Niel Hens
9.10-9.20	Rapid Talk 2	Estimating seasonal influenza attack rates from seroprevalence data	Adam Kucharski
9:20-9.30	Rapid Talk 3	Characterising seasonal influenza epidemiology using primary care surveillance data	Robert Cope
9.30-9:40	Rapid Talk 4	A comparison of approximate versus exact techniques for Bayesian parameter inference in non-linear ODE epidemiological models	Jennifer Flegg
9.40- 10.30	Panel Discussion	Methods for parameter estimation from data	
10:30-11:00		*Morning Tea*	
11.00-12.30	**Closing Session**	**Where to from here?**	**Chair: Jodie McVernon**
11:00-11:30	Speaker 1	What is the future for the management of biological systems?	Chris Baker
11:30-12:00	Speaker 2	TBC	Iadine Chades
12:00-12:30	Conference Close	Conference close and resolutions, where to next for PRISM?	Jodie McVernon
12:30-13.30		*LUNCH*	
14.00		**Departures**	