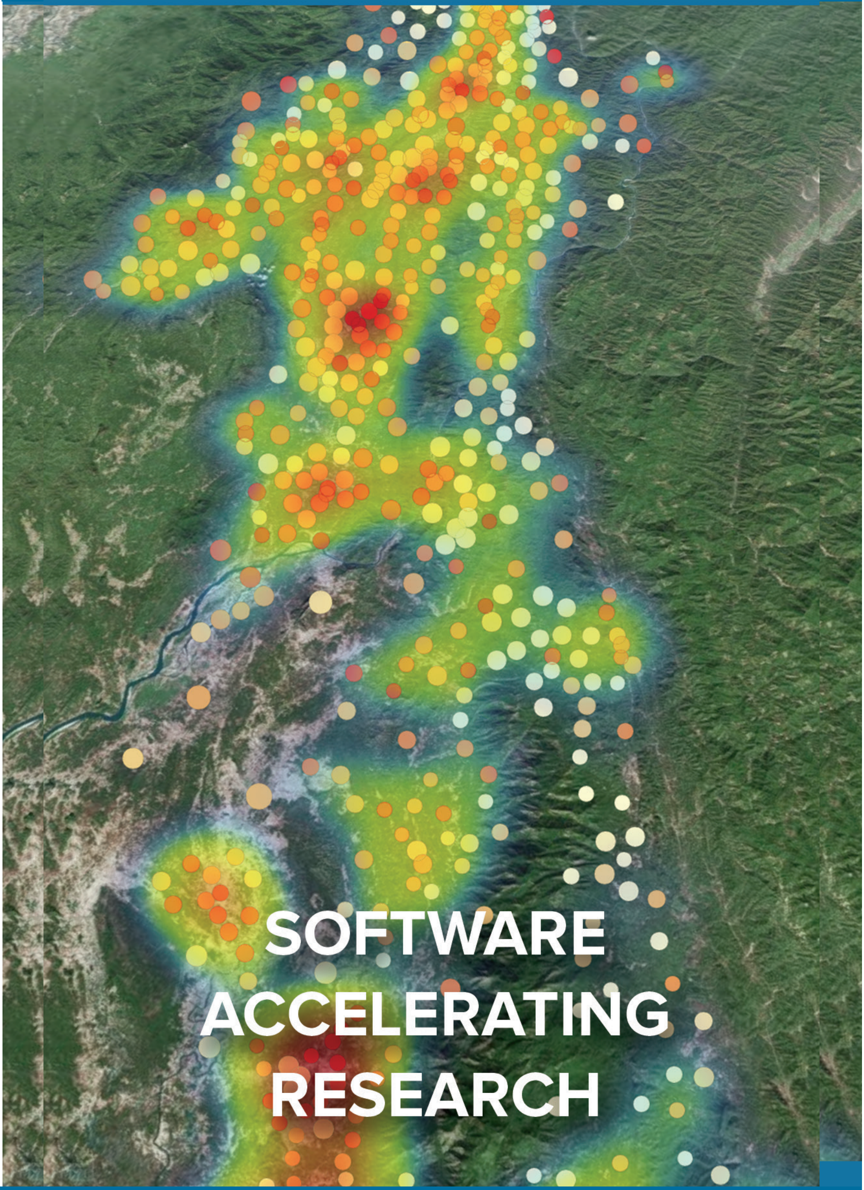
# 2018 6th Annual
# IDM Modeling Symposium



## SOFTWARE
## ACCELERATING
## RESEARCH

**INSTITUTE FOR DISEASE MODELING**

INTELLECTUAL VENTURES®

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# WELCOME

On behalf of the entire team at the Institute for Disease Modeling, I welcome you to our 6th Annual Modeling Symposium. This year's Symposium is particularly, although by no means exclusively, focused on the software tools developed and used by all of us in this community to model infectious disease and to guide our joint efforts toward control and eradication. It is exciting to see the continued growth in participation and attendance at this annual forum and we are pleased to sponsor and to help enable this gathering. I think we all value every opportunity to expand collaborations and share insights on the application of quantitative methods in global health efforts and that is a key objective of this meeting. Encouraging and enabling those efforts is a core, founding tenet of IDM. We all want to thank each of you for attending and contributing to our shared mission.

The Institute for Disease Modeling is a distinct and integral component of the Global Good initiative at Intellectual Ventures. Today, IDM is fast approaching 90 scientists and engineers focused on issues related to the eradication and control of infectious diseases and related global health missions. Our growth over the last 7 years has enabled us to increase our efforts on those diseases that have long been our focus, to broaden the suite of diseases which we can start to address, to address new cross-program initiatives and to implement our methods in shareable software. It has also helped grow collaborations outside of IDM. External collaborations are an important goal to IDM and, we believe, vital to positively impact global health.

We are thrilled to have roughly 250 attendees this year and over 80 speakers from 70 some organizations in global health. We look forward to an exciting, interesting and engaging three days together. As always, we greatly value your feedback and ideas both for our research program and to continue to make this annual Symposium better and hope that this will be the basis for strong future collaborations.

Sincerely,

Robert S. Hart
Vice President &
General Manager

# SESSION DESCRIPTIONS

## General Sessions

General sessions address the primary focus areas of the Symposium. They feature presentations targeted to explore a key area or finding and are highly engaging for all delegates.

## Breakout Sessions

Focusing on a single, clearly-defined topic or issue, speakers and delegates share experiences, contribute relevant research findings and brainstorm ideas to identify possible ways forward. Breakouts will also report on new findings and announce forthcoming research and new initiatives.

## Workshops

Software-focused workshops will feature demonstrations of the IDM software. Please bring a laptop to make the most of the workshops.

## Keynote

This session highlights emerging researchers doing exceptional work across a variety of fields within Global Health. IDM, in collaboration with a sponsorship from Public Library of Science (PLOS), has created a forum for students in the field of modeling and epidemiology to showcase their work, as well as provide them an opportunity to connect with prominent members of their communities.

*We are grateful for PLOS' support of our Symposium. PLOS (Public Library of Science) is a leading nonprofit Open Access publisher, innovator and advocacy organization dedicated to accelerating progress in science and medicine by leading a transformation in research communication.*

PLOS | NEGLECTED TROPICAL DISEASES

## Day 1 Overview

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|---|---|
| 7:30-8:45 | Registration & Breakfast |
| 8:45-9:00 | **Welcome**<br>Robert Hart, *IDM* |
| 9:00-10:30<br>*Auditorium* | **General Session 1; Software Tools**<br>David Aanensen, *Sanger Institute*<br>Mandy Izzo, *IDM*<br>Bobby Reiner, *IHME* |
| 10:30-11:00 | Break |
| 11:00-1:00<br>*Auditorium* | **Typhoid and Enteric Infections**<br>Myron Levine, *U of Maryland*<br>Jillian Gauld, *IDM*<br>Alicia Kraay, *U of Michigan*<br>Ben Lopman, *Emory University*<br>Virginia Pitzer, *Yale School of Public Health*<br>Brittany Hagedorn, *IDM* |
| 11:00-1:00<br>*Cottonwood* | **Introduction to Agent-Based Modeling**<br>Mandy Izzo, *IDM*<br>Jen Schripsema, *IDM* |
| 11:00-1:00<br>*Juniper* | **HIV Population Level**<br>Carol Camlin, *UC San Francisco*<br>Edinah Mudimu, *U of South Africa*<br>Kathryn Peebles, *International Clinical Research Center*<br>Alain Vandormael, *U of KwaZulu-Natal*<br>Graham Medley, *LSHTM* |
| 11:00-1:00<br>*Larch* | **Malaria in Low-Transmission Settings**<br>Mable Jerop, *Amref Health Africa*<br>William Pan, *Duke University*<br>Antonio Quispe, *Johns Hopkins*<br>Jennifer Flegg, *U of Melbourne*<br>Nguyen Tran, *Penn State University* |
| 11:00-1:00<br>*Laurel* | **Influenza and Pandemics**<br>Trevor Bedford, *Fred Hutch*<br>Joel Miller, *IDM*<br>David Pigott, *IHME*<br>Jonathan Read, *Lancaster University*<br>Lone Simonsen, *Roskilde University*<br>Alessandro Vespignani, *Northeastern University* |
| 11:00-1:00<br>*Madrona* | **Software Best Practices**<br>Christopher Lorton, *IDM* |
| 12:15-1:30 | Lunch Buffet at Eques Restaurant (*2nd Floor Lobby)* |
| 1:30-3:15<br>*Auditorium* | **General Session 2; Models 1**<br>Min Roh, *IDM*<br>Christopher Lorton, *IDM*<br>Thomas Smith, *Swiss TPH*<br>Dave Smith, *IHME*<br>Cecile Viboud, *Fogarty International* |
| 3:15-4:00 | Break |
| 4:00-5:00<br>*Auditorium* | **Keynote**<br>James Chirombo, *Lancaster University*<br>Poppy Miller, *Lancaster University*<br>Katie Owers, *Yale University*<br>Spener Fox, *UT Austin*<br>Molly Steele, E*mory University* |

## Sessions

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| **9:00-10:30**<br>*Auditorium* | **General Session 1; Software Tools**<br>*Chair: Jen Schripsema, IDM*<br>David Aanensen, *Wellcome Sanger Institute*<br>Mandy Izzo, *IDM*<br>Bobby Reiner, *IHME* |

### Data flow and analytics for Genomic Pathogen surveillance

David Aanensen, *Director, Centre for Genomic Pathogen Surveillance,* Wellcome Sanger Institute

Understanding the population and evolutionary biology of microorganisms can aid identification of lineages of risk. Genomic Surveillance aimed at identifying high risk clones, their risk assessment (through identification of correlates of resistance, virulence, etc) and the timely delivery of such information to decision makers can aid our efforts at infection control. During the presentation I will describe efforts in this area at The Wellcome Sanger Institute involving large scale sequencing to provide data and methodologies for the gathering, processing, and analytic and delivery of data through web and mobile applications to enhance and enable decision making.

### IDM Software overview

Mandy Izzo, *Senior Science Writer,* Institute for Disease Modeling

This presentation will be an overview of the software and tools created by IDM for epidemiological research. This is intended to help give a framework for other talks on specific software features, and to provide audience members with an understanding of what IDM's tools are capable of.

### Global Burden of Disease and geospatial tools at IHME: an overview

Bobby Reiner, *Assistant Professor,* Institute for Health Metrics and Evaluation

The GBD and geospatial teams at IHME use a multitude of tools to visualize both the data and results of their associated projects. Further, they leverage a small set of powerful computational programs to create the majority of their results. This talk will provide an overview of the visualization and modeling tools that are used at IHME.

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| **11:00-1:00**<br>*Auditorium* | **Typhoid and Enteric Infections**<br>*Chair: Jillian Gauld, IDM*<br>Myron Levine, *U of Maryland*<br>Jillian Gauld, *IDM*<br>Alicia Kraay, *U of Michigan*<br>Ben Lopman, *Emory University*<br>Virginia Pitzer, *Yale School of Public Health*<br>Brittany Hagedorn, *IDM* |

### Endemic typhoid fever in Samoa, a unique opportunity to assess the tools for typhoid elimination

Myron Levine, *Associate Dean for Global Health,* Vaccinology & Infectious Diseases, University of Maryland School of Medicine

The island country of Samoa has tenacious endemic typhoid fever, involving a mix of short-cycle (from chronic carriers) and long-cycle transmission. The relative isolation Samoa, the fact that all enteric fever is due to a local endemic antibiotic-sensitive *S. typhi* strain (no *S. Paratyphi* A or B), the limited population size (<200,000 inhabitants) and the motivation of the Ministry of Health are leading to a Samoan Typhoid Fever Control Program. The Program will quantify the human chronic carrier reservoir, identify specific modes of transmission, and assess interventions including mass vaccination with Vi conjugate vaccine and live oral vaccine in children and adults, respectively, and improvement of water supplies with the aim of interrupting transmission and achieving typhoid elimination.

### Typhoid fever in Blantyre, Malawi: Using spatial and genomic data to identify transmission pathways

Jillian Gauld, *Postgraduate Research Scientist*,
Institute for Disease Modeling

Since 2011, typhoid fever has been present in high endemic levels in Blantyre, Malawi, with the majority of cases being multi-drug resistant. Despite ongoing transmission, the dominant pathways of persistence remain unknown. A cohort and nested case control study were initiated to understand risk factors, explore the spatial patterns of incidence, and investigate genomic patterns of isolated *S. typhi* in relation to transmission. This presentation will review each of these components and their contribution to our understanding of typhoid fever in this setting.

### Direct, indirect, and overall effectiveness of Rotarix vaccination in rural Ecuador, 2008-2013

Alicia Kraay, *Postdoctoral Fellow,* University of Michigan

While rotavirus vaccine efficacy has been shown in randomized studies, its effectiveness in rural community settings with high barriers to vaccination is unclear. In particular, community-level estimates of direct and indirect vaccine effects are needed. Here we analyze eighteen months of all-cause diarrhea surveillance and ten years of serial population-based case-control data from rural Ecuador during the period of Rotarix vaccine introduction. We use this data to estimate direct, indirect, and overall effectiveness on all-cause diarrhea and rotavirus infection, including asymptomatic infection. We also consider the vaccine effects on older children and adults and consider the implications for rotavirus transmission in this and other endemic settings.

### Noroviruses: Ubiquitous, diverse and highly infectious... and soon to be vaccine preventable?

Ben Lopman, *Associate Professor,* Emory University

Norovirus is the number one cause of diarrheal the first year of life in developing countries. And, following the success of rotavirus vaccination, is becoming the primary cause of severe pediatric diarrheal disease but also causes considerable disease across the age range. In response to this burden, vaccines are in development and moving rapidly through the pipeline. However, the high burden across the age range, multiple transmission routes and genetic diversity of norovirus makes this a complex vaccine target. This presentation will review our statistical and mathematical studies of norovirus epidemiology and simulation of vaccination strategies.

### Cost-effectiveness of typhoid conjugate vaccines in Gavi-eligible countries

Virginia Pitzer, *Associate Professor*, Yale School of Public Health

We evaluated the cost-effectiveness of different delivery strategies for typhoid conjugate vaccines (TCVs) in Gavi-eligible countries. We used a transmission dynamic model to predict the impact of routine vaccination with TCVs with and without a catch-up campaign, and combined model predictions with information on typhoid treatment costs, vaccine-related costs and disability-adjusted life-years to identify the preferred strategy in each country. Routine vaccination including a catch-up campaign among children less than 15 years of age was the preferred strategy in most countries at willingness-to-pay values less than the gross domestic product, but there were large degrees of uncertainty. The main sources of uncertainty included the case fatality rate, underlying incidence of typhoid fever, and prevalence of antimicrobial resistance. Our results can be used to set research priorities and inform country-level decision-making around the introduction of TCVs.

### The value of environmental surveillance in prioritizing vaccination campaigns

Brittany Hagedorn, *Financial Analyst,* Institute for Disease Modeling

Typhoid incidence estimates have historically relied on case reporting; however, the heterogeneity of reporting makes it is difficult to know where the optimal place(s) to deploy vaccines are. Environmental surveillance offers an alternative and could be used to target vaccination campaigns. We consider the value of surveillance-responsive vaccination campaigns and identify conditions under which environmental surveillance is cost-effective.

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| **11:00-1:00** | **Introduction to Agent-Based Modeling** |
| *Cottonwood* | Mandy Izzo, *IDM*<br>Jen Schripsema, *IDM* |

### Introduction to agent-based modeling

Mandy Izzo, *Senior Science Writer*, Institute for Disease Modeling
Jen Schripsema, *Senior Technical Writer*, Institute for Disease Modeling

We will conduct a demo/breakout session with the Quick Start (aka the Training App). We will explore it's capabilities and demonstrate how we are simplifying the process of learning how to use EMOD for disease modeling. Participants will have an opportunity to be hands-on and test out the web-based application themselves.

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| **11:00-1:00**<br>*Juniper* | **HIV Population Level**<br>*Chair: Anna Bershteyn, IDM*<br>Carol Camlin, *UC San Francisco*<br>Edinah Mudimu, *U of South Africa*<br>Kathryn Peebles, *International Clinical Research Center*<br>Alain Vandormael, *U of KwaZulu-Natal*<br>Graham Medley, *London School of Hygiene & Tropical Medicine* |

### Gender, geographic mobility, and HIV/AIDS in Southern and East Africa

Carol Camlin, *Associate Professor in Residence*, UC San Francisco

I will provide a brief overview of the historical context of population geographic mobility in Southern and East Africa, the main drivers of this mobility, and how forms of mobility differ for men and women. I'll then share key findings of studies I have conducted with mixed research methods to better understand the pathways through which mobility contributes to HIV acquisition and transmission risks. I'll end with highlights of findings to date of a study of mobility and its impacts in the context of an ongoing HIV test and treat trial (SEARCH).

### Social, sexual network formation, and HIV transmission

Edinah Mudimu, *Senior Lecturer,* University of South Africa

Different social and sexual networks are observed in different societies. The formation of these networks depend on non-linear human behaviour. We present an algorithm that takes individuals seeking a "standard" heterosexual relationship from a virtual social network and individuals involved in commercial sex relationships. We superimpose the spread of HIV on the sexual network to analyse and identify the main drivers of HIV in the given virtual society.

### Modeling a partially effective HIV vaccine in South Africa: Viral adaptation, risk compensation, and cost-effectiveness

Kathryn Peebles, *Pre-doctoral Research Associate*, International Clinical Research Center

Introduction of a partially effective HIV vaccine may induce HIV viral adaptation, resulting in the reduction of population-level vaccine effectiveness over time. We use a model calibrated to the South African HIV epidemic to describe the rate and consequences of viral adaptation in response to a partially effective vaccine. We further describe the effect of risk compensation on the rate of viral adaptation, and the impact of both viral adaptation and risk compensation on the cost-effectiveness of an HIV vaccine.

### Estimating the incidence of HIV infection in a rural and hyper-endemic South African setting

Alain Vandormael, *Senior Lecturer,* University of KwaZulu-Natal, South Africa

Using data from one of Africa's largest population-based cohorts, we directly measure trends in the HIV incidence rate for males and females in a hyper-endemic South African setting since the roll-out of ART in 2004. These findings will be discussed.

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| **11:00-1:00**<br>*Larch* | **Malaria in Low-Transmission Settings**<br>*Chair: Amelia Bertozzi-Villa, IDM*<br>Mable Jerop*, Amref Health Africa*<br>William Pan, *Duke University*<br>Antonio Quispe, *Johns Hopkins Bloomberg School of Public Health*<br>Jennifer Flegg, *U of Melbourne*<br>Nguyen Tran, *Penn State University* |

### Spatial distribution of healthcare workers in malaria endemic zones in Kenya: Health system readiness for malaria pre-elimination

Mable Jerop, Monitoring, *Evaluation and Research Officer*, Amref Health Africa

It is essential to consider that available resources for health care are still a crisis in developing countries as global efforts in the fight against malaria continues towards elimination. Various international institutions have recommended effective strategies such as integrated community case management. This paper seeks to give a cross sectional description of the distribution of healthcare workers at facility and community levels and simulate the ideal quantity and distribution of health workers considering factors as malaria prevalence and accessibility to care in order to achieve the target to pre-elimination in the near future.

### An early warning system for malaria in the Amazon

William Pan, *Assistant Professor,* Duke University

Malaria is an important cause of morbidity and mortality worldwide. With support from NASA, our team has developed multiple quantitative methods that can be used to help future predict malaria cases with high spatial and temporal resolution.  Models interweave hydro-meteorological, land cover, demographic, and sur-veillance data to forecast malaria cases up to 12 weeks in advance using defined ecoregions of Peru and Ecuador for one-week time windows.

### Modeling surveillance data in the prospect of implementing a malaria elimination program in a low transmission setting

Antonio Quispe, *Senior Physician Researcher*, Johns Hopkins Bloomberg School of Public Health

Modeling surveillance data in the prospect of implementing malaria elimination programs in low transmission settings represent an increasing challenge for researchers and decision makers. From R0 models to multilevel multivariable models, different approaches have their own strengths and weaknesses. However, we can choose any of these approaches we certainly need to choose the one that serves the decision-makers the better. So in this presentation, I will present our latest efforts to model surveillance Peruvian data to inform the decision makers behind the malaria elimination program recently launched in Peru.

### Antimalarial resistance in Southeast Asia

Jennifer Flegg, *Senior Lecturer,* University of Melbourne

Malaria parasites have repeatedly evolved resistance to antimalarial drugs, thwarting efforts to eliminate the disease and contributing to an increase in mortality. In this talk, I will introduce several statistical and mathematical models for monitoring the emergence and spread of antimalarial drug resistance. For example, results will be presented from Bayesian geostatistical models that have quantified the space-time trends in drug resistance in Southeast Asia.

### Triple ACTs as the new paradigm for treatment of uncomplicated falciparum malaria

Nguyen Tran, *Postdoctoral Researcher,* Pennsylvania State University

Using the individual-based simulation to evaluate the long-term benefit of triple artemisinin combination therapy (TACT). The two evaluated TACTs were 3-day DHA-PPQ-MQ and 3-day AL-AQ. The model starts with a status quo drug distribution AL/ASAQ, AQ, CQ, and SP and then replaces the ACT with TACT in the year 2020. We found that employing TACT lowers the number of treatment failures compared to the status quo, and also delays the emergence of the K13-propeller resistance alleles in the population.

**11:00-1:00** **Influenza and Pandemics**
*Laurel*
*Chair: Joel Miller, IDM*
Trevor Bedford*, Fred Hutchinson Cancer Research*
Joel Miller, *IDM*
David Pigott, *Institute for Health Metrics and Evaluation*
Jonathan Read, *Lancaster University*
Lone Simonsen*, Roskilde University*
Alessandro Vespignani*, Northeastern University*

### Real-time genomic surveillance of pandemic threats

Trevor Bedford, *Associate Member*, Fred Hutchinson Cancer Research

Viral pathogens are an enduring threat to global public health. Here, I present efforts to characterize the evolutionary and epidemiological dynamics of RNA viruses with emphasis on challenges faced in pre-pandemic threats such as MERS-CoV and avian influenza as well as tracking virus spread after human-to-human becomes sustained. We've built phylogenetic models to characterize spillover frequency of MERS-CoV and to chart  geographic spread of Ebola and Zika. We are now working to deploy these inferences in a "real-time" fashion and inform planning and response by public health entities.

### Mathematical and computational methods to study early stages of a growing epidemic

Joel Miller, *Senior Research Scientist*, Institute for Disease Modeling

I will discuss the use of probability generating functions (PGFs) to describe the possible outcomes of an introduced infection in a large population.  I will also describe numerical tools we have developed to automate the application of PGFs to these problems. The methods are much more efficient than performing a large number of stochastic simulations.

### Improving the evidence-base for pandemic preparedness

David Pigott, *Assistant Professor,* Institute for Health Metrics and Evaluation

The potential for widespread epidemics to have severe consequences on human populations has been repeatedly demonstrated. Arguably the recent analytical paradigm has been focused in two key areas—identification of hotspots of disease emergence and the detection of novel threats, and event-based modelling to dynamically assess patterns of risk during an ongoing outbreak. With the Global Health Security Agenda, there has been renewed emphasis on the International Health Regulations and pre-emptive preparedness for outbreaks from a multitude of conditions, rather than specific protocols for specific diseases. I will discuss some approaches that can be used to inform these preemptive assessments, attempting to define the inherent variation in the potential for pathogenic transmission at various scales, and contextualize this potential within existing evaluations of specific pathogen emergence. By placing equal emphasis on what can be done prior to outbreaks as we do on providing resources once cases are reported the hope is that the impact of such outbreaks can be mitigated.

### Quantifying influenza transmission risks for school-age children: The role of community, social networks and school structures

Jonathan Read, *Senior Lecturer in Epidemiology,* Lancaster University

Schools are known to be important settings for influenza transmission, but it is not clear why. This talk presents a transmission modelling analysis of observed influenza B infections in a school-based cohort study in Pittsburgh, USA. The analysis identifies the relative role of different transmission routes (community, social, school) and school attendance on infection risk throughout a seasonal epidemic. Implications for public health interventions, such as school closures, are discussed.

### Pandemics of the past—Pandemics of the future

Lone Simonsen, *Professor*, Roskilde University, Denmark

Identifying epidemiological patterns and drawing on lessons from historic pandemic experiences can inform public health response to future pandemics. Over the last decade, researchers representing many fields have spent considerable efforts studying the 1918 Spanish influenza pandemic, the most devastating pandemic in modern history. In this talk, I will review those insights and discuss key unresolved issues unresolved.

### Big data and epidemic modeling

Alessandro Vespignani, *Distinguished Professor*, Northeastern University

Large-scale data-driven models of infectious diseases are not only valuable because they predict where and how an epidemic might spread in the next few weeks, but also because they provide rationales and quantitative analysis to support public health decisions and intervention plans. At the same time, the non-incremental advance of the field presents a broad range of challenges: algorithmic (multiscale problem), scalability, parallelization, and real-time integration of novel digital data stream (social networks, participatory platform for disease monitoring, human mobility, etc.). I will review and discuss recent results and challenges in the area, ranging from applied analysis for public health practice to foundational computational and theoretical challenges.

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| **11:00-1:00**<br>*Madrona* | **Software Best Practices**<br>Christopher Lorton, *IDM* |

### Software best practices

Christopher Lorton, *Managing Principal Software Engineer,*
Institute for Disease Modeling

The Institute for Disease Modeling is an unusual research organization with a full-time professional software development team dedicated to supporting the software needs of the research staff. In this session, members of the development team will present short overviews of several software development techniques which will improve the quality and reach of your software and can be put into practice by anyone involved in writing code.

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| **1:30-3:15**<br>*Auditorium* | **General Session 2; Models 1**<br>*Chair: Hil Lyons, IDM*<br>Min Roh, *IDM*<br>Christopher Lorton, *IDM*<br>Thomas Smith, *Swiss TPH*<br>Dave Smith, *Institute for Health Metrics and Evaluation*<br>Cecile Viboud, *Fogarty International* |

### Stochastic compartmental modeling with the IDM-CMS

Min Roh, *Research Scientist*, Institute for Disease Modeling
Christopher Lorton, *Managing Principal Software Engineer,*
Institute for Disease Modeling

In this talk, we present IDM's Compartmental Modeling Software (IDM-CMS) that allows for easy construction and simulation of stochastic compartmental models. Complex epidemiological dynamics such as spatial spread of a disease, impact of vaccination, and probability for extinction/resurgence can be conveniently modeled in this framework. After an introduction of the software and solvers offered in the IDM-CMS, we demonstrate how to create a simple SIR system and run it to obtain output trajectories.

### The OpenMalaria microsimulation platform

Thomas Smith, *Professor*, Swiss Tropical and Public Health Institute

The presentation will use the example of the OpenMalaria platform for modelling *Plasmodium falciparum* epidemiology and malaria interventions. This will entail comparing the rationale for microsimulation modeling with that of compartment models; it will consider the importance and challenges of sound model parameterization and discuss the contrast between silico experimentation and computer representation of the real world.

### Robust analysis and modular simulation for malaria

David Smith, *Professor*, Institute for Health Metrics and Evaluation, University of Washington

Robust analysis for malaria policy requires propagating uncertainty: 1) the spatial and temporal distribution of malaria transmission intensity; 2) the distribution of vectors; 3) the process of infection and immunity; and 4) the recent history of malaria control and operations. I will introduce a software platform called MASH (Modular Analysis and Simulation for Health) for dealing with some of these problems, along with some of the modules, algorithms and utilities that make it possible.

### Transmission dynamics of pandemic influenza

Cecile Viboud, *Senior Research Scientist*,
Fogarty International Center, National Institutes of Health

We will discuss a variety of historical modeling studies that highlight the signature epidemiological features of influenza pandemics and inform preparedness for future pandemics. The talk will particularly focus on the 1918 and 2009 pandemics. We will review how the age patterns of cases and deaths relates to the background immune profile of the population, compare the transmission potential of different pandemic seasons in different locations, and discuss spatial transmission models for pandemic influenza.

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| **4:00-5:00**<br>*Auditorium* | **Keynote**<br>*Chair: Robert Hart, IDM*<br>James Chirombo, *Lancaster University*<br>Spener Fox, *UT Austin*<br>Poppy Miller, *Lancaster University*<br>Katie Owers, *Yale University*<br>Molly Steele, E*mory University* |

### Spatio-temporal modelling of climate and non-climate impacts on malaria incidence in Malawi

James Chirombo, *PhD Student*, Lancaster University/ Malawi Liverpool Wellcome Trust Clinical Research Programme

Climate variation is thought to be a significant driver of vector-borne disease transmission, such as malaria. I present a spatio-temporal generalized linear mixed model and a Bayesian inferential framework to quantify the contribution of climatic, environmental, and socio-economic factors to district-level variation in malaria infection risk in Malawi. The resulting risk maps can aid malaria control programmes in resource allocation.

### Seasonality in risk of pandemic influenza emergence

Spencer Fox, *PhD Student*, The University of Texas at Austin

Influenza pandemics emerge via genomic reassortment between circulating human and animal strains. The risk of pandemic emergence should therefore be high during the flu season, when viruses are abundant and conditions favor transmission. However, the six pandemics on record since 1889 all emerged in the Northern Hemisphere following the flu season, suggesting that other forces may predictably constrain pandemic risk. We find that seasonal influenza epidemics leave a wake of immunity that impedes pandemic emergence. This transient refractory period is consistent with the spring-summer emergence, multiple wave dynamics of recent pandemics, and may cause initial underestimation of the viral transmission rate. These findings may improve pre-pandemic risk assessments and real-time situational awareness, particularly as we gain greater insight into the extent of immunity.

### Quantifying leptospirosis risk factors in urban slums

Poppy Miller, *PhD Student*, Lancaster University

Leptsospirosis emerged as a disease of urban slums in Brazil 20 years ago and has flourished in the tropical slums exacerbated by open sewers and rubbish dumps, and high numbers of rats. We modeled the spatio-temporal distribution of rats and leptospirosis cases to assess the impact of nearby high rat activity (and other social and environmental factors) on risk of leptospirosis infection. The results show that whilst increased rat activity significantly increases the risk of leptospirosis, other social and environmental factors had a much larger effect. These results will be used to implement targeted interventions to reduce leptospirosis risk in urban slums.

### Spatiotemporal dynamics and determinants of leptospirosis transmission in northeastern Thailand, 2000-2014

Katie Owers, *PhD Candidate*, Yale University

We characterized the timing, spatial distribution, and district-level determinants of leptospirosis cases over a 15-year period in northeastern Thailand. This period covers an epidemiologic transition from a major outbreak to persistent high endemic transmission, and we capture features of both. The persistent transmission in this region had previously been poorly managed due to a lack of understanding of the heterogeneities in infection. This project not only characterized leptospirosis, but also identified avenues for improved public health response to the disease.

### Targeting pediatric versus elderly populations for norovirus vaccines: A model-based analysis of mass vaccination options

Molly Steele, *PhD Candidate,* Emory University

Noroviruses are the leading cause of acute gastroenteritis and foodborne diarrheal disease in the United States. Norovirus vaccine development has progressed in recent years, but critical questions remain regarding which age groups should be vaccinated to maximize population impact. We developed a deterministic, age-structured compartmental model of norovirus transmission and immunity and simulated mass immunization of both pediatric and elderly populations to estimate age-specific and population-level impacts.

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| **5:00-6:00**<br>*Auditorium* | **Software Open Forum Discussion**<br>Gene Oates, *IDM* |

The Software Open Forum is an opportunity to meet the IDM software team and discuss the various tools created for internal and external researchers. The forum seeks to create an open and collaborative environment for all software related topics, including future collaboration opportunities, software development and training. Software team members from the various project groups will be available for these discussions.

## Day 2 Overview

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| 7:30-8:45 | Registration & Breakfast |
| 9:00-10:30<br>*Auditorium* | **General Session 3; Risk Maps**<br>Guillaume Chabot-Couture, *IDM*<br>Stephane Vouillamoz, *Novel-T*<br>Arend Voorman, *BMGF* |
| 10:30-11:00 | Break |
| 11:00-1:00<br>*Auditorium* | **Risk Mapping**<br>Graham Medley, *LSHTM*<br>Bobby Reiner, *IHME*<br>Vince Seaman, *BMGF*<br>Qinghua Long, *IDM* |
| 11:00-1:00<br>*Juniper* | **Evolutionary Epidemiology**<br>Gytis Dudas, *Fred Hutch*<br>Katia Koelle, *Emory University*<br>John McCrone, *U of Michigan*<br>Katherine Xue, *UW*<br>Mike Famulare, *IDM* |
| 11:00-1:00<br>*Laurel* | **Compartmental Modeling Software**<br>Min Roh, *IDM* |
| 11:00-1:00<br>*Madrona* | **HIV & TB Within Host**<br>Miles Davenport, *Kirby Institute*<br>Alison Feder, *Stanford University*<br>Shuyi Ma, *Center for Infectious Disease Research*<br>Somdatta Sinha, *U of British Columbia*<br>Kirsten Wiens, *IHME* |
| 12:15-1:30 | Lunch buffet at Eques Restaurant *(2nd floor lobby)* |
| 1:30-2:30<br>*Auditorium* | **General Session 4; Models 2**<br>Jaline Gerardin, *IDM*<br>Britta Jewell, *UC Berkeley* |
| 2:30-9:00 | IDM hosted excursion and dinner |

## Sessions

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| **9:00-10:30**<br>*Auditorium* | **General Session 3; Risk Maps**<br>*Chair: Benoit Raybaud, IDM*<br>Guillaume Chabot-Couture, *IDM*<br>Stephane Vouillamoz, *Novel-T*<br>Arend Voorman, *BMGF* |

### Rapid risk mapping for programmatic use: RiskMapper platform

Guillaume Chabot-Couture, *Director of Global Development Research,* Institute for Disease Modeling

Disease control and eradication programs must prioritize the deployment of their resources, i.e., vaccines delivery, surveillance efforts, and technical assistance, to maximize their impact. Risk maps are a programmatic tool that can compile multiple risk indicators into an optimal prediction of where the disease is going to be in the near future. We present on our experience building risk maps, and how we are working on a platform to make the creation of risk maps easier and faster.

### Supporting Polio eradication through the use of geographic information systems

Stephane Vouillamoz, *Co-Founder and Solutions Engineer,* Novel-T

This presentation will cover how mobile and geospatial data and analytics can power the planning, monitoring, and assessment of public health interventions.

### Creating an information system for the Global Polio Eradication Initiative and the programmatic implications

Arend Voorman, *Program Officer,* Bill & Melinda Gates Foundation

The quantity of data that are collected by the Global Polio Eradication Initiative (GPEI) is unlikely to be matched by any other public health program.  The Polio Information System (PolIS) was created to harmonize and consolidate multiple datasets collected across the globe and make the data and information available to GPEI partners. This presentation will describe the objectives of POLIS, the process employed to meet the objectives, and the programmatic implications.

**11:00-1:00** *Auditorium*

**Risk Mapping**
*Chair: Guillaume Chabot-Couture, IDM*
Graham Medley, *London School of Hygiene & Tropical Medicine*
Bobby Reiner, *Institute for Health Metrics and Evaluation*
Vince Seaman, *Bill & Melinda Gates Foundation*
Qinghua Long, *IDM*

### Short-term prediction of visceral leishmaniasis epidemic risk in India

Graham Medley, *Professor of Infectious Disease Modelling*, London School of Hygiene & Tropical Medicine

Visceral leishmaniasis (VL) is being successfully controlled on the Indian subcontinent, with the target of “elimination as a public health problem” likely to be achieved in 2020. Historically, VL has demonstrated widespread, devastating epidemics, and in the current situation substantial outbreaks have been observed at the village level. We believe that there is a substantial risk that the current success in reducing transmission will increase the possibility of future epidemics. The aim of this work is to develop a framework that will enable the spatial risk of outbreaks/epidemics to be predicted so that resources can be focussed more efficiently, and we are using the RiskMapper software as the basis for this work. As the work has only just started, the focus will be on the ideas rather than results.

### Mapping existing and potential infection risk zones of yellow fever worldwide

Bobby Reiner, *Assistant Professor,* Institute for Health Metrics and Evaluation

Given the recent yellow fever outbreaks and the expanding range of the primary vector *Aedes aegypti,* there is a great risk for future outbreaks internationally. To identify the contemporary distribution of yellow fever and identify those locations that may experience outbreaks in the future, we conducted a series of analyses. First, we estimated global yellow fever vaccination coverage by age from 1970 through 2016. Second, we combined this with environmental and biological explanatory covariates, and spatial variability in disease reporting rates, to map sub-national variation in incidence of yellow fever across at-risk countries. Our results can be used to quantify the number of cases averted by vaccination worldwide, and provide an evidence base for targeting vaccination campaigns within the risk zones.

### GRID3: Supporting the generation of high-quality geospatial reference data in developing countries

Vincent Seaman, *Deputy Director - Strategy, Data & Analytics,* Bill & Melinda Gates Foundation

The GRID3 project provides support to developing countries to collect/validate the basic geospatial reference layers (settlement names/locations and key points of interest, administrative boundaries, and GIS-based population estimates independent of census and other administrative data), along with GIS/data management capacity building, to ensure governments have the ability to use, manage, and sustain the GRID3 data. Examples and applications from completed datasets in Nigeria, along with a progress report for 2018 countries (Ethiopia, DRC, Tanzania, and Zambia) will be presented.

### Riskmap architecture

Qinghua Long, *Research Software Engineer,*
Institute for Disease Modeling

An overview of the architecture and building blocks of the Riskmap project. Discover the technologies and techniques supporting the workflow.

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| **11:00-1:00**<br>*Juniper* | **Evolutionary Epidemiology**<br>*Chair: Mike Famulare, IDM*<br>Gytis Dudas, *Fred Hutchinson Cancer Research Center*<br>Katia Koelle, *Emory University*<br>John McCrone, *U of Michigan*<br>Katherine Xue, *UW*<br>Mike Famulare, *IDM* |

### Genomic epidemiology and population genetics of emerging RNA viruses

Gytis Dudas, *Postdoctoral Fellow*, Fred Hutchinson Cancer Research Center

Sequencing technologies have allowed outbreaks of emerging RNA viruses to be investigated in unparalleled detail. Over the decades sequence data have been used successfully to understand evolutionary dynamics of many viruses across multiple scales.

### The effect of genetic linkage on influenza virus adaptation and disease spread

Katia Koelle, *Associate Professor,* Emory University

Phylodynamic studies of rapidly evolving viral pathogens often focus on only beneficial mutations or on the use of putatively neutral mutations to infer disease spread. Further, they often focus on only a part of a viral genome. Here, I will present results from a series of studies focused on influenza virus that show that linkage effects occur and may be an important factor in this virus's epidemiological spread, and that (purifying) selection on this virus's non-antigenic gene segments occurs and may, through linkage effects, impact the rate of viral adaptation, and thereby modulate rates of disease incidence.

### Influenza evolution at host scales: A case for stochastic processes

John McCrone, *Postdoctoral Researcher,* Department of Microbiology and Immunology, University of Michigan

We have defined the dynamics of influenza A virus populations in human hosts through next generation sequencing of 249 specimens from 200 individuals collected over 6290 person-seasons of observation. We used viral sequence data from 35 serially sampled

### Parallel evolution of influenza across multiple spatiotemporal scales

Katherine Xue, *Graduate Student*, University of Washington / Fred Hutchinson Cancer Research Center

The rapid global evolution of influenza viruses begins with de novo mutations that arise in individual infected hosts, but it remains unclear how influenza's within-host genetic diversity affects its global evolution. We used deep sequencing to track influenza's evolution in a cohort of immunocompromised patients with long-term infections. A small set of mutations arose recurrently in independent patients in our study, and many of these recurrent mutations also reached a high global frequency in the decade following the patient infections. Our results demonstrate striking similarities in influenza's evolution at the within- and between-host scales.

### Beyond reversion: Evolutionary epidemiology of vaccine-derived poliovirus transmission

Mike Famulare, *Senior Research Scientist,* Institute for Disease Modeling

Mass vaccination with the attenuated oral polio vaccine (OPV) has prevented millions of cases of childhood paralysis over the last sixty years, but it has also created a unique model system for emerging human pathogens. Circulating vaccine-derived poliovirus (cVDPV) outbreaks occur rarely, at a rate of roughly one per year per hundred million doses delivered. The low cVDPV emergence rate contrasts with the high reversion rates of attenuating substitutions in OPV recipients. To better understand the separation of scales between cVDPV emergence and its underlying microevolution, I conducted a comprehensive reanalysis of published poliovirus sequences sampled from vaccine recipients, transmitting cVDPV and wild-type outbreaks, and immunocompromised chronic shedders. The results highlight that virulence, within-host fitness, and between-host transmissibility are not equivalent.

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| **11:00-1:00** | **Compartmental Modeling Software** |
| *Laurel* | Min Roh, *IDM* |

### Stochastic compartmental modeling applications and methods

Min Roh, *Research Scientist,* Institute for Disease Modeling

Interdisciplinary collaboration in computer science, mathematics, and epidemiology has enabled development and analyses of advanced epidemiological models to improve our understanding of diseases. This session will discuss various applications of stochastic compartmental simulation methods as well as modeling and algorithmic challenges. We invite you to share your modeling experience and help define are for future research.

**11:00-1:00** **HIV & TB Within Host**
*Madrona*
*Chair: Stewart Chang, IDM*
Miles Davenport, *Kirby Institute*
Alison Feder, *Stanford University*
Shuyi Ma, *Center for Infectious Disease Research*
Somdatta Sinha, *U of British Columbia*
Kirsten Wiens, *Institute for Health Metrics and Evaluation*

## Modelling the within-host dynamics of HIV infection and immunity

Miles Davenport, *Professor and Head, Infection Analytics Program,* Kirby Institute, UNSW Australia

Epidemiological models of infection control are often dependent on a variety of assumptions about both biological mechanisms and parameter values of processes occurring within the infected host. In HIV infection, a genetic bottleneck at transmission results in only one or a small number of “founder” viruses establishing infection. This clonal viral population rapidly diversifies through mutation and recombination, and “immune escape” variants are rapidly selected by the host immune system.

The work presented will use modelling to dissect the mechanisms of transmission, immune control, and viral evolution, based on analysis of SIV viral dynamics and host immunity in rhesus and pigtail macaques, coupled with in vitro and clinical studies of HIV evolution. This work provides insights into the within-host arms race between virus and immune control, which can be used to inform multi-scale modeling of the HIV epidemic.

## Characterizing the within-host spatial structure of Simian-HIV drug resistance evolution

Alison Feder, *Graduate Student*, Stanford University

Evolution of pathogens within the body (to the immune system, drugs, or to new hosts) is increasingly understood to be a heterogeneous process in space. Nevertheless, our understanding of this evolution is limited by our sampling ability, which is often at a single time point taken from the blood. To bridge this gap, we analyze viral sequences from Siman-HIV-infected macaques sampled spatially (from five tissue types) and temporally over the course of treated infection. Using this data, we characterize the intra-patient environment, including quantifying the viral migration rate between tissues and the selective pressure imposed by drug treatment. Detailed parametrization of this intra-patient environment contributes to ongoing modeling efforts including those to understand the mechanisms of HIV multi-drug resistance evolution.

### Data-driven Inference of drug synergy in Mycobacterium tuberculosis

Shuyi Ma, *Postdoctoral Scientist,* Center for Infectious Disease Research

Combination therapy is an important strategy for treating tuberculosis (TB), which kills almost 2 million people each year, and there is pressing need for rational approaches to prioritize new drug regimens for clinical trials. To begin addressing this problem, we adapted a computational tool that we recently created—INferring Drug Interactions using chemoGenomics and Orthology, (INDIGO)—which accurately predicts drug synergy/antagonism in *E. coli* based on the available high resolution chemogenomic data available for that organism. We modified INDIGO to predict synergy/antagonism in 15,753 drug pairs involving 178 compounds in *Mycobacterium tuberculosis* (MTB) by leveraging publicly available transcriptomics data. Experimental validation of predicted drug pair interactions by checkerboard assay revealed concentration shifts upon inclusion of both drugs that were consistent with the in silico prediction. INDIGO shows great promise for efficiently selecting novel TB drug regimens by prioritizing combinations based on extent of synergy or antagonism.

### Host-pathogen co-evolution through HIV-1 whole genome analysis

Somdatta Sinha, *Professor*, Maths/UBC/Vancouver/Canada & IISER Mohali/India

Host-pathogen interactions underlie one of the most complex evolutionary phenomena resulting in continual adaptive genetic changes, where pathogens exploit the host's molecular resources for growth and survival, while hosts try to eliminate the pathogen. Deciphering the molecular basis of host–pathogen interactions is useful in understanding the factors governing pathogen evolution and disease propagation. We considered the Human Immunodeficiency Virus (HIV) type 1 and its human host to search for evolutionary signatures in the viral genome. In this study, we analyze the codon usage patterns of HIV-1 genomes across all subtypes and clades sequenced over a period of 23 years. We show presence of unique temporal correlations in the codon bias of three HIV-1 genes illustrating differential adaptation of the HIV-1 genes towards the host preferred codons. Our results point towards gene-specific translational selection to be an important force driving the evolution of HIV- 1 at the population level.

### Geographic variation in mycobacterial genotypes and tuberculosis disease

Kirsten Wiens, *Postdoctoral Fellow*, Institute for Health Metrics and Evaluation, University of Washington

The host and microbial factors that contribute to variation in tuberculosis (TB) disease are complex and incompletely understood. Recent evidence suggests that one driver of variation in TB is the local ecology of mycobacterial genotypes or strains. This presentation will focus on a project to 1) map the global distribution and virulence of mycobacterial strains that cause TB disease, and 2) test whether geographic strain variation can be used to improve global models of TB incidence, prevalence, and mortality.

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| **1:30-2:30**<br>*Auditorium* | **Geneneral Session 4; Models 2**<br>*Chair: Niket Thakkar, IDM*<br>Jaline Gerardin, *IDM*<br>Britta Jewell, *UC Berkeley* |

### A road to malaria elimination in Zambia

Jaline Gerardin, *Senior Research Manager*, Institute for Disease Modeling

What types of operations are effective at achieving malaria elimination in African settings? How do programmatic needs differ based on local conditions such as pre-elimination transmission intensity, population density, and importation rate? We develop a household-level model to characterize fine spatial scales of transmission and intervention coverage and use that model to devise a stratification framework to guide elimination strategies.

### Modeling HIV in the SEARCH trial using EMOD

Britta Jewell, *Postdoctoral Fellow*, UC Berkeley

I will discuss my experience as an “embedded modeler” within the SEARCH trial. I plan to present results from my modeling work with SEARCH (predicting trial results) as well as some trial-specific analytical projects on PrEP implementation.

# Symposium Excursion

**IDM hosted tour at the Museum of Flight and dinner**

Please join us for the IDM hosted Symposium excursion and dinner. This year's excursion will be at Seattle's exclusive Museum of Flight. Guests will get to experience the wonder of aeronautics; enjoying over 175 aircraft and spacecrafts plus countless artifacts and photographs. Climb aboard a retired Concord jet, test your piloting skills in a flight simulator, and peruse the flying oval office that served Eisenhower, Kennedy, Johnson and Nixon. Guests will also have private access after museum hours to the Apollo exhibit with optional guided docent tours.

The fun doesn't end there! Join us for IDM's hosted reception and dinner catered by McCormick and Schmick's in the museum's main gallery. Guests will dine on a varied menu of fresh, seasonal, northwest ingredients. Transportation will be provided by IDM.

Dress is business casual.

**Schedule of Events**

**2:00:** Buses depart from the Hyatt Regency Lobby

**3:00:** Arrive at Museum of Flight

**3:00-5:00:** Enjoy the Museum of Flight

**5:00:** Reception and Hors d'oeuvres

**6:00-9:00:** Dinner

**7:45:** First bus departs back to Hyatt

**8:30:** Second bus departs back to Hyatt

**9:15:** Last bus departs back to Hyatt

## Day 3 Overview

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| **7:30-8:45** | Registration & Breakfast<br>*Auditorium Foyer, Olympic Tower* |
| **9:00-10:30**<br>*Auditorium* | **General Session 5; Epidemiological Databases & Modeling Toolsets**<br>Peter Diggle, *Lancaster University*<br>Benoit Raybaud, *IDM*<br>Dan Klein, *BMGF*<br>Wilbert Van Panhuis, *U of Pittsburgh* |
| **10:30-11:00** | Break |
| **11:00-1:00**<br>*Auditorium* | **Small Area Estimation in Public Health and Demography**<br>Monica Alexander, *UC Berkeley*<br>Laura Dwyer-Lindgren, *IHME*<br>Jon Wakefield, *UW*<br>Katie Wilson, *UW* |
| **11:00-1:00**<br>*Juniper* | **Access, Treatment, and All-Cause Mortality**<br>Patrick Munywoki, *CDC Kenya*<br>Assaf Oron, *IDM*<br>Travis Porco, *UC San Francisco*<br>Bobby Reiner, *IHME*<br>Abraham Flaxman, *IHME*<br>Laura Lamberti, *BMGF* |
| **11:00-1:00**<br>*Larch* | **TB Population Level**<br>Mike Osberg, *Linksbridge*<br>Per Liljenberg, *BMGF*<br>Cliff Kerr, *Burnet Institute*<br>Romesh Abeysuriya, *Burnet Institute*<br>Sarah Metzger, *BMGF*<br>Adrienne Shapiro, *UW*<br>Jennifer Ross, *UW* |
| **11:00-1:00**<br>*Laurel* | **Measles**<br>Allison Portnoy, *Harvard TH Chan School of Public Health*<br>Laura Sampson, *Penn State University*<br>Niket Thakkar, *IDM*<br>Anne Rimoin, *UCLA* |
| **12:15-1:30** | Lunch Buffet at Eques Restaurant (*2nd Floor Lobby)* |
| **1:30-3:30**<br>*Auditorium* | **Panel Discussion**<br>Ruanne Barnabas, *UW*<br>Tom Smith, *Swiss TPH*<br>Stephane Vouillamoz, *Novel-T*<br>Adrienne Shapiro, *UW*<br>Sahar Zangenah, *Fred Hutch* |
| **3:30-4:30**<br>*Auditorium* | **Software Open Forum**<br>Gene Oates, *IDM* |

## Sessions

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| **9:00-10:30**<br>*Auditorium* | **General Session 5; Epidemiological Databases & Modeling Toolsets**<br>*Chair: Christopher Lorton, IDM*<br>Peter Diggle, *Lancaster University*<br>Benoit Raybaud, *IDM*<br>Dan Klein, *Bill & Melinda Gates Foundation*<br>Wilbert Van Panhuis, *U of Pittsburgh* |

### A tale of two parasites: Statistical modelling to support LF control in Africa

Peter Diggle, *Professor*, CHICAS, Lancaster University, UK

A key strategy for LF control is mass distribution of ivermectin in high-prevalence areas. A potential obstacle is that in areas co-endemic for LF and Loa loa, people who have high levels of Loa loa infection are at risk of serious adverse reaction to ivermectin. I will describe how statistical modelling can be used to map Loa loa prevalence and to identify high-risk communities.

### DTK tools and BHM

Benoit Raybaud, *Research Software Engineering Manager,* Institute for Disease Modeling
Dan Klein, *Senior Program Officer,* Bill & Melinda Gates Foundation

Presentation of the dtk-tools framework intended to strengthen and simplify the interaction between researchers and the EMOD model.

### Project Tycho: Improving data access for epidemic modeling in global health

Wilbert Van Panhuis, *Assistant Professor of Epidemiology and Biomedical Informatics*, University of Pittsburgh

Epidemics are a constant threat to global health, but limited data access and inefficient data systems challenge progress in epidemic prevention and control strategies. We have represented over a century of infectious disease data for the US and decades of data for dengue-related conditions for other countries in a standard format, and have made all data publicly available through the Project Tycho repository. We recently released Project Tycho 2.0 that aims to improve compliance with FAIR (Findable, Accessible, Interoperable, Reusable) guiding principles for data management in global health. We will present advanced data standardization, machine-interpretable metadata, and improved discoverability for global health data through Project Tycho.

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| **11:00-1:00**<br>*Auditorium* | **Small Area Estimation in Public Health and Demography**<br>*Chair: Laina Mercer, IDM*<br>Monica Alexander, *UC Berkeley*<br>Laura Dwyer-Lindgren, *Institute for Health Metrics and Evaluation*<br>Jon Wakefield, *UW*<br>Katie Wilson, *UW* |

### A Bayesian hierarchical model to estimate subnational populations of women of reproductive age

Monica Alexander, *PhD Candidate*, Demography, UC Berkeley

Accurate estimates of subnational-level populations are important for policy formulation and monitoring key population health indicators. However, in many developing countries, data on population counts are limited and are of poor quality, and so levels are unclear. We present a Bayesian hierarchical model to estimate female populations at the subnational level. The model incorporates available data on population counts, builds on characteristic mortality schedules and estimates migration patterns to obtain robust population estimates, projections and uncertainty levels.

### The local burden of HIV: Estimating subnational HIV prevalence in Africa

Laura Dwyer-Lindgren, *Assistant Professor*, Global Health,
Institute for Health Metrics and Evaluation, University of Washington

Despite recent successes, HIV/AIDS remains a major cause of death and ill health throughout much of sub-Saharan Africa. Subnational, local information on HIV/AIDS is increasingly necessary in order to effectively target interventions and track progress. This talk will discuss using Bayesian geostatistical methods to estimate HIV prevalence at a 5x5-km resolution in sub-Saharan Africa.

### Small-area estimation using complex survey data

Jon Wakefield, *Professor*, University of Washington

I will describe how data from complex surveys can be used for small-area estimation when combined with space-time smoothing models. I will give an overview of area- and point-based approaches, and give examples in the context of under-5 mortality. Combining different types of data (full birth history, summary birth history, censuses) will also be discussed.

### Child mortality estimation incorporating summary birth history data

Katie Wilson, *Graduate Student,* University of Washington

Reducing the number of deaths in children under five remains a key public health issue. Child mortality tends to be concentrated in developing regions where much of the information needed to assess achievement of this goal comes from surveys, such as the Demographic and Health Survey or Multiple Indicator Cluster Survey, or from census. In the surveys, mothers are asked about their birth histories with varying degrees of detail. We describe an approach that can be used to accommodate summary birth history data, which contains only the total number of children born and total number of children who died for each mother.

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| **11:00-1:00**<br>*Juniper* | **Access, Treatment, and All-Cause Mortality**<br>*Chair: Hao Hu, IDM*<br>Patrick Munywoki, *CDC Kenya*<br>Assaf Oron, *IDM*<br>Travis Porco, *UC San Francisco*<br>Bobby Reiner, *Institute for Health Metrics and Evaluation*<br>Abraham Flaxman, *Institute for Health Metrics and Evaluation*<br>Laura Lamberti, *Bill & Melinda Gates Foundation* |

### Evaluation of the health impact of an innovative aerial distribution system for safe drinking water in Kibera Informal settlement, Kenya

Patrick Munywoki, *Public Health Epidemiologist*, CDC Kenya

The focus will be on spatiotemporal analysis of the incidence of diarrheal diseases in relation to Skywater use and coverage in Kibera Informal Settlement in Nairobi, Kenya. The data arise from a population-based infectious disease surveillance (PBIDS) system which has been ongoing since 2006 to date.

### Scenarios and strategies for overall childhood mortality reduction: An emerging IDM activity

Assaf Oron, *Senior Research Scientist,* Institute for Disease Modeling

Moving beyond IDM's traditional focus on modeling individual diseases or a group of closely related disease, we have recently begun to address questions related to overall childhood mortality reduction.
I will describe these emerging efforts and ideas for future progress.
Discussion and insight from the audience will be welcome.
Work with Dennis Chao and Hao Hu.

### Mass administration of azithromycin: Challenges and the road ahead

Travis Porco, *Professor*, UCSF

Are potential benefits of mass azithromycin in select settings (such as rural Ethiopia) offset by selection for drug resistance? We will review available evidence, both empirical and from mathematical modeling studies.

### Local variation in childhood lower respiratory infection morbidity and mortality in Africa, 2000-2016

Bobby Reiner, *Assistant Professor,* Institute for Health Metrics and Evaluation

More than 327,000 children were estimated to have died from lower respiratory infections (LRIs) in Africa in 2016, ranking second only to malaria on the continent. Though these largely avertable deaths are substantial, this represents a 64% decline from the 507,000 children who died due to LRI in 2000. The rate of this decline, as well as the current burden of LRI, vary considerably across Africa, both between and within countries. Previous efforts to understand the spatiotemporal burden of LRIs lacked either spatial breath or fine spatial resolution. Here, we present the first yearly estimates of LRI prevalence, severe incidence, and mortality at a 5km2 resolution across Africa from 2000 and 2016.

### Planning strategic health interventions from Global Burden of Disease estimates

Abraham Flaxman, *Associate Professor,* Institute for Health Metrics and Evaluation

The Global Burden of Disease Study quantifies health loss from hundreds of diseases, injuries, and risk factors, so that health systems can be improved and disparities can be eliminated. But moving from identifying the problems to planning the solutions requires strategic analytics beyond the descriptive epidemiologic toolset GBD currently employs. This presentation will demonstrate some of our initial work in using GBD estimates to answer “what if” questions about national policies to reduce child mortality rates. A benefit of doing this based on the GBD is that it is straightforward to expand to other diseases, age group, and locations.

### Evolving trends in U5MR and strategies for addressing residual mortality

Laura Lamberti, *Program Officer,* Bill & Melinda Gates Foundation

This session will focus on global and regional trends in mortality among children under-five over the past 15 years.In particular, the evolving epidemiology and shifting composition of residual mortality will be highlighted. Strategies to address residual mortality will also be discussed.

**11:00-1:00** **TB Population Level**
*Larch*
*Chair: Brad Wagner, IDM*
Mike Osberg, *Linksbridge*
Per Liljenberg, *Bill & Melinda Gates Foundation*
Cliff Kerr, *Burnet Institute*
Romesh Abeysuriya, *Burnet Institute*
Sarah Metzger, *Bill & Melinda Gates Foundation*
Adrienne Shapiro, *UW*
Jennifer Ross, *UW*

### Patient pathway analysis for better understanding the misalignment between service delivery and patient preferences

Mike Osberg, *Senior Associate,* Linksbridge

The methods for developing patient pathways from population-based datasets will be described. Results from six countries and their programmatic implications will be discussed.

### Optimizing a portfolio of tuberculosis investments to reach strategic goals

Per Liljenberg, *Senior Program Officer,*
Bill & Melinda Gates Foundation

The Bill & Melinda Gates Foundation are funding investments in research and development of new interventions as well as improving delivery of existing interventions. Program Strategy Teams aim to achieve strategic goals for each disease by balancing investments of different types of new and existing interventions such as drugs, vaccines, or diagnostics, as well as by investing in different delivery interventions. We will present the outcomes of optimizing portfolio investments for tuberculosis in South Africa and India, including the impact these have on disease dynamics and health outcomes and the resources required to reach a given set of strategic goals.

### Determining optimal tuberculosis investments in the presence of uncertainties

Cliff Kerr, *Senior Research Associate*, Burnet Institute
Romesh Abeysuriya, *Senior Research Officer*, Burnet Institute

One of the major limitations in determining optimal resource allocations is the presence of uncertainties and missing data. These challenges are compounded when evaluating interventions that are either new or not implemented to scale in a given context. Here we present a method, an extension of the Optima TB model, for determining optimal resource allocations to improve tuberculosis-related health outcomes in South Africa and India. We focus on the issue of uncertainties and how these impact both model projections and the choice of strategic goals.

### Integrated Portfolio Management Valuation: A tool to support decision making, strategic thinking, and resource allocation

Sarah Metzger, *Program Officer*, Bill & Melinda Gates Foundation

Large organizations such as the Bill & Melinda Gates Foundation (BMGF) are forced to make trade-off decisions across investments and priorities to maximize impact. Launched in fall 2013, the Integrated Portfolio Management (IPM) program is a strategic initiative to support data-driven decisions regarding the prioritization and allocation of resources across the BMGF Global Health and Global Development product portfolios. In this talk, we will explore the systematic approach used to estimate and compare the cost-effectiveness, impact, and risks of different interventions at BMGF.

### New approaches to TB detection and prevention in people with HIV

Adrienne Shapiro, *Senior Fellow*, University of Washington

TB preventive therapy can prevent TB disease and reduce mortality in persons with HIV. Despite international and national guidelines recommending its use, less than 40% of HIV-infected persons in South Africa receive preventive therapy. This presentation will describe two interventions targeting two stages of the TB Care Cascade to improve uptake of TB preventive therapy.

### Small area estimation of TB and HIV deaths in Brazil, 2001-2015

Jennifer Ross, *Acting Instructor/Senior Fellow,* UW Division of Allergy and Infectious Diseases and Institute for Health Metrics and Evaluation

Brazil is a high-burden country for TB and HIV-TB co-infection that is also characterized by high levels of inequality in social and health indicators. However, TB and HIV deaths counts are low in individual geographic areas, leading to difficulty in separating true geographic differences in risk from stochastic noise. Addressing this challenge, we modeled TB and HIV mortality at the level of the administrative municipality (n=5477) using a small area estimation approach and comprehensive cause of death assignment from the Global Burden of Disease Study. We also evaluated relationships between social and health indicators and the outcomes of TB and HIV mortality.

**11:00-1:00** *Laurel*

**Measles**
*Chair: Kevin McCarthy, IDM*
Allison Portnoy, *Harvard TH Chan School of Public Health*
Niket Thakkar, *IDM*
Laura Sampson, *Penn State University*
Anne Rimoin, *UCLA*

### Considerations for measles control impact

Allison Portnoy, *Doctoral Candidate*, Harvard T.H. Chan School of Public Health

There is continued uncertainty about the current burden of measles and the impact of measles vaccination. Determining who is reached by supplementary immunization activities (SIAs) is vital to understanding their effectiveness, as well as measure progress towards measles control. Additionally, the assessment of the measles mortality burden is highly dependent on estimates of measles case fatality ratios (CFRs), which vary according to geography, health systems infrastructure, prevalence of underlying risk factors, and measles endemicity. The objective of this study is to conduct a systematic review of measles CFRs for both community-based and hospital-based cases and to develop a predictive model to estimate measles CFRs across heterogeneous groupings. We also examine the degree to which current SIA outreach efforts have proven to be effective. By developing estimates of measles CFRs and providing information on the proportion of zero-dose children reached by SIAs, we can provide improved inputs for future economic analyses.

### Age-specific patterns in lab confirmation of measles cases

Laura Sampson, *Postdoctoral Scholar*, Penn State University

Syndromic surveillance systems tasked with documenting cases are understandably designed to be sensitive, but are also unavoidably imprecise, which presents challenges in the evaluation of vaccination program performance. The febrile rash surveillance system that is the primary source of spatio-temporal data on measles incidence reflects, in practice, a mixture of both true measles cases, which should be impacted by measles vaccination efforts, and other infections (e.g. rubella) that should not be affected by measles vaccination efforts. Laboratory confirmation, through IgM serology, provides a highly specific indicator that is expected to change as a function of vaccination coverage. We show that the age-specific IgM confirmation rate is a reliable indicator of program performance and further illustrate that it is more robust to realistic biased reporting rates than both incidence and mean-age of case as indicators of vaccination program performance.

### Estimating and optimizing measles vaccination campaign efficacy

Niket Thakkar, *Research Scientist,* IDM

Measles vaccination is already recognized as one of the most successful public health interventions ever undertaken; however, vaccine distribution remains a challenge in high-burden settings. In many of these contexts, mass vaccination campaigns (SIAs) are the primary vaccine distribution method, raising key policy questions related to optimizing campaign timing, setting sub-national prioritization, and estimating SIA performance in retrospect. Answering these questions will require novel approaches, and in this talk, I'll describe recent progress on mechanistic and statistical modeling efforts for optimizing future SIAs and inferring the efficacy of past campaigns.

**1:30-3:30** **Panel Discussion**
*Auditorium* *Chair: Mandy Izzo, IDM*
Ruanne Barnabas, *UW*
Tom Smith, *Swiss TPH*
Stephane Vouillamoz, *Novel-T*
Adrienne Shapiro, *UW*
Sahar Zangenah, *Fred Hutchinson Cancer Research*

Join us for an engaging panel discussion focusing on novel methods for estimating, reaching, and treating missing populations in public health.

**3:30-4:30** **Software Open Forum**
*Auditorium* Gene Oates, *IDM*

The Software Open Forum is an opportunity to meet the IDM software team and discuss the various tools created for internal and external researchers. The forum seeks to create an open and collaborative environment for all software related topics, including future collaboration opportunities, software development and training. Software team members from the various project groups will be available for these discussions.

# Biographies

**David Aanensen**
**Director, Centre for Genomic Pathogen Surveillance**
**Wellcome Sanger Institute**
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David is Director of The Centre for Genomic Pathogen Surveillance (CGPS) at the Wellcome Genome Campus and Senior group leader at the Oxford Big Data Institute. CGPS aims to understand the distribution and spread of high-risk clones of pathogens through large-scale contextual surveys, whole genome sequencing (WGS), and the provision of data for decision making through the use of web applications and statistical and data analytic methods. Within the NIHR Global Health Research Unit of Genomic Surveillance of Antimicrobial Resistance, his team are enhancing local capacity for WGS at sites in The Phillipines, India, Colombia and Nigeria to enhance local, national, and international surveillance of priority AMR pathogens.

**Romesh Abeysuriya**
**Senior Research Office**
**Burnet Institute**
**romesh.abey@gmail.com**

Romesh Abeysuriya is a Senior Research Officer at the Burnet Institute in Melbourne, Australia. Romesh holds a PhD in Physics from the University of Sydney, where he worked on models of resting state neural activity. After working on development for the Optima HIV project, he completed his postdoctoral training at the Oxford Centre for Human Brain Activity, using dynamical systems approaches to simulate neural activity in network models. His work in epidemiology now applies these same approaches to population models of TB and HCV.

**Monica Alexander**
**PhD Candidate, Demography**
**UC Berkeley**
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Monica Alexander is a PhD candidate in demography at UC Berkeley. Her research interests include statistical demography and health and mortality inequalities. She has Master's degrees in Statistics (from Berkeley) and Social Research (from the Australian National University). She has worked on global health and demographic research with organizations such as UNICEF, the World Health Organization, and the Human Mortality Database.

**Ruanne Barnabas**
**Assistant Professor**
**University of Washington**
**rbarnaba@uw.edu**

Dr. Barnabas is an Assistant Professor in Global Health and Medicine at the University of Washington and affiliate at the Fred Hutchinson Cancer Research Center. Her research focuses on interventions for HIV treatment and prevention, specifically on community-based strategies to increase access to antiretroviral therapy (ART) for HIV. She is the protocol chair of the Delivery Optimization for ART Study, which will evaluate the effectiveness and cost-effectiveness of decentralized, community-based ART initiation and follow-up compared to clinic-based care. She leads the cost-effectiveness evaluation of other projects, including: 1) partner services for clients with sexually transmitted infections in Seattle, 2) cervical cancer screening among HIV-positive women in the US and in low and middle income countries, 3) scale-up of PrEP delivery in Africa, and 4) lottery incentives to increase the coverage of ART among men (for which she serves as the protocol co-chair). Her projects use empiric data, costs, and mathematical models to estimate the potential impact of HIV interventions.

**Trevor Bedford**
**Associate Member**
**Fred Hutchinson Cancer Research**
**trevor@bedford.io**

Dr. Trevor Bedford is an Associate Member in the Vaccine and Infectious Disease Division at the Fred Hutchinson Cancer Research Center. Dr. Bedford's research integrates population genetics, phylogenetics and epidemiological modeling to understand virus evolution and transmission patterns. He works across a variety of viral systems including influenza, Ebola, Zika, dengue, mumps virus, and MERS-CoV. Recently, he has lead "real-time" approaches to dissemination of results in an open, online fashion in an effort to make analyses actionable by public health entities.

**Anna Bershteyn**
**Senior Research Manager**
**Institute for Disease Modeling**
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Anna Bershteyn is a Senior Research Manager of the HIV/TB center at the Institute for Disease Modeling, and an Affiliate Assistant Professor of Global Health at the University of Washington. She has a PhD in Materials Science and Engineering from the Massachusetts Institute of Technology (MIT), where she studied lipid self-assembly at nanoparticle surfaces as a biomimetic approach to vaccine development. Her modeling research focuses on HIV transmission dynamics and impact evaluation of biomedical and programmatic improvements to HIV care and prevention.

**Amelia Bertozzi-Villa**
**Postgraduate Research Scientist**
**Institute for Disease Modeling**
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Amelia is a Postgraduate Research Scientist at IDM focused on malaria dynamics in Southeast Asia. She is also guest faculty at the University of Washington Information School.

**Carol Camlin**
**Associate Professor In Residence**
**University of California, San Francisco**
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Carol Camlin, PhD MPH, is Associate Professor in Residence in the UCSF Department of Obstetrics, Gynecology and Reproductive Sciences and affiliated with the UCSF Bixby Center for Global Reproductive Health and Center for AIDS Prevention Studies. Her research crosses the disciplines of social demography, sociology, and public health, and focuses on gender, HIV, and population mobility. She is Principal Investigator of a 5-year study to examine the impact of mobility on HIV transmission dynamics and care cascade outcomes in communities participating in the Sustainable East Africa Research in Community Health (SEARCH) trial. She also uses mixed methods approaches and behavioral and social theory to inform HIV intervention and implementation studies in health systems and communities in sub-Saharan Africa, as Investigator of several other randomized controlled trials in the region.

**Guillaume Chabot-Couture**
**Director of Global Development Research**
**Institute for Disease Modeling**
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Guillaume Chabot-Couture is research coordinator for the analysis and model usage center. His work focuses on polio eradication, measles elimination, and the value of disease surveillance and of monitoring and evaluation efforts.

**Stewart Chang**
**Research Scientist**
**Institute for Disease Modeling**
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Stewart Chang received his PhD in Bioinformatics from the University of Michigan and did postdoctoral research at the University of British Columbia and the University of Washington before coming to IDM in 2012. His research interests are in geospatial analysis of tuberculosis data and models of the immune response to tuberculosis.

**James Chirombo**
**PhD student**
**Lancaster University/ Malawi Liverpool Wellcome Trust Clinical Research Programme**
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James Chirombo a PhD student at Lancaster University in the Centre for Health Informatics, Computing and Statistics (CHICAS) supervised by Dr. Jonathan Read, Professor Peter Diggle and Dr. Diane Terlouw. For his PhD, he is working on modelling spatial processes of infectious disease transmission. A key component is in understanding how human commuting and travel behaviour generate patterns of mobility and incorporate this information to understand the spread of infectious diseases. He is also working on modelling climatic impacts on climate-sensitive diseases such as malaria in order to help in designing effective control interventions.

**Miles Davenport**
**Professor and Head, Infection Analytics Program**
**Kirby Institute, UNSW Australia**
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Professor Miles Davenport is Head of the Infection Analytics Program at the Kirby Institute, in Sydney Australia. His background is as an MD-PhD (MB BS, D.Phil), and he now directs an interdisciplinary team applying mathematical and computational approaches to understand infection dynamics. His research focus is on understanding and modeling host-pathogen interactions in chronic infections like HIV, and malaria, and in neonatal infection. He has a wide variety of experimental collaborations both within Australia and overseas, which aim to combine theory and modeling to better understand experimental data. These projects range from bioinformatics approaches to understanding immune recognition and viral evolution, through to mathematical modeling of host-pathogen interactions in human and animal infection. Professor Davenport was President of the Australasian Society for Immunology in 2009-10, and is currently Section Editor at Journal of Immunology, and a member of the Editorial Board of Journal of Virology. He has published nearly 200 papers in infection and immunity.

**Peter Diggle**
**Professor**
**CHICAS, Lancaster University, UK**
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Peter Diggle is Distinguished University Professor of Statistics in the Faculty of Health and Medicine, Lancaster University. He also holds adjunct positions at Johns Hopkins, Yale, and Columbia Universities; and he was president of the Royal Statistical Society from July 2014 to December 2016. His research involves the development of statistical methods for spatial and longitudinal data analysis, motivated by applications in the biomedical, health, and environmental sciences.

**Gytis Dudas**
**Postdoctoral Fellow**
**Fred Hutchinson Cancer Research Center**
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Gytis Dudas is a postdoctoral fellow in Trevor Bedford's group at Fred Hutchinson Cancer Research. During his PhD with Andrew Rambaut at the University of Edinburgh he was fortunate enough to work with many groups deployed to West Africa during the 2013-2015 Ebola virus epidemic. He uses sequence data to understand epidemiological dynamics of RNA virus outbreaks through inference of population structure and flux of viral lineages between population compartments.

**Laura Dwyer-Lindgren**
**Assistant Professor, Global Health**
**Institute for Health Metrics and Evaluation**
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Laura Dwyer-Lindgren is an Assistant Professor at the Institute for Health Metrics and Evaluation at the University of Washington. Her research interests are small area estimation and geostatistical modeling methods, spatial patterns of health outcomes, and geographic health disparities. Her research is currently focused on mapping HIV prevalence, incidence, and mortality.

**Mike Famulare**
**Senior Research Scientist**
**Institute for Disease Modeling**
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Mike Famulare has a PhD in Physics from the University of Washington, Seattle, and a Bachelor of Science in Physics Education from New York University. His doctoral thesis was in Computational Neuroscience and focused on the mathematics and biophysics of single neuron information processing. Mike has a strong science education and community education focus and spent some time as a physics teacher at Stuyvesant High School in Manhattan, NYC. before turning to research. Mike's current research focuses on live polio vaccine transmission and genetic instability, polio immunity, molecular epidemiology, and transmission dynamics in heterogeneous populations.

**Alison Feder**
**Graduate Student**
**Stanford University**
**afeder@stanford.edu**

Alison Feder is a PhD student in Dmitri Petrov's lab in the Department of Biology at Stanford, where she has been supported by an NSF Graduate Research Fellowship, a Gerald J. Lieberman Fellowship and a CEHG Graduate Fellowship. She combines evolutionary theory with clinically- and experimentally-derived data to study the dynamics of intra-patient HIV drug resistance evolution through space and time. Alison holds an MSc (Res) in Statistics from the University of Oxford and a BA in Mathematics from the University of Pennsylvania.

**Abraham Flaxman**
**Associate Professor**
**Institute for Health Metrics and Evaluation**
**abie@uw.edu**

Abraham Flaxman, PhD, is Associate Professor of Global Health at the Institute for Health Metrics and Evaluation (IHME) at the University of Washington. He is currently leading the development of new methods for cost effective analysis with microsimulation and is engaged in methodological and operational research on verbal autopsy. Dr. Flaxman has previously designed software tools such as DisMod-MR that IHME uses to estimate the Global Burden of Disease, and the Bednet Stock-and-Flow Model, which has produced estimates of insecticide-treated net coverage in sub-Saharan Africa. This work uses Integrative Systems Modeling to combine a system dynamics model of process with a statistical model of data to bring together all available sources of information.

**Jennifer Flegg**
**Senior Lecturer**
**University of Melbourne**
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Dr. Jennifer Flegg is a Senior Lecturer in the School of Mathematics and Statistics at the University of Melbourne. In her research, she applies mathematics and statistics to biomedical problems in areas such as wound healing, tumour growth, and infectious diseases. Jennifer was awarded a PhD in 2009 from Queensland University of Technology in applied mathematics. From 2010 to 2013, she was at the University of Oxford developing statistical models for the spread of resistance to antimalarial drugs. From 2014 to April 2017, Jennifer was a Lecturer in the School of Mathematical Sciences at Monash University. In May 2017, she joined the School of Mathematics and Statistics at the University of Melbourne as a Senior Lecturer in Applied Mathematics.  She started an Australian Research Council Discovery Early Career Research Award in 2016 to study and mathematically model venous leg ulcers.

**Spencer Fox**
**PhD Student**
**University of Texas at Austin**
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Spencer Fox (@foxandtheflu) is a PhD student at the University of Texas at Austin under Dr. Lauren Ancel Meyers. His research focuses on statistical and computational methods for understanding emerging infectious disease dynamics. Apart from research he teaches data science techniques in R and runs a computational epidemiology blog (https://sjfox.github.io/).

**Jillian Gauld**
**Postgraduate Research Scientist**
**Institute for Disease Modeling**
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Jillian Gauld has a Master of Science in Population and Public Health from the University of British Columbia, along with a Bachelor of Science (Honours) in Biology from Queen's University. She received funding from the Canadian Institutes of Health Research for her master's thesis, which focused on the development of contact networks in the hospital setting, and modeling the transmission of respiratory pathogens between healthcare workers. Prior to joining IDM, Jillian was an environmental health scientist at the BC Centre for Disease Control in Vancouver, Canada. As a member of the IDM research team, Jillian is working on transmission network development and epidemiology to inform vaccination policies and control strategies for enteric and respiratory diseases.

**Jaline Gerardin**
**Senior Research Manager**
**Institute for Disease Modeling**
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Jaline Gerardin is a research manager on the malaria team at IDM. Her work has focused on the role of drug-based strategies in malaria elimination and how heterogeneity impacts intervention success.

**Brittany Hagedorn**
**Financial Analyst**
**Institute for Disease Modeling**
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Brittany Hagedorn is a financial analyst for the Institute for Disease Modeling. She collaborates with multiple disease teams to estimate the cost of proposed interventions and to assess their value in comparison to alternative strategies for disease control. Brittany is interested in questions around the value of information in helping policy makers design more cost-effective strategies, as well as the trade-offs between alternative intervention strategies under budgetary constraints. Prior to joining IDM, Brittany worked with North American healthcare delivery systems to optimize their workflows to improve safety and clinical outcomes while simultaneously reducing cost. She has also advised healthcare technology companies on product design and development. Brittany is an ASQ-certified Six Sigma Black Belt and holds a BS in Systems Engineering and Masters of Business Administration (MBA) from Washington University in St. Louis.

**Robert Hart**
**Vice President and General Manager**
**Institute for Disease Modeling**
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Robert S. Hart is the Vice President and General Manager of IDM, sponsored by Global Good at Intellectual Ventures. Robert has a PhD in Geophysics as well as a Master of Science degree in Geophysics from the California Institute of Technology (CalTech), and a Bachelor of Science degree in Earth and Planetary Sciences from the Massachusetts Institute of Technology (MIT). He has over thirty years of experience founding and managing high technology-based software firms as an executive officer and venture investor, as well as serving as a board director. He was most recently a founder and the CEO of Veratect Corporation, an open source data mining and analysis firm providing the earliest possible indicators of the emergence of infectious disease worldwide, but with a particular focus on the developing world. Prior to Veratect, highlights of Robert's career include tenure as the CEO of Corazonx, a cardiac ultrasound software firm; General Partner at Sea-Point Ventures, a venture capital firm focusing on the wireless telecom industry; CEO of Tegic Communications, the developer of the predictive text input software used in most cellular phones; CEO of Optimas Corporation, a digital image analysis firm; and founder and CEO of Sierra Geophysics, a leading provider of applications software to the global oil and gas industry. Robert currently serves on a number of corporate and non-profit boards.

**Hao Hu**
**Senior Research Manager**
**Institute for Disease Modeling**
**hhu@idmod.org**

Hao Hu leads the Epidemiology Section at the Institute for Disease Modeling (IDM). Currently, he is focused on modeling the persistence and elimination feasibilities of *S. Pneumoniae* and typhoid fever, understanding the transmission pathways of several enteric pathogens, exploring ways to reduce all-cause childhood mortality, and modeling the role of household structure and contact heterogeneities on disease transmission dynamics. His previous work at IDM included creating data-driven district-level polio outbreak risk maps in Nigeria and Pakistan, analyzing the spatial and temporal trends of the 2014 Ebola outbreak in West Africa, as well as modeling the transmission and persistence dynamics of polio.

**Mandy Izzo**
**Senior Science Writer**
**Institute for Disease Modeling**
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Mandy Izzo is the Senior Science Writer for the Institute for Disease Modeling, where she leverages her experience in research to contribute scientific content to web resources and facilitate communication both within IDM and with external collaborators. She is involved in outreach and training, and serves as a contact point at IDM to connect people with appropriate resources. She earned a BA in Integrative Biology from the University of California, Berkeley; an MS in Biology from California State University, Northridge; and a PhD in Ecology and Evolutionary Biology from the University of Michigan. Her training was furthered during postdoctoral positions at the University of California, Davis, first in the Department of Entomology and Nematology, and then in the Department of Fish, Wildlife, and Conservation Biology. She has over 11 years of field and lab experience in the biological sciences that include the design, oversight, execution, and analysis of projects.

**Mable Jerop**
**Monitoring, Evaluation and Research Officer**
**Amref Health Africa**
**Jeropmable@gmail.com**

Mable Jerop is a data scientist currently working with Amref Health Africa organization, which provides various health programmes to the most vulnerable communities in Africa. Mable has a professional background in statistics, with research interests on modelling of various health interventions for infectious diseases, which is a key element for health planning in low and middle income countries. She has contributed to various health projects and research funded through donor institutions including USAID, Global Fund, and Bill & Melinda Gates Foundation, covering seven countries in East and West Africa regions.

**Britta Jewell**
**Postdoctoral Fellow**
**UC Berkeley**
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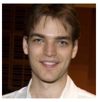
Britta Jewell is a postdoctoral fellow, joint between UC Berkeley, UCSF, and IDM. Her research focuses on modeling the SEARCH trial in Kenya and Uganda as well as understanding barriers to PrEP use. She holds a PhD in infectious disease epidemiology from Imperial College London, an MSc from the University of Oxford, and a BA from UC Berkeley where she studied European history and the history of medicine. Britta has spent the last 6 years in the fields of infectious disease epidemiology and mathematical modeling, and her PhD focused on optimizing the impact and cost-effectiveness of oral PrEP for serodiscordant couples in East Africa.



**Cliff Kerr**
**Senior Research Associate**
**Burnet Institute**
**ck@thekerrlab.com**

Cliff Kerr is a Senior Research Associate at the Burnet Institute in Melbourne, Australia, and a co-founder of the Optima Consortium for Decision Science, where he is the team leader for software and model development. He holds a Ph.D. in theoretical physics from the University of Sydney and completed his postdoctoral training at the State University of New York's Downstate Medical Center. In addition to his work on public health, he is currently leading both a computational neuroscience research group at the University of Sydney and a data analytics consulting firm.

**Dan Klein**
**Senior Program Officer**
**Bill & Melinda Gates Foundation**
**dan.klein@gatesfoundation.org**

Daniel J. Klein is an Interim Senior Program Officer in the Strategy, Data, and Analytics team within Global Development at the Bill and Melinda Gates Foundation. His research develops and applies machine learning techniques to challenges in global development to extract insights from a combination of new and classical data sources. At the end of 2018, Dan will be returning to the Institute for Disease Modeling (IDM), where he was a Senior Research Manager and Chair of the Applied Mathematics team. At IDM, he split time between HIV modeling and algorithm development for stochastic model optimization, calibration, and parameter space exploration. Dan earned Ph.D. and M.S. degrees in control theory from the Aeronautics and Astronautics department at the University of Washington, and a B.S. degree with Honors in Mechanical Engineering from the University of Wisconsin, Madison. He also enjoyed the sunshine of Santa Barbara, CA as a postdoctoral scholar with the Center for Control and Dynamical Systems in the Electrical and Computer Engineering department at UCSB.

**Alicia Kraay**
**Postdoctoral Fellow**
**University of Michigan**
**amullis@umich.edu**

Alicia Kraay is a postdoctoral fellow at University of Michigan. She has a strong interest in infectious disease epidemiology, with a deeper focus on both waterborne and vector-borne pathogens. She is particularly interested in the mechanisms of spatial spread in epidemics and how these patterns may be modified by climate factors and other circulating pathogens. She uses both regression and mathematical simulation modelling approaches to help answer these questions.

**Laura Lamberti**
**Program Officer**
**Bill & Melinda Gates Foundation**
**laura.lamberti@gatesfoundation.org**

Dr. Laura Lamberti leads the Strategic Data Analytics & Synthesis initiative of the Bill & Melinda Gates Foundation's Maternal, Newborn and Child Health Discovery & Tools (MNCH D&T) team. Laura is an epidemiologist with experience in child health in low- and middle-income countries. Prior to the Gates Foundation, Laura was an Assistant Scientist in the Department of International Health at the Johns Hopkins Bloomberg School of Public Health where she focused on statistical analysis and modelling of child health interventions, risk factors and global burden of all-cause and pathogen-specific mortality. She was also co-primary investigator on a large-scale effectiveness evaluation of pediatric diarrhea treatment in Bihar, Uttar Pradesh and Gujarat, India. Laura holds a PhD and Master of Health Science (MHS) in Global Disease Epidemiology and Control from the Johns Hopkins Bloomberg School of Public Health and a Bachelor of Science (BS) in Biomedical Engineering from Columbia University.

**Myron Levine**
**Associate Dean for Global Health, Vaccinology & Infectious Diseases**
**University of Maryland, School of Medicine**
**mlevine@som.umaryland.edu**

Myron Levine has worked on infectious disease research since 1970. He co-founded the Center for Vaccine Development in 1974 and was Director until December 2014. Throughout his career Dr. Levine has spent considerable time in developing countries working on the epidemiology, treatment, and prevention of infectious diseases and he applies this field experience toward studies of the pathogenesis of such infections and the development and testing of vaccines. Dr. Levine has 47 years of continual involvement in conducting Phase 1, 2, 3, and 4 clinical trials to evaluate the safety, immunogenicity, and efficacy of a wide array of vaccines. Besides serving as a clinician in vaccine testing (for both adults and children) and designing and supervising epidemiologic studies (conducted in the U.S. and abroad), he spends time supervising research activities in the laboratory. These projects focus on the construction and characterization of attenuated *Salmonella Typhi, S. Paratyphi A*, and *Shigella* to serve as live oral vaccines. Dr. Levine has long experience studying the epidemiology of typhoid fever and helped establish the Typhoid Fever Control Program of the Ministry of Health of Chile, which succeeded in interrupting transmission of *S. Typhi* in Santiago, Chile. He has carried out large-scale field trials of Ty21a vaccine in ~495,000 Chilean schoolchildren in four randomized controlled trials. Dr. Levine is board-certified in Pediatrics and Preventive Medicine and also trained in tropical public health. He is author or co-author of 645 peer review publications and a member of the National Academy of Medicine and its Board of Global Health.

**Per Liljenberg**
**Senior Program Officer**
**Bill & Melinda Gates Foundation**
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Per Liljenberg is currently leading the Integrated Portfolio Management Team, advancing portfolio management practices within the Global Heath division at the Bill & Melinda Gates Foundation. Prior to joining BMGF, as a Business Operations Director at AstraZeneca, he was running the governance body managing the portfolio of research projects in the area of Respiratory, Inflammation and Autoimmunity. Per is a theoretical physicist by training and has a MSc from Imperial College and PhD from Chalmers University of Technology, Sweden.

**Qinghua Long**
**Research Software Engineer**
**Institute for Disease Modeling**
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Qinghua has a MS in Public Administration from Illinois Institute of Technology and BS in Science Engineering from Queen Mary, University of London. Qinghua has experience with web applications such as a prosecution system that recorded hunting violations, citation information and fine amount. As part of IDM's team Qinghua will be designing and querying large data for climate, demographic and transportation as inputs for IDM's modeling software as well as conducting data reduction and analysis of simulations reports, and designing and implementing usability testing for enhanced user experience.

**Ben Lopman**
**Associate Professor**
**Emory University**
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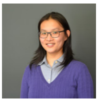
Ben Lopman, PhD, is Associate Professor of Epidemiology at the Emory University Rollins School of Public Health.  Previously, he worked for seven years with the Division of Viral Diseases at CDC.  His work focuses on the epidemiology of enteric viruses and their control using vaccination.

**Christopher Lorton**
**Managing Principal Software Engineer**
**Institute for Disease Modeling**
**clorton@idmod.org**

Christopher Lorton has a Master of Science in Computer Science from Washington University, St. Louis, where he also obtained a Bachelor of Science in Physics. His master's thesis focused on the parallel computation of neural networks (NN) for the recognition of handwritten characters. Christopher's past work includes machine vision systems, digital media processing, cross-platform managed code runtime development, and the accelerated rendering of graphical user interfaces (GUI). Christopher's current responsibilities as a development lead include heading up the team responsible for IDM's compartmental and agent-based modeling engines and the team responsible for IDM's data repositories.

**Hil Lyons**
**Research Manager**
**Institute for Disease Modeling**
**hlyons@idmod.org**

Hil Lyons has a PhD in Statistics, as well as a Master of Science degree in Statistics, and a Bachelor of Science in Mathematics, from the University of Washington, Seattle. Hil's research has included the stochastic modeling of the growth and death processes in tree stand data, as well as spatial point processes and applications of applied statistics. He has also worked extensively as a statistical consultant for a variety of academic research groups and departments, including a position as Assistant Director of the Department of Statistics consulting center at the University of Washington. As a result, he has expertise with a wide variety of modeling and applied statistics topics and methods. Within IDM, Hil's work is focused on polio eradication efforts, where he provides statistical modeling, analysis, and interpretation of diverse data for robust and timely decision support.

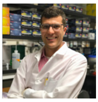


**Shuyi Ma**
**Postdoctoral Scientist**
**Center for Infectious Disease Research**
**shuyi.ma@cidresearch.org**

Shuyi Ma works at the interface of computational and experimental systems biology, combining these approaches to drive discovery. She did her graduate work with Nathan Price at the University of Illinois and the Institute for Systems Biology, where she harnessed statistical machine learning tools to identify transcriptome-based biomarkers that could diagnose multiple lung diseases, and modeled genome-scale metabolism and transcriptional regulation in the lung pathogen, Mycobacterium tuberculosis (MTB), which kills 1.8 million people each year. As a postdoctoral scientist with David Sherman at the Center for Infectious Disease Research, she has integrated novel omics-based experimental strategies with modeling approaches to reveal how MTB responds to drugs acting individually and in combination, in order to inform therapy design.

**Kevin McCarthy**
**Research Manager**
**Institute for Disease Modeling**
**kmccarthy@idmod.org**

Kevin McCarthy is the Research Manager for the measles research team at the Institute for Disease Modeling. Kevin has a PhD in Physics from the Massachusetts Institute of Technology as well as a Bachelor degree in both Physics and Electrical Engineering from the University of California, San Diego. His research focus is on optimizing burden control activities and helping to clarify critical vaccination policy decisions relevant to achieving and maintaining measles eradication. Kevin joined the Institute in 2013, and before leading the measles effort, he worked on both malaria and polio. As a member of the polio team, Kevin developed methods to calibrate a spatio-temporal polio model investigating the dynamics of eradication in northern Nigeria, the potential risk of accidental or intentional oral polio vaccine use after synchronized cessation, and the consequences of localized inaccessibility for surveillance and vaccination activities. In malaria, he worked on calibration of the IDM intra-host malaria model and malaria vaccine efficacy studies. These calibrated models can be used to evaluate the expected efficacy of potential intervention campaigns and provide decision support to global health policymakers. Prior to IDM, Kevin's research focused on astrophysics and particle physics, and his doctoral research was performed as a member of the Cryogenic Dark Matter Search collaboration.



**John McCrone**
**Postdoctoral Researcher**
**Department of Microbiology and Immunology,**
**University of Michigan**
**mccrone@umich.edu**

JT McCrone is a recent graduate from the the department of Microbiology and Immunology at the University of Michigan. He is broadly interested understanding the forces that shape the evolutionary trajectories of human pathogens, in particular viruses. His dissertation work has combined deep sequencing and population genetics to explore the role of stochastic processes in influenza evolution within individuals during acute infections and between individuals during transmission.

**Graham Medley**
**Professor of Infectious Disease Modelling**
**London School of Hygiene & Tropical Medicine**
**graham.medley@lshtm.ac.uk**

Graham Medley is Professor of Infectious Disease Modelling at the London School of Hygiene and Tropical Medicine. He is working on neglected tropical diseases as part of the NTD Modelling Consortium (leprosy, schistosomiasis) and SPEAK India (visceral leishmaniasis) and a separate project on diagnostics for soil-transmitted helminths. He is also modelling the social processes involved in HIV transmission. Graham's first degree was in Biology and Computer Science (University of York, 1982), and although computer science has moved on (paper tape is quite rare these days), this combination gave him an early insight into modelling biological populations. He has been working on infectious disease transmission dynamics since his PhD at Imperial College, London. Graham has worked on many different pathogens (viruses, bacterial, protozoa, helminths) in many different hosts and vectors, and has about 180 peer-reviewed publications. He is particularly interested in understanding how interventions are and should be designed to control infectious disease – the definition of "interventions" includes both the natural (e.g. immune response) and societal action (e.g. immunisation). Mathematical models are tools for understanding, just as much tools for prediction. Graham is currently an editor of Epidemics, a handling editor for Mathematical Biosciences and on the board of reviewing editors for Science. He was recently appointed as chair of SPI-M to provide advice to the UK government on epidemic control.

**Laina Mercer**
**Research Statistician**
**Institute for Disease Modeling**
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Laina Mercer is a Research Statistician at the Institute for Disease Modeling working to support initiatives related to polio eradication, vaccine delivery, and reproductive health.

**Sarah Metzger**
**Program Officer**
**Bill & Melinda Gates Foundation**
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Sarah Metzger is a Program Officer specializing in portfolio management at the Bill & Melinda Gates Foundation. Sarah is a mathematician and epidemiologist dedicated to inspiring collaboration and bringing mathematical modeling to the fingertips of decision makers to catalyze improvements in global health. Sarah holds a BS in Mathematics from Southern Methodist University and a MSPH in Global Disease Epidemiology and Control from the Johns Hopkins School of Public Health.

**Joel Miller**
**Senior Research Scientist**
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Joel received his PhD studying fluid dynamics at Cambridge University and followed that with postdocs focused on disease control at Los Alamos, the U British Columbia Centre for Disease Control, and the Harvard School of Public Health. His research now focuses on applications of network models to disease control. He has coauthored a book (Mathematics of Epidemics on Networks) and developed a Python package (EoN) focused on diseases in networks. He is a published poet and has lived in 7 countries on 4 continents. On average he can be found about a short distance southwest of Hawaii.

**Poppy Miller**
**PhD Student**
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Poppy began her academic life training to be a microbiologist, at Massey University in New Zealand, as she was fascinated by genetics and infectious diseases. She soon realised that lab work was not for her, instead, she enjoyed learning about infectious diseases by teasing patterns out of datasets. She changed her major to statistics, graduated with a BSc (Hons), then moved to the UK to do a PhD in Statistics and Epidemiology with Peter Diggle and Chris Jewell. She has worked on many statistical projects including developing a novel class of source attribution models for human campylobacteriosis cases (sourceR), developing SIR-SI models for leptospirosis in sheep and abattoir workers, and using spatio-temporal models to investigate disease risks. Her work is focused by a goal to improve human and animal health by increasing knowledge about infectious diseases whilst developing novel statistical methods.

**Edinah Mudimu**
**Senior Lecturer**
**University of South Africa**
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Edinah Mudimu is a senior lecturer at the University of South Africa in South Africa. She has been in academia since 2004. Edinah completed her PhD research in 2016 from the University of South Africa, MSc in Operations research (2004) and BSc Honours in Applied mathematics (2001) from the National University of Science and Technology in Zimbabwe.  For her PhD research, Edinah used agent-based simulation modelling to model human social behaviour and HIV progression in a human society. Her research interests include studying human (social) behaviour at the societal level, the different social and sexual network structures that emerge in human populations and the effect that such networks have in the spread of infectious diseases using agent-based simulation techniques. She is currently on a Vision Keepers programme for researchers sponsored by the University of South Africa. You can reach her at emudimu@gmail.com or mudime@unisa.ac.za.

**Patrick Munywoki**
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Patrick Munywoki is a Public Health Epidemiologist working with CDC's Division of Global Health Protection (DGHP) in Kenya. He has over 10 years research experience and has led several studies investigating the epidemiology and transmission dynamics of Respiratory Syncytial Virus (RSV) and other respiratory viruses. Patrick has a background in BSc Nursing (Moi University, Kenya) and a MSc in Public Health in Developing Countries (London School of Hygiene of Tropical Medicine, UK). He got his PhD from Open University, UK in 2013 and completed his PostDoc at KEMRI-Wellcome Trust Research Programme in Kilifi, Kenya. Patrick's current interests are in establishing a career in public health with ability to combine different perspectives (epidemiology, transmission dynamics, public health, and economics) in providing evidence to guide in decision-making by governments and international agencies, which dovetails with CDC's DGHP vision.

**Gene Oates**
**Director of Software Engineering**
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Gene Oates is the Senior Software Engineering Manager at the Institute for Disease Modeling (IDM). With over thirty years of experience in the software industry, he has developed products in the telecommunications and network management fields, as well as in the financial and transportation domains, and has one patent as a result. While Gene has pursued traditional software education to advance his knowledge (DeVry, University of Lincoln, other courses), his expertise has been gained from the ground up and honed through working on cutting-edge technologies. For example, he was a senior developer on the Open Application Interface (OAI), as well as designed and developed the first non-SNA implementation of the NetView Operational Architecture. He also contributed to the first ever project that allowed peripheral processors the capability to interact with Cellular Home Switches to detect cellular call progress, cellular phone status and cellular text messages – a joint effort between US West, Motorola, Octel, and Accessline, and a key feature that eventually led to the "One Number" telephone service taken for granted today. Gene also contributed heavily to the success of Concur's SaaS implementation for Expense and Travel Management. As one of the principal engineers, he architected and developed the central control mechanisms for all client access, as well as utilities to migrate thousands of databases for software upgrades, and the architecture required to take an enterprise analytics solution into the "Cloud". Gene developed a prototype of a data driven semantic technology based engine that provided the capability of data sharing via the Ontology Web Language (OWL). At IDM, Gene utilizes his years of experience leading software development teams of all sizes heading up the software development projects within IDM.

**Assaf Oron**
**Senior Research Scientist**
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Assaf Oron is a senior research scientist at IDM's epidemiology team. He has a BSc in physics from the Hebrew University, an MSc in environmental science from the Weizmann Institute, and a PhD in statistics from the University of Washington. He has broad experience at the interface between science, medicine, mathematical models, and statistical models, in industry, applied research and, academic research. Assaf's focus at IDM is overall strategy development for maternal, newborn, and child health, in particular mortality reduction.

**Katie Owers**
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Katie Owers is a PhD candidate in Epidemiology of Microbial Disease at Yale University, where she is advised by Albert Ko. She is broadly interested in using advanced quantitative methods to answer questions of disease ecology, and is particularly interested in the spatial patterns that both produce and result from disease processes. Her doctoral research uses a variety of spatiotemporal modeling techniques to address questions about the transmission dynamics and determinants of leptospirosis, an environmentally-transmitted zoonotic pathogen, in complex ecological settings.

**Mike Osberg**
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Mike is a senior associate at Linksbridge. He has an MPP in advanced policy analysis, economic and community development from the University of Minnesota Humphrey School of Public Affairs.

**William Pan**
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William Pan is Assistant Professor of Global Environmental Health at Duke University with appointments in the Duke Global Health Institute and Nicholas School of Environment. He has over 15 years of experience studying the impact of human-environment dynamics on health, focusing on tropical regions in low- and middle-income countries (LMICs). He is a biostatistician with expertise in spatial analysis, demography and environmental epidemiology from the University of North Carolina at Chapel Hill. He is Director of the Duke-Peru Priority Partnership Location, Executive Steering Member of the North Carolina One Health Collaborative, member of the Emerging, Infectious and Zoonotic Diseases Research Core for the Center for Comparative Medicine and Translational Research, and Review Editor for EcoHealth. His research focuses on understanding dynamic relationships between humans and the (natural, social, built) environment with a particular interest in health outcomes resulting from these relationships. His work is highly interdisciplinary, ranging from climate change and child growth, mercury toxicity, infectious diseases and vaccines, and determinants of human fertility and migration. He currently leads four ongoing studies based in the Peruvian, Ecuadorian, and Brazilian Amazon regions that collectively address health impacts of resource extraction coupled with environmental change. He has served as the primary mentor to over 20 postdoctoral and doctoral students and has been recognized as a leading biostatistician in global health research with the 2012 James E. Grizzle Distinguished Alumni Award from UNC-Chapel Hill and the 2015 NIH Fogarty International Center Director's Award.

**Kathryn Peebles**
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Kathryn is a PhD student in the department of Epidemiology at the University of Washington. Her previous research experience includes evaluation of tobacco control policy among United States adolescents and assessing predictors of HIV and hepatitis B co-infection among a pediatric population in Zambia. Her current research focuses on the use of mathematical models to evaluate the impact of biomedical HIV prevention interventions, including the estimation of efficacy dilution attributable to behavioral risk factors and cost effectiveness of pre-exposure prophylaxis in implementation settings.

**David Pigott**
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David Pigott, DPhil, is Assistant Professor at the Institute for Health Metrics and Evaluation (IHME) at the University of Washington. He is a faculty member in the Geospatial team, focusing on improving the spatial resolution at which disease burden and metrics are considered, expanding and refining existing techniques to a wider number of pathogens and sequelae. He also leads work defining at-risk areas for a number of pathogens with pandemic potential and quantifying heterogeneities in global response capacity. Dr. Pigott studied at the University of Oxford, UK, first for an undergraduate degree in Biological Sciences, then a DPhil investigating the spatial epidemiology of a variety of pathogens, including the leishmaniases and a number of zoonotic hemorrhagic fevers.

**Virginia Pitzer**
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Virginia Pitzer, ScD, is an Associate Professor in the Department of Epidemiology of Microbial Diseases at Yale School of Public Health. She received her ScD in Epidemiology from Harvard School of Public Health, and was a postdoctoral fellow at Princeton University and Fogarty International Center/National Institutes of Health prior to joining the Yale faculty in 2012. Her research focuses on mathematical modeling of the transmission dynamics of enteric diseases, including rotavirus and typhoid fever. She studies how interventions such as vaccination, improved treatment of cases, and improvements in sanitation affect disease transmission at the population level.

**Travis Porco**
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T. C. Porco is Professor of Epidemiology and Biostatistics at the UCSF FI Proctor Foundation and works as a clinical trial statistician and infectious disease mathematical modeler.

**Allison Portnoy**
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Allison is a third year doctoral student in the Department of Global Health and Population at the Harvard T.H. Chan School of Public Health. Her research interests include economic modeling of public health interventions, decision sciences, vaccine costs and financing, and the impact of vaccination on population health and economic outcomes, particularly in examining the evidence base on the broader economic impact and value of vaccination. Prior to joining Harvard, Allison worked as a health economist at the International Vaccine Access Center at Johns Hopkins, and conducted research projects with the World Health Organization, Agency for Healthcare Research and Quality, and the University of Washington in Seattle. Her previous education includes a MSPH in Health Policy & Management from the Johns Hopkins Bloomberg School of Public Health and a BA in International Relations from Stanford University.

**Antonio Quispe**
**Senior Physician Researcher**
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Dr. Quispe is a physician researcher, epidemiologist, and statistician that, in the last decade, has successfully contributed to the mission of several national and international organizations, in both the public and the private sectors. Founding his own company, studying, and working overseas, managing local and international grants, and consulting with impactful agencies have been experiences that allowed him to grow professionally and personally.  Consequently, his dream and lifetime goal is to take advantage of my training and personal strengths to contribute to the public health of Peru and the Americas, as well as to pursue a long, productive life as a senior researcher.

**Benoit Raybaud**
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Benoit Raybaud has previously worked in the banking and nuclear industries, managing a wide variety of application development projects. While working for the University of Notre Dame, he managed the software development portfolio at the Center for Research Computing, providing development work to the university faculty. There he was immersed in the biology of Malaria and vector-borne diseases working on several modeling projects. Benoit was heavily involved with working on the VecNet project, which provided a modeling platform using both EMOD and OpenMalaria modeling software. Benoit joins the software team at IDM as a software manager, to assist researchers with their unique software projects.

**Jonathan Read**
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After an apprenticeship in theoretical ecology, Jon moved into infectious disease modelling at the Universities of Cambridge and Warwick as a postdoc with Professor Matt Keeling. He is currently a Senior Lecturer at Lancaster Medical School, Lancaster University, and holds an honorary Senior Lectureship at the University of Liverpool. He has designed and established epidemiological field studies on influenza in China, USA, and Vietnam, as well as conducting the largest national survey of social mixing behaviour in the UK. His research interests lie at the interface of field work and modelling of infectious diseases, in particular the quantification of human behaviours relevant to the transmission of pathogens. Other interests include measuring and understanding the structure of contact networks,  the ecology and evolutionary dynamics of influenza, and the development of more fully parameterized models of infectious diseases.

**Bobby Reiner**
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Bobby Reiner is an Assistant Professor at the Institute of Health Metrics and Evaluation in the department of Global Health in the Schools of Medicine and Public Health at the University of Washington. His research interests span multiple pathogens at various spatial and temporal scales. He is interested in developing novel modeling frameworks that incorporate and leverage "individual-level" data to assess questions of interest at the scales where policy decisions are made.

**Anne Rimoin**
**Associate Professor**
**University of California, Los Angeles**

Anne W. Rimoin, Ph.D., M.P.H. is an Associate Professor in the Department of Epidemiology at UCLA School of Public Health. She received her training at Middlebury College (B.A. African History, 1992), UCLA School of Public Health (M.P.H, International Health and Nutrition, 1996), and the Johns Hopkins Bloomberg School of Public Health (Ph.D. International Health, Division of Disease Prevention and Control, 2003). In 2004, she founded the UCLA-DRC Research program in the Democratic Republic of the Congo, where the vast majority of her research is based. She collaborates closely with the DRC Ministry of Health, the Institut National de Recherche Biomedicale (National Institute of Biomedical Research and DRC National Reference Laboratory) and the Kinshasa School of Public Health. Dr. Rimoin's main research focus is on the design and implementation of disease surveillance systems in remote rural areas to detect novel pathogens of animal origin that are crossing species into human populations in central Africa and to understand the epidemiology and ecological factors that influence transmission and spread of these diseases. Her ongoing work aims to elucidate the epidemiology of Monkeypox and other emerging infectious diseases (EIDs) through active disease surveillance in remote regions of central Africa with subsistence hunters and other individuals at who live and work at the human-animal interface and are at high risk for cross species disease transmission. These individuals represent an important sentinel population for monitoring viral disease emergence in a region from which numerous EIDs, including Ebola, Monkeypox, and Marburg have been known to recur.

**Min Roh**
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Min K. Roh is a research scientist at the IDM's Applied Mathematics group. Her research involves development of stochastic compartmental simulation algorithms, focusing on rare event probability estimation and parameter optimization. Min obtained her PhD from University of California Santa Barbara, where she published numerous papers on rare event characterization. Her recent work at IDM includes event-based parameter estimation and data-driven modeling.

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Jennifer Ross, MD, MPH is Acting Instructor/Senior Fellow in the Division of Allergy and Infectious Diseases at the University of Washington. Her research focuses on modeling approaches to reduce morbidity and mortality from other pathogens in persons with HIV infection. At IHME, she works with the Local Burden of Disease research team to develop models for tuberculosis (TB) and HIV/TB co-infection. Prior to joining IHME in 2017, she was a National Institutes of Health Fogarty Global Health Research Fellow investigating relationships between scale-up of HIV care and malaria burden in Uganda and Kenya. Dr. Ross studied for her bachelor's degree in Genetics and Cell Biology at Dartmouth College, and medical and public health degrees at Oregon Health and Science University. She completed clinical training at the University of California, San Francisco (Internal Medicine) and the University of Washington (Infectious Diseases). She also serves as an attending physician at Harborview Medical Center in Seattle.

**Laura Sampson**
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Laura Sampson earned her PhD in Physics from Montana State University in 2015, and then moved on to a postdoc at Northwestern University working as a member of the LIGO collaboration on the detection of gravitational waves. She made the leap into the modeling of disease dynamics as a postdoc working with Matthew Ferrari at Pennsylvania State University in April of 2017, and continues that work today. She specializes in time-series analysis and Bayesian inference, and has been working on spatial and temporal predictions of measles incidence. Sampson was named one of the 2016 L'Oreal USA for Women in Science Fellows.

**Jen Schripsema**
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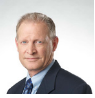
Jen Schripsema is a technical writer with a strong background in both software and biology. She has an MS in User Centered Design and Engineering from the University of Washington and BA in Biology from the Colorado College. She is interested in the role science communication plays in furthering the goals of research. Jen also has experience setting up content management systems that allow for greater collaboration with research and development teams.



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Vince Seaman currently works at the Bill & Melinda Gates Foundation in Seattle, Washington, where he is the Interim Deputy Director for the Strategy, Data and Analytics team. In that role, he supports the use of geospatial data, analytics, and technology to enable better decision-making and more effective interventions in the global development community. Prior to joining the Gates Foundation, Dr. Seaman spent 7 years at the U.S. Centers for Disease Control (CDC), and was detailed to Nigeria for three years as a secondee to the World Health Organization, supporting polio and other vaccine-preventable disease programs. Vince completed his MS and PhD in Pharmacology and Toxicology at the University of California, Davis in 2006, after spending 15 years practicing as a licensed pharmacist and 8 years as a public high school science teacher in California.

**Adrienne Shapiro**
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Adrienne Shapiro, MD, PhD, is an infectious disease clinician and epidemiologist. Her research focuses on approaches to decrease the burden of HIV-associated TB in resource-limited settings through improved diagnostic tools, strategies for case-finding, and improving TB prevention. She received her MD and PhD in Epidemiology at Johns Hopkins and is currently a senior fellow in the Division of Infectious Diseases at the University of Washington.

**Lone Simonsen**
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Lone Simonsen is a professor of population health sciences, at Dept of Science & Environment at Roskilde U. in Denmark, following 3 years as a Marie Curie visiting professor at U. Copenhagen. She also holds a position as Research Professor in Global Health at George Washington U, Washington DC. She pursued a PhD in population genetics from University of Massachusetts, Amherst and later trained at the Centers for Disease Control (CDC) in infectious disease epidemiology. She is an elected member of the Danish Royal Academy of Sciences & Letters and the American Epidemiological Society AES. Over the past 20+ years she has worked as a researcher at the CDC, World Health Organization (WHO) and NIH on issues including unsafe medical injections, global patterns of HIV/AIDS, tuberculosis drug resistance, SARS, pandemic influenza, e-health data, surveillance systems, and vaccine program evaluation. Before moving to academia in 2007, she was a senior epidemiologist at the National Institutes of Health-NIAID. She was a senior fellow with the RAPIDD modeling research network hosted by Fogarty-NIH during 2009-2016. She has coauthored ~200 peer-reviewed papers, book chapters, and commentaries. Her research currently focuses on modeling the spread and burden of historic and contemporary pandemics and emerging infectious diseases, population transitions in health, other pandemic threats (ebola, SARS, etc), and impact of pneumococcal vaccine programs for the Gates Foundation. She co-edited a 2016 JID special issue on "big data" in health and a 2017 special issue in Epidemics on Ebola forecasting. H-index 63; I10-index 133; >19000 citations.

**Somdatta Sinha**
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After a Master's degree in Physics from Visva Bharati University, Santiniketan and a PhD in Theoretical Biology from School of Theoretical & Environmental Sciences, Jawaharlal Nehru University, India, Somdatta worked as a scientist and Group Leader at the CSIR-Centre for Cellular & Molecular Biology, Hyderabad, India for 28 years. She joined the Indian Institute of Science Education Research Mohali in 2011 as a full professor and has been involved in research and teaching in interdisciplinary topics in Mathematical and Computational Biology. Since 2016 she is continuing as a visiting professor at IISER Mohali. Her research is focused on understanding the logic and design of biological processes at multiple spatiotemporal scales using tools and concepts from Mathematics, Physics, Nonlinear Dynamics and Complex Systems. One major interest is in modeling infectious diseases at different scales—from genome analysis to epidemiology. Along with epidemiological models in malaria, she has also been interested in prevalence data analysis using standard regression models and spatiotemporal visualization. She is currently a Visiting Professor at the Department of Mathematics, and an International Visiting Research Scholar (2018) at the Peter Walls Institute of Advanced Studies, University of British Columbia, Vancouver, Canada.

**David Smith**
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David L. Smith is Professor of Global Health at the Institute for Health Metrics and Evaluation (IHME) at the University of Washington. Professor Smith studied Ecology and Evolutionary Biology at Princeton University with Professor Simon A. Levin before moving into epidemiology and global health. Prof. Smith's scientific research has been on the ecology, epidemiology, and evolution of infectious diseases. Prof. Smith has published extensively on the epidemiology, dynamics, and control of malaria, influenza, cholera, rabies, *Staphylococcus aureus*, and nosocomial pathogens; the evolution of resistance to antibiotics in nosocomial pathogens; the evolution of resistance to antimalarial drugs; malaria elimination and eradication; and the bioeconomics of infectious diseases. Prof. Smith was one of the original members of the Malaria Atlas Project, which has published evidence-based global maps of *Plasmodium falciparum* and *P. vivax*.

**Thomas Smith**
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Thomas Smith is the head of the Infectious Disease Modeling unit at the Swiss Tropical and Public Health Institute, where his main focus is on modeling malaria intervention strategies. He has three decades of experience in the design and analysis of field studies and trials of malaria interventions, including 4 years based in Papua New Guinea, and numerous projects in East Africa. Since 2003 he has led the Swiss TPH group that developed and uses the OpenMalaria software for simulating malaria intervention strategies. He is also an adviser to the WHO Global Malaria Program.

**Molly Steele**
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Molly Steele is a PhD candidate working with Dr. Ben Lopman in the Environmental Health Sciences program at Emory University's Rollins School of Public Health. Molly earned her MPH in Epidemiology at the Rollins School of Public Health and her MSc in Ecology at the Pennsylvania State University's Center for Infectious Disease Dynamics. Molly's research is directed at understanding the epidemiology and transmission of norovirus, with a focus on predicting the potential impact of different vaccination strategies on norovirus gastroenteritis.

**Niket Thakkar**
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Niket Thakkar is a research scientist at the Institute for Disease Modeling, focusing on statistical and machine learning models of measles. He is particularly interested in using modeling to both inform policy making and understand the effects of policy decisions. He has a doctoral degree in applied mathematics from the University of Washington where he worked with Professor David Masiello on problems in nanoscale optics.

**Nguyen Tran**
**Post-doc Researcher**
**Pennsylvania State University**
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Nguyen Tran is currently a postdoc researcher at the Pennsylvania State University. He's spent several years on the development of the population-level malaria microsimulation and it now explicitly tracks parasitaemia levels, pharmacokinetics, pharmacodynamics, host immunity, variable biting rates, and multiple drug-resistant alleles. The original purpose of this model was to evaluate if using multiple first-line therapies (MFT) at a population level has beneficial long-term health outcomes. He is currently working on subsequent phases of this modeling work, looking at optimal treatment course durations when several treatments are available and optimal ways to introduce new antimalarial combinations into population-level use when they become available.

**Alain Vandormael**
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Alain Vandormael was awarded his PhD in Sociology and MSc in Statistics from the University of Minnesota, USA. His PhD examined the preventive and survival benefits of antiretroviral (ART) use in the AHRI study area of Somkhele, northern KwaZulu-Natal. Alain is interested in understanding why some HIV prevention strategies are falling short and providing insight into how these strategies can be optimized in the future.

**Wilbert Van Panhuis**
**Assistant Professor of Epidemiology and Biomedical Informatics**
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Wilbert Van Panhuis is an assistant professor of Epidemiology and Biomedical Informatics at the University of Pittsburgh. He received his MD from the Free University in Amsterdam and his PhD from Johns Hopkins. Wilbert currently works at the interface of epidemiology and global health informatics to improve the use of data for strategies against infectious disease transmission. He is particularly interested in strategies that involve global cooperation to counter cross-border transmission and common determinants of infectious diseases, such as climate change, inequality, and urbanization. Funded by NIH, the Gates Foundation, and others, I am principal investigator of the Project Tycho (www.tycho.pitt.edu) Data Repository for Global Health. Project Tycho data has been searched over 1 million times by 3000+ users from 90 countries. Together with colleagues, he has used historical disease data to estimate that vaccination in the US has prevented over 100 million cases of childhood disease (NEJM, New York Times), and that El-Niño is related to dengue epidemics in Southeast Asia (PNAS). Moving forward, he aims to improve access and availability of global health data for research and policy through development of data systems compliant with FAIR (Findable, Accessible, Interoperable, and Reusable) guiding principles for data management. Researchers and students around the world should be able to help improve global health by contributing innovative technology and new scientific discoveries without being impaired by inefficient data systems.

**Alessandro Vespignani**
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Alessandro Vespignani is the Sternberg Family Distinguished University professor at Northeastern University. He is the founding director of the Network Science Institute and leads the Laboratory for the Modeling of Biological and Socio-technical Systems. Vespignani's recent work focuses on data-driven computational modeling and forecast of emerging infectious diseases, resilience of complex networks, and collective behavior of techno-social systems. Vespignani is elected fellow of the American Physical Society, member of the Academy of Europe, and fellow of the Institute for Quantitative Social Sciences at Harvard University. He served in the board/leadership of a variety of professional association journals and the Institute for Scientific Interchange Foundation.

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**Fogarty International Center, NIH**
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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 modeling. 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.

**Stephane Vouillamoz**
**Co-Founder and Solutions Engineer**
**Novel-T**
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Stéphane Vouillamoz is a co-founder and solutions engineer at Novel-T. He has worked for the World Health Organization as a Software Engineer on Health and Geographical Information Systems for close to 10 years, helping the organization with its data and information management needs.

**Arend Voorman**
**Program Officer**
**Bill & Melinda Gates Foundation**
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Arend Voorman is a Program Officer at the Bill and Melinda Gates Foundation, working on polio eradication. He used statistical modeling to analyze polio epidemiology, risk and program performance. He earned his PhD in Biostatistics in 2014 from the University of Washington, developing machine learning methods to turn the large data sets produced in modern genetics into biological insights.

**Bradley Wagner**
**Research Scientist**
**Institute for Disease Modeling**
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Research Scientist at the Institute for Disease Modeling working primarily on dynamic models of TB transmission and pathogenesis. He was previously a postdoctoral research fellow at the David Geffen School of Medicine, UCLA and has a PhD in Applied Mathematics from McMaster University.

**Jon Wakefield**
**Professor**
**University of Washington**
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Jon Wakefield has worked extensively in the general area of spatial epidemiology and was formerly a member of the Small Area Health Statistics Unit (SAHSU) at Imperial College in London. He has particular interests in the sources and alleviation of ecological (or aggregation) bias and has worked on study designs for supplementing ecological information. His other interests include spatial-temporal models for infectious disease data, cluster detection, disease mapping, spatial regression, Bayesian methods in biostatistics and epidemiology, and genetic epidemiology. He has received the Guy medal in Bronze from the Royal Statistical Society, is a Fellow of the American Statistical Association, and is a former chair of the Department of Statistics at the University of Washington.

**Kirsten Wiens**
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Kirsten Wiens, PhD is a Postdoctoral Fellow at the Institute for Health Metrics and Evaluation (IHME) at University of Washington. She is a member of the Local Burden of Disease research team, focusing on geospatial mapping of tuberculosis (TB). Dr. Wiens completed her doctoral work at New York University School of Medicine, where she studied how different strains of the Mycobacterium tuberculosis complex interact with the host immune response. She is interested in understanding how these strain differences impact the global distribution and epidemiology of TB.

**Katie Wilson**
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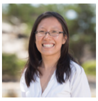
Katie is a 5th year PhD student studying Biostatistics at the University of Washington advised by Dr. Jon Wakefield. Her research interests include spatial statistics and cancer epidemiology. Currently, she is working on methods for analyzing survey data.



**Katherine Xue**
**Graduate student**
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Katherine Xue is a graduate student in Jesse Bloom's laboratory at the University of Washington and Fred Hutchinson Cancer Research Center. She works to characterize the evolutionary dynamics of influenza within human hosts using high-throughput sequencing.

**Sahar Zangeneh**
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Sahar Zangeneh holds a PhD in Statistics from the University of Michigan. She is currently a Staff Scientist in the HIV Prevention Network at the Vaccine and Infectious Disease Division of Fred Hutch Research Center. Sahar is broadly interested in Population Health Sciences. As a staff scientist at FHCRC she brings her expertise in statistical analysis with missing data and analyzing data collected through complex sampling designs, such as sample survey data, to population health sciences. Her research has been recognized by several awards from the American Statistical Association.

# Notes

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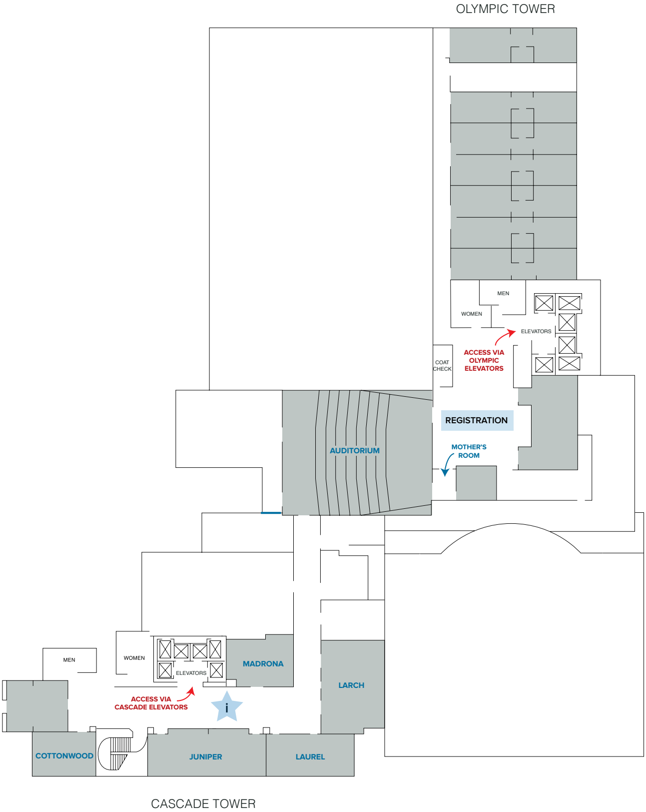

**There is a mother's room available near registration. Please see event staff to access.