2017 5th Annual IDM Modeling Symposium

INSTITUTE FOR DISEASE MODELING

INTELLECTUAL VENTURES®

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WELCOME

On behalf of the entire team at the Institute for Disease Modeling, we want to welcome you to our 5th Annual Modeling Symposium. We greatly appreciate, and are honored by your attendance–particularly to those contributing presentations. We value this oppor-tunity to provide a venue for collaboration and to help extend the science of quantitative modeling in disease eradication and control around the globe. It is exciting to see this forum continue to grow so rapidly and effectively over the past five years, and we look for-ward to continuing the tradition. Encouraging and fostering collaboration in global health is a core value at IDM and your research, ideas, suggestions and interactions with your colleagues at this venue are of tremendous value to developing global health policies, programs and campaigns. For IDM itself, your feedback and interaction is extremely valued.

The Institute for Disease Modeling is a distinct and integral com-ponent of the Global Good initiative at Intellectual Ventures. Today, IDM has over 75 scientists and engineers focused on issues related to the eradication and control of infectious diseases. That expansion in staff 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, and to implement our cross-disease methods in shareable software. This expansion has also aided us in growing our collaborations outside of IDM. External collaborations are an important goal to IDM and, we believe, vital to positively impact global health.

Collaborations over the past year have included developing models for diseases new to IDM, such as pneumonia and typhoid, as well as refining existing disease models. Our shared software was used as the base for new models of dengue and other vector-borne diseases developed elsewhere. Collaborations drove forward on new method development for calibration of individual-based models, utilization of disease surveillance data (including genetics), and more. Vaccine trial designs were informed, and field data were interpreted, through a dynamic model lens in partnership with vari-ous institutions. Finally, we recognize that modeling cannot achieve impact on its own; all real-world impact will be achieved through collaborations with individuals and institutions on the ground. Thus we especially appreciate our collaborators who are directly getting rid of disease in the field, and we value our interactions focused on assisting towards accelerating these declines in disease.

As always, we greatly value your feedback and ideas, and hope that this will be the basis for strong future collaborations.

Sincerely,

Robert S. Hart
Vice President &
General Manager

Philip Welkhoff
Senior Director of Research

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

The keynote addresses the primary theme of the symposium and summarizes key findings for the global health community.

Day 1 Overview		
7:30-8:45	Auditorium Foyer (Olympic Tower)	Registration & Breakfast
8:45-9:00	Welcome **Auditorium**	Robert Hart, IDM
9:00-11:45	Pneumonia 1 **Madrona**	Ben Althouse, IDM Stefan Flasche, LSHTM Marc Lipsitch, Harvard University Dan Weinberger, Yale University
9:00-11:45	Risk Mapper Tool Workshop Value of Information **Auditorium**	Guillaume Chabot-Couture, IDM M Elizabeth Halloran, Fred Hutch Natalia Molodecky, Imperial College London Roland Sutter, WHO Jon Wakefield, UW
9:00-11:45	Calibration of Individual-Based Models **Larch**	Daniel Klein, IDM Graham Medley, LSHTM Zelda Zabinksy, UW Ian Vernon, Durham University Michael Goldstein, Durham Univ.
9:00-11:45	Works-In-Progress **Cottonwood**	Dennis Chao, IDM Adam Akullian, IDM Alicia Kraay, University of Michigan
11:45-1:00	Eques Restaurant (2nd Floor Lobby)	Lunch Buffet
1:00-2:30	General Session 1 **Auditorium**	Robert Reiner, IHME Maya Petersen, UC Berkeley Mark Hatherill, SATVI
2:30-3:15	Break	
3:15-4:45	General Session 2 **Auditorium**	Keith Klugman, BMGF Myron Levine, Univ. of Maryland Flaminia Catterucia, Harvard Univ.
5:00-6:00	General Session **Laurel**	Software Open Forum
5:00-6:00	Keynote **Auditorium**	Emerging Researchers

SESSIONS

7:30-8:45	Registration	Auditorium Foyer
Registration and full service breakfast		

8:45-9:00	Welcome	Auditorium
Welcome to IDM's 5th Annual Disease Modeling Symposium		
Robert Hart, *Vice President and General Manager, Institute for Disease Modeling*		

9:00-11:45	Breakout	Madrona
Pneumonia Chair: Ben Althouse, *Research Scientist , Institute for Disease Modeling*		

How can modeling address open questions in *S. pneumococcus* epidemiology

Ben Althouse, *Research Scientist, Institute for Disease Modeling*

We will discuss open questions in the epidemiology of *S. pneumococcus* and focus on how modeling can and is addressing these questions.

Optimizing pneumococcal vaccination programs

Stefan Flasche, *Assistant Professor, London School of Hygiene & Tropical Medicine*

With the observed strong indirect effect of pneumococcal conjugate vaccination programs, there is scope for reduced dose programs to offer similar protection. Using transmission dynamic models for various settings, I investigate who mainly infects infants, the age group potentially under less protection in reduced dose schedules.

Pneumococcal biology and its relevance for modeling, with applications

Marc Lipsitch, *Professor, Center of Communicable Disease Dynamics, Harvard School of Public Health*

This talk will describe key features of pneumococcal biology that are of direct relevance to modeling the impact of interventions, such as vaccines. It will also describe some key uncertainties about pneumococcal biology that may change the construction of such models when they are resolved. Finally, I will present one or more applications of an individual-based model to vaccine trial design or other topics.

Estimating the impact of vaccines using synthetic controls

Dan Weinberger, *Assistant Professor, Yale School of Public Health*

Quantifying the impact of pneumococcal conjugate vaccines

(PCVs) on pneumonia is challenging due to time trends unrelated to the vaccine. We use a method developed for website analytics and economics, called "synthetic controls," to disentangle changes in pneumonia rates caused by the vaccine from changes caused by unrelated factors. We found that PCVs significantly reduce all-cause pneumonia hospitalizations in young children and reduce hospitalizations for invasive pneumococcal disease and pneumococcal pneumonia in children and adults. In contrast to previous studies, we did not detect a decline in all- cause pneumonia hospitalizations in older adults in any of the five countries following the introduction of the vaccine in children.

9:00-10:00	Breakout	Auditorium

Risk Mapper Tool Workshop

Guillaume Chabot-Couture, *Senior Research Manager , Institute for Disease Modeling*

The Risk Mapper Tool Workshop will demonstrate IDM's new online disease case mapping and risk modeling tool prototype. Participants will have an opportunity to work with the tool by using their own disease data or with some sample data provided. Additional information will be provided to attendees upon registration of this workshop.

10:00-11:45	Breakout	Auditorium

Value of Information

Chair: Guillaume Chabot-Couture, *Senior Research Manager , Institute for Disease Modeling*

Estimating population effects of vaccination from routinely collected data

M Elizabeth Halloran, *Professor, Fred Hutchinson Cancer Research Center/University of Washington*

Establishing that vaccination provides population-level effects that go beyond the direct effects in the vaccinated individuals can have important consequences for public health policy. However, implementing formal studies in the field to evaluate the different effects of vaccination can be expens-ive, of limited generalizability, or unethical. We consider challenges and opportunities of using routinely collected databases.

The value of accurate surveillance data to inform polio risk, vaccination planning, and policy

Natalia Molodecky, *PhD Candidate, Imperial College London*

Globally, cases of poliomyelitis are detected through national acute flaccid paralysis (AFP) surveillance systems. Although these data's primary utility is to capture daily incidence of poliomyelitis, a majority of AFP cases are not poliomyelitis and therefore provide a representative sample of the population. As a result, these data have been used to estimate spatially and temporally heterogeneous predictors of polio risk, such as vaccine-induced population immunity and immunization coverage. I will briefly describe the AFP surveillance system and the capabilities of these data. I will then provide examples of mathematical models incorporating estimates from these data and their implications on informing polio risk, vaccination strategy and policy decisions.

Data quality for polio eradication: Accuracy & reliability

Roland Sutter, *Coordinator, Research, Policy & Containment (RPC), World Health Organization*

This presentation will focus on which data sources likely provide accuracy for the control and eradication of diseases. In other words, which data sources can we trust for modeling and program management decisions.

Spatio-temporal modeling of infectious disease count data

Jon Wakefield, *Professor, Departments of Statistics and Biostatistics, University of Washington*

We review recent advances in modeling space-time infectious disease data. We emphasize attempts to understand age-gender disease dynamics, spatial effects, neighborhood weighing schemes and the effect of vaccination. We also link the models to more traditional infectious disease models.

9:00-11:45	Breakout	Larch

Calibration of Individual-Based Models

Chair: Daniel Klein, *Senior Research Manager, Institute for Disease Modeling*

Calibration of individual-based models

Daniel Klein, *Senior Research Manager, Institute for Disease Modeling*

Fitting and optimizing individual based models can be a challenging task. In this brief talk, I will discuss some of the approaches that we have developed for this challenging task. Specific examples from IDM research will be presented. Finally, Python-based tools for optimization and a basic calibration will be introduced and demonstrated.

Model-based decision-making: does it matter how good the model is?

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

Mathematical modeling of transmission dynamics of infectious pathogens are increasingly used to support decision-making in public health. All models in biology are approximations, and it is impossible to include all sources of heterogeneity. Consequently, model fitting and model validation are often proposed as essential steps in order to provide some confidence in the model results. But a well-fitting model is not necessarily "correct" and validation is not always possible and does not guarantee "correctness". Modelers put increasing effort into development of more complex models and more sophisticated fitting methods, but relatively little consideration is given to whether the model is "useful" for the question being asked. There is no doubt that models need to be tested to ensure that they support the correct decision–fitting and validation are intermediate technical steps–but they do not actually address the accuracy of the model- based decision directly.

In this presentation, I use a combination of real examples and toy models to address the issue of how the processes of fitting and validation impact on the decision being addressed.

Global optimization

Zelda Zabinksy, *Professor, University of Washington*

Global optimization methods are needed when the problem is ill-structured, non-convex, and possibly discontinuous, and will be discussed briefly. A new global optimization algorithm (Probabilistic Branch and Bound) has been applied to two problems in health care, and preliminary results will be presented. The first problem is allocation of a new technology, and involves a simulation and multiple objectives. The second problem is a Markov decision process with constraints, and the algorithm can provide a type of sensitivity analysis.

Uncertainty analysis for complex models

Ian Vernon, *Lecturer, Durham University*

Michael Goldstein, *Professor, Durham University*

An overview of methodology for handling the main sources of uncertainty for complex real-world systems modeled by computer simulators. Topics covered to include model emulation, assessment of structural discrepancy, history matching and forecasting.

9:00-11:45	Breakout	Cottonwood

Works-In-Progress

Chair: Dennis Chao, *Senior Research Scientist , Institute for Disease Modeling*

Seasonality of cholera

Dennis Chao, *Senior Research Scientist, Institute for Disease Modeling*

In endemic settings, cholera outbreaks can occur regularly. However, the actual burden of cholera can be difficult to estimate. We believe that by using weather data and the age-specific incidence of diarrheal disease, we can have sufficiently accurate cholera incidence data even in the absence of lab testing.

Modeling the decline of typhoid fever in an urban slum in Kenya

Adam Akullian, *Postdoctoral Research Scientist, Institute for Disease Modeling*

We present an overview of a multi-disciplinary project with CDC-Kenya that uses epidemiological, environmental, social, and molecular biological analysis to elucidate typhoid fever transmission dynamics in an urban slum. Mathematical and statistical modeling will be used to explain the dramatic decline in incidence, and to quantify uncertainty around its potential reemergence to epidemic levels. Understanding the primary drivers of this decline can help inform the strategic implementation of prevention interventions, including vaccination campaigns in this and other high-burden urban settings.

Rainfall and diarrheal disease: Evaluating the concentration dilution hypothesis for all-cause diarrhea

Alicia Kraay, *Student , University of Michigan, Ann Arbor*

Although rainfall is thought to be an important driver of diarrheal disease, the mechanisms by which rainfall affects diarrhea are not well-understood. One hypothesis, called the concentration dilution hypothesis, suggests that heavy rainfall is a risk when it follows a dry period because the event can concentrate pathogens in the local water supply but reduces risk when following a wet period by diluting the water reservoir. Using a spatially-explicit transmission model based on time series all-cause diarrhea data from rural Ecuador, we systematically test this hypothesis and illustrate how the effects of rainfall and temperature on disease risk might vary by pathogen.

11:45 -1:00	Lunch	Eques

2nd floor near the Hyatt's grand staircase

1:00-2:30	General Session	Auditorium

General Session 1

Chair: Anna Bershteyn, *Senior Research Manager, Institute for Disease Modeling*

The global burden of disease: Diarrhea and lower respiratory infections

Robert Reiner, *Assistant Professor, Institute for Health Metrics and Evaluation, University of Washington*

Globally, lower respiratory infections (LRI) and diarrheal diseases are among the top contributors to mortality and morbidity. LRI and diarrhea are the two leading causes of death amongst infectious diseases across all ages,and spe-cifically in children under the age of 5. In 2015, they caused an estimated 4 million deaths, with 1.3 million of those in children. Across all causes of death, they rank 4th and 9th respectively across all ages and 3rd and 4th in children. While at the global level deaths attributable to these diseases have reduced over the last 25 years, progress has varied by country, with many, largely preventable, deaths still occurring. In this talk I will present the results from the 2015 Global Burden of Diseases, Injuries, and Risk Factors (GBD) Study, focusing on both mortality and morbidity attributable to LRI and diarrheal diseases. Finally, I will also present our preliminary efforts to refine the resolution of burden estimation from the country level to the $5km^2$ pixel level, enabling us to provide quantitative evidence at the same scales at which policy decisions occur.

The SEARCH Study: A cluster randomized HIV prevention and treatment trial in rural Kenya and Uganda

Maya Petersen, *Associate Professor, UC Berkeley School of Public Health*

The Sustainable East Africa Research in Community Health Study (SEARCH; NCT01864683) is an ongoing cluster randomized trial enrolling 32 communities of approximately 10,000 persons each in rural Uganda and Kenya. The first phase of the study (2013-2017) will evaluate the health, economic, and HIV prevention impacts of an HIV "test and treat" strategy, compared to country-specific standard-of-care. Intervention communities receive annual population- based multi-disease testing, including HIV, universal ART eligibility for all HIV+ individuals, and facilitated linkage to care and streamlined ART delivery. The second phase of the study (2017-2020) will evaluate the added health and prevention benefits of delivering targeted PrEP, HIV testing, and suppression interventions in the context of universal ART eli-gibility and streamlined delivery. This presentation will provide an overview of the study, highlight key results to date (including interim evolution in population-level viral suppression in the intervention communities), and describe the targeted PrEP strategy currently being deployed in the second phase of the study.

Using prognostic biomarkers to target TB preventive therapy

Mark Hatherill, *Professor, SATVI, University of Cape Town*

Mass TB preventive therapy in endemic countries where more than half the adult population is infected by *M. tuberculosis* is not feasible or affordable. A host blood-based RNA signature that identifies individuals at high risk of progression to TB disease within 12-18 months of testing has been developed and validated. An ongoing clinical trial (CORTIS) will test whether targeted preventive therapy using a 1-weekly, 12-dose isoniazid/rifapentine regimen protects high risk (RNA biomarker+) adults against TB disease. The CORTIS clinical trial design and future implementation considerations will be discussed.

2:30-3:15	Break	Foyer

3:15-4:45	General Session	Auditorium

General Session 2

Chair: Hao Hu, *Senior Research Manager, Institute for Disease Modeling*

Saving children from death due to pneumonia

Keith Klugman, *Director, Pneumonia, Bill & Melinda Gates Foundation*

Even as global child deaths have declined from 12.6 million to 6.6 million over the last two decades, pneumonia has remained the world's leading cause of death among children under age 5. Despite available interventions, pneumonia claimed the lives of 1.3 million children in 2011 and was responsible for 18 percent of child deaths worldwide–nearly all of them in developing countries, particularly in Sub-Saharan Africa and South Asia. Because pneumonia can be caused by a number of viruses and bacteria, multiple interventions are needed to reduce childhood mortality from the disease.

Childhood deaths from pneumonia are preventable using vaccines, diagnostic tools, and treatments, but issues of availability, access, and cost remain obstacles in the developing world. Nearly half of early childhood deaths from pneumonia are estimated to result from lack of, or delay in, appropriate diagnosis and treatment.

Volunteer challenge studies providing insights on enteric disease epidemiology

Myron Levine, *Associate Dean, University of Maryland School of Medicine*

Volunteer challenge studies with *Vibrio cholerae* O1, *Shigella*, and enterotoxigenic *Escherichia coli* have provided key information that have provided insights to explain the epidemiology of these enteric infections, including their modes of transmission and human biological risk factors.

Targeting *Anopheles-Plasmodium* interactions to help malaria eradication

Flaminia Catterucia, *Associate Professor, Harvard TH Chan School of Public Health*

Nearly 200 million people are infected every year by malaria parasites, and more than 10 million people have already died because of malaria infections since the turn of this century, mostly young children in sub-Saharan Africa. According to the World Health Organization, "mosquito control is the only intervention that can reduce malaria transmission from very high levels to close to zero". Consistently, extraordinary efforts are being made to control *Plasmodium* transmission by the *Anopheles* mosquito using long lasting insecticide treated nets (LLINs) and indoor residual spraying (IRS). The increased application of both interventions over the last decade, however, has inevitably led to the emergence and spread of insecticide resistance in natural mosquito populations, making the generation of alternative strategies that can reduce disease transmission a high priority.

Here we present studies on the molecular and genetic mechanisms that shape the interplay between reproductive biology and *Plasmodium* development in *Anopheles* mosquitoes. Specifically, we show how the malaria parasite exploits the physiological environment created by mating and blood feeding in the female *Anopheles* to achieve its own transmission. Increasing knowledge of mosquito biology and mosquito-*Plasmodium* interactions will contribute novel tools and concepts for malaria control.

5:00-6:00	General Session	Room

Software Open Forum Discussion

Gene Oates, *Director of Software Engineering, Institute for Disease Modeling*

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.

5:00-6:00	Keynote	Auditorium

Emerging Researchers

Chair: Philip Welkhoff, *Senior Director of Research, Institute for Disease Modeling*

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.

Day 2 Overview		
7:30-8:45	Auditorium Foyer (Olympic Tower)	Registration & Breakfast
9:00-10:30	Pneumonia 2 **Cottonwood**	Gail Rodgers, BMGF Ron Dagan, Ben-Gurion University Imran Nisar, Aga Khan University Stephen Pelton, Boston University Kimberly Shea, Boston University
9:00-10:30	Enteric Disease **Juniper**	Duncan Steele, BMGF Ben Lopman, Emory University Joe Eisenberg, University of Michigan Andrew Brouwer, University of Michigan
9:00-10:30	Measles 1 **Larch**	Sheng Li, City University of New York Amy Winter, Princeton University Kurt Frey, IDM Saki Takahashi, Princeton University
9:00-10:30	Malaria 1 **Auditorium**	Amy Wesolowski, Princeton University Dave Smith, IHME John Huber, University of Notre Dame Bryan Greenhouse, UC San Francisco
9:00-10:30	HIV **Madrona**	Diego Cuadros, U of Cincinnati Susan Cassels, UC Santa Barbara Ying Huang, Fred Hutch Zindoga Mukandavire, LSHTM
9:00-10:30	Software Tutorial **Laurel**	Benoit Raybaud, IDM Dan Bridenbecker, IDM Milen Nikolov, IDM
10:30-10:45	Break	
10:45-11:45	General Session 3 **Auditorium**	Jen Gardy, BCCDC Dan Neafsey, Broad Institute
11:45-4:00	Woodinville Wine Excursion and IDM-hosted lunch	
4:30-5:45	Break	
5:45-9:00	Daniel's Broiler, IDM-hosted dinner	

SESSIONS

7:30	Registration	Auditorium Foyer
Registration and full service breakfast		

9:00-10:30	Breakout	Cottonwood

Pneumonia 2

Chair: Hao Hu, *Senior Research Manager, Institute for Disease Modeling*

Current status of alternate dosing strategy studies

Gail Rodgers, *Senior Program Officer, Bill & Melinda Gates Foundation*

This talk will provide an overview of the PCV Alternate Dose Strategy including design and status of ongoing trials.

Alveolar pneumonia – Is it all pneumococcal? The vaccine probe approach

Ron Dagan, *Professor, Ben-Gurion University of the Negev*

Alveolar pneumonia is often considered pneumococcal, but the extent of pneumococcal involvement is unclear. In a series of studies starting during the pre-PCV7 period and continuing during the PCV7 and PCV13 periods, we have been attempting to demonstrate the extent of *S. pneumoniae* involvement as the causative organism in alveolar pneumonia.

Indirect effect of 10-valent pneumococcal vaccine on nasopharyngeal carriage in children under 2 years of age in rural Matiari, Pakistan

Imran Nisar, *Senior Instructor, Department of Pediatrics, Aga Khan University*

The presentation is about the direct and indirect effects of PCV10 on nasopharyngeal carriage in children under 2 years of age in Matiari Sindh .We will look at the carriage rate and serotype distribution in immunized and unimmunized chil-dren. We will also look at risk factors associated with carriage of PCV10-specific serotypes.

Impact of PCV13 vaccination on *S. pneumoniae* nasopharyngeal colonization in urban Boston children from 2010 – 2016.

Stephen Pelton, *Professor of Pediatrics and Epidemiology, Boston University School of Medicine and Public Health*

We have completed analysis of impact of PCV13 on pneumonia in children less than 5 years of age following introduction of PCV13. We will present analysis in both "healthy children" and those with comorbid conditions.

Impact of PCV13 vaccination on all-cause pneumonia in urban Boston children: A time-series analysis

Kimberly Shea, *Assistant Professor, Boston University*

Bacterial pneumonia occurs more frequently in urban, minority children, resulting in increased morbidity and mortality. We used a large de-identified health information database to evaluate the impact of PCV13 on incidence of pneumonia in pediatric patients at a large urban safety-net hospital network in Boston by comparing population-based estimates of pneumonia incidence before (2007-2009) and after (2011-2013) the introduction of PCV13.

9:00-10:30	Breakout	Juniper

Enteric Disease

Chair: Dennis Chao, *Senior Research Scientist, Institute for Disease Modeling*

Norovirus: Ubiquitous, diverse, infectious and hard to control

Ben Lopman, *Associate Professor, Emory University Rollins School of Public Health*

The epidemiology of enteric viruses is complex due to multiple transmission routes, incomplete immunity, pathogen diversity and heterogeneity in host susceptibility. With vac-cines in the pipeline, it is becoming increasingly urgent to understand norovirus epidemiology and estimate key para-meters governing transmission. In this talk, I will discuss how he have used transmission models to understand the (a) role of symptomatic and asymptomatic infection, (b) duration of immunity, and (c) genetically-determined susceptibility in order to simulate potential vaccination strategies. Implications for norovirus control in developing countries, where the burden is greater but data are sparser, will be con-sidered.

Environmental modes of transmission for enteric pathogens

Joe Eisenberg, *Chair and Professor*, *Department of Epidemiology, University of Michigan*

The traditional risk factor paradigm has characterized the proximate risks of enteric infection and diarrheal disease, and has supported mitigation of these risks over the past four decades. However, the application of this knowledge has not gained traction, largely due to the complex social and eco-logical factors that impact intervention effectiveness. For example, communities are faced with changing climatic con-ditions (increasing flooding and droughts) and social struc-tures (urbanization, travel and migration patterns) that can largely determine which of the many transmission pathways enteric pathogens exploit. Unraveling the mechanisms behind how these factors impact the highly interdependent transmission pathways requires moving beyond an individual-based risk factor paradigm to a

systems perspective that accounts for dynamic population-level processes. In this talk, I will present a systems framework that accounts for mul-tiple modes of environmentally-mediated transmission and environmental processes that govern pathogen fate and transport.

Dose-response relationships for environmentally-mediated infectious disease transmission models

Andrew Brouwer, *Research Investigator, Department of Epidemiology, University of Michigan*

Environmentally-mediated infectious disease transmission models provide a mechanistic approach to examining environmental interventions for outbreaks, such as water treat-ment or surface decontamination. The shift from the classical SIR framework to one incorporating the environment requires codifying the relationship between exposure to environmental pathogens and infection, i.e. the dose-response relationship. There has been little research examining the consequences of the choice of functional form in the context of transmission dynamics. We find that middle- and high-dose data do not constrain the low-dose response, and different dose-response forms that are equally plausible given the data can lead to significant differences in simulated outbreak dynamics. However, identifiability analysis offers a way to manage multiple sources of uncertainty and leverage environmental monitoring to make inference about infectivity. By applying an environmentally-mediated infectious disease model to the 1993 Milwaukee *Cryptosporidium* outbreak, we demonstrate that environmental monitoring allows for inference regarding the infectivity of the pathogen and thus improves our ability to identify outbreak characteristics such as pathogen strain.

9:00-10:30	Breakout	Larch

Measles 1

Chair: Kevin McCarthy, *Senior Research Scientist, Institute for Disease Modeling*

Demographic transition, immunization, and the dynamics of measles in China

Sheng Li, *Assistant Professor, City University of New York, School of Public Health*

Industrialization and demographic transition generate non-stationary dynamics in human populations that can affect the transmission and persistence of infectious diseases such as measles. Based on a national 30-year measles dataset, we explored the spatial-temporal patterns of measles in China. A novel, time-varying catalytic model was developed to explain that a combination of demographic transition and reduced prevalence due to improved vaccination, has shifted the age distribution of susceptibility to measles throughout China.

Integrating data, demography, and dynamics to inform vaccination policy: Measles and rubella in a changing world

Amy Winter, *Postdoctoral Fellow, Princeton University*

Human demography directly and significantly affects measles and rubella transmission dynamics. The non-linear effects of population dynamics on disease transmission suggest that our policy-driven vaccination thresholds may be non-applicable across regions. This presentation draws on examples from the Americas and Africa to show that measles and rubella vaccination control techniques must cater to local population dynamics.

Role of supplementary immunization activity scheduling on measles incidence in Nigeria

Kurt Frey, *Research Engineer, Institute for Disease Modeling*

Around 40% of Nigerian children under two years of age receive measles containing vaccine via routine immunization (RI). National and subnational supplementary immunization activities (SIAs) are used to enhance immunity levels and reduce measles incidence. Measles infectivity in Nigeria demonstrates pronounced seasonal forcing with infectivity peaking during periods of low rainfall. This study examines the role of SIA scheduling on measles incidence, and seeks to identify an optimal timetable for deploying SIAs.

The geography of measles vaccination in the African Great Lakes region

Saki Takahashi, *PhD Student, Princeton University*

Expanded access to measles vaccination was among the most successful public health interventions of recent decades. All WHO regions currently target measles elimination by 2020, yet continued measles circulation makes that goal seem elusive. Clustering of low vaccination areas may allow for pockets of susceptibility that sustain circulation despite high overall (i.e., regional or national) coverage. Using data from Demographic and Health Surveys, we quantify spatial patterns of measles vaccination in ten countries in the African Great Lakes region between 2009-2014, identify "coldspots" where vaccine coverage is below the WHO target of 80%, and estimate the local effect of supplementary immunization activities. Characterizing heterogeneities in susceptibility that cross administrative boundaries is especially important since targeting at-risk areas and trans-national coordination are likely required to eliminate measles in the region.

9:00-10:30	Breakout	Auditorium

Malaria 1

Chair: Caitlin Bever, *Senior Research Scientist, Institute for Disease Modeling*

Inferring sources and sinks of malaria importations in Madagascar

Amy Wesolowski, *Postdoctoral Fellow, Princeton University*

Humans are able to introduce malaria parasites beyond the limits of mosquito dispersal. Understanding the dynamic nature of sources and sinks of human connectivity and malaria parasites will be key to assessing the feasibility of control and elimination. Here, we focus on identifying these sources and sinks using a range of connectivity measures in Madagascar. In particular, we focus on the temporal and spatial dimensions of the risk of malaria being reestablished on the high plateau. We also identify how simple mathematical models can be used to identify areas where the reported cases may be misaligned with the underlying transmission dynamics, perhaps suggesting that other factors such as importations may be playing a role in the epidemiology.

The ecology of malaria

Dave Smith, *Professor, IHME, University of Washington*

The ecology of malaria transmission is the study of complex interactions between humans, parasites, mosquitoes, and the environment that allow parasites to persist. Malaria transmission can be affected by various kinds of "noise." While it is often assumed this noise is merely a nuisance, it can have surprisingly large effects.

Quantitative, model-based estimates of variability in the generation and serial intervals of *Plasmodium falciparum* malaria

John Huber, *Undergraduate Student, University of Notre Dame*

The serial interval is a fundamentally important quantity in infectious disease epidemiology that has numerous applications, such as inferring transmission linkages between reported cases of *P. falciparum* malaria in near-elimination settings. Despite its importance, the serial interval for *P. falciparum* malaria is poorly understood quantitatively. To obtain a quantitative estimate of its serial interval, the sum of the components of the *P. falciparum* transmission cycle was taken based on a combination of mathematical models and empirical data. During this process, a number of factors were identified that account for substantial variability in its serial interval across different contexts. The implications of this variability for inferences about transmission linkages between reported cases will be discussed.

Sharpening malaria surveillance with next-generation antibody assays

Bryan Greenhouse, *Associate Professor, University of California, San Francisco*

Antibodies directed against malaria parasites are inexpensive and easy to measure but remain an underutilized surveillance tool due to a lack of consensus on what to measure and how to interpret results. High throughput screening of antibodies from well-characterized cohorts offers a means to rationally choose the most informative sets of responses and analytical methods. Recent data suggest that high-resolution data on malaria exposure, reported as interpretable metrics such as incidence, can be obtained from a handful of antibody responses if chosen and analyzed appropriately.

9:00-10:30	Breakout	Madrona

HIV

Chair: Anna Bershteyn, *Senior Research Manager, Institute for Disease Modeling*

The HIV epidemic in sub-Saharan Africa: Why do we need maps, and why aren't we good at it?

Diego Cuadros, *Assistant Professor, University of Cincinnati*

HIV continues to ravage many parts of Africa with millions of people infected. In order to reverse the HIV epidemic, the rate of new HIV infections has to be dramatically reduced. This will require an aggressive and smart implementation of the control intervention strategies currently available. Recent work has uncovered the extraordinary heterogeneity in HIV risk by geography in generalized epidemic settings, running contrary to early expectations at the start of the epidemic. There is real opportunity to exploit those geographical heterogeneities for epidemic control by intervening in the most vulnerable populations. Current knowledge, remaining gaps, and future of the geography of the HIV epidemic in Africa will be discussed during this talk.

HIV self-testing for men who have sex with men

Susan Cassels, *Assistant Professor, University of California, Santa Barbara*

HIV self-testing kits are now available over the counter, and some health departments have already started implementing programs to increase their use. However, the potential impact of these tests on the HIV epidemic among men who have sex with men (MSM) is unknown. Using data from two different epidemiologic settings in the U.S., Seattle and Atlanta, we use stochastic network-based HIV transmission models to estimate how different strategies of HIV self-testing at the individual and partnership levels affects HIV incidence. Our models help identify the most effective strategies for promotion, including targeting sub-populations and combining self-testing with continued clinic-based testing.

Predicting overall vaccine efficacy in a new setting by re-calibrating baseline covariate and immune response endpoint effect modifiers of genotype-specific vaccine efficacy

Ying Huang, *Associate Member, Fred Hutchinson Cancer Research Center*

We discuss the Gilbert and Huang (2016, Epidemiologic Methods) transport formula for predicting overall cumulative vaccine efficacy through time t (VE(t)) to prevent clinically sig-nificant infection with a genetically diverse pathogen (e.g., HIV infection) in a new setting for which a Phase III pre-ventive vaccine efficacy trial that would directly estimate VE(t) has not yet been conducted. The formula integrates data from (1) a previous Phase III trial or trials, (2) a Phase I/II immune response biomarker endpoint trial in the new setting where a follow- up Phase III trial is planned, (3) epidemiological data on background HIV infection incidence in the new setting, and (4) genomic epidemiological data on HIV sequence distributions in the previous and new settings. For (1), the randomized vaccine versus placebo Phase III trial yields estimates of vaccine efficacy to prevent particular genotypes of HIV in participant subgroups defined by baseline covariates X and immune responses to vaccination S(1) measured at a fixed time point post-vaccination that modify genotype-specific vaccine efficacy. For (2), the Phase I/II trial tests the same vaccine in a new setting, or a refined new vaccine in the same or new setting, and measures the same baseline covariates and immune responses as the ori-ginal Phase III trial. For (3), epidemiological data in the new setting are used to project overall background HIV infection rates in the baseline covariate subgroups in the planned Phase III trial, hence re- calibrating for HIV incidence dif-ferences in the two settings; whereas for (4), databases of HIV sequences measured from HIV infected individuals are used to re-calibrate for differences in the distributions of the circulating HIV genotypes in the two settings. The methods are applied to current HIV vaccine trials and possibly to other infectious diseases such as dengue.

Modelling impact of targeted HIV pre-exposure prophylaxis in Zimbabwe

Zindoga Mukandavire, *Assistant Professor, London School of Hygiene & Tropical Medicine*

Modeling results on Zimbabwe suggest that with good planning and programming, PrEP could be an important addition to the existing HIV prevention package in Zimbabwe. In general our findings demonstrate that PrEP programmes should target high-risk individuals. An individual's age is also important in targeting of PrEP and our results suggest that it is always better to target younger individuals of equal risk.

9:00-10:30	Breakout	Laurel

Software Tutorial

Benoit Raybaud, *Research Software Engineering Manager, Institute for Disease Modeling*

IDM researchers use software tools and workflows in order to create and manage analysis based on IDM's Epidemiological MODeling (EMOD) software model. This session will introduce EMOD and the ecosystem of tools and features used internally. Those include: the Python pre- and post-processing features, the sweep and visualization capabilities of DTK-Tools, and an example of dashboard visualization for malaria. Tools presented will be made available for attendees.

IndividualProperties and InterventionStatus

Dan Bridenbecker, *Senior Software Engineer, Institute for Disease Modeling*

This session will provide a short introduction on IndividualProperties and how these will be used with an upcoming new feature called InterventionStatus (formerly known as CascadeState).

Binding epidemiology to visual elements: Flexible presentation of EMOD simulation outputs.

Milen Nikolov, *Postdoctoral Research Scientist, Institute for Disease Modeling*

Visualization of disease models features and outputs is important for effective communication of results, debugging, and thorough understanding of complex model behavior. We showcase client-side visualization tools, in development at IDM, allowing flexible binding of epidemiological components to generic configurable visual elements in the browser. We present a set of examples which visually highlight various epidemiologically relevant model characteristics (e.g. mobility of infected individuals in the context of malaria outbreaks, and targeted interventions in simulations) demonstrating the amplification of important but otherwise subtle epidemiology dynamics, via straightforward visual elements templates a click away from simulation execution.

10:30-10:45	Break	Foyer

10:45-11:45	General Session	Auditorium

General Session 3

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

All your base are belong to us: Using genomics to solve public health problems

Jen Gardy, *Senior Scientist, BC Centre for Disease Control*

Fast and cheap genome sequencing technology has unlocked a world of possibility in public health, from rapid dia-

gnosis and personalized medicine to more accurate reconstruction of disease transmission networks. Using TB as an example, I'll share how our TB genomics projects, now at over 1500 genomes and counting, are helping guide public health policy and practice in British Columbia and beyond.

Fulfilling the potential of genomic epidemiology of malaria

Dan Neafsey, *Associate Director, Genomic Center for Infectious Disease, Broad Institute*

As with other deadly disease, our knowledge of malaria has greatly benefited in recent years from new genomic data and analytical tools to interpret those data. Drug resistance, vaccine efficacy, and transmission dynamics are examples of themes that have become rapidly more tractable due to advances in genomic technology. Further progress in the genomic epidemiology of malaria will come from the maturation of tools and models to interpret genomic data, and the capacity to generate such data more quickly and in disease-endemic settings.

11:45-4:00	Lunch and Excursion	Woodinville, WA

Lunch will be hosted by IDM. IDM will also provide transportation to and from Woodinville. After lunch explore the bounty of Washington's premier wineries: Chateau Ste. Michelle, Columbia, and Novelty Hill/Januik. You may also take advantage of the Red Hook Brewery, Woodinville Distillery, or Sammamish River Trail. You must be registered to attend.

For the itinerary and map, see the following pages.

5:45-9:00	Dinner	Daniel's Broiler

Dinner at Daniel's Broiler, hosted by IDM

Please join us for hors d'oeuvres and wine starting at 5:45, dinner service will begin promptly at 6:15. You must be registered to attend.

Daniel's Broiler is on the 21st floor of Bank of America tower, which can be accessed by the Hyatt elevators towards the Sky Bridge.

SYMPOSIUM EXCURSION

Lunch and Tour of Woodinville Wine County: 12:00 - 4:00

IDM will host lunch at Columbia Winery for registered excursion attendees from 12:30pm to 1:30pm. Afterwards, attendees will be allowed to freely explore the Woodinville Wine Country including Woodinville Whiskey Distillery, Redhook Brewery, and the Sammamish River Trail.

The city of Woodinville (~20-minute drive from Bellevue) is a friendly community in a scenic agricultural valley where people are drawn to one of the finest wine tasting experiences anywhere and boasts over more than 100 wineries and tasting rooms.

How it Works

If you are registered for the excursion, you will find an excursion ticket located with your name badge that includes the following benefits:

- Chartered bus transportation to and from the wineries in Woodinville and the Hyatt in Bellevue
- IDM-hosted lunch
- Discounted wine flights available with cash purchases at featured wineries.

Each ticket will indicate your starting point to explore Woodinville Wine Country. We kindly ask that you start there to evenly distribute attendees and allow for easy access to wine tastings. If you do not intend to visit the wineries, please feel free to explore the area on your own.

1. Chateau Ste. Michelle
2. Columbia Winery
3. Novelty Hill Januik

Schedule of Events

- 12:00: Buses depart from the Hyatt Regency Lobby for Woodinville
- 12:30: Arrive at Columbia Winery
- 12:30 - 1:30: Lunch at Columbia Winery
- 1:30: First stop on your ticket (if attending the wineries)
- 2:30 - 3:45: Explore Woodinville at your leisure and schedule
- 4:00: Buses depart from Columbia Winery
- 4:45: Buses return to the Hyatt Regency, Bellevue

WOODINVILLE WINE COUNTRY

1 **START HERE**
Columbia Winery

Columbia Winery offers a rich collection of grape varieties in the state.

2 **Chateau Ste. Michelle**

Chateau Ste. Michelle features award-winning wines and unparralled tasting experience.

3 **Novelty Hill Januik**

Novelty Hill Januik is a favorite Woodinville winery with a sleek, modern winery design, expansive gardens and outdoor patio.

4 **Woodinville Whiskey Company**

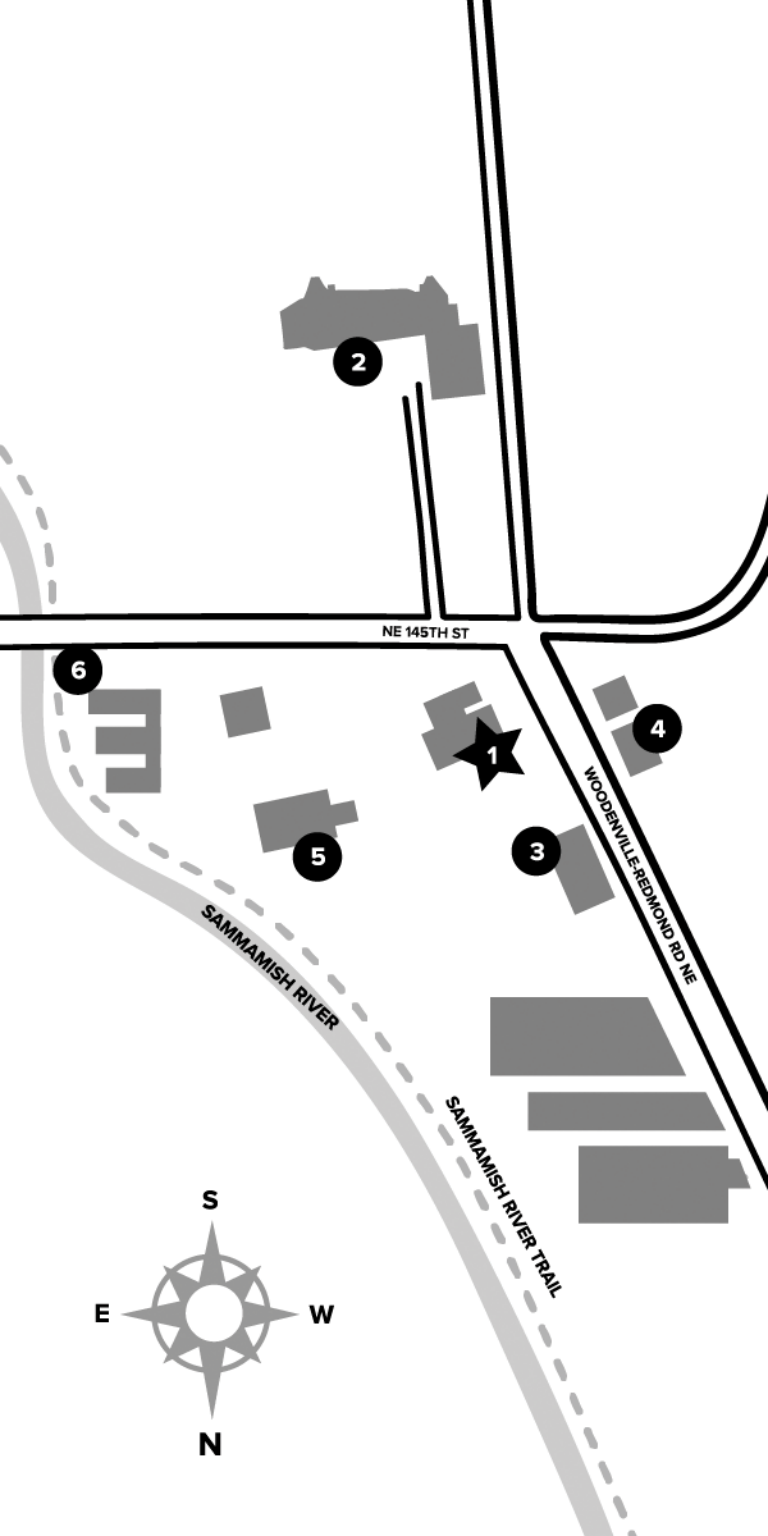
State-of-the-art distilling equipment, pure ingredients, pristine water and unique aging conditions make Washington an ideal place for distilling.

5 **Redhook Brewery**

A gorgeous brewery reminiscent of the old Bavarian brew houses, Redhook Brewery is one of the finest craft brew makers located in the heart of Woodinville, Washington.

6 **Sammamish River Trail Entrance**

Sammamish River Trail is paved and offers extraordinary views of the river, the broad Sammamish River Valley, Cascade foothills and Mt. Rainier.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Day 3 Overview		
7:30-8:45	Auditorium Foyer (Olympic Tower)	Registration & Breakfast
9:00-10:30	General Session 4 **Auditorium**	Jillian Gauld, IDM Samson Kiware, Ifakara Health Institute
10:30-11:15	Break	
11:15-12:15	Panel Discussion **Auditorium**	From data to decisions: the role of modeling in optimizing resource allocation in the fight against disease.
12:15-1:30	Eques Restaurant (2nd Floor Lobby)	Lunch Buffet
1:30-3:00	Tuberculosis **Madrona**	Nimalan Arinaminpathy, Imperial College London Zoë McLaren, Univ. of Michigan Walter Beyeler on behalf Patrick Finley, Sandia National Laboratories Damion Dooley, UBC/BCCDC
1:30-3:00	Malaria 2 **Auditorium**	Ruben Conner, PATH Katherine Battle, Univ. of Oxford Emilie Pothin, Swiss TPH Andre Lin Ouedraogo, IDM
1:30-3:00	COMPS: Software Service for Research **Cottonwood**	John Sheppard, IDM
1:30-3:00	Advances in Applied Math for Infectious Diseases **Juniper**	Kyle Gustafson, IDM Ewan Cameron, Univ. of Oxford Mauricio Santillana, Harvard Univ. Niall Mangan, UW
1:30-3:00	Dengue **Larch**	Isabel Rodriguez-Barraquer, Johns Hopkins University Katia Koelle, Duke University Alex Perkins, Univ. of Notre Dame
1:30-3:00	Measles 2 **Laurel**	Nita Bharti, Penn State Univ. Matthew Ferrari, Penn State Univ. Mark Jit, LSHTM
3:00-3:45	Break	
3:45-5:45	General Session 5 **Auditorium**	Ruanne Barnabas, UW Todd Noel on behalf of Carrie McNeil, Sandia National Laboratories Claudia Emerson, McMaster University

SESSIONS

7:30	Registration	Auditorium Foyer
Registration and full service breakfast		

9:00-10:30	General Session	Auditorium

General Session 4

Chair: Laina Mercer, *Research Statistician, Institute for Disease Modeling*

Typhoid fever in Santiago, Chile: Modern insights where historical data meet mathematical modeling

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

The mechanisms of typhoid transmission remain largely unknown in most modern-day settings. Although the disease is broadly correlated with a lack of clean drinking water and sanitation, Santiago, Chile, had nearly universal access to treated drinking water and widespread sewage coverage, yet had high endemic levels of typhoid in the 1970s. Prior to vaccination and other interventions in the early 1980s, high-resolution data were collected to shed light on cases, chronic carriers, and mechanisms of disease transmission, data that are rarely available in combination in modern settings. Investigating historical sites where typhoid has been successfully controlled can provide valuable insight for modern intervention planning. By understanding the significance of unknowns that remain within a site where we understand the burden of chronic carriers, mechanisms of transmission, and incidence, we are more prepared to quantify potential risks for control planning we may face in modern settings.

Attacking the mosquito on multiple fronts: Insights from vector control optimization model (VCOM) for malaria elimination

Samson Kiware, *Research Scientist, Ifakara Health Institute*

Despite great achievements by insecticide-treated nets (ITNs) and indoor residual spraying (IRS) in reducing malaria transmission, it is unlikely these tools will be sufficient to eliminate malaria transmission in many settings today. For-tunately, field experiments indicate that there are many prom-ising vector control interventions that can be used to complement ITNs and/or IRS by targeting a wide range of biological and environmental mosquito resources. We present the Vector Control Optimization Model (VCOM), which is a computational tool to predict the impact of combined vector control interventions at the mosquito population level in a range of eco-epidemiological settings. The model predicts specific combinations of vector control tools to achieve local malaria elimination and can assist researchers and program decision-makers on the design of experimental or operational research to test vector control interventions.

10:30-11:15	Break	Auditorium Foyer

11:15-12:15	General Session	Auditorium

Panel Discussion

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

From data to decisions: The role of modeling in optimizing resource allocation in the fight against disease

12:15 -1:30	Lunch	Eques

2nd floor near the Hyatt's grand staircase

1:30-3:00	Breakout	Madrona

Tuberculosis

Chair: Bradley Wagner, *Research Scientist, Institute for Disease Modeling*

Diagnostic delays in the control of tuberculosis: Looking for keys under the lamp-post?

Nimalan Arinaminpathy, *Senior Lecturer, Mathematical Epidemiology, Imperial College London*

In country settings such as India, TB patients typically visit a series of providers before finally being diagnosed. There has been much attention around these delays in diagnosing TB, and what we might do to reduce these delays in order to reduce TB transmission. However, there is increasing evidence that patient behaviour, as well as the quality of TB diagnosis, can be an important driver in TB transmission. In this context I will describe recent perspectives from India, and possible implications for critical needs in addressing TB transmission.

A new method for estimating disease prevalence: An application to multi-drug resistant tuberculosis

Zoë McLaren, *Assistant Professor, University of Michigan*

This work develops an innovative, low-cost, data-driven method to estimate disease prevalence from routinely-collected data from diagnostic laboratories. We demonstrate that approximately one-quarter of multi-drug resistant tuberculosis cases were undiagnosed between 2004-2010 in South Africa. We discuss the wide applicability of our method for using routinely-collected data to monitor population prevalence can guide evidence-based policy making.

Modeling to create sustainable point of care HIV/TB testing networks for developing countries

Walter Beyeler on behalf of Patrick Finley, *Computer Science R&D, Sandia National Laboratories*

Developing countries rely on lab testing to assess and treat individuals for both acute and chronic illnesses. Point-of-care (POC) testing offers opportunities to improve convenience

and decrease time needed for diagnosis, but effectively introducing POC testing into the public health and healthcare infrastructure is challenging. It requires commitments to training, equipment maintenance, and supply logistics that can be hard for developing countries to sustain. Working closely with in-country partners, we have modeled the tradeoffs of centralized and POC testing to enable more efficient and effective implementation. Specifically, we evaluate alternative implementation strategies being considered for POC testing in the TB and HIV programs in Cambodia, deriving system-performance metrics including cost, accuracy, turnaround time, and patient access. Additionally, we model the potential benefits of integrating program-specific implementation plans to identify cooperative strategies that may be more sustainable and more effective than current disease-centric approaches.

Model based assessment of reactive interventions for the elimination and control of malaria

Damion Dooley, *Scientific Programmer, Department of Pathology, University of British Columbia/BCCDC*

GenEpiO is a consortium-driven OWL ontology project that provides a comprehensive controlled vocabulary for infectious disease surveillance and outbreak investigations. GenEpiO leverages a number of its companion OBO Foundry family of ontologies in order to cover clinical, environmental, genomic sequencing, and epidemiology-related terminology. The ontology germinated from the IRIDA.CA food-borne pathogen sequencing and analysis mission in 2014, but has since branched out to cover tuberculosis sample metadata. We seek to demonstrate the utility of ontology and related tools to facilitate data exchange and analysis between health agencies at a local and global level.

1:30-3:00	Breakout	Auditorium

Malaria 2

Chair: Jaline Gerardin, *Research Manager, Institute for Disease Modeling*

Co-chair: Caitlin Bever, *Senior Research Scientist, Institute for Disease Modeling*

Ongoing programs and impact in Southern Province, Zambia

Ruben Conner, *Research Officer, PATH*

PATH-MACEPA and the NMCC have been engaged in various activities to reduce transmission in Southern Province of Zambia. Most recently, this has included a randomized controlled trial of mass drug administration. This program combined with enhanced standard of care, resulted in a 93% reduction in malaria prevalence from 2012 to 2015. This presentation will focus on ongoing work in Southern Province along with a deep-dive into some of the research results.

Mapping malaria in low-transmission settings

Katherine Battle, *Postdoctoral researcher, Malaria Atlas Project, University of Oxford*

Mapping malaria in low-transmission settings presents new challenges with regards to the modeling methodologies employed. The data available for such models vary widely in type and source and may be sparse. The type of modeling framework used depending on the type and quality of data will be discussed.

Using models to inform operational planning in the context of malaria elimination

Emilie Pothin, *Statistical Modeler in Epidemiology, Swiss Tropical and Public Health Institute /CHAI*

In order to achieve elimination, countries will have to target their interventions to areas where they will be the most impactful. This will require data-driven decisions. Data, with the addition of mathematical models, can help National Programs better plan their strategies. Malaria dynamics can be dissected into a set of metrics that can be mapped using newly developed geostatistical approaches, and linked to the suitability for different malaria intervention packages with mathematical models. Application of the methodology for Haiti will be presented to illustrate how the theoretical and modeling framework for stratification can be applied to inform design of sustainable and accelerated elimination strategies.

Modeling the effectiveness of seasonal malaria chemoprevention in a high and seasonal malaria transmission setting

André Lin Ouedraogo, *Resident Scholar, Institute for Disease Modeling*

Current seasonal malaria chemoprevention (SMC aims at reducing the incidence of malaria in children aged 3- 59 months in seasonal transmission settings. Although SMC was proven very successful in clinical trials, the heterogeneity of its effectiveness in operational campaigns has never been investigated.

1:30-3:00	Breakout	Cottonwood

COMPS Software Service for Research

John Sheppard, *Managing Principal Software Engineer, Institute for Disease Modeling*

The COmputational Modeling Platform Service (COMPS) is a toolset allowing users to leverage the power of High-Performance Computing clusters to generate and explore large modeling domains via the web. This session will show how to create the input data needed by the simulation, produce and organize large sets of simulations, explore and find previously generated simulation sets, and visualize the outputs.

1:30-3:00	Breakout	Larch

Dengue

Chair: Ben Althouse, *Research Scientist, Institute for Disease Modeling*

Challenges in the interpretation of dengue vaccine trial results

Isabel Rodriguez-Barraquer, *Research Associate, Johns Hopkins Bloomberg School of Public Health*

The first dengue vaccine has been licensed for use in multiple countries after large Phase 3 studies. However, there are still fundamental uncertainties regarding the vaccine's mode of action. These uncertainties limit our capacity to model the potential impact that this vaccine may (or may not!) have if rolled-out at the population level.

Should we expect dengue virulence evolution in response to Dengvaxia vaccination?

Katia Koelle, *Associate Professor, Duke University*

Theory underlying the evolution of virulence indicates that many pathogens should evolve to an intermediate level of virulence given the trade-offs between transmissibility and the duration of infectiousness. Further research indicates that imperfect viral vaccines that do not prevent infection have the potential to select for "hotter" viruses, i.e., those having higher propensities to cause severe disease in unvaccinated individuals. Here, using a combination of within-host dengue models fit to data and published assumptions about the mode of action of Sanofi Pasteur's Dengvaxia® vaccine, we evaluate whether selection for greater dengue virulence is a possibility in regions with high vaccination coverage.

This work is in collaboration with Dr. Rotem Ben-Shachar.

Statistical and biological uncertainties associated with vaccine efficacy estimates and their implications for dengue vaccine impact projections

Alex Perkins, *Eck Family Assistant Professor, University of Notre Dame*

Given the limited effectiveness of strategies based solely on vector control to reduce dengue virus transmission, it is expected that an effective vaccine could play a pivotal role in reducing the global disease burden of dengue. Dengvaxia® from Sanofi Pasteur recently became the first dengue vaccine to become licensed in select countries and to achieve WHO recommendation for use in certain settings, despite the fact that a number of uncertainties about the vaccine's efficacy and mode of action complicate projections of its potential impact on public health. We used a new stochastic individual-based model for dengue transmission to perform simulations of the impact of Dengvaxia® in light of two key uncertainties: statistical uncertainty about the numerical value of the vaccine's efficacy against disease, and biological uncertainty about the extent to which its efficacy against dis-

ease derives from the amelioration of symptoms, blocking of dengue infection, or some combination thereof. Our results suggest that projections of the vaccine's public health impact may be far more sensitive to biological details of how the vaccine protects against disease than to statistical details of the extent to which it protects against disease. Under the full range of biological uncertainty that we considered, there was nearly three-fold variation in the population-wide number of disease episodes averted. These differences owe to variation in indirect effects of vaccination arising from uncertainty about the extent of onward transmission of dengue from vaccine recipients. These results demonstrate important limitations associated with the use of symptomatic disease as the primary endpoint of dengue vaccine trials and highlight the importance of considering multiple forms of uncertainty in projections of a vaccine's impact on public health.

1:30-3:00	Breakout	Juniper

Advances in Applied Math for Infectious Diseases

Chair: Joshua Proctor, *Senior Research Scientist, Institute for Disease Modeling*

Spatial models of country-scale stochastic outbreaks using a Levy process

Kyle Gustafson, *Postdoctoral Research Scientist, Institute for Disease Modeling*

Disease outbreaks in naive populations can spread quickly and widely according to pathogen infectivity and host social network structure. Predictions of spatiotemporal outbreak dynamics are difficult and rarely deterministic, partly because host social networks are complex and time-dependent. We compare stochastic models of outbreak dynamics based on Levy flights and use the 2014-15 Ebola outbreak in Sierra Leone as a case study for testing a new method to improve the efficacy of intervention strategies.

Some recent advances in applied spatial statistics

Ewan Cameron, *Senior Computational Statistician, Malaria Atlas Project, University of Oxford*

In this talk I will highlight two key problems in the application of spatial statistical models to contemporary datasets with examples drawn from the disease mapping literature. Namely, the development of efficient methods for Gaussian process priors with sophisticated covariance functions and the treatment of covariate selection for down-scaling (or multi-scale) models.

Tracking and forecasting epidemic outbreaks using Internet searches, social media, and news reports

Mauricio Santillana, *Faculty member, Harvard University*

Novel disease surveillance systems based on information from: Internet search engines, social media, new reports, cloud-based EHRs, and crowd-sourced systems, have emerged as new ways to monitor

public health events and provide estimates of disease activity in near real-time. I will discuss how these novel systems compare to traditional healthcare-based disease surveillance systems for influenza, dengue, and Zika.

Data-driven discovery of disease dynamics using sparse selection and information criteria

Niall Mangan, *Acting Assistant Professor, University of Washington*

Rapidly inferring the structure and dynamics of disease networks is critical to identifying outbreaks and designing intervention. I present a framework for model selection using Sparse Identification of Nonlinear Dynamics (SINDy and Information Criteria. SINDy is a data-driven method for inferring nonlinear dynamical systems, which allows generation of data-supported candidate models from a combinatorially large number of possibilities. We demonstrate proof of concept for the method on a few dynamical systems, including a simulated Susceptible-Exposed-Infected-Recovered (SEIR network. The time-series data required to infer the SEIR model is representative of a single outbreak, suggesting that SINDy can recover the structure and dynamics of a disease network from a relatively small amount of data.

1:30-3:00	Breakout	Laurel

Measles 2

Chair: Kevin McCarthy, *Senior Research Scientist, Institute for Disease Modeling*

Measuring dynamic populations to reduce measles burden

Nita Bharti, *Assistant Professor, Pennsylvania State University*

Despite the existence of a cheap and effective measles vaccine, gaps in vaccination often occur because target population size estimates are inaccurate and populations are constantly changing. Measuring dynamic populations and rapid changes in population sizes is necessary to distribute sufficient doses of measles vaccines where they are needed. We've developed methods based on satellite imagery and other remotely-acquired data to measure both rapid and gradual changes in populations. In addition to informing current and future immunization strategies, we have used these methods to measure populations retrospectively and update estimated immunity profiles of previously vaccinated populations and reassess their risks of measles outbreaks and immunization priorities.

Better with age: Insights on measles surveillance and control

Matthew Ferrari, *Associate Professor, Pennsylvania State University*

Time series of case-counts are a staple data-source for studying epidemic dynamics, forecasting, and evaluating control. Variation in reporting rates over short (intra-epidemic)

or long (annual or decadal) can confound the interpretation of trends. Trends in reporting can obscure the interpretation of dynamic transitions, such as the emergence of outbreaks or the transition to elimination. Age-specific records can help identify biases caused by time-varying reporting and clarify trends in time-series reporting. We illustrate the application of age-specific surveillance to clarify temporal trends, evaluate the impact of vaccination programs, and infer vaccination response targets during outbreak response using case studies from sub-Saharan Africa and Asia.

Can timely administration of measles vaccines save lives?

Mark Jit, *Professor, London School of Hygiene & Tropical Medicine*

The World Health Assembly aimed to reduce global measles mortality by 95% between 2000 and 2015. The target was missed despite improvements in measles-containing vaccine (MCV coverage. Poor timeliness of MCV administration may have contributed to continued measles mortality, but the importance of MCV timeliness is not well-understood. Hence we used DynaMICE (Dynamic Measles Immunization Calculation Engine to explore the impact of improved timeliness of MCV administration in low and lower-middle income countries. Results suggest that improved timeliness of MCV administration could reduce measles mortality by up to 80,000 deaths annually.

3:00-3:45	Break	Auditorium Foyer

3:45-5:45	General Session	Auditorium

General Session 5

Chair: Edward Wenger, *Senior Research Manager, Institute for Disease Modeling*

Utilizing implementation science to address barriers along the HIV care continuum

Ruanne Barnabas, *Assistant Professor, University of Washington*

This presentation will describe the key messages from implementation science studies that address gaps in the HIV continuum of care. Central to improving access to care are simplified, decentralized services which are evaluated for impact on health and cost.

Strengthening one health coordination using participatory-based tabletop exercises

Todd Noel on behalf of Carrie McNeil, *Project Lead, Sandia National Laboratories, International Biological and Chemical Threat Reduction*

Integration of participant- based data collection and eval-

uation in tabletop exercises provides an effective, unique approach for identifying strengths and gaps in outbreak preparedness across animal and public health sectors. The presentation will include a demonstration of novel, web-based technology developed for data collection and report development during in-person and virtual multi-player tabletop exercises.

The ethics of epistemology of disease modeling: A few considerations

Claudia Emerson, *McMaster University*

Presentation information not provided.

BIOGRAPHIES

Adam Akullian
Postdoctoral Research Scientist
Institute for Disease Modeling
aakullian@idmod.org

Adam Akullian has a PhD in Epidemiology from the University of Washington and an ScB in Environmental Science from Brown University. As a doctoral candidate, Adam studied the evolutionary ecology and spatial epidemiology of emerging enteric diseases in rural and urban Kenya, as well as the geography of HIV in rural areas of Kenya and Uganda. He is also a recipient of a National Science Foundation (NSF Graduate Research Fellowship. Before graduate school, Adam worked as a research scientist at the University of California, Berkeley where he investigated the ecology and spatial patterns of *Schistosoma japonicum* in China. As a member of the IDM's research team, Adam is focused on mathematical and epi-demiological modeling of HIV in sub-Saharan Africa with the goal of informing effective public health interventions.

Ben Althouse
Research Scientist
Institute for Disease Modeling
balthouse@idmod.org

Ben Althouse has brought his enjoyment of the dynamic, intellectually challenging and inherently collaborative nature of the scientific process to the IDM Epidemiology team as a Research Scientist, where he will explore pneumococcal pneumonia vaccines, the dynamics of enteric diseases, and the role of complex human contact structures on disease transmission. He holds a PhD in Epidemiology and a Master of Science in Biostatistics from the Johns Hopkins Bloomberg School of Public Health where he was awarded an NSF Graduate Research Fellowship, and holds Bachelor of Science degrees in Mathematics and Biochemistry from the University of Washington. His previous work has included mathematical modeling of sylvatic dengue virus transmission in nonhuman primates in Senegal, examining the role of antimicrobial use on the evolution of drug resistance, using Twitter as a model system of co-infection dynamics, and using novel data sources (such as Google searches, Twitter, and Wikipedia article views) for population-level surveillance of infectious and chronic diseases. Ben is an Affiliate Faculty member in the Department of Biology at New Mexico State University, Las Cruces, and a Guest Lecturer in the Information School at UW.

Nimalan Arinaminpathy
Senior Lecturer, Mathematical Epidemiology
Imperial College London
nim.pathy@imperial.ac.uk

A mathematical modeler interested in the spread and control of human tuberculosis (TB). A large part of his work focuses on TB in India and the South East Asian region, where control priorities have to be formulated in the context of complex healthcare systems.

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.

Katherine Battle
Postdoctoral researcher
Malaria Atlas Project, University of Oxford
katherine.battle@well.ox.ac.uk

Katherine works as a post-doctoral researcher with the Malaria Atlas Project in Oxford. She provides technical support to the Clinton Health Access Initiative (CHAI) to develop risk maps in countries working towards malaria elimination. Her previous work focused on estimating the global burden of *Plasmodium vivax* malaria, for which she analyzed geographic variation in relapse rates as well as the relationship between the prevalence of infection and incidence of clinical disease.

Anna Bershteyn
Senior Research Manager
Institute for Disease Modeling
abershteyn@idmod.org

Anna Bershteyn is a Senior Research Manager and Associate Principal Investigator at the Institute for Disease Modeling, where she leads the immunology, pathology, and within-host dynamics team. 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. In addition to other awards for her research, Anna was an Ida M. Green fellow, a Paul and Daisy Soros fellow, a Fannie and John Hertz fellow, and a National Science Foundation Gradu-ate Research fellow. Her modeling research focuses on HIV transmission dynamics and impact evaluation of biomedical and programmatic improvements to HIV care and prevention.

Caitlin Bever
Senior Research Scientist
Institute for Disease Modeling
cbever@idmod.org

Caitlin Bever has a PhD in Biological Engineering from the Massachusetts Institute of Technology (MIT), along with a Bachelor's degree (BSc) with Combined Honors in Physics and Astronomy from the University of British Columbia (UBC. Caitlin received a Medtronic Fellowship for her post-graduate work at MIT and the Rudy Haering Medal for outstanding graduating physics student from UBC. Her academic research focused on understanding how to select useful predictions from uncertain mathematical models of biology. Prior to joining IDM, Caitlin worked on a team at Entelos that built a novel model of atherosclerosis in mouse, paired with an analogous model of cardiovascular disease in human, which improved the design of pre-clinical experiments and identified key indicators for translating results from mouse to human. Caitlin was on assignment in Switzerland for a year and a half as a consultant for Entelos, after which she worked with the malaria modeling group at the Swiss Tropical and Public Health Institute. In her role there, she developed new methods for spatial modeling of entomological inoculation rates and co-wrote a WHO report on how country-specific considerations contribute to the impact of malaria vaccines. As a member of IDM's research team, Caitlin leads the projects on malaria vaccines and human African trypanosomiasis (HAT with a focus on disease eradication.

Walter Beyeler
Sandia National Laboratories
ebeyel@sandia.gov

Nita Bharti
Assistant Professor
Pennsylvania State University
nita@psu.edu

Nita Bharti is an assistant professor of Biology at Pennsylvania State University in the Center for Infectious Disease Dynamics. Her research focuses on the links between human behavior and health; in particular the impact of movement and dynamic pop-ulation sizes on access to health care and infectious diseases. She integrates various data sources, including satellite imagery, mobile phones, surveys, andviral genome sequences, to quantify the dynamics of human populations, land use, access to health care, and disease transmission.

Dan Bridenbecker
Senior Software Engineer
Institute for Disease Modeling
dbridenbecker@idmod.org

As one of the EMOD developers, Mr. Bridenbecker has done extensive work on demographics, reporters, and numerous Malaria and HIV features. Prior to joining IDM, Dan spent most of his career in the defense field including over 10 years on air-to-air combat simulations and tools.

Andrew Brouwer
Research Investigator
Department of Epidemiology,
University of Michigan
brouweaf@umich.edu

Andrew Brouwer is a research investigator in the Department of Epidemiology at the University of Michigan. He received his BA in mathematics and chemistry and MA in mathematics from the SUNY College at Potsdam (2009) and his MS in environmental science and engineering from Clarkson University (2011). Andrew also earned his MS in applied and interdisciplinary mathematics (2013), MA in statistics (2015), and PhD in applied and interdisciplinary mathematics (2015) at the University of Michigan. He was a postdoctoral research fellow in the Department of Epidemiology at the University of Michigan before joining their faculty as a research investigator.

Ewan Cameron
Senior Computational Statistician
Malaria Atlas Project, University of Oxford
dr.ewan.cameron@gmail.com

After postdoctoral research in extra-galactic astronomy (in Switzerland and Bayesian statistics (in his homeland, Australia, Dr Cameron joined the Malaria Atlas Project at the University of Oxford in 2014 as a senior computational statistician. His recent work has focused on the calibration of individual simulation models for malaria transmission and on the spatio-temporal mapping of malaria on a global scale.

Susan Cassels
Assistant Professor
University of California, Santa Barbara
scassels@geog.ucsb.edu

Susan Cassels is an assistant professor in the Geography department at the University of California Santa Barbara, although her work spans the disciplines of demography and epidemiology as well. Her research interests are in the areas of population health, migration, epidemic modeling, HIV/AIDS, and sexual networks. Current disease modeling is focused on innovative HIV testing strategies to reduce HIV incidence among men who have sex with men. Other work is focused on immigration and residential mobility in Southern California and its effects on sexual risk behavior, sexual network structure, and HIV transmission.

Flaminia Catteruccia
Associate Professor
Harvard TH Chan School of Public Health
fcatter@hsph.harvard.edu

Dr. Flaminia Catteruccia is Associate Professor at the Department of Immunology and Infectious Diseases in the Harvard T.H. Chan School of Public Health. Her lab studies the biology of mosquitoes that transmit malaria, a disease that kills half a million people each year. In particular, her research focuses on how mosquitoes reproduce and transmit the disease to humans. Her goal is to reduce the malaria burden by identifying where we can interfere with the mosquito's ability to transmit deadly malaria parasites.

Flaminia trained as a molecular entomologist at Imperial College London, where she achieved the first genetic manipulation of *Anopheles* mosquitoes. She has since contributed numerous molecular and genetic studies that have expanded our understanding of mosquito biology and mosquito-parasite interactions. Her work includes field studies in a number of African countries to bridge laboratory findings to the implementation of novel strategies for malaria elimination.

Guillaume Chabot-Couture
Senior Research Manager
Institute for Disease Modeling
gcouture@idmod.org

Guillaume Chabot-Couture is a Senior Research Manager at IDM, and leads the analysis and model usage center. He has a PhD in Applied Physics from Stanford University. Guillaume's research interests include vaccination campaign data analysis and modeling, disease risk estimation, financial projections, and weather modeling.

Dennis Chao
Senior Research Scientist
Institute for Disease Modeling
dennisc@idmod.org

Dennis Chao studies the epidemiology of enteric disease. He has been with IDM for a little over a year.

Ruben Conner
Research Officer
PATH
rconner@path.org

Ruben Conner has been working with PATH for the past three years, where he has been involved in research coordination, costing, impact evaluation and visualization of data. He currently resides in Seattle, WA but enjoys regular trips to Zambia and Senegal.

Diego Cuadros
Assistant professor
University of Cincinnati
diego.cuadros@uc.edu

Diego earned his PhD degree in Biology at the University of Kentucky and hold a BSc degree in Biology from the National University of Colombia. His research focused in medical geography and quantitative epidemiology. Early during his career his research focused on understanding the role of biological cofactors as drivers of the variability in HIV transmission and epidemic trajectory across sub-Saharan Africa. During his postdoctoral training at Weill Cornell Medical College in Qatar, he has focused on understanding the spatial patterns of geo-graphical distribution of infectious diseases such as HIV and hepatitis C virus. He is currently working with the Africa Centre for Population Health investigating the drivers of the geo-graphical distribution of HIV infection in South Africa.

Ron Dagan
Professor
Ben-Gurion University of the Negev
rdagan@bgu.ac.il

Ron Dagan is Distinguished Professor of Pediatrics and Infectious Diseases at the Ben- Gurion University of the Negev, Beer- Sheva, Israel. He founded the Pediatric Infectious Disease Unit at the Soroka University Medical Center in Beer-Sheva and served as its director from 1987 to June 2014. He is a Founding Member of the World Society of Pediatric Infectious Diseases (WSPID, Member of the Executive Committee of the International Society of Infectious Disease (ISID and a Fellow of the Infectious Diseases Society of America (IDSA. He served as President of the European Society for Paediatric Infectious Diseases (ESPID from 2004 to 2006 and as President of the World Society for Pediatric Infectious Diseases (WSPID from 2006 through 2009. He has chaired the board of the International Symposia on Pneumococcus and Pneumococcal Diseases (ISPPD from 2010 to 2016. Prof. Dagan has contributed over 500 original articles, reviews and book chapters, and has presented over 500 papers at national and international scientific meetings. He has earned international recognition for his research, which has focused largely on vaccine preventable diseases, with particular emphasis on pneumococcal vaccines, the epidemiology of respiratory infections in children and pathogenesis, treatment and prevention of otitis media.

Damion Dooley
Scientific Programmer
Department of Pathology, University of British Columbia/BCCDC
damion.dooley@bccdc.ca

Damion is a scientific programmer in the Hsiao BC Public

Health Reference Laboratory, British Columbia Centre for Disease Control, which is affiliated with the University of British Columbia Department of Pathology and Laboratory Medicine. He has been the lead ontology developer of the Genome Canada funded IRIDA.CA project since 2015, and now leads GE2M, an open source project to enable the reuse of ontologies in software and datasets. Past work as CTO of his consultancy, Learningpoint.ca, and his web services company Communicopia Inc. (est. 1998), led to key roles in several startups including Ecotagious.ca, focusing on electricity conservation, and Jitsulab.com, providing academic-grade survey software.

Joe Eisenberg
Chair and Professor
Department of Epidemiology, University of Michigan
jnse@umich.edu

Dr. Eisenberg is the Chair and Professor of Epidemiology and the John G. Searle Professor of Public Health in the School of Public Health at the University of Michigan. Dr. Eisenberg received his PhD in Bioengineering in the joint University of California, Berkeley/University of California, San Francisco program, and an MPH from the School of Public Health at the University of California, Berkeley. He is an expert in water- and vector- borne transmission modeling, infectious disease epi-demiology, and microbial risk assessment. His broad research interests integrate infection transmission models and epidemiology studies to study environmental determinants of infectious disease. Dr. Eisenberg is the Chair and Professor of Epidemiology and the John G. Searle Professor of Public Health in the School of Public Health at the University of Michigan. Dr. Eisenberg received his PhD in Bioengineering in the joint University of California, Berkeley/University of California, San Francisco program, and an MPH from the School of Public Health at the University of California, Berkeley. He is an expert in water- and vector-borne transmission modeling, infectious disease epidemiology, and microbial risk assessment. His broad research interests integrate infection transmission models and epidemiology studies to study environmental determinants of infectious disease.

Claudia Emerson
McMaster University
emersoc@mcmaster.ca

Mike Famulare
Senior Research Scientist
Institute for Disease Modeling
mfamulare@idmod.org

Mike Famulare has a PhD in Physics from the University of Washington, Seattle, and a Bachelor of Science in Physics Edu-

cation 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, N.Y.C. 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.

Matthew Ferrari
Associate Professor
The Pennsylvania State University
mferrari@psu.edu

Dr. Matthew Ferrari is an Associate Professor of Biology and Statistics at the Center for Infectious Disease Dynamics at The Pennsylvania State University. His research combines population dynamic models and computational statistical methods to study the dynamics of pathogen transmission in space and time in human, animal, and plant systems. For the last decade, Dr. Ferrari has employed these methods to develop quantitative models to assess the performance of vaccination programs using surveillance data and forward projections of candidate vaccination strategies to facilitate decision and policy making.

Patrick Finley
Computer Science R&D
Sandia National Laboratories
pdfinle@sandia.gov

Patrick Finley is a computer scientist at Sandia National Laboratories in Albuquerque, New Mexico. As part of the Complex Systems group, Patrick applies computational modeling and data analytics to public health and disease outbreak control in the US and in developing countries. His current research interests include uncertainty analysis of disease models and applying artificial intelligence methods to improve biosurveillance in developing countries.

Stefan Flasche
Assistant Professor
London School of Hygiene & Tropical Medicine
Stefan.Flasche@lshtm.ac.uk

Stefan Flasche is an Assistant Professor at LSHTM.

Kurt Frey
Research Engineer
Institute for Disease Modeling
kfrey@idmod.org

Kurt Frey has a doctorate in Chemical Engineering from the Massachusetts Institute of Technology (MIT), as well as a Master of Science in Chemical Engineering Practice from MIT, and a Bachelor of Science in Chemical Engineering from Ohio State University. Kurt has worked for a variety of research groups, and was most recently at Argonne National Laboratory, supporting efforts on environmental processes for nuclear waste, both in recycling and disposal.

Jennifer Gardy
Senior Scientist
BC Centre for Disease Control
jennifer.gardy@bccdc.ca

Jennifer Gardy is a Senior Scientist at the BC Centre for Disease Control and an Assistant Professor at UBC's School of Population and Public Health, where she holds a Canada Research Chair in Public Health Genomics. When not doing science, she can be found talking about science on Canadian TV, regular guest-hosting shows such as The Nature of Things and Daily Planet.

Jillian Gauld
Postgraduate Research Scientist
Institute for Disease Modeling
jgauld@idmod.org

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
Research Manager
Institute for Disease Modeling
jgerardin@idmod.org

Jaline Gerardin has a PhD in Biophysics from the University of California, San Francisco, along with a Bachelor's degree (BA) in Chemistry and Physics from Harvard University. She is also an NSF Graduate Research Fellowship recipient. As a doctoral candidate, Jaline researched how cells use signaling

circuits to distinguish between long and short stimuli. By searching a large library of potential circuit designs, Jaline identified five families of architectures that can effectively measure the duration of a stimulus. Her research explained how small circuits can be designed to filter noisy input, decode information stored in dynamical profiles, and coordinate a series of events in time. Jaline has published papers on a wide variety of topics in such journals as Cell, Proceedings of the National Academy of Sciences, Journal of Chemical Physics, and Physics Letters.

As part of the research team at IDM, Jaline studies how antimalarial drugs can be deployed to reduce malaria transmission. Building on IDM's sophisticated malaria model, her work investigates the best campaign strategies for effective interventions with drugs in the context of other tools for malaria control and elimination.

Michael Goldstein
Professor
Durham University
michael.goldstein@durham.ac.uk

Bayesian statistician. Developed the Bayes linear approach for dealing with problems of sufficient size and complexity that standard Bayesian methods face serious practical and computational difficulties. Many years of experience in applying these methods to problems of uncertainty quantification for complex physical systems modelled by computer simulators.

Bryan Greenhouse
Associate Professor
University of California, San Francisco
Bryan.greenhouse@UCSF.edu

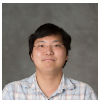
Dr. Bryan Greenhouse is an Associate Professor at the University of California, San Francisco in the Division of HIV, Infectious Diseases, and Global Health at Zuckerberg San Francisco General Hospital. Dr. Greenhouse completed his MD at the University of Pennsylvania School of Medicine and his MA in Biostatistics at the University of California, Berkeley. Dr. Greenhouse's research program is focused on understanding the epidemiology and biology of malaria by applying laboratory and analytical methods to field studies, primarily in Africa. Specifically, his current projects focus on understanding the development of naturally acquired immunity to malaria, creating novel serologic tools to measure malaria exposure and immunologic protection, and using parasite population genetics and spatial data to understand parasite transmission and evolution.

Kyle Gustafson
Postdoctoral Research Scientist
Institute for Disease Modeling
kgustafson@idmod.org

Kyle Gustafson joined IDM full-time in January 2016 as a postdoctoral research scientist advised by Joshua L. Proctor in the Applied Math group. His previous studies in magnetized plasma turbulence and mammalian gene regulation inform a unique perspective on disease dynamics in human populations. Kyle earned his PhD in Physics with Bill Dorland at the University of Maryland as a Fellow of the Fannie and John Hertz Foundation.

M Elizabeth Halloran
Professor
Fred Hutchinson Cancer Research Center/
University of Washington
betz@fhcrc.org

Professor M. Elizabeth (Betz) Halloran is an expert in novel designs and analysis of vaccine studies that go beyond evaluating protective efficacy. She is Director of the NIGMS-MIDAS Center for Inference and Dynamics of Infectious Disease and Director of the Summer Institute for Statistics and Modeling of infectious Diseases held each summer at the University of Washington.



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

Hao Hu leads the Epidemiology Section at 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, 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.

Prior to joining IDM, Hao performed research in the Laboratory for the Modeling of Biological and Social-technical Systems (MoBS) at Indiana University (now at Northeastern University). His was part of the team modeling spatial spread of infectious diseases in a structured population. He is also involved in the real-time modeling of the A/H1N1 pandemic in 2009, calculating the short-term virus importation trajectories and projecting seasonal transmission potential based on empirical transportation networks.

Hao has a PhD in Biophysics from Indiana University, and a Bachelor of Science degree in Applied Physics from the University of Science and Technology of China (USTC).

Robert Hart
Vice President and General Manager
Institute for Disease Modeling
rhart@idmod.org

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 firm 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 SeaPoint 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.

Mark Hatherill
Professor
SATVI, University of Cape Town
mark.hatherill@uct.ac.za

Mark Hatherill is Professor and Director of the South African Tuberculosis Vaccine Initiative (SATVI) at the University of Cape Town. Trained as a pediatrician and critical care subspecialist, since 2005 he has focused on the design and implementation of clinical trials of novel TB vaccines and therapeutic regimens in children and adults. His current research focuses on the use of biomarkers to target TB preventive therapy.

Ying Huang
Associate Member
Fred Hutchinson Cancer Research Center
yhuang@fhcrc.org

Ying Huang is an Associate Member at the Vaccine & Infectious Diseases Division of the Fred Hutchinson Cancer Research Center. She is also an Affiliate Associate Professor at the Department of Biostatistics at the University of Washington. Dr. Huang's research interests center on the statistical design and analysis of biomarker studies for application in infec-

tious diseases and cancer. Her primary interest in HIV vaccine research is in developing and evaluating immune correlates of vaccine's protective effect for selecting and refining vaccine regimens and for predicting vaccine's protective effect in future efficacy trials.

John Huber
Undergraduate Student
University of Notre Dame
jhuber3@nd.edu

John Huber is a senior at the University of Notre Dame, studying Applied and Computational Mathematics and Statistics. He is an undergraduate researcher in the lab of Dr. Alex Perkins. His research is focused on using mathematical models to understand transmission dynamics for vector-borne diseases.

Mandy Izzo
Senior Science Writer
Institute for Disease Modeling
mizzo@idmod.org

Mandy Izzo is a Senior Science Writer for the Institute for Disease Modeling, where she develops scientific content for the global health community. 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 post-doctoral 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. Trained as an Evolutionary Ecologist with specialization in the Behavioral Ecology of insects, Mandy's work on insects has spanned topics such as the evolution of cricket song in the presence of an acoustically-orienting parasitic fly; the evolution of signals mediating inter- and intra-sexual selection in paper wasps; how multi-modal signals interact to mediate social interactions among dominance hierarchies in social insects; and how social interactions maintain honesty in communication. In addition to her work on insects, she has forayed into other taxa as well, examining the functionality of zebra stripes and studying the social, hormonal, and genetic basis of aggressive behavior of female tree swallows. Mandy is passionate about science communication, and aims to help make science more accessible between fields as well as to the general public. Her enjoyment of engaging others in science is manifest in her numerous publications and award-winning presentations. She holds a long-standing interest in public health and epidemiology, and is extremely excited for the opportunity to participate in the scientific process with a group that strives towards increasing transparency in science.

Mable Jerop
Student
Amref Health Africa in Kenya
jeropmable@gmail.com

Mable is a Monitoring and Evaluation expert for the Global Fund Malaria grant under Amref Health Africa in Kenya where she coordinates community interventions on Malaria control in endemic zones in Kenya. With a professional background in Statistics, her research interests focus on population health research through modelling of various health interventions. With over 5 years experience, she has contributed to various health programs and research in Kenya funded through donor institutions including the U.S. Agency for International Development (USAID) and Bill & Melinda Gates Foundation.

Mark Jit
Professor
London School of Hygiene & Tropical Medicine
mark.jit@lshtm.ac.uk

Mark Jit is professor in vaccine epidemiology at the London School of Hygiene & Tropical Medicine (LSHTM) and senior scientist in the Modelling and Economics Unit of Public Health England (PHE). His research focuses on epidemiological and economic modelling of infectious disease control interventions such as vaccination, to support evidence-based public health decision making. He has published over 100 papers covering a range of vaccine antigens including measles, HPV, pneumococcus, rotavirus, influenza, dengue and EV71, as well as methodological papers advancing the ways vaccines are evaluated. This has influenced many of the major changes to the UK's immunization schedule over the past ten years, informed vaccine policy in several other countries (both developed and developing) and supported global guidance and decision-mak-ing by WHO and Gavi, the Vaccine Alliance.

Samson Kiware
Research Scientist
Ifakara Health Institute
skiware@ihi.or.tz

Samson Kiware (BA, MSc, PhD) is a Research Scientist and a Wellcome Trust Fellow at the Ifakara Health Institute in Tanzania. His main research interests are based on developing bioinformatics system for mosquito studies and mathematical models that can be used to optimize vector control tools for malaria elimination.

Daniel Klein
Sr. Research Manager
Institute for Disease Modeling
dklein@idmod.org

Daniel Klein is a Chair of the Applied Math group and Senior Research Manager at IDM. His background is in control theory and networked dynamic systems.

Keith Klugman
Director, Pneumonia
Bill & Melinda Gates Foundation
keith.klugman@gatesfoundation.org

Keith Klugman leads the Bill & Melinda Gates Foundation's work to improve the development and delivery of pneumonia vaccines and expand the use of antibiotic treatments and diagnostic tools. Klugman is a leading expert on antibiotic resistance in pneumonia pathogens and helped develop the pneumococcal vaccine that is part of the immunization regimen for children born in the US, which is also being rolled out globally. Klugman previously served as a Professor of Global Health and Professor of Epidemiology in the Rollins School of Public Health at Emory University and Professor of Medicine in the Division of Infectious Diseases at the Emory School of Medicine. He serves as Honorary Professor in the Respiratory and Meningeal Pathogens Research Unit at the University of the Witwatersrand in South Africa.

Katia Koelle
Associate Professor
Duke University
katia.koelle@duke.edu

Katia Koelle is an ecologist and evolutionary biologist whose research focuses on understanding the disease dynamics and evolutionary dynamics of viral pathogens affecting humans. Her research spans from understanding the processes regulating within-host viral dynamics and evolution to understanding the interplay between viral spread and evolution at the population level. Her research focuses on influenza virus, including its antigenic evolution, and on dengue virus.

Alicia Kraay
Student
University of Michigan-Ann Arbor
amullis@umich.edu

Alicia Kraay is a doctoral candidate in the department of epidemiology at the University of Michigan, Ann Arbor. She has a broad 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 modeling approaches to help answer these questions.

Myron Levine
Associate Dean
University of Maryland School of Medicine
mlevine@medicine.umaryland.edu

Director of the Center for Vaccine Development from 1974 to 2014. Long experience in communicable disease epidemiology and vaccinology.

Sheng Li
Assistant Professor
City University of New York, School of Public Health
sheng.li@sph.cuny.edu

Sheng Li is an Assistant Professor of Systems Science and Epidemiology at City Univ. of New York School of Public Health. His graduate training was in Epidemiology and Complex Systems Science from the Center for The Study of System Science (CSCS) and School of Public Health in the University of Michigan at Ann Arbor. Before that, he was infectious epidemiologist and physician in governmental agencies. Sheng's current research is focused on modeling measles, rubella, HIV and childhood obesity.

Marc Lipsitch
Professor
Center for Communicable Disease Dynamics, Harvard Chan School of Public Health
mlipsitc@hsph.harvard.edu

Marc Lipsitch is Professor of Epidemiology and Director, Center for Communicable Disease Dynamics, Harvard T.H. Chan School of Public Health. His pneumococcal research combines experimental, population genomic, epidemiologic and mathematical modeling approaches to understand serotype and genetic diversity and the impact of interventions. More generally he is interested in the application of quantitative approaches to improve observational and randomized study design, study the impact of interventions on infectious diseases, and study the interrelationship of pathogen evolution, host immunity and human disease.

Ben Lopman
Associate Professor
Emory University, Rollins School of Public Health
blopman@emory.edu

Ben Lopman, PhD MSc is an infectious disease epidemiologist whose research is directed at understanding the epidemiology of enteric viruses and developing an evidence base for their control. Prior to joining the Epidemiology Faculty at the Emory University Rollins School of Public Health in 2016, Dr. Lopman worked for 7 years with the Division of Viral Disease at CDC. His post-graduate work was at the London School of Hygiene & Tropical Medicine and Imperial College London.

Isaac Lyatuu
Research Scientist
Ifakara Health Institute
ilyatuu@ihi.or.tz

Isaac Lyatuu is a research scientist from Ifakara Health Institute with a background in computer science coupled with data, health informatics and mathematics. He was in charge of data system design and implementation of the SAVVY project parallel to overseeing project activities. Mr. Lyatuu currently works in the Data Systems Unit of the Ifakara Health Institute and oversees different project's data management aspects.

Ayesha Mahmud
Graduate Student
Princeton University
mahmud@princeton.edu

Ayesha Mahmud is a PhD student in Demography at Princeton University and is a member of the Metcalf lab. She is broadly interested in using historical datasets and demographic and epidemiological models to understand the interplay between human demography and infectious disease dynamics. Her dissertation examines the causes and consequences of seasonality in the transmission and incidence of common childhood infectious diseases in a variety of contexts. Ayesha received a BA in Physics and Economics from Carleton College, Minnesota.

Niall Mangan
Acting Assistant Professor
University of Washington
niallmm@gmail.com

Niall M. Mangan received her PhD in Systems Biology from Harvard University, Cambridge, MA, in 2013. She is currently an Acting Assistant Professor of applied mathematics at the University of Washington. Her current research interests include data-driven discovery of mechanistic models for disease dynamics, metabolic and regulatory networks, and renewable energy systems.

Zoë McLaren
Assistant Professor
University of Michigan
zmclaren@umich.edu

Zoë McLaren is an Assistant Professor at the University of Michigan School of Public Health. Her research examines the impact of health status on economic outcomes in developing countries. Her recent work has focused on developing health and economic policy for HIV/AIDS and tuberculosis in sub-Saharan Africa. Prof. McLaren holds a PhD in Public Policy and Economics from the University of Michigan.

Kevin McCarthy
Senior Research Scientist
Institute for Disease Modeling
kmccarthy@idmod.org

Kevin McCarthy has a PhD in Physics from the Massachusetts Institute of Technology (MIT) as well as a Bachelor's degree in both Physics and Electrical Engineering from the University of California, San Diego (UCSD). While at MIT, Kevin was a member of the founding team of the MIT Entrepreneurship Review (MITER). He served as the managing editor to a team of five writers focusing on innovations in energy technology and "clean tech", and as a member of the MITER executive board.

Kevin's doctoral research was performed as a member of the Cryogenic Dark Matter Search collaboration which searches for interactions between atomic nuclei and a hypothetical dark matter particle termed the Weakly Interacting Massive Particle (WIMP). Prior to his graduate work, Kevin's research experience included work on diboson production at the Collider-Detector at Fermilab, study of the electrical properties of magnetically doped amorphous semiconductors, and an investigation of the potential for new physics searches at the Laser Interferometer Gravitational Wave Observatory (LIGO).

Kevin's research at IDM focuses on calibration of a spatio-temporal disease model to describe endemic conditions in northern Nigeria and calibration of the IDM intra- host malaria model. These calibrated models can be used to evaluate the expected efficacy of potential intervention campaigns and provide decision support to global health policymakers.

Carrie McNeil
Project Lead
Sandia National Laboratories, International Biological and Chemical Threat Reduction
csmcnei@sandia.gov

Carrie McNeil DVM MPH provides IBCTR/SNL expertise in One health, infectious diseases, outbreak response, and emergency management. Prior to coming to Sandia, she worked as an Epidemic Intelligence Service Officer and emergency plan-ner with the Centers for Disease Control and Prevention, an emergency veterinary clinician and responder, an environmental health nonprofit director, and legislative consultant. She completed her Global Environmental Health MPH at Emory University in 2012 and DVM at University of California Davis in 2004.

Graham Medley
Professor
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 also working on modelling the social processes involved in HIV transmission, and has current projects on neglected tropical

diseases (leprosy, visceral leishmaniasis and soil-transmitted helminths.

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 175 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. immunization). 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.

Laina Mercer
Research Statistician
Institute for Disease Modeling
lmercer@idmod.org

Laina Mercer holds a PhD in Statistics from the University of Washington. Her dissertation research was related to statistical methods for space-time smoothing of surveillance and complex survey data with applications in demography and public health. While at the University of Washington, Laina was a fellow at the Center for Studies in Demography and Ecology and she served as Chair of Statistics in the Community (StatCom), a student-run volunteer organization that provides statistical consulting services free of charge to non-profit community and governmental groups. Laina also holds an MS in Biostatistics from the University of Washington and a BS in Mathematics from Western Washington University. She worked for two years at Seattle Children's Research Institute in the Children's Core for Biomedical Statistics, specifically in medical research for pediatric transplantation and surgery. She also spent two years at Fred Hutch in the Tobacco and Health Behavior Science Research Group, investigating behavioral interventions for smoking cessation. As a member of IDM's analysis and model usage center, Laina is working to support polio eradication efforts through statistical modeling of programmatic, clinical trial and cluster survey data. Laina is most interested in how diverse data sources can be used in a timely fashion to inform public health policy decisions.

Natalia Molodecky
Doctoral Student
Imperial College London
n.molodecky@imperial.ac.uk

Natalia Molodecky is a PhD student in the Vaccine Epidemiology Research Group at Imperial College London. Her research is focused on using mathematical and statistical models to understand transmission dynamics of poliovirus in Pakistan to inform vaccination strategies.

Zindoga Mukandavire
Assistant Professor
London School of Hygiene & Tropical Medicine
zindoga.mukandavire@lshtm.ac.uk

Dr. Mukandavire is a member of the Social and Mathematical Epidemiology Group (SaME) in the Department of Global Health and Development. His research involves the use mathematical theories and methods as tools to understand infectious disease transmission dynamics in order to establish efficient and cost effective ways to control their spread and identifying the mechanisms that facilitate their spread across populations and heterogeneous landscapes.

His current research is on modeling HIV transmission dynamics in West Africa and assessing the utility of different inter-ventions (condom use, pre-exposure prophylaxis and antiretroviral treatment) targeted at high-risk groups (female sex workers, clients and pimps) and the general population.

Daniel Neafsey
Associate Director, Genomic Center for Infectious Disease
Broad Institute
neafsey@broadinstitute.org

Daniel Neafsey joined the Broad Institute of MIT and Harvard in 2004 and is now associate director of the Broad Institute's Genomic Center for Infectious Diseases, where he leads a group focusing on the genomics of malaria parasites and mosquito vectors. He is excited by the potential for new technology and information types to turn the tide against diseases like malaria.

Neafsey's current projects involve the application of comparative genomic and population genetic analyses to *Plasmodium* malaria parasites and *Anopheles* mosquitoes to study population structure, natural selection, and genomic factors underlying parasite and vector phenotypes that impact public health. Neafsey's interests also include the use of pathogen polymorphism data to inform vaccine design and understand vaccine efficacy, analysis of drug resistance mechanisms and evolution, the use of clinical genotyping data to interpret disease transmission dynamics, and the development of new genomic protocols and informatics tools to address key questions in infectious disease and global health.

Milen Nikolov
Postdoctoral Research Scientist
Institute for Disease Modeling
mnikolov@idmod.org

Milen Nikolov is a Postdoctoral Researcher at the Institute for Disease Modeling, Bellevue, WA, where he's currently working on developing dynamical spatial malaria models and understanding the conditions required for the disease eradication in the context of spatially connected vector and human pop-ulations. He completed his PhD and MS degrees in Elec-trical and Computer Engineering at Cornell University, where his doctoral work covered various topics in networks' structure and information processing. His research has been published in a number of leading journals and international conference proceedings in the fields of networks, computational biology, and epidemiology.

Muhammad Imran Nisar
Senior Instructor
Department of Pediatrics, Aga Khan University
imran.nisar@aku.edu

Dr. Imran Nisar is a Senior Instructor (Research) in the Department of Pediatrics and Child Health at Aga Khan University. He holds and MBBS and a Master of Science degree in Epidemiology and Biostatistics. He is principal investigator of a study measuring indirect effect PCV10 on nasopharyngeal carriage of pneumococcus in Matiari, Pakistan funded by Bill & Melinda Gates Foundation. He is currently enrolled in the PhD in Population and Public Health program at Aga Khan University, Pakistan

Todd Noel
Software Engineer
Sandia National Laboratories
tgnoel@sandia.gov

After obtaining his degree in Computer Science, Todd Noel joined Sandia National Labs as a Software Engineer for the International Nuclear Security Engineering group (INSE). Todd's main focus has been creating virtual training tools to help mitigate threats from the nuclear, biological, and chemical spheres. This experience includes extensive work in tabletops including the development of a 3D tabletop recorder for protection of facilities and a decision-based tabletop recorder for higher level exercises. He is also the lead developer on the Virtual Zoonotic Preparedness Simulation, which is a multiplayer, decision-based exercise that takes users through a simulated zoonotic outbreak and records the results in an after action report. Todd is a full-stack developer, in that he can create every aspect of an application, from the database to the API to the user interface. He also works in the 3D realm, creating models and simulations for use in virtual or augmented reality. His experience also has led him around the world where he has helped conduct training exercises using his tools and trained others to use them.

Gene Oates
Director of Software Engineering
Institute for Disease Modeling
goates@idmod.org

Gene Oates is the Director of Software Engineering at the Institute for Disease Modeling. He leads the development of epidemiological modeling, software tools, and software services that are intended to support infectious disease eradication cam-paigns worldwide.

Gene has over 30 years in the software industry where he has developed products in telecommunications, network man-agement, financial, and transportation domains. He was the senior developer on the Open Application Interface (OAI) allowing peripheral computers the ability to provision users and observe call progress with the Intecom DPBX. Gene designed and developed the first non-SNA implementation of the NetView Operational Architecture enabling DECnet resources to appear in NetView as manageable entities allow-ing operations staff the capability to manage DECnet from NetView. As part of this effort he developed the RUNCMD architecture used to issue commands to non- SNA com-ponents. In another large scale project Gene contributed to Motorola's first implementation that allowed peripheral pro-cessors the capability to interact with cellular home switches to detect cellular call progress, cellular phone status and cel-lular text messages. This project was a joint effort between US West, Motorola, Octel and Accessline. This was a key feature in the early stages of "One Number" telephone service that res-ulted in a patent for Accessline. Gene is no stranger to cloud computing. He contributed heavily to the success of Concur's SaaS implementation for expense and travel management. As one of the principle engineers, he architected and developed the central control mechanisms for all client access, utilities to migrate thousands of databases for software upgrades, and the architecture taking an Enterprise Analytics solution into the cloud. He developed a prototype of a data driven semantic technology based engine providing the cap-ability of data sharing via the Ontology Web Language (OWL). Gene brings with him years of experience in leading/managing software development teams of varying size.

André Lin Ouedraogo
Resident Scholar
Institute for Disease Modeling
aouedraogo@idmod.org

André Lin has a PhD in Medical Sciences. He works to identify and organize input data in order to refine and apply models to conduct sensitivity analyses as well as explore trade- offs among multiple interventions in support of elimination and eradication of malaria.

Stephen Pelton
Professor of Pediatrics and Epidemiology
Boston University Schools of Medicine and Public Health
spelton@bu.edu

Stephen Pelton is chief of Pediatric Infectious Diseases as Boston Medical Center. He has been invested in treatment and prevention of respiratory tract infection for more than two decades. Currently, one of his focuses is impact of PCV13 on AOM and pneumonia burden in children and whether impact is different in those with comorbidity.

Alex Perkins
Eck Family Assistant Professor
University of Notre Dame
taperkins@nd.edu

Alex Perkins is the Eck Family Assistant Professor of Biological Sciences and Concurrent Assistant Professor of Applied and Computational Mathematics and Statistics at the University of Notre Dame. His research interests span a range of questions in mosquito-borne disease epidemiology involving the spatial dynamics of transmission across a range of spatial scales and how models can be used to guide assessments of novel interventions and projections of their epidemiological impact. His PhD research in Population Biology at the University of California, Davis was supported by a Department of Energy Computational Sciences Graduate Fellowship, and his postdoctoral research was supported by a Research and Policy for Infectious Disease Dynamics Fellowship through the Fogarty International Center at the National Institutes of Health.

Maya Petersen
Associate Professor
UC Berkeley School of Public Health
mayaliv@berkeley.edu

Maya Petersen, MD, PhD is Associate Professor of Biostatistics and Epidemiology at the School of Public Health of the University of California, Berkeley. Dr. Petersen's methodological research focuses on the development and application of novel causal inference methods to problems in health, with an emphasis on longitudinal data and adaptive treatment strategies (dynamic regimes), machine learning methods, and study design and analytic strategies for randomized trials. Her applied work focuses on developing and evaluating improved HIV prevention and care strategies in resource-limited settings. Maya is currently co-PI (with Diane Havlir and Moses Kamya) of the SEARCH Trial, a large "test and treat" HIV prevention trial in East Africa, and co-PI (with Elvin Geng) of the AdaPT-R Trial, a sequential multiple assignment randomized trial to develop adaptive strategies that optimize retention in HIV care in Kenya.

Emilie Pothin
Statistical modeller in epidemiology
Swiss TPH/CHAI
emilie.pothin@unibas.ch

Dr. Emilie Pothin has a background in mathematical modeling and epidemiology of malaria. Her research combines the use of mathematical models and statistical methods to simulate transmission dynamics, estimate its intensity, and apply these results to improve malaria control and elimination. One of her primary activities is to provide support to malaria control programs in countries by simulating impact of malaria interventions in given settings.

Joshua Proctor
Senior Research Scientist
Institute for Disease Modeling
jproctor@idmod.org

Joshua Proctor has a PhD in Mechanical and Aerospace Engineering from Princeton, as well as a Bachelor of Science in Aeronautics and Astronautics Engineering, and a Bachelor of Arts in English Literature, both from the University of Washington, Seattle. His doctoral research was on the effects of neural feedback on rapidly running insects (cockroaches), and focused heavily on developing mathematical models that would describe the locomotion of the subjects all the way from the neural level to their body-environment interactions. These studies were then translated into robotic designs as a way to improve the control of legged robots.

As a member of IDM's research team, Joshua focuses on mathematical model and numerical algorithm development, namely the mathematical modeling of disease transmission as well as ways to potentially arrest the spread of disease through control interventions, such as vaccination campaigns.

Benoit Raybaud
Research Software Engineering Manager
Institute for Disease Modeling
braybaud@idmod.org

Benoit is the manager of the research software development team. He and his team are responsible for providing support to the researchers with their needs in term of tools enabling them to efficiently use the model and the computational resources available at IDM and in the cloud. The team has also been involved in providing training and support for IDM external collaborators.

Robert Reiner
Assistant Professor
IHME, University of Washington
bcreiner@uw.edu

Bobby Reiner is an Assistant Professor at the Institute for 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.

Gail Rodgers
Senior Program Officer
Bill & Melinda Gates Foundation
gail.rodgers@gatesfoundation.org

Gail Rodgers is a Senior Program Officer on the Pneumonia Team at the Bill & Melinda Gates Foundation. Since October 2014 she has led the Pneumococcus Initiative with a focus on development of a low cost pneumococcal vaccine, assessment of alternate dosing strategies of pneumococcal conjugate vaccine (PCV), and assessment of impact of PCVs in GAVI Alliance countries. Gail also leads the Strategic Information and Risk Factors Initiative that focuses on understanding the etiology of pneumonia to be able to better address these pathogens via preventive and/or treatment efforts and, importantly, the role of household air pollution (HAP) on pneumonia in children and interventions that can be done to decrease pneumonia due to HAP.

Isabel Rodriguez-Barraquer
Research Associate
Johns Hopkins Bloomberg School of Public Health
isabelr@jhu.edu

Infectious disease epidemiologist. I am iinterested in applying novel epidemiological and statistical methods to understand the dynamics of infectious diseases, with a focus on vector-borne diseases.

Mauricio Santillana
Faculty member
Boston Children's Hospital, Harvard Medical School
msantill@g.harvard.edu

Mauricio Santillana, a physicist and applied mathematician with expertise in mathematical modeling and scientific computing, is a faculty member in the Computational Health Informatics Program at Boston Children's Hospital, an Instructor at Harvard Medical School, and an associate at the Harvard Institute for Applied and Computational Sciences.

Kimberly Shea
Assistant Professor
Boston University
kimshea@bu.edu

Kimberly Shea, PhD, MPH, is Assistant Professor in the Department of Epidemiology at the Boston University School

of Public Health. Her primary research interest is the epidemiology of vaccine- preventable diseases, especially post-licensure effectiveness of vaccination. She is currently engaged in evaluating the impact of pediatric pneumococcal vaccination–including changes in overall disease burden and changes in pneumococcal serotypes known to cause disease and be present in nasopharyngeal colonization–through clinical studies, use of healthcare claims data, and disease surveillance activities shared with the Massachusetts Department of Public Health. As it has become increasingly apparent that some populations remain vulnerable to pneumococcal disease despite widespread vaccination, much of her recent work focuses on pneumococcal disease risk among high-risk populations such as those suffering from one or more comorbidities. In addition, Dr. Shea teaches multiple global health and epidemiological methods courses at BUSPH including a seminar course on the epidemiology of vaccine-preventable diseases.

John Sheppard
Managing Principal Software Engineer
Institute for Disease Modeling
jsheppard@idmod.org

John Sheppard is a member of the IDM software development team and brings over 16 years of experience in software development and engineering excellence. He has worked in biodiversity informatics, bioinformatics, and data analytics, as well as search technology and large-scale distributed systems. John is also the co-author of multiple patents related to search and data analytics technologies. With a long history in the field as well as wide interests that span most of computer science, he has been involved in various open source projects, including projects for rules engines, peer mesh networks, and language runtimes. Within IDM, John leads the development efforts focused on creating the operational infrastructure for IDM's modeling solvers.

David Smith
Professor
IHME, University of Washington
smitdave@uw.edu

David L Smith's research addresses a range of questions about the epidemiology and control of infectious diseases and the evolution of resistance. Malaria has been a major focus of his research for more than a decade. He has been a member of the Malaria Atlas Project, the Malaria Elimination Group, Research and Policy and Policy for Infectious Disease Dynamics (RAPIDD), and the Malaria Eradication Research Agenda (malERA). Other interests include rabies, antibiotic resistance in nosocomial pathogens, MRSA, influenza, and cholera.

Roland Sutter
Coordinator, Research, Policy & Containment (RPC)
World Health Organization
sutterr@who.int

Coordinator responsible for Research, Policy and Containment for the Global Polio Eradication Initiative at the World Health Organization in Geneva, Switzerland since 2002. Before that, he served as the Chief of the Polio Eradication Branch, Global Immunization Division at the Centers for Disease Control and Prevention.

Saki Takahashi
PhD Student
Princeton University
sakit@princeton.edu

Saki Takahashi is currently a PhD student in the Department of Ecology and Evolutionary Biology at Princeton University, advised by Dr. Jessica Metcalf and Dr. Bryan Grenfell. She is broadly interested in clarifying the spatial distribution as well as the ecological and evolutionary dynamics of viral infections and their control measures across epidemiological scales. She received her AB in Applied Mathematics from Harvard University and ScM in Epidemiology from the Johns Hopkins Bloomberg School of Public Health.

Ian Vernon
Lecturer
Durham University, UK
i.r.vernon@durham.ac.uk

Ian Vernon is a Bayesian statistician interested in applying Bayesian statistics to complex physical systems modeled by computer simulators. He works on developing Bayesian methodology that allows a full uncertainty analysis of both the computer model and the real system it represents. This facilities history matching (and model calibration), model checking/validation and the design of future system experiments. He has successfully applied these techniques to the areas of cosmology, systems biology, epidemiology, geology and environmental science.

Jon Wakefield
Professor
Departments of Statistics and Biostatistics, University of Washington
jonno@uw.edu

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. His interests include spatial-temporal models for infectious disease data, small area estimation, cluster detection, disease mapping and spatial regression.

Dan Weinberger
Assistant Professor
Yale School of Public Health
daniel.weinberger@yale.edu

Dan Weinberger is an Assistant Professor of Epidemiology at Yale School of Public Health. His research group studies the biology and epidemiology of pathogens that infect the respiratory tract, including pneumococcus and RSV. We use diverse quantitative and laboratory approaches to understand, predict, and optimize public health interventions.

Philip Welkhoff
Senior Director of Research
Institute for Disease Modeling
peckhoff@idmod.org

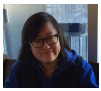
Philip Welkhoff leads all research efforts at IDM. He received his PhD from Princeton University in Applied and Computational Mathematics, and has dual undergraduate degrees in Mathmatics and Aerospace Engineering from the University of Texas, Austin. At Princeton, Philip's work focused on computational neuroscience and biophysics-motivated models of decision making. Also while at Princeton, he began working on malaria and mathematical models of disease transmission.

Philip's interest in disease transmission, particularly malaria, began early on. As a child, he frequently suffered from malaria while growing up at a humanitarian hospital on the north coast of Haiti. In 2009, Philip received a Special Achievement Award by a Hertz Fellow for his work on malaria modeling. He also serves on the board of directors for the Fannie and John Hertz Foundation and as an interviewer for its graduate fellowship program. Additionally, he serves as an external reviewer for the Bill & Melinda Gates Foundation (BMGF) and as a pro bono external adviser for BMGF programs in Global Health and Global Development. Beyond modeling disease eradication, Philip's research interests include technologies for improved public health in the developing world, as well as other global development issues, such as vaccine delivery, developing world nutrition and agriculture, and improved sanitation.

Edward Wenger
Senior Research Manager
Institute for Disease Modeling
ewenger@idmod.org

Dr. Edward Wenger directs the malaria research program at IDM. His team develops and exercises sophisticated infectious disease models to inform rational, cost-effective intervention campaigns aimed at reducing the burden of disease and achieving eradication.

Before joining the disease modeling program in 2011, Dr. Wenger worked on the CMS heavy-ion program at CERN outside Geneva. He graduated from Dartmouth College and received his PhD in Physics from MIT.



Amy Wesolowski
Postdoctoral Fellow
Princeton University
amywesolowski@gmail.com

Amy Wesolowski is a postdoctoral fellow in the Department of Ecology and Evolutionary Biology at Princeton University. Her work focuses on quantifying and understanding the role of human travel on the spatial spread of various infectious diseases. Previously, she was a postdoctoral fellow at the Harvard TH Chan School of Public Health in the Center for Communicable Disease Dynamics. She obtained her PhD in Engineering and Public Policy from Carnegie Mellon University.

Amy Winter
Postdoctoral Fellow
Princeton University
awinter@princeton.edu

Amy holds a MPH from Emory University and a PhD from Princeton University in Demography. She currently works at Princeton University as a postdoctoral fellow in the Jess Metcalf lab. Her research interests lie at the intersection of human demography, infectious disease epidemiology, and health policy. Her current postdoctoral work explores rubella and measles disease dynamics, the effects of vaccine control programs, and potential for novel data sources to inform key knowledge gaps.

Zelda Zabinsky
Professor
University of Washington
zelda@u.washington.edu

Dr. Zelda B. Zabinsky is a Professor in the Department of Industrial and Systems Engineering at the University of Washington, with adjunct appointments in the departments of Electrical Engineering, Mechanical Engineering, and Civil and Environmental Engineering. She is an IIE Fellow. Professor Zabinsky has published numerous papers, appearing in Mathematical Programming, Journal of Global Optimization, Operations Research, and her book, Stochastic Adaptive Search in Global Optimization, describes research on theory and practice of algorithms useful for solving problems with multimodal objective functions in high dimension. Her research has been funded by federal agencies including NSF, NASA, FAA, and ONR, and local industry including Boeing, Microsoft, and Port of Tacoma.

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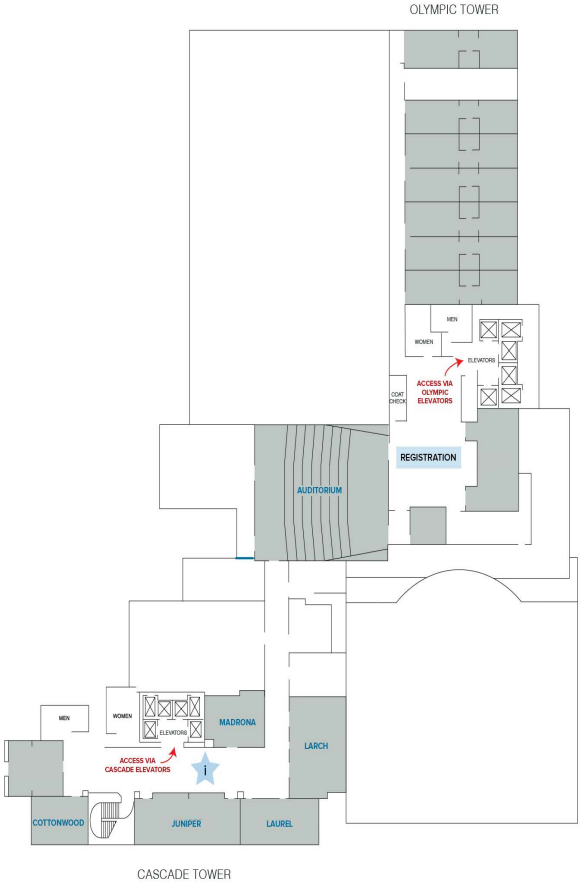
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