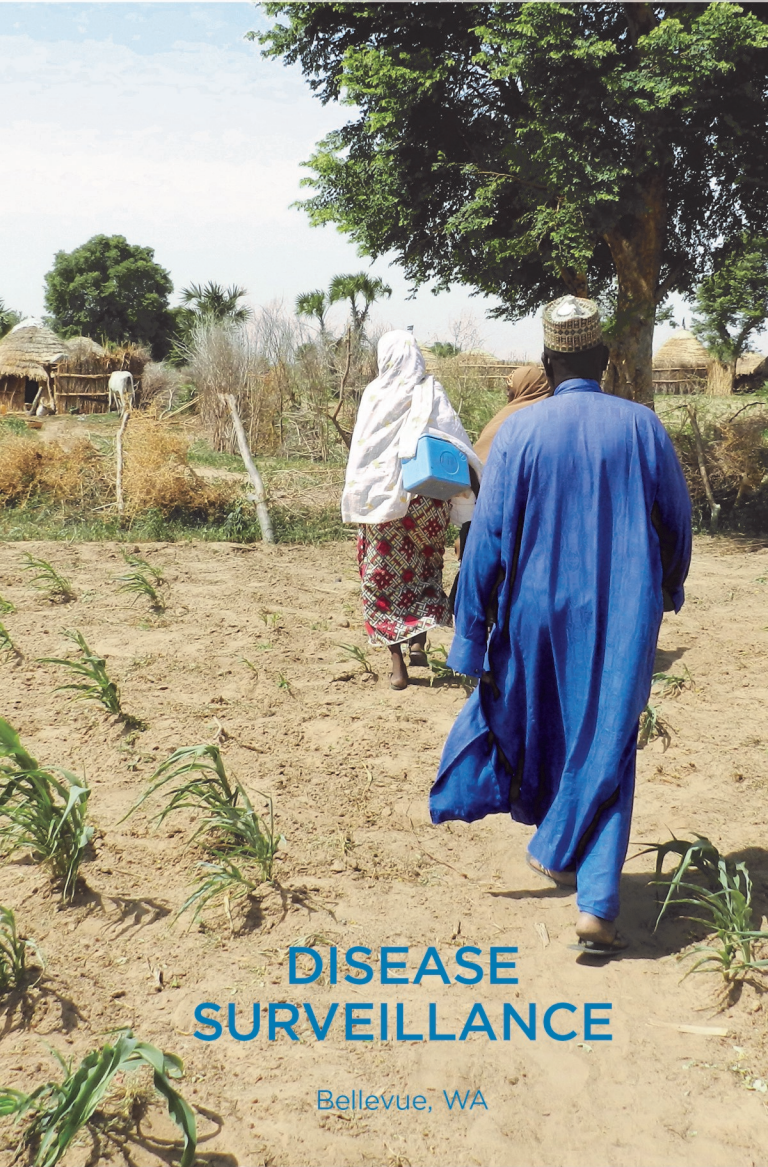# 2016 4th Annual
IDM Modeling Symposium

DISEASE
SURVEILLANCE

Bellevue, WA

INSTITUTE FOR DISEASE MODELING

INTELLECTUAL VENTURES®

TABLE OF CONTENTS

WELCOME

On behalf of the entire team at the Institute for Disease Modeling, we want to welcome you to the 2016 Symposium and express our appreciation for your attendance – particularly to those contributing presentations. We are grateful for the opportunity 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 grow so rapidly and effectively over the past four years and we look forward 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 part of the IV Global Good organization. We have grown to roughly 60 scientists and engineers which has enabled us to broaden our disease focus. This focus has aided us in achieving a network of extensive collaborators, reaching over 60 partners at the end of 2015. We continue to work to extend this significant collaborative network, fostering new scientific relationships that can positively impact global health.

As always, providing access to IDM's software tools to the entire community is an important component of IDM's mission. Today we are announcing the v2.5 release of our core EMOD software, available for download from IDM's GitHub repository. EMOD v2.5 now provides the ability to extend EMOD functionality with Python, simulate micro-spatial modeling at household level, model spatial migration of disease vectors with greater control, run multicore (HPC) simulations for all disease types, and enables you to interact with the disease tutorials through Excel. For those developing the EMOD source code, you can now create disease specific builds and we have removed the need to build boost. These improvements allow for greater developer productivity. Moreover, an enhanced version of our COMPS software platform is also available for collaboration. The first day of this Symposium is devoted to several software workshops to aid users in accessing and utilizing the IDM software suite. Additional software workshops are incorporated during the second and third day.

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 Eckhoff
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 hands- on 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.

MONDAY AGENDA

7:45	Registration	Juniper Foyer
Registration and continental breakfast.		

8:30-12:00	Workshop	Juniper
EMOD Basics		
Dan Bridenbecker, *Senior Software Engineer*		

8:30-12:00	Workshop	Laurel
COMPS Basics		
John Sheppard, *Senior Software Engineer Manager* Aaron Roney, *Software Engineer*		

12:00 -1:00	Lunch	Juniper Foyer
Buffet located in the Juniper Foyer.		

1:00-3:30	Workshop	Juniper
EMOD: Python Pre and Post Processing		
Jonathan Bloedow, *Senior Software Engineer*		

1:00-5:30	Workshop	Laurel
COMPS: Parameter sweeps, RESTful API and CSMT		
Aaron Roney, *Software Engineer,* Jeff Steinkraus, *Senior Software Engineer* Gene Oates, *Senior Software Engineer Manager* John Sheppard, *Senior Software Engineer Manager*		

TUESDAY AGENDA

7:30	Registration	Auditorium Foyer
Registration and full service breakfast.		

8:45-9:00	Welcome	Auditorium
Welcome to IDM's 4th Annual Disease Modeling Symposium		
Robert Hart, *Vice President and General Manager at IDM*		

9:00-10:30	Auditorium	General Session
General Session 1		
Chair: Mike Famulare, *Senior Research Scientist at IDM*		
Dylan George, *Member of Technical Staff, In-Q-Tel, formerly White House Office of Science and Technology Policy*		
Scott Dowell, *Deputy Director for Surveillance and Epidemiology, Bill and Melinda Gates Foundation*		
Busiku Hamainza, *Epidemiologist, Ministry of Health, National Malaria Control Centre, Zambia*		

10:45-12:15	Auditorium	General Session
General Session 2		
Chair: Hao Hu, *Senior Research Manager at IDM*		
Vince Seaman, *Senior Program Officer, Polio, Bill and Melinda Gates Foundation*		
Sarah Volkman, *Principal Research Scientist, Harvard T. H. Chan School of Public Health*		
Bryan Greenhouse, *Assistant Professor, University of California, San Francisco*		

12:15 -1:15	Lunch	Eques
Lunch at Eques		
Eques is located on the 2nd floor near the Hyatt's grand staircase.		

1:20-2:50	Breakout	Auditorium

Surveillance
Chair: Ben Althouse, *Research Scientist at IDM*

Neil Abernethy, *Associate Professor, University of Washington*

Trevor Bedford, *Assistant Member Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Cente*

Sam Scarpino, *Assistant Professor of Mathematics and Statistics, University of Vermont, Santa Fe Institute*

Jarad Niemi, *Assistant Professor Department of Statistics, Iowa State University*

Ewan Cameron, *Senior Computational Statistician, University of Oxford*

1:20-2:50	Breakout	Juniper

HIV Cascade of Care
Chair: Anna Bershteyn, *Senior Research Manager at IDM*

Peter Gilbert, *Research Professor Department of Biostatistics, University of Washington & Fred Hutchinson Cancer Research Center*

Dobromir Dimitrov, *Senior Staff Scientist, Fred Hutchinson Cancer Research Center*

Christian Selinger, *Research Scientist, Institute for Disease Modeling*

Ruanne Barnabas, *Assistant Professor in Global Health and Medicine, University of Washington*

Elvin Geng, *Associate Professor of Medicine, University of California, San Francisco*

Stefano Bertozzi, *Dean, School of Public Health, University of California, Berkeley*

1:20-2:50	Breakout	Laurel

Serious Gaming Initiative
Chair: Nick Karnik, *Senior Software Engineer at IDM*

Nick Karnik, *Senior Software Engineer, Institute for Disease Modeling*

Andy South, *Consultant, Liverpool School of Tropical Medicine*

Gene Oates, *Senior Software Engineer Manager, Institute for Disease Modeling*

1:20-2:50	Workshop	Cottonwood
EMOD		

EMOD as Open Source Software
Christopher Lorton, *Senior Software Manager at IDM*

3:00-4:30	Breakout	Auditorium
Malaria Genetics and Parasitology		
Chair: Caitlin Bever, *Senior Research Scientist at IDM*		

Edward Wenger, *Senior Research Manager at IDM*

Roberto Amato, *Staff Scientist, University of Oxford*

Wes Wong, *Ph.D Candidate, Harvard School of Public Health*

Peter Gilbert, *Research Professor Department of Biostatistics, University of Washington & Fred Hutchinson Cancer Research Center*

André Lin Ouedraogo, *Visiting Research Scholar, Institute for Disease Modeling*

3:00-4:30	Breakout	Juniper
Dengue, Chikungunya, Zika, and Aedes aegypti		
Chair: Laina Mercer, *Research Statistician*		

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

Quirine ten Bosch, *Doctoral Researcher in Infectious Disease Dynamics, University of Notre Dame*

Bobby Reiner, *Assistant Professor, Department of Epidemiology and Biostatistics, University of Indiana School of Public Health*

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

3:00-4:30	Breakout	Laurel

Advances in Applied Mathematics for Complex Systems and Surveillance

Chair: Josh Proctor, *Senior Research Scientist at IDM*

Nathan Kutz, *Professor Applied Mathematics Department, University of Washington*

Bing Brunton, *Professor Biology Department, University of Washington*

Eric Shea-Brown, *Professor Applied Mathematics Department, University of Washington*

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

Josh Proctor, *Senior Research Scientist, Institute for Disease Modeling*

3:00-4:30	Breakout	Cottonwood

Typhoid

Chair: Jillian Gauld, *Post Graduate Research Scientist*

Jason Andrews, *Assistant Professor, Stanford University*

Nick Feasey, *Senior Lecturer, Liverpool School of Tropical Medicine*

Paul Arora, *Epidemiologist & Visiting Scholar. The Hospital for Sick Children*

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

4:35-5:20	Keynote	Auditorium

Keynote Address

Peter Gething, *Associate Professor Malaria Atlas Project, University of Oxford*

6:00-9:00	Dinner	Bank of America

Dinner at Daniel's Broiler

Please join us for hors d'oeuvres and wine starting at 6:00pm and dinner at 7:00 pm. You must be registered to attend.

WEDNESDAY AGENDA

7:30	Registration	Auditorium Foyer
Registration and full service breakfast.		

8:30-10:30	Auditorium	General Session

General Session 3

Chair: Jaline Gerardin, *Senior Research Scientist at IDM*

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

Melissa Penny, *Project Leader, Health Systems Research and Dynamical Modeling, Swiss Tropical and Public Health Institute*

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

Joseph Eisenberg, *Professor and Chair of Epidemiology, University of Michigan*

10:45-12:45	Auditorium	General Session

General Session 4

Chair: Edward Wenger, *Senior Research Manager at IDM*

Deirdre Hollingsworth, *Associate Professor, Coordinator Neglected Tropical Diseases, University of Warwick*

Hugh Sturrock, *Spatial Epidemiologist, University of California, San Francisco*

Samson Kiware, *Research Scientist/Wellcome Trust Fellow, Ifakara Health Institute Tanzania*

Duncan Earle, *Associate Professor of International Development, MACEPA*

12:45 -1:40	Lunch	Eques
Lunch at Eques		
Eques is located on the 2nd floor near the Hyatt's grand staircase.		

1:45-3:45	Breakout	Auditorium

Malaria Elimination

Chair: Philip Eckhoff, *Director of Research at IDM*

Samir Bhatt, *Senior Computational Statistician, University of Oxford*

Adam Bennett, *Programmatic Lead, Malaria Elimination Initiative, Global Health Group, University of California, San Francisco*

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

Gerry Killeen, *Resident Guest Scientist, Ifakara Health Institute*

Casey Ferris, *Graduate Researcher, University of Notre Dame*

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

1:45-3:45	Breakout	Juniper

Enteric Diseases

Chair: Dennis Chao, *Senior Research Scientist at IDM*

Duncan Steele, *Deputy Director and Strategic Lead for Enteric Vaccines, Bill and Melinda Gates Foundation*

Kurt Long, *Research Scientist, Swiss Tropical and Public Health Institute*

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

Andrew Brouwer, *Postdoctoral Research Fellow in the Department of Epidemiology, University of Michigan*

Alicia Kraay, *Doctoral Student , University of Michigan*

1:45-3:45	Workshop	Laurel

IDM Software

Jonathan Bloedow, *Senior Software Engineer, Institute for Disease Modeling*

Open Session, *IDM Software Team*

7:45	Registration	Juniper Foyer

Registration and continental breakfast.

8:30-12:00	Workshop	Juniper

EMOD

EMOD Basics Workshop

Dan Bridenbecker, *Senior Software Engineer*

At IDM, one of the key tools used for quantitative analysis is the Epidemiological MODeling software (EMOD). EMOD is an individual-based, stochastic simulation that supports disease campaign planning, data gathering, new product development, and policy decisions. This workshop will introduce attendees to disease modeling, discuss why and when to use EMOD, and present an overview of the model components. Attendees will learn how to run the model and view the simulation results through Excel, and then explore the next steps for using EMOD. Please bring a laptop.

8:30-12:00	Workshop	Laurel

COMPS

COMPS Overview

John Sheppard, *Senior Software Engineer Manager*

COMputational Platform Service (COMPS) provides access to a High Performance Computing (HPC) environment and various modeling tools, including EMOD. This presentation will discuss what COMPS is and why you would want to use it for your modeling research.

COMPS Basics Workshop

Aaron Roney, *Software Engineer*

The COMPS workshop includes input file creation (demographics, temperature, humidity and rainfall), simulation creation, simulation execution, output visualization, and how to run a parameter sweep. Please bring a laptop.

12:00 -1:00	Lunch	Juniper Foyer

Buffet located in the Juniper Foyer.

1:00-3:30	Workshop	Juniper

EMOD

Advanced DTK: Python Pre and Post Processing

Jonathan Bloedow, *Senior Software Engineer*

This session will discuss and demonstrate new capabilities within the DTK that allow for extending the DTK functionality with Python. New in version 2.5, DTK users and developers can write Python scripts that will run as part of the DTK execution during either start-up, shutdown, or both. This allows for a huge variety of options for pre- and post-processing, including input file reformatting, and output file transformation. With this capability, input files no longer have to be in JSON format, and output files can be in a preferred format, aggregated, or merged. Please bring a laptop.

1:00-5:30	Workshop	Laurel

COMPS

Running a Parameter Sweep

Aaron Roney, *Software Engineer*

Using the simulation created in the morning workshop, you will add a parameter sweep across a bounded parameter space, graph the inset chart output of simulation, view the various channels of output, and graph multiple simulations inset chart output. Please bring a laptop.

RESTful API and Client Side Modeling Tools

Jeff Steinkraus, *Senior Software Engineer*

This session demonstrates how you can use your favorite scripting language or software tool to utilize and harness the power of COMPS via the RESTful API.

Collaboration Opportunities

Gene Oates, *Senior Software Engineer Manager*

John Sheppard, *Senior Software Engineer Manager*

Discussion on the opportunity for collaborators to access COMPS in 2016.

7:30	Registration	Auditorium Foyer

Registration and full service breakfast.

8:45-9:00	Welcome	Auditorium

Welcome to IDM's 4th Annual Disease Modeling Symposium

Robert Hart, *Vice President and General Manager at IDM*

9:00-10:30	Auditorium	General Session

General Session 1

Chair: Mike Famulare, *Senior Research Scientist at IDM*

Policy Modeling support for infectious disease outbreak decision making – examples from Ebola

Dylan George, *Member of Technical Staff, In-Q-Tel, formerly White House Office of Science and Technology Policy*

Modeling results have been developed during several infectious disease outbreaks including FMD in the UK, H1N1 pandemic, Ebola Virus Disease epidemic in West Africa, and now for the Zika Virus outbreak. Using modeling results for decision making during outbreaks has become more common. In this presentation I will review examples of how modeling results influenced preparedness and response activities.

Disease Surveillance Priorities at the Gates Foundation

Scott Dowell, *Deputy Director for Surveillance and Epidemiology, Bill and Melinda Gates Foundation*

Surveillance in general – how the term is used at BMGF and elsewhere, what surveillance activities we support, categories of disease surveillance; 2-3 examples of how good disease surveillance can guide effective public health; childhood mortality and why we are investing so much in CHAMPS; some other surveillance needs and opportunities - epidemic detection, antimicrobial resistance.

Current Malaria Surveillance Systems in Zambia – An intervention for Malaria Elimination

Busiku Hamainza, *Epidemiologist, Ministry of Health, National Malaria Control Centre, Zambia*

The presentation will discuss the malaria surveillance systems currently in use in Zambia and how these systems have been operationally built up to enable granular epidemiological awareness to guide program implementation with Malaria elimination as the guiding goal.

10:45-12:15	Auditorium	General Session

General Session 2

Chair: Hao Hu, *Senior Research Manager at IDM*

The use of Geospatial Data and Reference Layers to Enhance Disease Surveillance

Vince Seaman, *Senior Program Officer, Polio, Bill and Melinda Gates Foundation*

I will discuss how the basic geospatial reference layers (settlements, boundaries, roads, population) and geo- coded data can combine to enhance the collection, visualization, and analysis of disease surveillance activities. I will use the rich data set in Nigeria used to support polio AFP and environmental surveillance as an example.

Genetic Indicators for Malaria Transmission

Sarah Volkman, *Principal Research Scientist, Harvard T. H. Chan School of Public Health*

Informing malaria surveillance with molecular tools

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

Traditional epidemiologic surveillance has informed malaria control and elimination for more than a century. Over the last few decades, analysis of the Plasmodium genome has provided additional answers to fundamental questions about parasite biology, but has been utilized relatively infrequently to augment our understanding of transmission and epidemiology, and even less frequently to inform control efforts in real- time. I will discuss some potential applications where molecular data can be used to validate, augment, or revise our understanding of malaria epidemiology transmission as understood by traditional surveillance, tools to support these applications, and remaining challenges.

12:15 -1:15	Lunch	Eques

Lunch at Eques

Eques is located on the 2nd floor near the Hyatt's grand staircase.

1:20-2:50	Breakout	Auditorium

Surveillance

Chair: Ben Althouse, *Research Scientist at IDM*

BASTION: Tools to Promote Sharing of Epidemic Model Parameters and Data

Neil Abernethy, *Associate Professor, University of Washington*

The epidemic modeling and disease surveillance research communities increasingly need to share data and software tools. The BASTION project seeks to support this exchange with a web- based repository of source data, parameters, inputs, citations, versioning, and annotations for epidemic models. The prototype user interface and API facilitate collaboration on the development and evaluation of models and epidemic scenarios. We demonstrate the system using epidemic models of avian influenza, HIV, and Rift Valley Fever, and discuss future implications for model interoperability.

Real-time surveillance of virus evolution

Trevor Bedford, *Assistant Member Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Center*

Owing to rapid mutation, the evolution of RNA viruses such as influenza, Ebola and Zika occurs on a human timescale; rather than being forced to infer past evolutionary events, we can observe them in near real- time. In these cases of pathogens of intense public health relevance, an accurate and timely picture of ongoing evolution is especially important. Here, I present tools that continually ingest publicly available sequence data to give a near real- time view of viral evolutionary dynamics. I also present methods to visualize adaptive evolution, geographic spread and to forecast future strain turnover.

1:20-2:50	Breakout	Auditorium

Surveillance

Chair: Ben Althouse, *Research Scientist at IDM*

Data Blindspots: High-tech Disease Surveillance Misses the Poor

Sam Scarpino, *Assistant Professor of Mathematics and Statistics, University of Vermont, Santa Fe Institute*

Individuals in low socioeconomic brackets are considered at-risk for developing influenza-related complications and exhibit higher than average influenza-related hospitalization rates. This disparity has been attributed to various factors, including poor access to preventative and therapeutic health-care, limited sick leave, and household structure. Adequate influenza surveillance in these at-risk populations is a critical precursor to accurate risk assessments and effective inter-vention. However, the United States of America's primary national influenza surveillance system (ILINet) monitors out-patient healthcare providers that may be largely inaccessible to lower socioeconomic populations. Recent initiatives to incorporate internet-source and hospital electronic medical records (EMR) data into surveillance systems seek to improve the timeliness, coverage, and accuracy of outbreak detection and situational awareness. Here, we use a flexible statistical framework for integrating multiple surveillance data sources to evaluate the adequacy of traditional (ILINet) and next generation (BioSense 2.0 and Google Flu Trends) data for situational awareness of influenza, across poverty levels. We find that zip codes in the highest poverty quartile are a crit-ical blind-spot for ILINet that the integration of next gen-eration data fails to ameliorate.

Stochastic dynamic models for low count observations

Jarad Niemi, *Assistant Professor Department of Statistics, Iowa State University*

We build a stochastic dynamic model with Poisson transitions and binomial observations. These models are flexible enough to model a simple single location or sub-population SIR model to a multiple location, multiple population SEIRD model and beyond. Parameters and states in the model are efficiently estimated using particle learning. We investigate aspects of this model to understand the types of data col-lection that are necessary for reasonable public health decision making in real-time. I will discuss some potential applications where molecular data can be used to validate, augment, or revise our understanding of malaria epi-demiology transmission as understood by traditional sur-veillance, tools to support these applications, and remaining challenges.

1:20-2:50	Breakout	Auditorium

Surveillance
Chair: Ben Althouse, *Research Scientist at IDM*

Embedding Inhomogeneous Markov Process Models in the Bayesian Geostatistical Framework

Ewan Cameron, *Senior Computational Statistician, University of Oxford*

I will describe recent work to model patient serological status as the end point of an inhomogeneous, continuous time Markov process (describing the acquisition and loss of immunity over a lifetime) within a Bayesian geostatistical framework. Key issues regarding computational efficiency and identification of system parameters will be discussed and some novel solutions presented

1:20-2:50	Breakout	Juniper

HIV Cascade of Care
Chair: Anna Bershteyn, *Senior Research Manager at IDM*

Projected effectiveness of mass HIV vaccination with multi-dose regimens to be tested in South Africa

Peter Gilbert, *Research Professor Department of Biostatistics, University of Washington & Fred Hutchinson Cancer Research Center*

Dobromir Dimitrov, *Senior Staff Scientist, Fred Hutchinson Cancer Research Center*

Christian Selinger, *Research Scientist, Institute for Disease Modeling*

Multiple promising HIV vaccine regimens are planned for testing in vaccine efficacy trials in South Africa. They target an average efficacy of at least 50% over 24 months which may warrant deployment. We use mathematical model to estimate the impact of a vaccination program accounting for uncertainties in the vaccine efficacy profile and in adherence to a five-dose regimen scaled over 12 months. The model, calibrated to the most recent epidemiological data, stratifies vaccinated individual by immune response and explores different formulations of time-dependent efficacy. Our results indicate that even a partially effective vaccine would have a substantial impact on the HIV epidemic in South Africa with uncertainties in the temporal vaccine efficacy profile having a little influence on the vaccine effectiveness.

1:20-2:50	Breakout	Juniper

HIV Cascade of Care
Chair: Anna Bershteyn, *Senior Research Manager at IDM*

Cost-effectiveness of community-based strategies to strengthen the continuum of HIV care

Ruanne Barnabas, *Assistant Professor in Global Health and Medicine, University of Washington*

The presentation describes how cost-effectiveness of community-based strategies for HIV testing and linkage is estimated using empiric data from trials and mathematical models predicting the impact of interventions on HIV incidence.

Specification of interventions in implementation sciences

Elvin Geng, *Associate Professor of Medicine, University of California, San Francisco*

Implementation strategies are needed to enhance the global response to HIV, but specifying and measuring such strategies is not always fully transparent. A standardized approach to design, specification and measurement is needed advance the field of implementation science and enhance the global response to HIV.

Using Bigger Data, Better: Precision Public Health

Stefano Bertozzi, *Dean, School of Public Health, University of California, Berkeley*

1:20-2:50	Breakout	Laurel

Serious Gaming Initiative
Chair: Nick Karnik, *Senior Software Engineer at IDM*

Introduction to Serious Gaming

Nick Karnik, *Senior Software Engineer, Institute for Disease Modeling*

In 2011, four gamers with no scientific background solved an AIDS-related research problem in 10 days that had eluded scientists for 15 years. Similar efforts have succeeded at harnessing the power of gaming for knowledge and insight into solving real-world problems. We will delve into the history of gaming, present examples of serious gaming applications, and explore the various learning approaches through tangential learning, gamification, game-based learning, and serious gaming.

1:20-2:50	Breakout	Laurel

Serious Gaming Initiative

Chair: Nick Karnik, *Senior Software Engineer at IDM*

ResistanceSim: a serious game to support training in Insecticide Resistance Management for malaria vector control programs in Africa

Andy South, *Consultant, Liverpool School of Tropical Medicine*

Insecticide resistance in mosquitoes threatens successes in malaria control achieved through bednets and indoor residual spraying, currently the main vector control interventions. Good Insecticide Resistance Management practices have been promoted to address the rise in resistance but these are not always well understood and prioritized by vector control programs. We describe the development of a 'serious game' (ResistanceSim) to support training in Insecticide Resistance Management for vector control programs in Africa. The game is explicitly a learning support tool and not a decision support tool. Players conduct entomological monitoring which determines what data they see, then choose interventions which influence mosquito abundance, resistance and community health

EMOD as a Serious Game

Gene Oates, *Senior Software Engineer Manager, Institute for Disease Modeling*

Learning the complexities and assumptions built into the IDM open source Disease Transmission Kernel (DTK) modeling software is a challenging endeavor. Today individuals desiring this level of knowledge are required to understand the source code, read numerous publications and allocate the time to achieve this knowledge. IDM explored using a "serious gaming" approach to learning the DTK using an engaging experience.

1:20-2:50	Workshop	Cottonwood

EMOD

EMOD as Open Source Software

Christopher Lorton, *Senior Software Engineer Manager, Institute for Disease Modeling*

Source code for EMOD has been publicly available for a number of years. The source code is now available on GitHub. This session will cover: where to find the code on the web, how to get the code to your machine, building the code on Windows or Linux, and running the model to verify that you've built it correctly.

3:00-4:30	Breakout	Auditorium

Malaria Genetics and Parasitology

Chair: Caitlin Bever, *Senior Research Scientist at IDM*

Using parasite genetic information to monitor progress and inform strategies for malaria elimination

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

The distribution of multi-strain infections and genetic relatedness encodes information on the transmission intensity and connectedness of different regions. By modeling transmission and parasite recombination dynamics, we can compare modeled features with geo-localized sequences and infer characteristic transmission properties and migration-based coupling.

Population genetics of malaria drug resistance

Roberto Amato, *Staff Scientist, University of Oxford*

Malaria parasites are constantly evolving to escape the immune system, but also to elude our attempts to control the disease by chemotherapy. Monitoring and understanding this evolutionary process is crucial for informing and evaluating the success of elimination campaign. Genomic data represent a powerful and irreplaceable resource to directly observe these changes as they happen and to generate actionable knowledge.

3:00-4:30	Breakout	Auditorium

Malaria Genetics and Parasitology

Chair: Caitlin Bever, *Senior Research Scientist at IDM*

Relatedness of P. falciparum polygenomic Infections Suggest that the Co-transmission of Genetically Related Parasites is Common in Senegal

Wes Wong, *Ph.D Candidate, Harvard School of Public Health*

Polygenomic infections are composed of multiple distinct parasite strains and the relatedness between them can be used to better understand transmission dynamics within the greater population. In general, there are two competing hypotheses of polygenomic infection formation in malaria: the superinfection hypothesis, which posits that polygenomic infections are the result of a series of independent mosquito bites, and the co-transmission hypothesis, which posits that polygenomic infections are the result of a single mosquito injecting multiple parasite strains into the human host. Understanding the relative contribution of superinfection and co-transmission has important public health consequences, since the superinfection hypothesis predicts that the genetic diversity within polygenomic infectious serve as useful proxies for declining transmission rates. However, if co- transmission is common, then it undermines the usefulness of these metrics for inferring declining transmission rates. I take a two-pronged approach to this problem, utilizing genetic sequences collected from the field as well as developing computational models to understand the prevalence of co-transmission and the patterns of relatedness within polygenomic infections following superinfection or co-transmission.

Parasite Genetic Diversity Affects Protective Efficacy in a Phase 3 Trial of the RTS,S/AS01 Malaria Vaccine Pending

Peter Gilbert, Research Professor Department of Biostatistics, University of Washington & Fred Hutchinson Cancer Research Center

Modeling the burden of P. falciparum oocysts in the mosquito vector and the dynamics of transmission reducing immunity to estimate the true infectious reservoir for malaria

André Lin Ouedraogo, *Visiting Research Scholar, Institute for Disease Modeling*

It is acknowledged that naturally acquired immunity may interfere with Plasmodium sporogonic development and therefore should be taken into consideration while modeling malaria transmission. The EMOD model was calibrated to field data on oocyst distribution and on human immune responses to P. falciparum gametocytes allowing a dynamic projection of the infectious reservoir.

3:00-4:30	Breakout	Juniper

Dengue, Chikungunya, Zika, and Aedes aegypti

Chair: Laina Mercer, *Research Statistician*

Model-based projections of Zika virus infections in the Americas

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

The potential magnitude of the ongoing Zika epidemic is exceedingly difficult to gauge based on existing data, due to a number of uncertainties that cloud the relationship between observed cases and true infections. As an alternative to methods that depend on case data, we developed and applied a new method that leverages highly spatially resolved data about drivers of Zika transmission to project that 57.1 (48.5-94.0) million infections could occur before the first wave of the epidemic concludes. Strengths, limitations, and uncertainties associated with this approach will be discussed, as will practical implications such as the method's possible utility as a way to target surveillance efforts.

Contributions from the silent majority to dengue transmission

Quirine ten Bosch, *Doctoral Researcher in Infectious Disease Dynamics, University of Notre Dame*

The unknown contribution of asymptomatic and clinically inapparent infections to the transmission of emerging mosquito-borne viruses raises questions about the effectiveness of current practices for detecting and responding to outbreaks of viruses such as Zika and dengue. Despite estimates that each year 293 million people have asymptomatic or clinically inapparent dengue virus (DENV) infections, these have been assumed to contribute little to DENV transmission. Recently it was shown, however, that people with silent DENV infections are capable of infecting mosquitoes. Using models of within-host viral dynamics and demographic projections, we quantified the contributions of asymptomatic, clinically inapparent, and clinically apparent DENV infections to overall transmission. Our findings emphasize the need to reorient current practices for responding to outbreaks of dengue and Zika viruses to more directly address the contributions of people with asymptomatic, clinically inapparent, and pre-symptomatic infections to transmission.

3:00-4:30	Breakout	Juniper

Dengue, Chikungunya, Zika, and Aedes aegypti

Chair: Laina Mercer, *Research Statistician*

The curious case of the 2010-2011 DENV-2 outbreak in Iquitos, Peru: Incomplete homologous protection?

Bobby Reiner, *Assistant Professor, Department of Epidemiology and Biostatistics, University of Indiana School of Public Health*

Dengue is caused by any of four dengue virus serotypes (DENV-1 through DENV-4), and once an individual experiences an infection by a DENV serotype, they are assumed to be immune to homologous infections for life. Using a variety of data sources from Iquitos, Peru over 16 years, we investigate the validity of this assumption. In 1995, an American genotype of DENV-2 caused a large outbreak of febrile illness in Iquitos, Peru (the first time DENV-2 was detected in Iquitos). In 2010, an Asian-American genotype of DENV-2 invaded Iquitos, causing an unprecedented outbreak, with a confusing age signature: an unexpectedly high percent of the cases appearing in clinics were individuals 25 and older. This and other data from Iquitos indicates that protection from homologous DENV re-infection may be incomplete. This finding has significant implications for our understanding of dengue epidemiology and for dengue vaccine formulation, which may need to consider multiple genotypes of each serotype.

Assessing the Threat of Establishing a Sylvatic Zika Virus Cycle in South America

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

I review potential non-human primate and mosquito species capable of Zika virus transmission, and present a mathematical model of Zika virus transmission. I find high chances of establishing a sylvatic Zika virus transmission cycle across a broad range of biologically-realistic parameters. A sylvatic cycle of Zika virus would make future elimination efforts in the Americas practically impossible, and would paint a dire situation for the epidemiology of Zika virus and ending the ongoing outbreak of congenital Zika syndrome.

3:00-4:30	Breakout	Laurel

Advances in Applied Mathematics for Complex Systems and Surveillance

Chair: Josh Proctor, *Senior Research Scientist at IDM*

Data-driven approaches to dynamical networks: Integrating equation-free methods, machine learning and sparsity

Nathan Kutz, *Professor Applied Mathematics Department, University of Washington*

Modern science is allowing researchers from tremendously diverse academic disciplines (CS, EE, AMATH, PBIO, BIO, PHYS, etc.) to participate in rich interdisciplinary activities that are shaping our fundamental understanding of how dynamical network activities function across micro- and macro- spatial and temporal scales. This talk is concerned with highlighting emerging methods from the mathematical sciences that are centered around a (networked) dynamical systems perspective. The integration of these various concepts (reduced- order modeling, equation- free, machine learning, sparsity, networks, multi-scale physics and adaptive control) are critical to formulating successful modeling strategies that perhaps can say something meaningful about the myriad of interactions in biological systems.

Sparse sensor placement optimization for classification (SSPOC)

Bing Brunton, *Professor Biology Department, University of Washington*

Choosing a limited set of sensor locations to characterize or classify a high-dimensional system is an important challenge in engineering and surveillance design. Given a fixed budget of sensors, where should they be placed to optimally inform a decision? Traditionally, optimizing the sensor locations involves a brute- force, combinatorial search, which is NP-hard and is computationally intractable for even moderately large problems. Using recent advances in sparsity- promoting techniques, we present a novel algorithm to solve this sparse sensor placement optimization for classification (SSPOC) that exploits low- dimensional structure exhibited by many high-dimensional systems.

Assembling collective activity in (neural) networks

Eric Shea-Brown, *Professor Applied Mathematics Department, University of Washington*

Experimental breakthroughs are yielding an unprecedented view of the connectivity of biological networks and of their collective activity. But how does the former lead to the latter? We use graphical and point process methods to show how surprisingly local features of network connectivity govern their global dynamics.

3:00-4:30	Breakout	Laurel

Advances in Applied Mathematics for Complex Systems and Surveillance

Chair: Josh Proctor, *Senior Research Scientist at IDM*

Low dimensional models of SI(R) disease spread on static and dynamic networks

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

If we try to model SIR disease spreading in an N-node network, the number of possible states is 3^N. For large values of N, we must consider approximate models. Standard "pair-approximation" models require O(K) equations where K is the maximum degree. Surprisingly, by changing the focus from a node-based to an edge-based approach, we can reduce the model to a single governing ODE. The resulting model accurately predicts the large-population limit of disease spread in random networks of given degree distribution. The simplicity of the resulting models allows us to consider partnerships changing in time. This allows us to include partnership duration as a parameter in our disease models. I will discuss how these models can be developed and some applications.

Discovering reduced-order-models from dynamic, infectious disease data

Josh Proctor, *Senior Research Scientist, Institute for Disease Modeling*

Equation-free methods are becoming increasingly ubiquitous in the analysis of dynamically evolving, complex systems. The recent surge in popularity of these methods stems from a number of distinct advantages including the ability to handle high-dimensional measurement data, discover reduced-order models, and importantly, analyze systems where the governing equations may not be well characterized. In this talk, I discuss how recently developed equation-free methods can be applied to the field of computational epidemiology. Equation-free methods are becoming increasingly ubiquitous in the analysis of dynamically evolving, complex systems. The recent surge in popularity of these methods stems from a number of distinct advantages including the ability to handle high-dimensional measurement data, discover reduced-order models, and importantly, analyze systems where the governing equations may not be well characterized. In this talk, I discuss how recently developed equation-free methods can be applied to the field of computational epidemiology.

3:00-4:30	Breakout	Cottonwood

Typhoid

Chair: Jillian Gauld, *Post Graduate Research Scientist*

Challenges in estimating disease burden for typhoid

Jason Andrews, *Assistant Professor, Stanford University*

There is a paucity of data on typhoid incidence globally, particularly outside of urban settings. This presentation will discuss some of the challenges in measuring typhoid burden, review various approaches to efficiently estimating incidence, and present data from surveillance sites in Nepal.

Three epidemics of invasive Salmonella Disease

Nick Feasey, *Senior Lecturer, Liverpool School of Tropical Medicine*

Blantyre, Malawi is home to MLW, one of the Wellcome Trust's five major overseas programs. MLW has offered diagnostic microbiology to adult and pediatric patients presenting with suspected sepsis for almost 20-years. This longitudinal bacteraemia surveillance has permitted the identification of multiple epidemics of invasive Salmonella Disease. In this talk, I will review the approaches we have taken to modeling these epidemics in the past and the novel strategies that we are developing for the future.

Trends in Typhoid: Global patterns and surveillance systems

Paul Arora, *Epidemiologist & Visiting Scholar, The Hospital for Sick Children*

Typhoid has declined globally over the past 10-20 years depending on specific location. The reasons for these declines are not entirely clear. The "Trends in Typhoid" (T2) project aims to describe reported longitudinal data on typhoidal salmonella in literature and from specific sites in case countries. Surveillance systems for typhoid vary in their comprehensiveness and methods. Various reported patterns in typhoidal salmonella will be reviewed from surveillance systems and compared with contextual data on changes in water, sanitation and hygiene and other potentially important contextual factors. These patterns and sources of data may be of use to various modeling exercises to explain global and local changes in typhoidal salmonella.

3:00-4:30	Breakout	Cottonwood

Typhoid

Chair: Jillian Gauld, *Post Graduate Research Scientist*

Modeling the mechanisms of persistence and control of typhoid fever in Santiago, Chile

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

Typhoid fever control on a global scale poses a challenge in public health, given heterogeneities between populations with regards to transmission routes, amplification, burden, and drug resistance. Historical data from Santiago, Chile has provided a case study for the need to capture these dynamics for the design of effective control programs. This presentation will outline modeling work that captures mechanisms of persistence and control in Santiago, as well as discuss unknowns that remain significant to modeling typhoid both within the Santiago context and on the global scale.

4:35-5:20	Keynote	Auditorium

Keynote Address

Malaria surveillance for elimination: the role of geospatial modeling

Peter Gething, *Associate Professor Malaria Atlas Project, University of Oxford*

The capacity to reliably measure malaria transmission and disease, stratify risk, and evaluate the impact of control strategies is now accepted as integral to the success of malaria control and elimination. Where malaria surveillance has historically been weak, geospatial modeling has played a key role in compensating for limited data and providing richer and more robust evidence to support decision making. However, malaria surveillance systems are rapidly evolving and the granularity, reliability and richness of malariometric data increase year-on-year. This data explosion presents enormous opportunities for more precise, evidence-based malaria control and elimination strategies, and this talk will consider the challenges in geospatial modeling that must be met if these are to be realized.

6:00-9:00	Dinner	Bank of America

Dinner at Daniel's Broiler

Please join us for hors d'oeuvres and wine starting at 6:00, dinner service will begin promptly at 7:00. You must be registered to attend.

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

7:30	Registration	Auditorium Foyer

Registration and full service breakfast.

8:30-10:30	Auditorium	General Session

General Session 3

Chair: Jaline Gerardin, *Senior Research Scientist at IDM*

Systematic disease surveillance: stories from polio eradication and weather forecasting

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

Many of us work on building blocks of an integrated, quantitative disease surveillance system that doesn't yet exist. This talk will explore possible features of that system and the routes to its creation. From polio, we'll look at examples of the uses and challenges of integrating a global, representative surveillance strategy with quantitative analysis and disease control. The talk will close with a brief telling of the history of weather forecasting to provide a model of scope and scale of the needed progress ahead of us.

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

Melissa Penny, *Project Leader, Health Systems Research and Dynamical Modeling, Swiss Tropical and Public Health Institute*

As many countries and decision makers plan pre- elimination intervention and surveillance strategies, multiple data sources and quantitative analysis are required to make informed decisions, including from an economic perspective. In this presentation we will explore the role of different mathematical models and their complexity in providing evidence of both optimal and alternative strategies, and metrics to assess success. Analysis for Zambia and Tanzania will be presented and operational constraints discussed.

Spatial Dynamics & Heterogeneous Transmission of Malaria

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

Most models of malaria assume that parasite transmission follows the law of mass action within a population, but transmission in most natural settings is likely to be highly heterogeneous. In this talk, I will discuss reasons what is known about heterogeneous transmission, and how models with heterogeneous transmission are different from models assuming transmission is well-mixed.

8:30-10:30	Auditorium	General Session

General Session 3

Chair: Jaline Gerardin, *Senior Research Scientist at IDM*

Environmental determinants of Infectious diseases: Roads and diarrheal disease

Joseph Eisenberg, *Professor and Chair of Epidemiology, University of Michigan*

Road construction in northern coastal Ecuador has caused both ecological and social changes. After observing these changes over the past 13 years, we now have a clearer understanding of how these environmental drivers impact disease transmission of enteric pathogens and how to mitigate these changes through water and sanitation interventions. I will first present data on regional-level patterns of infection and antibiotic resistance, and then examine some social and ecological drivers that may explain these patterns.

10:45-12:45	Auditorium	General Session

General Session 4

Chair: Edward Wenger, *Senior Research Manager at IDM*

Providing useful insights on control and elimination when working on a neglected tropical disease

Deirdre Hollingsworth, *Associate Professor, Coordinator Neglected Tropical Diseases, University of Warwick*

Neglected tropical diseases (NTDs) are a group of infections which predominantly affect the "bottom billion", or the poorest people in the world. They are responsible for chronic suffering as well as mortality in these hard to reach populations. In recent years there has been a drive to reduce the burden of these diseases through an international effort to roll out interventions at a global scale. NTDs are neglected not only in terms of their public health burden, but also in our limited understanding of their biology and life cycles, with remarkably few epidemiological studies from which to parameterise or, in some cases, even simple mathematical models can capture much of the qualitative behaviour of these systems, but developing, validating and testing models which can be used to give detailed policy guidance is more challenging.

10:45-12:45	Auditorium	General Session

General Session 4

Chair: Edward Wenger, *Senior Research Manager at IDM*

DiSARM – A Disease Surveillance And Risk Mapping platform for malaria elimination

Hugh Sturrock, *Spatial Epidemiologist, University of California, San Francisco*

DiSARM is an online mapping platform, able to generate automated risk maps in near real-time. Leveraging the power and library of satellite derived environmental and climatological variables in Google Earth Engine, DiSARM gives disease control programs the ability to predict disease risk at high spatial resolution through time. Currently, DiSARM is being developed for malaria elimination settings and is being implemented in Swaziland and Zimbabwe. This presentation will give an overview of the core functions of the platform and will describe plans for expansion.

Informatics tools applicable to diverse entomological studies of mosquitoes

Samson Kiware, *Research Scientist/Wellcome Trust Fellow, Ifakara Health Institute Tanzania*

Standardized schemas, databases, and public data repositories are needed for the studies of malaria vectors. These studies encompass a remarkably diverse array of designs and rapidly generate large data volumes, often in resource-limited tropical settings lacking specialized software or informatics support. We will present 1) paper and electronic based data collection forms based on a generic schema that can be used to collect data in standardized formats from majority of entomological studies and 2) a repository that can be used to store, link, share entomological

Malaria Surveillance and Drug Based Strategies in Zambia, Senegal, and Ethiopia

Duncan Earle, *Associate Professor of International Development, MACEPA*

A synthesized review of the most recent results on malaria surveillance and drug based strategies in Zambia, Senegal, and Ethiopia.

12:45 -1:40	Lunch	Eques

Lunch at Eques

Eques is located on the 2nd floor near the Hyatt's grand staircase.

1:45-3:45	Breakout	Auditorium

Malaria Elimination

Chair: Philip Eckhoff, *Director of Research at IDM*

Stacked Generalisation for malaria mapping

Samir Bhatt, *Senior Computational Statistician, University of Oxford*

The canonical statistical technique of spatial statistics is the Gaussian stochastic process – an extremely flexible class of functions that exploits correlations inherent in spatial data. Most research on Gaussian processes have concentrated on trying to characterise the structure of complex correlations but very few have tried to add complexity to the underlying mean of the process. My new model seeks to keep the advantages of Gaussian process models but also allow for simple flexibility in parameterising the mean.

Surveillance for high risk populations in malaria elimination settings

Adam Bennett, *Programmatic Lead, Malaria Elimination Initiative, Global Health Group, University of California, San Francisco*

In many malaria elimination settings, a large proportion of malaria transmission is thought to be driven by high risk population groups that may be mobile and difficult for malaria programs to identify and target with interventions. This talk will introduce and discuss methods to identify these groups and potential strategies to engage them in routine surveillance strategies, drawing on ongoing work in Asia and southern Africa.

"Discovering" Chipepo High School and other learnings from the Lake Kariba surveillance data

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

The Zambia National Malaria Control Centre has been conducting an elimination campaign in the Lake Kariba region in Southern Province, with widespread scale-up of drug campaigns and vector control. In the process, they have collected a rich dataset on the demographics, seasonality, and geography of who gets sick, and who doesn't, and how that's impacted by the various interventions. We take a look at some of the expected and unexpected learnings derived from the data and discuss the resulting implications for future campaign operations.

| 1:45-3:45 | Breakout | Auditorium |

Malaria Elimination

Chair: Philip Eckhoff, *Director of Research at IDM*

Simple, accessible, illustrative models for bridging the gap between specialist modelers and field surveillance practitioners: Interpreting entomological indicators of malaria vector control needs and intervention opportunities as a motivating example

Gerry Killeen, *Resident Guest Scientist, Ifakara Health Institute*

Complex mathematical models are often essential to accurately capture real-world process that are correspondingly complex in nature. Unfortunately, their mechanistic basis and plausibility typically require specialist skills to assess critically, making them opaque to most field surveillance practitioners. This inaccessibility to critical appraisal results in the most important end user group interpreting the results and conclusions with either too little confidence or too much. Faced with such uncertainty about their accuracy, public health practitioners and policy makers often select between discordant modeling studies on the basis of how palatable the different results and conclusions are. Here I give several concrete examples of how simple models can be used to help surveillance practitioners exploit the results of more complex modeling studies, by allowing them to conceptualize a biological rationale for measuring practical entomological field indicators which define malaria vector control targets and identify emerging opportunities for more effective, innovative intervention strategies.

A Climate-Driven Approach to Modeling Mosquito Larval Habitat

Casey Ferris, *Graduate Researcher, University of Notre Dame*

In mosquito modeling, successfully modeling the life cycle depends on the complexity of the interactions between the mosquito, the local population, and its environment. For this research, we focus on modeling the mosquito larval habitat, which directly determines the amount of adult mosquitoes available to transmit disease. More specifically, we developed a model intended to represent all of the possible climate-driven larval habitats available throughout the world. In order to evaluate our model, we replaced EMOD's current mosquito larval habitat module with our own custom module. Our larval habitat model design will be presented, along with some of our preliminary results.

1:45-3:45	Breakout	Auditorium

Malaria Elimination

Chair: Philip Eckhoff, *Director of Research at IDM*

Modeling malaria transmission at small spatial scales

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

Small spatial scales are highly relevant when considering the role of reactive case management in eliminating malaria. A household-level model of malaria transmission in a Zambian community is implemented in EMOD and used to understand how surveillance quality affects a region's ability to achieve and maintain elimination

1:45-3:45	Breakout	Juniper

Enteric Diseases

Chair: Dennis Chao, *Senior Research Scientist at IDM*

Surveillance for Enteric Diseases: Burden to Policy

Duncan Steele, *Deputy Director and Strategic Lead for Enteric Vaccines, Bill and Melinda Gates Foundation*

A discussion of the various surveillance projects that the Bill and Melinda Gates foundation has funded for enteric diseases (e.g., rotavirus, cholera, and typhoid), and how this data can be used to influence global policy and decision making by countries.

Causal models of the epidemiology of enteric pathogen co-infections among children < 59 months in Mirzapur, Bangladesh

Kurt Long, *Research Scientist, Swiss Tropical and Public Health Institute*

Enteric pathogen co-infections may be contributing significantly to the burden of childhood diarrheal disease in low-to-middle income countries. The prevalence and epidemiology of co-infections are to be presented for children aged < 59 months with moderate-to-severe diarrhea (MSD) and matched healthy controls enrolled in the Bangladeshi component of the Global Enteric Multicenter Study (GEMS). Approximately, 84.7 percent and 66 percent of stools collected from case and control children, respectively, were positive for at least pathogen while 43 percent and 22.7 percent of these two groups had stools positive for > 2 pathogens. Structural equation models (SEM) will be presented which identify the underlying risk factors and causal pathways that determine the high burden of co-infections in this population.

1:45-3:45	Breakout	Juniper

Enteric Diseases

Chair: Dennis Chao, *Senior Research Scientist at IDM*

Modeling the effectiveness of cholera vaccination in Bangladesh

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

Cholera continues to impose a high burden in many parts of the developing world. Bangladesh, the homeland of cholera, is considering mass vaccination on a scale larger than has ever been attempted for this disease. We will present some preliminary modeling results and burden estimates that could inform vaccination policy for populations where cholera is endemic.

The Role of the Environmental Processes in Infectious Disease Dynamics

Andrew Brouwer, *Postdoctoral Research Fellow in the Department of Epidemiology, University of Michigan*

For many infectious pathogens, the environment plays an important role in transmission from one host to another. This environmental mediation may occur through a number of media, including water, air, food, and fomites. Mitigation, therefore, often involves environmental-based interventions, including water treatment, surface decontamination, and hand hygiene. Persistence of pathogens in the environment and their movement through various media, water in particular, has been extensively studied by hydrologists and microbiologists. Likewise, the functional relationship between exposure to pathogens in the environment and infection is an important part of characterizing transmission. The structure of transmission models incorporating these environmental processes has been varied in the literature. We rigorously examine the dynamics of the pathogen die-off in the environment, as well as different functional forms of the dose-response process, in the context of risk characterization and pathogen transmission.

1:45-3:45	Breakout	Juniper

Enteric Diseases

Chair: Dennis Chao, *Senior Research Scientist at IDM*

Determinants of Short Term Movement in a Developing Region and Implications for Disease Transmission

Alicia Kraay, *Doctoral Student , University of Michigan*

Although it is known that human mobility is important for infectious disease spread, reasons for movement and how this heterogeneity in travel may impact infectious disease risk has not been well characterized. To address these questions, we analyzed 10 years of survey data from 15 communities in a remote but rapidly changing region in rural coastal Ecuador to identify determinants of travel and then incorporate these predictors in a rotavirus transmission model. We find that accounting for differences in attack rates and travel patterns by age and baseline remoteness impacts transmission dynamics and allows for pathogen invasion even when there otherwise would not be an outbreak. Accounting for heterogeneity in risk also leads to increased attack rates among children and concentration of disease risk in more remote regions. Furthermore, we show that the joint effects for heterogeneity in transmission and travel is greater than individually modeled effects.

1:45-3:45	Workshop	Laurel

IDM Software

Pythoid/Toyphoid for Prototyping

Jonathan Bloedow, *Senior Software Engineer at IDM*

This session will cover new capabilities within the EMOD 2.5 release that are made possible due to the addition of embedded Python. Just as Python scripts can be used for pre- and post-processing as extensions to the DTK, simple new disease models can also prototyped entirely within Python. This session will demonstrate the "ToyPhoid" model as an example, and show exactly how modelers without expert C++ programming skills can work with this powerful new capability.

Open Session with the IDM Software Team

The IDM software team will be available to discuss and answer questions about COMPS, EMOD and the Serious Gaming Initiative.

| 1:45-3:45 | Breakout | Cottonwood |

Connecting HIV Networks with Surveillance Data
Chair: Dan Klein, *Senior Research Manager at IDM*

Mathematical models to inform effective home-use HIV testing strategies for men who have sex with men

Susie Cassels, *Assistant Professor of Geography, University of California, Santa Barbara*

The U.S. Food and Drug Administration (FDA) approved the first over- the- counter home-use HIV test in 2012. Public health departments have started to implement 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. The aim of this research is to inform public health approaches to promote safe and effective home-use HIV testing strategies for diverse populations of MSM.

Evaluating the impact of HIV pre-exposure prophylaxis (PrEP) and condom use among female sex workers

Zindoga Mukandavire, *Social and Mathematical Epidemiology Group, London School of Hygiene and Tropical Medicine, London, UK*

Female sex workers (FSWs) are an important group for tar-geted interventions to reduce HIV transmission in many set-tings. In order to understand the role HIV pre- exposure prophylaxis (PrEP) could play in controlling HIV transmission amongst FSWs, it is important to understand how its impact compares with scaling- up condom use. We developed a dynamic compartmental model for HIV transmission amongst FSWs, their clients and pimps to compare the pro-tection provided by PrEP with FSWs increasing their condom use with clients and/or pimps. For different HIV prevalence scenarios and baseline condom use, we estimated the cov-erage of PrEP that gives the same reduction in endemic FSW HIV prevalence or HIV infections averted as different increases in condom use. Our results suggest that condom promotion interventions should remain the mainstay HIV pre-vention strategy for FSWs, with PrEP only being imple-mented once condom interventions have been maximised or to fill prevention gaps where condoms cannot be used.

1:45-3:45	Breakout	Cottonwood

Connecting HIV Networks with Surveillance Data

Chair: Dan Klein, *Senior Research Manager at IDM*

A New Method for Estimating HIV Incidence Using Public Health Surveillance and Viral Genetic Data

Sandy Rutherford, *Scientific Director Complex Systems Modeling Group, the IRMACS Centre and Department of Mathematics, Simon Fraser University*

Evaluation of HIV testing and treatment programs require accurate estimates of true HIV incidence, and not simply the number of new HIV diagnoses. We present a new method for addressing this problem using readily available public health surveillance data and viral genetic data obtained from genotypic drug resistance tests of infected individuals. Optimization methods are used to combine a compartmental disease transmission model with a model of population- level viral genetic distance. This method is applied to the HIV epidemic in British Columbia, Canada. However, the model has the potential for wide application, because the data required is routinely collected in many jurisdictions.

Observability Based Approach to Optimal Design of Networks

Atiye Alaeddin, *Doctoral Graduate, University of Washington*

Utilizing the concept of observability from control theory, and some tools from graph theory and optimization, the topic of this presentation is to develop algorithms in networked system design that meet the specified control objectives' guarantees. Here, the objective is to design an optimal set of weights in the dynamics induced by the communication graph to maximize the privacy of nodes in the network. We solve the most private configuration of a network efficiently. We propose an observability- based design of communication topology in the network which improves the privacy in the network whenever the network is threatened by a foreigner. This adaptive network responds to this attack by changing the topology of the network online to reduce the information being exposed to the foreigner.

1:45-3:45	Breakout	Madrona

Vaccine-Preventable Diseases

Chair: Guilluame Chabot-Couture, *Senior Research Manager*

Machine learning techniques for measles risk prediction

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

We will discuss the application of random forest classification and regression to spatiotemporal measles risk prediction. The aims of the project are to predict the probability that at least one measles case will be reported, as well as the relative risk of large outbreaks occurring, in a given administrative district and time period. The model is calibrated to historical measles case count data from Nigeria and Ethiopia. The risk rankings produced by the model may assist the planning of resource allocation among subnational administrative units during measles supplemental immunization activities (SIAs).

Rubella Surveillance in Low-Resource Settings: Limitations, Biases, and Potential for Strengthening

Amy Winter, *Doctoral Graduate, University of Washington*

Rubella and Congenital Rubella Syndrome (CRS) cases in low-resource settings are highly under-reported. Modelers rely on patching sources of data together to estimate rubella dynamics and the burden of CRS, resulting in biased estimates. Population based age-structured serological surveys can be used to help strengthen CRS estimates in poor surveillance settings.

Spatial Model for Risk Prediction and Sub-National Prioritization to Aid Poliovirus Eradication in Pakistan

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

Pakistan is one of only two countries where poliovirus circulation remains endemic. For the Pakistan polio eradication program, identifying high risk districts is essential to target interventions and allocate limited resources. Using a hierarchical Bayesian framework we developed a spatial Poisson hurdle model to jointly model the probability of one or more cases, and the number of cases which would be detected in the event of an outbreak. The results of this model have been used to inform which sub-national areas in Pakistan should receive additional immunization activities, additional monitoring, and other special interventions.

1:45-3:45	Breakout	Madrona

Vaccine-Preventable Diseases

Chair: Guilluame Chabot-Couture, *Senior Research Manager*

Polio surveillance: methods to improve detection of large outbreaks

Isobel Blake, *Research Fellow, Imperial College London*

Prompt detection of polio outbreaks is critical to allow a fast response and interrupt transmission. Here I will give an overview of global polio surveillance and the delays that can occur at different stages of the programme. I will then describe a statistical method that could be routinely used to detect clusters of paralysis cases with the aim of providing an early warning of large polio outbreaks. In particular this method would have provided an early warning of an outbreak in Tajikistan and Republic of Congo 39 and 11 days before official confirmation.

Leveraging Data from the Polio Surveillance Network for Planning Immunization Activities

Arie Voorman, *Analyst, Polio Team, Bill and Melinda Gates Foundation*

In order for polio eradication to be successful, supplementary immunization activities need to be carried out in much of the world to mitigate risk of poliovirus spread. These activities are both epidemiologically and financially important, accounting for about 40% of resources spent on polio eradication. Knowledge of population immunity is crucial for planning these activities, but is imperfectly measured through dose histories, which are collected passively through the polio surveillance network. I'll discuss some previously unrecognized shortcomings of this data, with consequences for how global polio immunization activities are planned.

| 1:45-3:45 | Breakout | Madrona |

Vaccine–Preventable Diseases

Chair: Guilluame Chabot-Couture, *Senior Research Manager*

The use of surveillance data to understand spatial and temporal dynamics of poliovirus transmission in Pakistan to inform vaccination strategies for eradication

Natalia Molodecky, *Doctoral Student, Imperial College London*

Pakistan currently provides the greatest challenge to global polio eradication. Understanding the spatio-temporal dynamics of poliovirus transmission in Pakistan would support evidence-based planning for mass vaccination campaigns. I will describe a statistical model fit to routine surveillance data recording the presence of poliomyelitis associated with wild-type 1 poliovirus (WPV1) in districts of Pakistan to predict the geographic distribution of poliomyelitis incidence. I then describe the geographic distribution of serotype-2 population immunity in Pakistan (estimated from surveillance data) at the time of global withdrawal of serotype-2 oral polio vaccine (OPV2) in April 2016, based on various vaccination scenarios. Finally, building on these pieces of work, I describe a validated transmission model of poliovirus in Pakistan for WPV1 and adapted to the serotype-2 vaccine-derived poliovirus (VDPV2) context; used to inform vaccination strategies to mitigate risk following global withdrawal of OPV2.

BIOGRAPHIES

Neil Abernethy
Associate Professor
University of Washington

Neil Abernethy applies biomedical informatics to study infectious disease epidemiology at the University of Washington, where he is an Associate Professor in the division of Biomedical and Health Informatics, with a joint appointment in Health Services.

Atiye Alaeddini
Ph.D Graduate
University of Washington

Atiye Alaeddini has a Ph.D in Aeronautics and Astronautics from the University of Washington, Seattle. Her doctoral thesis was Observability-Based Approach to Design, Analysis and Optimization of Dynamical Systems. She also has a Master of Science in Computer Engineering from University of California, Santa Cruz. She is a control scientist with research experience on different applications of control theories on real systems. Some few examples are design a network with privacy guarantee, localization of a swarm of small ground robots, and active sensing of a limited sensing ground robot.

Ben Althouse
Research Scientist
Institute for Disease Modeling

Ben Althouse brings his enjoyment of the dynamic, intellectually challenging and inherently collaborative nature of the scientific process to the IDM Epidemiology team, where he explores pneumococcal pneumonia vaccines, the dynamics of enteric diseases, and the role of complex human contact structures on disease transmission. He was an Omidyar Fellow at the Santa Fe Institute, and holds a Ph.D 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 non-human 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.

Roberto Amato
Staff Scientist
University of Oxford

Roberto Amato is a Staff Scientist involved in the analysis of natural genetic variation in the Plasmodium parasites that cause malaria. His primary focus is at the intersection of theoretical and empirical approaches aimed at characterizing and understanding the evolution of the malaria parasite and its clinical consequences such as the emergence of drug resistance. The ultimate goal is to create a framework where genomic data can be used to identify in near real-time relevant changes in the parasite populations and to guide public health interventions. Based at the Wellcome Trust Sanger Institute in Cambridge, UK, Roberto works closely with the colleagues at the Wellcome Trust Centre for Human Genetics at University of Oxford and supports several global collaborations including the MalariaGEN P. falciparum Community Project and Pf3k.

Jason Andrews
Assistant Professor
Stanford University

Jason Andrews is an Assistant Professor in the Division of Infectious Diseases and Geographic Medicine at Stanford University.

Paul Arora
Epidemiologist & Visiting Scholar
The Hospital for Sick Children, Toronto

Dr. Paul Arora is an epidemiologist by training and currently serves as Epidemiologist and Visiting Scholar at the Centre for Global Child Health at The Hospital for Sick Children. Paul's primary research interests are in the application and development of knowledge synthesis and quantitative epidemiologic methods to address the global burden of diseases and longitudinal patterns of change. Paul will be presenting this work on behalf of the T2 collaborators group.

Ruanne Barnabas
Assistant Professor in Global Health and Medicine
University of Washington

Dr. Ruanne Barnabas is an infectious diseases physician and assistant professor in global health and medicine at the University of Washington. She also conducts research on HIV treatment and prevention in southern Africa. The ultimate aim of her work is to estimate the effectiveness and cost-effectiveness of HIV treatment and prevention interventions to inform public health policy. She completed her medical training at the University of Cape Town, her doctorate in mathematical modeling at the University of Oxford, and her infectious diseases training at the University of Washington.

Biographies

Trevor Bedford
Assistant Member, Vaccine and Infectious Disease Division
Fred Hutchinson Cancer Research

Trevor Bedford is an Assistant Member at the Fred Hutchinson Cancer Research Center affiliated with the Vaccine and Infectious Disease Division and with the Computational Biology Program. Dr. Bedford works at the interface of evolution, epidemiology and immunology. His research applies computational and statistical methods to understand viral dynamics. He is interested in using pathogen sequence data to make detailed inferences of pathogen transmission patterns. Previous research has focused on understanding antigenic drift in influenza virus, geographic spread of Ebola and within-host evolution of HIV.

Adam Bennett
Programmatic Lead for the Malaria Elimination Initiative and Global Health Group
University of California, San Francisco

Dr. Adam Bennett is an Assistant Professor of Epidemiology and Biostatistics at the University of California, San Francisco, and Programmatic Lead for the Malaria Elimination Initiative (MEI). Adam completed his MA in medical anthropology at the University of Colorado-Denver, and a Ph.D in international health and development at the Tulane University School of Public Health and Tropical Medicine. Adam is leading the MEI's surveillance efforts to develop and recommend new and efficient strategies for identifying, tracking and targeting populations at high risk of malaria in elimination settings.

Anna Bershteyn
Senior Research Manager
Institute for Disease Modeling

Anna Bershteyn leads the immunology, pathology, and within-host dynamics team at IDM. She has a Ph.D 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 Graduate Research fellow. Her modeling research focuses on HIV transmission dynamics and impact evaluation of biomedical and programmatic improvements to HIV care and prevention.

Stephano Bertozzi
Dean, School of Public Health
University of California, Berkeley

Dr. Stefano M. Bertozzi is dean and professor of health policy and management at the UC Berkeley School of Public Health. Previously, he directed the HIV and tuberculosis programs at the Bill and Melinda Gates Foundation. Dr. Bertozzi worked at the Mexican National Institute of Public Health as director of its Center for Evaluation Research and Surveys. He was the last director of the WHO Global Programme on AIDS and has also held positions with UNAIDS, the World Bank, and the government of the DRC. He is currently co-chair of the Health Working Group for the UC-Mexico Initiative and co-editor of the Disease Control Priorities (DCP3) volume on HIV/AIDS, Malaria & Tuberculosis. He has served on governance and advisory boards for WHO, UNAIDS, the Global Fund, PEPFAR, the NIH, Duke University, the University of Washington and the AMA. He has advised NGOs, and ministries of health and social welfare in Asia, Africa and Latin America. He holds a bachelor's degree in biology and a Ph.D in health policy and management from the Massachusetts Institute of Technology. He earned his medical degree at UC San Diego, and trained in internal medicine at UC San Francisco.

Caitlin Bever
Senior Research Scientist
Institute for Disease Modeling

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.

Samir Bhatt
Senior Computational Statistician
University of Oxford

Samir Bhatt is a senior computational statistician at the Malaria atlas project. His background is in statistical genetics and spatial statistics. As part of the malaria atlas project Samir has led the mapping of malaria prevalence in Africa.

Isobel Blake
Research Fellow in the Vaccine Epidemiology Research Group
Imperial College London

Isobel Blake is a Research Fellow in the Vaccine Epidemiology Research Group at Imperial College London. Her research is focused on using mathematical and statistical methods to understand and quantify the spread of polio and other infectious diseases.

Jonathan Bloedow
Senior Software Engineer
Institute for Disease Modeling

Jonathan H.H. Bloedow is the EMOD development lead for the IDM software development team. He has a Masters of Engineering from Cornell. Jonathan's current activities within IDM include managing the EMOD software development cycle as well as architecting and developing several key areas of EMOD.

Dan Bridenbecker
Senior Software Engineer
Institute for Disease Modeling

Daniel Bridenbecker has a Bachelor of Science (B.S.) from Lewis and Clark College in Portland, Oregon, and majored in both Math and Physics. Additionally, Daniel completed Master of Science course work in Mathematics at Georgia State University. Prior to working at IDM, Daniel was the Software Engineering Manager at Cloud Cap Technology that developed fully autonomous autopilots and pan/tilt/zoom camera systems for small unmanned air vehicles. Daniel came to Cloud Cap after his partner and he sold their custom software development company, Solution Engineering, Inc., to the Goodrich Corporation. At Solution Engineering, Daniel worked on numerous projects ranging from precision measurement to decision support software. Daniel also brings over 10 years of experience developing air-to-air combat simulations for Lockheed Martin. This experience includes pilot decision logic, integrated avionics system, and numerous data analysis tools. As a member of the IDM software team, Daniel's primary focus is on developing EMOD software

Andrew Brouwer
Postdoctoral Research Fellow in the Department of Epidemiology
University of Michigan

Andrew Brouwer is a postdoctoral research fellow in the Department of Epidemiology at the University of Michigan. Andrew completed his Ph.D in applied and interdisciplinary mathematics at the University of Michigan in 2015 and also holds master's degrees in mathematics, applied mathematics, statistics, and environmental science and engineering.

Bing Brunton
Professor, Biology Department
University of Washington

Bing Brunton is a Washington Research Foundation Innovation Assistant Professor in Neuroengineering at the University of Washington (UW) Department of Biology. She is also a Data Science Fellow of the UW Science Institute and a faculty member of the Graduate Program in Neuroscience. She holds a B.S. in Biology from Caltech and a Ph.D in Neuroscience from Princeton. Her research interests combine data-driven analytic techniques and ideas from dynamical systems to understand big, complex data measuring neural activity.

Ewan Cameron
Senior Computational Statistician
University of Oxford

Ewan researches the geospatial distribution of the global malaria burden within Peter Gething's group. The diverse suite of contemporary statistical techniques he applies to this challenge is informed by his past research in astronomy (University of St Andrews; ETH Zurich) and Bayesian statistics (Queensland University of Technology). Ewan is currently focusing on the refinement of ensemble prediction strategies for modeling the relationship between prevalence and incidence in areas of high (P. falciparum) malaria endemicity. His other interests include sequential Monte Carlo methods for approximate Bayesian computation and recursive algorithms for Bayesian model selection under (infinite-dimensional) stochastic process priors.

Susie Cassels
Assistant Professor of Geography
UC Santa Barbara

Susan Cassels, Ph.D, MPH is an assistant professor of Geography and a research associate in the Broom Center for Demography at the University of California Santa Barbara. Her work spans many disciplines, including demography, epidemiology, and geography. Cassels' research interests are in the areas of population health, migration, epidemic modeling, HIV/AIDS, and sexual networks. Currently, her research is focused on migration and residential mobility and its effects on sexual risk behavior, sexual network structure and HIV transmission. She has ongoing projects among heterosexuals in Ghana and among men who have sex with men in Seattle and Los Angeles.

Guillaume Chabot-Couture
Senior Research Manager
Institute for Disease Modeling

Guillaume Chabot-Couture is a Senior Research Manager in the IDM program, and leads the analysis and model usage section. He has a Ph.D in Applied Physics from Stanford University, where he focused on experimental and theoretical cuprate superconductor research, as evidenced by his dissertation, "Synchrotron X-ray Scattering Studies of Anomalous Oxygen Order in Superconducting Mercury Barium Copper Oxide & of Charge-transfer Excitations in Related Undoped Lamellar Copper Oxides". Guillaume has received two national post-graduate scholarships from the Natural Sciences and Engineering Research Council of Canada and has also published several papers in such journals as the New Journal of Physics and Physical Review. In his spare time, Guillaume has served as a lecturer and leader for the Canadian Physics Olympiad. 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

Dennis Chao holds a Ph.D from the University of New Mexico and a BSE from Princeton University. Prior to IDM, Dennis was a Staff Scientist in the Vaccine and Infectious Disease Division at the Fred Hutchinson Cancer Research Center. He developed models of infectious disease transmission for influenza, cholera, and dengue in order to better understand the epidemiology of these pathogens and to predict the effectiveness of potential intervention strategies. His prior projects included research on threats from bioterrorism and emerging infectious diseases as well as modeling the effects of mass cholera vaccinations in Haiti and Africa. Dennis joins IDM's Epidemiology team as a research scientist to continue his work with enteric diseases and modeling.

Dobromir Dimitrov
Senior Staff Scientist
Fred Hutchinson Cancer Research Center

Dr. Dimitrov is a Senior Staff Scientist at the Vaccine and Infectious Disease Division at Fred Hutchinson Cancer Research Center. He is using mathematical models to study the public-health impact of biomedical interventions for HIV prevention including oral and topical pre-exposure prophylaxis, treatment for prevention, HIV vaccines and HIV cure. Dr. Dimitrov is leading the modeling effort on various projects supporting the research agenda of the HIV Prevention Trial Network and the HIV Vaccine Trial Network.

Scott Dowell
Deputy Director for Surveillance and Epidemiology
Bill and Melinda Gates Foundations

Duncan Earle
MACEPA PATH

Philip Eckhoff
Director of Research
Institute for Disease Modeling

Philip Eckhoff leads all research efforts at IDM. He received his Ph.D 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 and 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.

Joseph Eisenberg
Professor and Chair of Epidemiology
University of Michigan

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 Ph.D 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.

Mike Famulare
Senior Research Scientist
Institute for Disease Modeling

Mike Famulare has a Ph.D in Physics from the University of Washington, Seattle, and a Bachelor of Science in Physics Education from New York University. His doctoral thesis was in Computational Neuroscience and focused on the mathematics and biophysics of single neuron information processing. Mike has a strong science education and community education focus and spent some time as a physics teacher at Stuyvesant High School in Manhattan, 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.

Nick Feasey
Senior Lecturer
Liverpool School of Tropical Medicine

Nick Feasey is a UK and Malawi based infectious disease physician and medical microbiologist, whose research interests include the clinical features and epidemiology of invasive Salmonella disease in Africa and the global phylogeny of Salmonella Enteritidis. His ongoing research involves a detailed description of the current epidemic of Typhoid Fever in Blantyre.
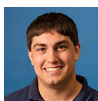
Casey Ferris
Graduate Researcher
University of Notre Dame

Casey Ferris is a Graduate Researcher at the University of Notre Dame, working under Greg Madey and Frank Collins. Their research includes Agent-Based Modeling and Simulation, with a focus on malaria transmission modeling.

Jillian Gauld
Postgraduate Research Scientist
Institute for Disease Modeling

Jillian Gauld has a Master of Science in Population and Public Health from the University of British Columbia, along with a Bachelor of Science (Honors) 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.

Elvin Geng
Associate Professor of Medicine
UC San Francisco

Elvin Geng is Associate Professor of Medicine and works in implementation science and the global HIV response.

Dylan George
Member of Technical Staff
In-Q-Tel, Office of Science and Technology Policy

Dylan provides strategic science and technical vision for establishing the IQT lab BiologyNext as a center of gravity for strengthening capacity to counter biological threats specifically for detecting and mitigating infectious disease epidemics. Prior to going IQT, Dylan served as a Senior Advisor for Biological Threat Defense at the White House Office of Science and Technology Policy.

Jaline Gerardin
Senior Research Scientist
Institute for Disease Modeling

Jaline Gerardin has a Ph.D in Biophysics from the University of California, San Francisco, along with a Bachelor's degree (B.A.) 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 anti-malarial 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.

Peter Gething
Associate Professor Malaria Atlas Project
University of Oxford

Pete Gething is Associate Professor at the University of Oxford, UK. With a background in geospatial modeling and epidemiology, he has worked on malaria and other vector borne disease since 2002. He now leads the Malaria Atlas Project (MAP), an international collaboration providing geospatial intelligence on global malaria epidemiology and control and his group is also the World Health Organization Collaborating Centre for Geospatial modeling.

Peter Gilbert
Research Professor Department of Biostatistics University of Washington & Fred Hutchinson Cancer Research Center

Peter is Principal Investigator at Statistical Data Management for the HIV Vaccine Trials Network. He is also a Research Professor at the University of Washington. Peter's current research interests center on the statistical design and analysis of HIV vaccine efficacy trials, with emphasis on assessing immune correlates of vaccine-induced protection including the "sieve analysis" of the HIV sequences infecting trial volunteers. While being motivated by HIV vaccine efficacy trials, this research contributes to general areas of statistical methods research including surrogate endpoint assessment, causal inference, survival analysis, and efficient randomized trial design. In collaboration with scientists from the Thai Ministry of Health and the United States Military HIV Research Program, Peter led the statistical design and analysis of an immune correlates study of the RV144 "Thai Trial" (published in 2012), which established a process for correlates discovery that may be useful for other vaccine trial settings. In addition, Peter led the statistical design of a sequential Phase 2b trial design for evaluating vaccine efficacy and immune correlates for multiple HIV vaccine regimens (published in 2011), which is planned for implementation and may be useful for other vaccine trial settings.

Bryan Greenhouse
Assistant Professor
University of California, San Francisco

Bryan Greenhouse, MD, MA is an Assistant Professor in the Division of HIV, Infectious Diseases, and Global Medicine at the University of California, San Francisco. His research program is focused on understanding the interactions between malaria parasites and the human host at individual and population levels, applying laboratory and analytical methods to study malaria primarily in Africa. His current projects focus on understanding the development of naturally acquired immunity, 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.

Busiku Hamainza
Epidemiologist Ministry of Health
National Malaria Control Centre, Zambia

Dr. Busiku Hamainza (BH) is a malaria epidemiologist with a large research background focusing on evaluations of malaria interventions, behavior change studies, surveillance, diagnostics, program management and advocacy. He has special interests in community based surveillance and health service delivery and innovations in routine surveillance. Dr. BH's core competencies include: a well-developed understanding of epidemiological research and presentation; knowledge of epidemiology, infectious diseases with particular focus on malaria and healthcare; experience in the development of program performance analysis and methodology; and sound ability to design innovative theories in relation to healthcare concerns associated with malaria parasite infections.

Robert Hart
Vice President and General Manager
Institute for Disease Modeling

Robert S. Hart is the Vice President and General Manager of IDM, sponsored by Global Good at Intellectual Ventures. Robert has a Ph.D 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.

Deirdre Hollingsworth
Associate Professor, Coordinator Neglected
Tropical Diseases
University of Warwick

Deirdre Hollingsworth is based in the Warwick Infectious Disease Epidemiology Research (WIDER) centre which works across the mathematics and life sciences departments at the University of Warwick. Dr. Hollingsworth leads the neglected tropical disease (NTD) modelling consortium (www.ntdmodelling.org), an international network of infectious disease epidemiologists working to improve the design of public health interventions to reduce the burden of these disease in the poorest populations of the world. Within NTDs, her research foci are lymphatic filariasis (elephantiasis), visceral leishmaniasis (or kala azar in the Indian sub-continent), and soil-transmitted helminths.

Hao Hu
Senior Research Manager
Institute for Disease Modeling

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

Nick Karnik
Senior Software Engineer
Institute for Disease Modeling

Nick Karnik has a Bachelor of Science degree in Computer Science from the University of Maryland, College Park, where his research project focused on Human Computer Interaction (HCI). With a passion for computer science, namely design patterns, complex data structures, machine learning (ML), natural language processing (NLP), and graph theory, as well as experience building large-scale distributed systems, Nick has earned accolades for his work. He has founded several startup companies, as well as built the Big-Data Validation Framework for Bing that resulted in a nomination for the Microsoft Engineering Excellence Award, and he has won several "hack day" awards in Bing for "Best Idea". He was also accepted at YCombinator, had his most recent startup venture awarded the "Investors Pick" at Startup Weekend, and has a patent pending in Intelligent Intent Detection from Social Network Messages.

Gerry Killeen
Resident Guest Scientist
Ifakara Health Institute

Dr. Killeen has been based at the Ifakara Health Institute (IHI) in Tanzania for the last 13 years. During that time he established the Environmental Health and Ecological Sciences department which is now led by two of his former students and hosts more than 30 projects and 20 principal investigators, including one of the largest malaria vector working groups in the world. He has directly supported three national malaria control programs (Zambia, mainland Tanzania and Zanzibar) and one local-scale malaria control program (Dar es Salaam City Council Urban Malaria Control Programme). He works on a variety of basic and applied aspects of malaria transmission control, especially vector control, with a strong emphasis upon quantitative ecology and mathematical modeling, as well as capacity strengthening at individual, systems and institutional levels.

Samson Kiware
Research Scientist/Wellcome Trust Fellow
Ifakara Health Institute Tanzania

Samson Kiware (B.A, MSc, Ph.D) is a Research Scientist and Wellcome Trust Fellow at the Ifakara Health Institute in Tanzania. His main research interests are based on developing bioinformatics system and mathematical models for improved understanding of malaria transmission, control, and elimination.

Dan Klein
Senior Research Manager
Institute for Disease Modeling

Daniel J. Klein has a Ph.D in Aeronautics and Astronautics from the University of Washington, where he also obtained a Master of Science. He also has a Bachelor of Science (Honors) in Mechanical Engineering from the University of Wisconsin, Madison, where his undergraduate thesis described the design and implementation of automated processing algorithms for retinal fundus and scheimpflug image analysis. Previous to IDM, Daniel was a postdoctoral scholar in the Electrical and Computer Engineering department at the University of California, Santa Barbara, where he worked on the theory and practice of multi-agent control systems. Daniel's past research includes coordinated control of unmanned aerial vehicles, distributed estimation leveraging cycles in the measurement topology, and infection-like information propagation in mobile ad-hoc networks. His work also includes the development of a nonlinear phase-coupled oscillator theory that enabled a group of airplane-like vehicles to track a target in a coordinated manner, which was demonstrated using a small school of free-swimming robotic fish.

At IDM, Daniel's time is split between developing the HIV model and building research tools. His HIV work focuses on building the contact network using ideas from feedback control to guide the dynamical relationship formation process. He is exploring structural assumptions in HIV modeling, HIV model calibration, the impact of interventions, and parameter sensitivity. The research tools he is developing allow researchers to run simulations in parallel on a supercomputer and view the results, as well as to explore large parameter spaces to find interesting regions, and to calibrate model parameters. In his spare time, Daniel guest lectures at the University of Washington, participates in the HIV Modeling Consortium and other related groups, and is a frequent presenter at conferences.

Alicia Kraay
Doctoral Candidate
University of Michigan, Ann Arbor

Alicia Kraay is a doctoral candidate in the department of epidemiology at the University of Michigan-Ann Arbor. She is broadly interested in infectious disease, with a focus on waterborne disease and environmental determinants of infectious disease. Her dissertation work combines and regression and transmission modeling approaches to understand the mechanisms of spatial spread of waterborne disease and how these processes might be modified by climate factors.

Nathan Kutz
Associate Professor
University of Washington

Nathan Kutz is professor of applied mathematics at the University of Washington. He develops data methods for reduced-order and equation-free modeling, machine learning and compressive sensing for applications across the sciences. Specifically the methods are used for characterizing complex, dynamical systems. The work has been driven by formative, interdisciplinary interactions with experimentalists across the engineering (gesture recognition, background subtraction algorithms), physical (optical and atomic physics) and biological sciences (neuroscience). More recently, he has committed a great deal of research effort towards modeling networked dynamical systems, formulating new approaches that accounts explicitly for the fundamental interaction dynamics along with its observed low-dimensional behavior.

Kurt Long
Research Scientist and Project Lead
Swiss Tropical and Public Health Institute

Kurt Long is a research scientist and project leader at Swiss Tropical where he leads research concerned with childhood health and nutrition.

Christopher Lorton
Senior Software Engineer Manager
Institute for Disease Modeling

Christopher Lorton has a Master of Science in Computer Science from Washington University, St. Louis, where he also obtained a Bachelor of Science in Physics. His master's thesis focused on the parallel computation of neural networks (NN) for the recognition of handwritten characters. Christopher's past work includes machine vision systems, digital media processing, cross-platform managed code runtime development, and the accelerated rendering of graphical user interfaces (GUI). Christopher's current responsibilities as a development lead include simulation engine software development for an upcoming compartmental modeling framework, as well as the rapid prototyping of disease transmission models for the efficient simulation of those models.

Kevin McCarthy
Senior Research Scientist
Institute for Disease Modeling

Kevin McCarthy has a Ph.D in Physics from the Massachusetts Institute of Technology (MIT) as well as a Bachelor 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 5 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.

Laina Mercer
Research Statistician
Institute for Disease Modeling

As a member of IDM's Polio team, Laina is working to support polio eradication efforts through disease mapping, statistical risk modeling, campaign impact evaluations, and campaign strategy optimization.

Joel Miller
Senior Research Scientist
Institute for Disease Modeling

Joel Miller is a Mathematical Modeler focused on the dynamic behavior of complex systems of interacting agents. Much of his work has focused on the spread of diseases through contact networks, with a recent emphasis on deriving low-dimensional models for disease spread in a population in which partnerships are neither permanent nor fleeting.

He is a Hertz Fellow. His Ph.D at Cambridge University in fluid dynamics was awarded the Vernon Harrison award from the British Society of Rheology for the top (UK) thesis in the field of rheology. He switched his focus to infectious disease spread during postdocs at Los Alamos, the University of British Columbia CDC, and a joint postdoc with the Harvard School of Public Health and Fogarty International Center. He has held faculty positions at Penn State University and Monash University (in Melbourne). He joined the applied mathematics group at IDM in March of 2016.

Natalia Molodecky
Doctoral Student
Imperial College, London

Natalia Molodecky is a Ph.D 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
Social and Mathematical Epidemiology Group
London School of Hygiene and Tropical
Medicine, London, UK

I am a member of the Social and Mathematical Epidemiology Group (SaME) in the Department of Global Health and Development. My 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.

My current research is on modeling HIV transmission dynamics in West Africa and assessing the utility of different interventions (condom use, pre-exposure prophylaxis and antiretroviral treatment) targeted at high-risk groups (Female Sex Workers, Clients and Pimps) and the general population.

Jarad Niemi
Assistant Professor Department of Statistics
Iowa State University

Jarad Niemi is an Assistant Professor in the Department of Statistics at Iowa State University. As a Bayesian statistician, his primary research interests are in computational statistics and particular in Markov chain Monte Carlo and sequential Monte Carlo approaches to statistical inference. His statistical methods are applied to disease outbreaks, including measles and influenza, as well as RNA sequencing experiments.

Gene Oates
Senior Software Engineer Manager
Institute for Disease Modeling

Gene Oates leads the software engineering team at IDM. With over thirty years of experience in the software industry, he has developed products in the telecommunications and network management fields, as well as in the financial and transportation domains, and has one patent as a result. Gene was a senior developer on the Open Application Interface (OAI), as well as designed and developed the first non-SNA implementation of the NetView Operational Architecture. He also contributed to the first ever project that allowed peripheral processors the capability to interact with Cellular Home Switches to detect cellular call progress, cellular phone status and cellular text messages – a joint effort between US West, Motorola, Octel and Accessline, and a key feature that eventually led to the "One Number" telephone service taken for granted today. Gene also contributed heavily to the success of Concur's SaaS implementation for Expense and Travel management. As one of the principal engineers, he architected and developed the central control mechanisms for all client access, as well as utilities to migrate thousands of databases for software upgrades, and the architecture required to take an enterprise analytics solution into the "Cloud". Additionally, Gene developed a prototype of a data driven semantic technology based engine that provided the capability of data sharing via the Ontology Web Language (OWL).

André Lin Ouedraogo
Visiting Research Scholar
Institute for Disease Modeling

André Lin has a Ph.D in Medical Sciences from the Radboud University Medical Centre, Netherlands, along with a Master's degree and a PhD in Applied Biology from the University of Ouagadougou. He was also awarded a graduate scholarship in Biology Engineering from the University of Sciences and Technology in Algiers where his interest lay in the biological and anti-bacterial properties of a cobalt-60's sterile irradiated amniotic membrane tissue. As a doctoral candidate, André Lin used sensitive molecular tools and first quantified the full extent of the human reservoir for gametocytes. Prior to joining IDM, André Lin was Principal Investigator of epidemiological and clinical studies at CNRFP, Ouagadougou. His work contributed novel and highly relevant findings about malaria low-density infections and immunity to accurately understand the composition and dynamics of the infectious reservoir to facilitate current and future malaria control and elimination efforts. He also acted as temporary advisor for WHO. As part of the research team at IDM, André 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. His concentration is optimizing disease eradication plans for time, cost, and robustness and developing novel diagnostic techniques in support of elimination and eradication of malaria.

Melissa Penny
Project Leader, Health Systems Research and Dynamical Modeling
Swiss Tropical and Public Health Institute

Dr. Melissa Penny is a senior member of the malaria modeling group at Swiss Tropical and Public Health Institute (Basel, Switzerland). Her work focuses on developing and using mathematical models to provide quantitative evidence to support malaria control and elimination decisions. With a focus on assessing the potential impact of malaria vaccines on transmission and clinical disease, she recently led the multi-institute collaboration that provided evidence to WHO and other stakeholders on the likely public health impact and cost-effectiveness of the malaria vaccine RTS,S.

Alex Perkins
Eck Family Assistant Professor
University of Notre Dame

Alex Perkins is the Eck Family Assistant Professor of Biological Sciences at the University of Notre Dame. His work seeks to apply mathematical modeling approaches to glean the most information possible from empirical data about vector-borne pathogen transmission, with an emphasis on spatial dynamics, transmission heterogeneity, and intervention evaluation and impact assessment.

Josh Proctor
Senior Research Scientist
Institute for Disease Modeling

Joshua Proctor is a Sr. Research Scientist at IDM. He has a Ph.D 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.

Bobby Reiner
Assistant Professor, Department of
Epidemiology and Biostatistics
University of Indiana, School of Public Health

Dr. Reiner's research interests mostly focus on the role and drivers of spatio-temporal variation in infectious disease transmission dynamics. Currently he is fixated on the disease ecology of the mosquito-borne pathogens malaria, dengue and West Nile virus, investigating the drivers of temporal variation (both seasonal and inter-annual variation) in incidence. Additionally, from a more methodological standpoint, he is interested in developing novel modeling frameworks to assess questions of interest that are designed to incorporate and leverage 'individual-level' data related to infectious diseases.

Aaron Roney
Software Engineer
Institute for Disease Modeling

Aaron Roney has a Bachelor of Science in Nuclear Engineering from Texas A&M University, where his research focused on massively parallel deterministic neutron transport software, specifically splitting and coalescing neutron energy bins for consumption. Despite a background in nuclear physics and engineering, Aaron moved to Seattle to pursue an opportunity with Microsoft as a software developer on the XAML Application Platform in the Operating Systems Group. He has founded a startup company which he manages with his wife, and he is currently pursuing a Master of Science in Computer Science from the University of Washington. As a member of IDM's software development team, Aaron is currently focused on providing rich, map-based services to researchers.

Sandy Rutherford
Scientific Director, Complex Systems Modeling Group
Simon Fraser University

Dr. Rutherford is the scientific director of Complex Systems Modeling Group, IRMACS Centre and Department of Mathematics, at Simon Fraser University. He holds a Ph.D in Mathematical Physics from the University of British Columbia and held postdoctoral fellowships at the Swiss Federal Institute of Technology (ETH) in Zurich, Switzerland, and the International School for Advanced Studies (SISSA) in Trieste, Italy. His research spans a wide range of fields within the mathematical sciences, including epidemiological modeling, operations research in health care, criminal justice system modeling, and quantum-mechanical many-body problems.

Sam Scarpino
Assistant Professor of Mathematics and Statistics
University of Vermont, Santa Fe Institute

Big Data alone can't solve our problems. This deceptively simple principle guides Sam's research and is motivated by two key insights from his dissertation. From these insights, Sam has developed a scientific research framework: to investigate pressing biological questions by integrating mathematical models and data with powerful statistical methods. Sam earned a B.Sc. in biology from Indiana University, Bloomington and a Ph.D in integrative biology from the University of Texas at Austin. His dissertation research was supported by a National Science Foundation Graduate Research Fellowship and a Doctoral Dissertation Improvement Grant. He attended the Santa Fe Institute's Complex Systems Summer School in 2010.

Vince Seaman
Senior Program Officer, Polio
Bill and Melinda Gates Foundation

Vince Seaman leads the GIS work for the polio team and supports. GIS applications across other programs at the Foundation. His past careers include working as a research chemist; a clinical pharmacist for 15 years; a high school science teacher, class adviser and coach for 8 years; and most recently, a six year stint as an epidemiologist at the Centers for Disease Control where he investigated public health emergencies resulting from environmental contamination and pollution. He moved to the Global Immunization Division in 2010, and after supporting the WHO EPI team in Liberia for 4 months, Vince was detailed to the WHO country office in Nigeria for 2.5 years to help combat vaccine preventable diseases. It was there that he recognized the need for more accurate maps for vaccination campaign microplanning, and embarked on an ambitious journey to map the entire northern half of the country. This work led to tracking vaccination teams and many related applications, which played an important role in the Nigeria polio eradication effort.

Christian Selinger
Research Scientist
Institute for Disease Modeling

Christian Selinger has a MSc in mathematics from the University of Vienna and a Ph.D in mathematics from the University of Luxembourg. He has also studied mathematics at the University of Paris 6. Christian has worked in the field of stochastic analysis, optimal transport theory, and systems biology of infectious diseases for 2 years. Prior to joining IDM, he analyzed host response to viral infections within the context of emerging pathogens (MERS CoV) and non-human primate AIDS vaccine studies (SIV). As a member of IDM's research team, he is focusing on polio immunity model calibration for IPV vaccination and modeling intra-host HIV drug resistance and adherence.

Eric Shea-Brown
Professor Applied Mathematics
University of Washington

Eric is an associate professor at the University of Washington Applied Mathematics Department, an affiliate investigator at the Allen Institute for Brain Science, and adjunct faculty in the Department of Physiology and Biophysics. His group works in mathematical neuroscience, aiming to connect circuit dynamics with basic computational and coding functions of the brain. This sparks both abstracted modeling and analysis and enthusiastic, close collaborations with experimental groups at UW and beyond. Before coming to UW, Eric was a postdoctoral fellow in mathematical neuroscience in the group of Prof. John Rinzel, at NYU's Courant Institute and Center for Neural Science. In 2004, he completed his Ph.D in Princeton's Program in Applied and Computational Mathematics, advised by Prof. Phil Holmes and co-advised by Prof. Jonathan Cohen.

John Sheppard
Senior Software Engineer Manager
Institute for Disease Modeling

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 run times. Within IDM, John leads the development efforts focused on creating the operational infrastructure for IDM's modeling solvers.

David Smith
Professor of Global Health
Institute for Health Metrics and Evaluation

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.

Andy South
Consultant
Liverpool School of Tropical Medicine

Andy South consults on the ResistanceSim serious gaming project for Insecticide Resistance Management. He developed the simple game model that determines how mosquito abundance and resistance react to player actions. He is a key member of the ETCH (Engaging Tools for Communication in Health) team, housed at the Liverpool School of Tropical Medicine. Andy has a PhD in ecological modeling and GIS and has since worked developing software for animal tracking data and analyzing spatial fisheries data for the UK government. He is now a consultant specializing in open-source software and data visualization in the statistical environment R, and working on a project modeling the development of insecticide and drug resistance.

Duncan Steele
Deputy Director and Strategic Lead for Enteric Vaccines
Bill and Melinda Gates Foundation

Duncan Steele, Deputy Director and strategic lead for enteric vaccines in the Enteric and Diarrheal Diseases team, is responsible for an integrated portfolio of vaccine research and development and implementation strategies for the control of diarrhea and enteric fever in vulnerable populations. He coordinates teams across Vaccine Development and Vaccine Delivery for improved and new vaccines against rotavirus, cholera, typhoid fever, enterotoxigenic E. coli (ETEC) and Shigella spp.

Before starting at the foundation in October 2011, Duncan was Senior Technical Advisor at PATH, a global health non-profit organization, where he worked across multiple diarrhea vaccine-related programs, including the Rotavirus Vaccine Program focused on disease burden and clinical trials in Africa and Asia; and in vaccine development for new alternative rotavirus vaccines; and for vaccines against ETEC and Shigella. Previously, as a scientist at the Initiative for Vaccine Research, Department of Immunization, Vaccines and Biologicals, World Health Organization, Dr. Steele was responsible for the diarrheal disease vaccines portfolio, where he coordinated a global strategic agenda for vaccine research for the major diarrheal and enteric diseases.

Duncan is a South African trained microbiologist with extensive experience in virology and microbiology, especially for diarrheal diseases, and has mentored students and postgraduates across the African continent. He is the author of more than 270 scientific publications on diarrheal diseases, epidemiology, clinical research and vaccine development.

Jeff Steinkraus
Senior Software Engineer
Institute for Disease Modeling

Jeff Steinkraus has a Master of Science degree in Computer Science and Engineering from the University of Michigan, as well as dual Bachelor of Science degrees in Computer Science and Honors Mathematics from the University of Michigan. Jeff's master's research focused on artificial intelligence (AI) and machine learning (ML). As a member of the IDM software team, Jeff has worked in a variety of areas, including input tools, disease model features and performance, and currently works on developing and enhancing an open, flexible infrastructure to support disease modeling.

Hugh Sturrock
Spatial Epidemiologist
University of California, San Francisco

Hugh Sturrock is a spatial epidemiologist in the Global Health Group's Malaria Elimination Initiative at UCSF and is lead of the DiSARM project.

Quirine ten Bosch
Doctoral Researcher in Infectious Disease
Dynamics
University of Notre Dame

Quirine ten Bosch is a Ph.D candidate at the University of Notre Dame. Her work is aimed at unraveling the complexities of dengue transmission using data-driven statistical and mathematical modeling approaches, and translating insights gained by those approaches into pragmatic tools for public health decision-making.

Sarah Volkman
Principal Research Scientist at Harvard T.H. Chan School of Public Health
Harvard School of Public Health

Sarah Volkman has over twenty years of experience in malaria biology with a primary research interest in the application of malaria population genetics to questions of malaria transmission and drug resistance. Her work is specifically focused on how genetic signals can be used to understand changes in malaria transmission dynamics, evaluate the impact of interventions, and define transmission networks and use of genetic signals to understand sources of new infections. She received her B.S. from the University of California, San Diego (cum laude), her Sc.D. from the Harvard School of Public Health, and did postdoctoral studies in malaria population genetics at Harvard University. Sarah Volkman is currently a principal research scientist in the Department of Immunology and Infectious Disease at the Harvard T.H. Chan School of Public Health and member of the Broad Institute. Dr. Volkman is also a Professor of Nursing at the School for Health Studies at Simmons College where she prepares nursing students in basic science content since 1989. She is a member of the WHO Technical Expert Group on Drug Efficacy and Response and the Scientific Advisory Committee for the WorldWide Antimalarial Resistance Network (WARN).

Arie Voorman
Analyst, Polio Team
Bill and Melinda Gates Foundation

Arie Voorman joined the Polio Team at the Gates Foundation in 2014, where he supports improvements in data quality and use in the eradication program. Prior to joining the Gates Foundation, he earned his PhD in Biostatistics at the University of Washington, focusing on novel statistical methods for machine learning and the genetics of complex diseases.

Edward Wenger
Senior Research Manager
Institute for Disease Modeling

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 Ph.D in Physics from MIT.

Biographies

Amy Winter
Doctoral Student
Princeton University

Amy Winter is a fifth-year graduate student in the Program in Population Studies at Princeton University's Office of Population Research. She holds a B.A. from the University of Georgia and a M.P.H in Global Health from the Rollins School of Public Health at Emory University. Prior to her graduate career, she worked with an Emory University research team investigating HIV/AIDS among MSM in the US. Her Masters' work focused on social epidemiology assessing negative health outcomes of intimate partner violence among women in India. Her current research lies at the intersection of human demography, infectious disease epidemiology, and health policy. Specifically, she explores rubella disease dynamics in endemic areas, the effects of vaccine introduction, and potential novel data sources for informing key knowledge gaps.
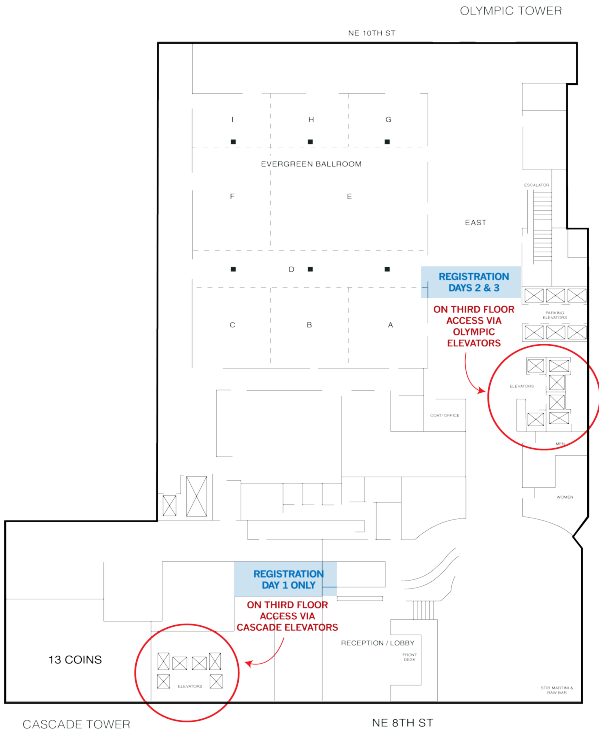
Wes Wong
Doctoral Candidate
Harvard School of Public Health

Wes is currently a third year doctoral candidate at the Harvard TH Chan School of Public Health, under the advisement of Dyann Wirth, Dan Hartl and Dan Neafseyas. He hopes to integrate population genomic analysis with mathematical modeling to better understand the population genetics and evolution of infectious diseases. He is particularly interested in understanding how populations change in response to decreasing population size, which becomes important as infectious diseases are driven toward extinction. His aim is to understand how our attempts to eradicate infectious disease change them and one day develop models that will predict how these populations will evolve over time.
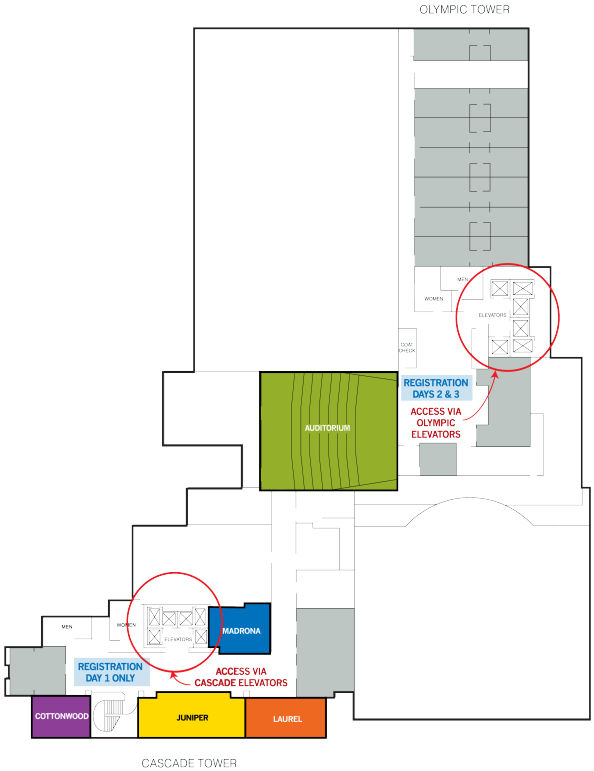
NOTES

HOTEL MAP

Lobby Level

CONFERENCE FLOOR PLAN

OLYMPIC TOWER

MEN
WOMEN
ELEVATORS
COAT CHECK

REGISTRATION DAYS 2 & 3

ACCESS VIA OLYMPIC ELEVATORS

AUDITORIUM

MEN
WOMEN
ELEVATORS

MADRONA

REGISTRATION DAY 1 ONLY

ACCESS VIA CASCADE ELEVATORS

COTTONWOOD
JUNIPER
LAUREL

CASCADE TOWER

Third Floor