



INSTITUTE FOR
DISEASE MODELING
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WELCOME

On behalf of the entire team at the Institute for Disease Modeling, we welcome you to our 7th Annual Modeling Symposium. IDM is a distinct institute within the Global Good Fund, a collaboration between Intellectual Ventures and Bill and Melinda Gates. Today, IDM has over 85 scientists and engineers focused on the eradication and control of infectious diseases, on achieving permanent improvement in child and maternal health, and in primary health care in the developing world. Our goal is to help shape global efforts in healthcare by developing, using, and freely sharing computational modeling tools and to advise policymakers, promote quantitative decision-making, and advance scientific methodologies.

We greatly appreciate and are honored by your attendance and particularly thank those contributing presentations and posters to this year's symposium. It is very gratifying to see your continued support and participation for this forum, and we look forward to continuing the tradition. We very much value this opportunity to provide a venue for collaboration and to help extend the quantitative modeling in disease eradication and control and global health. Collaboration in global health is a core value at IDM and your research, ideas, suggestions, and interactions with your colleagues are vital to developing global health policies, programs and campaigns. For IDM itself, your feedback and interaction are extremely valued.

IDM collaborations over the past year span multiple diseases, encouraging and improving surveillance methodologies, new computational methods and advanced genetic analysis, and new initiatives in primary healthcare and maternal and newborn health. We continue to engage in vaccine trial designs and field data interpretation. As all these efforts need the engagement and participation of many individual scientists and institutions, we are grateful for our collaborators and their unique contributions in this vital endeavor.

Thank you for your feedback and ideas; we hope that this symposium will again form a strong foundation for future progress.

Robert S. Hart
Vice President &
General Manager



Symposium Key Features

General Sessions

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

Breakout Sessions

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

Workshops

Software-focused workshops will feature demonstrations of IDM tools used by researchers for computational modeling. Please bring a laptop to make the most of the workshops. Released IDM tools are available freely on GitHub.

Poster Session

Poster Session is a graphic presentation of an author's research. Authors illustrate their findings by displaying graphs, photos, diagrams and a small amount of text on the poster boards.

Excursion

The excursion is offered to all attendees upon registration. IDM's excursion offers the opportunity for attendees to see the unique offerings of the PNW, and continue conversations in a more informal environment. Space is limited and subject to availability.

Dietary Restrictions

All meals have alternate options to accommodate dietary restrictions. Please see catering staff for meal option.

Mother's Room

IDM's Modeling Symposium has always proudly featured a mother's room, a private key accessible space with chairs and a refridgerator. Please see Symposium staff for access.

Day 1 Overview

8:00-8:45	Registration & Breakfast <i>Auditorium Foyer, Olympic Tower</i>
8:45-9:00	Welcome Robert Hart, <i>IDM</i>
9:00-10:30 <i>Auditorium</i>	General Session 1: Genetics <i>Chair: Josh Proctor, IDM</i> David Rasmussen, <i>North Carolina State University</i> Jennifer Gardy, <i>BMGF</i> Alison Mather, <i>Quadram Institute Bioscience</i>
10:30-11:00	Break
11:00-12:15 <i>Juniper</i>	Mapping MNCH trends <i>Chair: Assaf Oron, IDM</i> Roy Burstein, <i>IDM</i> Assaf Oron, <i>IDM</i> Kathryn Banke, <i>BMGF</i>
11:00-12:15 <i>Auditorium</i>	Advances in statistics and mathematics for the study of infectious disease spread <i>Chair: Josh Proctor, IDM</i> Niall Mangan, <i>Northwestern University</i> Samir Bhatt, <i>Imperial College London</i> Benjamin Brintz, <i>University of Utah</i> Kyle Gustafson, <i>US Navy</i>
11:00-12:15 <i>Laurel</i>	Understanding health seeking <i>Chair: Caitlin Bever, IDM</i> Marie-Reine Rutagwera, <i>PATH</i> Dorothy Echodu, <i>Pilgrim Africa</i> Dan Weiss, <i>Malaria Atlas Project, University of Oxford</i> Justin Cohen, <i>CHAI</i>
12:15-2:00	Lunch Buffet at Eques Restaurant (2nd Floor Lobby)
2:00-3:30 <i>Laurel</i>	Tuberculosis <i>Chairs: Bradley Wagner, IDM & Stewart Chang, IDM</i> Haylea Hannah, <i>UW</i> Jorge Ledesma, <i>IHME</i> Adrienne Shapiro, <i>UW</i> Jennifer Ross, <i>UW</i> Jessie Brown, <i>Linksbridge, SPC</i>
2:00-3:30 <i>Auditorium</i>	Data-driven operations <i>Chair: Amelia Bertozzi-Villa, IDM</i> Anna Bershteyn, <i>IDM</i> Ruben Conner, <i>Consultant</i> Daniel Citron, <i>IHME</i> Adolphus Clarke, <i>Ministry of Health, Republic of Liberia</i> Kate Battle, <i>Malaria Atlas Project</i>
2:00-3:30 <i>Juniper</i>	Measles <i>Chair: Kevin McCarthy, IDM</i> Amy Winter, <i>Johns Hopkins Bloomberg School of Public Health</i> Matt Ferrari, <i>Penn State University</i> Michael J Mina, <i>Harvard School of Public Health & Medical School</i> Kurt Frey, <i>IDM</i>
2:00-3:30 <i>Madrona</i>	Accelerating calibration and analysis using distributed computing <i>Chair: Benoit Raybaud, IDM</i> Jonathan Russell, <i>IDM</i> Benoit Raybaud, <i>IDM</i> Albert Lee, <i>IDM</i>
4:00-5:00 <i>Larch</i>	Poster Session

Sessions

9:00-10:30 General Session 1: Genetics

Chair: Josh Proctor, IDM

Auditorium David Rasmussen, North Carolina State University

Jennifer Gardy, BMGF

Alison Mather, Quadram Institute Bioscience

Phylogenetics in a world of rapidly adapting pathogens

David Rasmussen, *Assistant Professor*, North Carolina State University

By combining epidemiological modeling with phylogenetics, phylogenetics has given molecular epidemiology new power to track the spread of pathogens using genomic data. At the same time, phylogenetic models often ignore the singular feature of microbial populations that make them so difficult to control: their ability to rapidly adapt to new selective pressures such as host immune responses. I will present work on a new multi-type birth-death model that allows us to couple adaptive molecular evolution at the sequence level to the fitness of lineages in a phylogeny. Using Ebola virus as an example, I will show how this model can be used to infer the fitness of different pathogen strains and even the fitness effects of individual mutations.

Driving policy and practice change with genomic data: Lessons from TB

Jennifer Gardy, *Deputy Director, Surveillance, Data, and Epidemiology*, Bill & Melinda Gates Foundation

Genomic epidemiology has rapidly moved from proof-of-concept to routine implementation in well-resourced public health reference laboratories worldwide. In British Columbia, Canada, a unique retrospective analysis of over a decade's worth of tuberculosis genomic data revealed important insights into the epidemiology of TB in this low-incidence, pre-elimination setting; however, translating these insights into policy and practice change requires more than sequencing power. This presentation will discuss our work on this project and the big-picture lessons learned about successful implementation.

Genomic epidemiology of antimicrobial resistance — how best to understand transmission?

Alison Mather, *Research Leader*, Quadram Institute Bioscience

Antimicrobial resistance (AMR) is one of the greatest threats to human and animal health we face. In order to control AMR, it is essential to understand where it arises and how it spreads between populations, but bacterial evolution and biology are complex. In this talk, I will describe our work using whole genome sequencing and metagenomics, and the approaches to analyse those data, to investigate the sources, reservoirs, and transmission pathways of bacterial pathogens and AMR.

11:00-12:15 Mapping MNCH trends

Chair: Assaf Oron, IDM

Breakout *Roy Burstein, IDM*

Juniper Assaf Oron, IDM

Kathryn Banke, BMGF

Mapping neonatal, infant, and under-5 deaths and mortality rates in 103 countries from 2000 to 2017

Roy Burstein, *Research Scientist*, Institute for Disease Modeling, formerly Institute for Health Metrics and Evaluation

We quantified subnational variation in neonatal, infant, and under-5 mortality within 103 countries from 2000 to 2017, covering geographies where 97% of the world's child deaths occur. We extracted and geo-referenced data from over 500 household surveys and censuses and fit discrete hazard geostatistical models. We estimated that 85 million of the 132 million under-5 deaths in this period could have been averted in the absence of geographic inequality in mortality rates. Furthermore, as mortality for children aged 1–4 years has fallen faster than rates among neonates since 2000, a larger proportion of under-5 deaths took place during the first 28 days of life in most locations.

Squaring the circle? Comparing and combining child mortality data from surveys and surveillance districts

Assaf Oron, *Research Manager*, Institute for Disease Modeling

Improving mortality surveillance data in high mortality settings: Countrywide Mortality Surveillance for Action (COMSA)

Kathryn Banke, *Program Officer*, Bill & Melinda Gates Foundation

The Bill & Melinda Gates Foundation is supporting Countrywide Mortality Surveillance for Action (COMSA) demonstration projects in Mozambique and Sierra Leone. COMSA is a sample registration system where all births and deaths are continuously identified and reported from a representative sample of the population. Verbal autopsy interviews are completed for all deaths in the population under surveillance. COMSA's national and sub-national cause-specific mortality fractions are calibrated using paired MITS and verbal autopsy data from the Childhood Health and Mortality Prevention Surveillance (CHAMPS) Network, leading to a more accurate understanding of causes of death nationally. COMSA surveillance data are made rapidly and continuously available to the public and national and international stakeholders and used to inform public health policies and decision-making.

11:00-12:15 Advances in statistics and mathematics for the study of infectious disease spread

Breakout *Chair: Josh Proctor, IDM*
 Auditorium Niall Mangan, *Northwestern University*
 Samir Bhatt, *Imperial College London*
 Benjamin Brintz, *University of Utah*
 Kyle Gustafson, *US Navy*

Sparse model selection for structurally challenging infectious disease systems

Niall Mangan, *Assistant Professor, Northwestern University*

Inferring the structure and dynamical interactions of infectious and susceptible populations is critical to understanding outbreaks and designing interventions. Often these systems are heterogeneous in time and space. Hybrid systems are especially difficult to identify because the parameters and equation structure may vary across multiple dynamical regimes. I will discuss hybrid-SINDy, a method for combining clustering and sparse model selection. I demonstrate the success of these methods on a spring-mass model for locomotion and a simple infectious disease model with time-dependent transmission rates. If time permits, I will also discuss some recent results on the manifold learning of spatially heterogeneous disease dynamics.

New statistical approaches to spatial mapping

Samir Bhatt, *Lecturer in Geostatistics, Imperial College London*

In this talk, I will explore some of the new approaches I have developed in the field of spatial mapping. These include non-stationary processes, variationally auto encoded functions, and the merging of deep learning with spatial fields.

Predictive models of diarrhea etiology

Benjamin Brintz, *Postdoctoral Researcher, University of Utah*

Non-laboratory methods to more accurately assess etiology is needed for appropriate management of pediatric diarrhea. We used clinical and quantitative molecular etiologic data from the Global Enteric Multicenter Study (GEMS) to develop predictive models for etiology of diarrhea. Variables predictive of viral etiology included age, vomiting, BMI, bloody diarrhea, and breastfeeding. We then used a post-test odds method to improve model performance by incorporating site-specific aggregate climate data, and aggregate clinical data of previous patients.

Efficient classification of *P. falciparum* genomes by machine learning of optimal SNPs

Kyle Gustafson, *Scientist*, US Navy

Efficient and accurate classification of biological samples can improve the accuracy and timeliness of epidemiological models and interventions. Geolocalization and characterization of the regional genetic variants are both important for the allocation of resources during an eradication campaign as well as tracking the response of parasite populations to these campaigns. The careful application of antimalarials is crucial to advancing malaria control efforts in Africa and Southeast Asia that are currently at risk due to the expanding resistance. We present the application of a machine learning method to geoclassify field-derived samples of *P. falciparum* with a sparsely optimized set of SNPs. We show that this method can automatically learn new targeted sets of SNP loci, akin to existing barcode methods, that combine a high power of discrimination with low cost for customized assay development.

11:00-12:15 Understanding health seeking

Chair: Caitlin Bever, IDM

Breakout Marie-Reine Rutagwera, *PATH*

Laurel Dorothy Echodu, *Pilgrim Africa*

Dan Weiss, *Malaria Atlas Project, University of Oxford*

Justin Cohen, *CHAI*

Community health workers: A strategy to improve healthcare access for malaria elimination in Zambia

Marie - Reine I. Rutagwera, *Senior Malaria Surveillance Specialist*, PATH

Prompt access to health care services is key to malaria elimination in Zambia. Hence, the Ministry of Health has prioritized the engagement of Community Health Workers (CHWs) in malaria case management at community level, thereby reducing patient time for accessing health care services from the onset of the symptoms to diagnosis and treatment, which is vital in an elimination setting.

CRCT trial of iCCM vs ProCCM + PBO nets for control of resurgence post-IRS in Uganda: Can either combo maintain accelerated reduction?

Dorothy Echodu, *CEO, Pilgrim Africa (PI, Katakwi Rotary Malaria Project)*

A new two-year cluster-randomized controlled trial running 2/2019 to 2/2021 will compare the effectiveness of two different community case management of malaria techniques in NE Uganda. 55 villages, all of whom had 4 rounds of IRS with Actellic from 2016-2018, and half of whom also had 4 rounds of MDA with DP in the same time period, will be assigned either to the integrated community case management (iCCM) arm or to the proactive community case management (ProCCM) arm. iCCM is the national standard of care, and addresses under 5's only, in a passive context where caregivers of young children seek out community health workers (CHW's) in their homes. In the ProCCM arm, a catchment area of 30-35 households is assigned to each CHW, who sweeps them weekly, and adds in adult case detection for malaria to the integrated care for malaria, pneumonia and diarrhea in <5's.

Quantifying accessibility to healthcare facilities

Daniel Weiss, *Director of Global Malaria Epidemiology, Malaria Atlas Project, University of Oxford*

Long travel times to healthcare facilities can be an impediment for populations living in rural areas. We map travel time to emergency pediatric healthcare in Malawi to quantify geographic inequities in available care and to illustrate the utility of such maps for characterizing spatial patterns of accessibility. We also demonstrate how to create bespoke accessibility maps with relative ease using an established methodology.

Extending malaria case management to remote populations

Justin Cohen, *Vice President, Global Malaria, Clinton Health Access Initiative*

The Clinton Health Access Initiative supports over 20 countries strengthen their systems for malaria case management and disease surveillance. Expansion of high quality testing and treatment to underserved areas reduces the burden of disease, drives down transmission, and increases disease intelligence to enable improved resource allocation. This talk will describe the advances made by malaria programs across the Americas, sub-Saharan Africa, and Southeast Asia in increasing the accessibility of critical malaria case management services.

2:00-3:00

Tuberculosis

Chairs: Bradley Wagner, IDM & Stewart Chang, IDM

Breakout

Haylea Hannah, *UW*

Laurel

Jorge Ledesma, *IHME*

Adrienne Shapiro, *UW*

Jennifer Ross, *UW*

Jessie Brown, *Linksbridge, SPC*

Optimizing the population-level impact of integrating diagnostic algorithms for active tuberculosis into HIV testing in South Africa: A mathematical modeling analysis

Haylea Hannah, *PhD Student*, University of Washington

Most TB deaths are preventable with early diagnosis and treatment, and nearly 20% of TB cases go undiagnosed in South Africa. Point-of-care diagnostics integrated with HIV testing may improve case detection, thereby reducing TB incidence and mortality. This presentation will detail results from a mathematical modeling analysis assessing the population-level impact of concurrent HIV and TB testing in South Africa and identifying the diagnostic algorithm for active pulmonary TB that results in the greatest reduction in the TB burden. The diagnostic algorithms evaluated in this analysis pair standard-of-care screening and diagnostic tools with novel, point-of-care tests. Our results demonstrate a promising role for novel, point-of-care tests for TB for enhanced case finding in South Africa.

Global burden of Tuberculosis from 1990 to 2017: Findings from the 2017 global burden of disease study

Jorge Ledesma, *Post-Bachelor Fellow*, Institute for Health Metrics and Evaluation

Given the critical need to assess progress in reducing global tuberculosis burden, this presentation will highlight various methodologies used by the 2017 Global Burden of Disease study to derive location-, year-, age-, and sex-specific estimates of tuberculosis. In addition, key findings of the levels and trends of tuberculosis burden will be discussed.

Combining TB diagnostics and prevention to bend the epidemic curve

Adrienne Shapiro, *Senior Fellow/Acting Instructor*, University of Washington

Models of the TB and TB/HIV epidemics in multiple settings suggest that a multi-factorial approach, including improving TB diagnostic tests (non-sputum tests) for rapid detection of TB disease, and dramatically increasing TB preventive therapy coverage are necessary to decrease TB incidence. This presentation will review recent efforts in advancing diagnostic testing tools, diagnostic algorithms, and efforts to increase preventive treatment uptake, and propose new directions for exploring these combinations in high-burden settings.

Modeling geographic prioritization of TB case detection activities in Guatemala

Jennifer Ross, *Acting Assistant Professor*, University of Washington

This presentation will describe the role of active case detection in finding, diagnosing, and linking to care persons with undiagnosed tuberculosis. It will apply data collected as part of an active case detection exercise in Guatemala to compare modeled strategies for prioritizing active case detection to geographic areas with a high anticipated burden of persons with undiagnosed tuberculosis.

The PPA Wizard: A do-it-yourself online tool for countries to implement a Patient Pathway Analysis

Jessie Brown, *Associate*, Linksbridge, SPC

The Patient Pathway Analysis (PPA) methodology combines patient care seeking data with TB service availability data to assess the alignment of service delivery with patient preferences and identify key gaps in access to care. Linksbridge, SPC has collaborated with the Bill and Melinda Gates Foundation to develop the “PPA Wizard,” an online tool aimed to facilitate country-level PPA implementation. The presentation will focus on the process and considerations around designing an analytical tool to meet the programmatic needs of National Tuberculosis Programs (NTPs), while minimizing the need for technical assistance.

2:00-3:30 Data-driven operations

Chair: Amelia Bertozzi-Villa, IDM
Breakout Anna Bershteyn, IDM
Auditorium Ruben Conner, Consultant
Daniel Citron, IHME
Adolphus Clarke, Ministry of Health, Republic of Liberia
Kate Battle, Malaria Atlas Project

Data and dynamics to optimize the continuum of care and prevention for HIV in southern and eastern sub-saharan Africa

Anna Bershteyn, *Principal Scientist*, Sr. Research Manager, Institute for Disease Modeling

In the absence of an HIV cure, reducing HIV burden and incidence of new infections requires lifelong antiretroviral therapy (ART) for people living with HIV, as well as appropriately timed prevention services for those at risk. Care and prevention interventions are dynamic in and of themselves because of the multiple steps and services that must be undertaken and sustained over time. They also interact with the dynamics of HIV transmission and population demographics. We will discuss three examples of how routine data and dynamic modeling are combined to provide estimates and policy recommendations for HIV care and prevention.

Monday · April 15th**Data use in the field: Current barriers and future potential**Ruben Conner, *Epidemiologist*, Consultant

Modeling and other advanced quantitative uses of data have advanced markedly in the last 20 years. However, many non-governmental organizations continue to rely on simpler techniques for analysis and decision-making, such as working primarily in Excel. This talk explores some of the barriers to using more advanced methods. We also discuss how to reduce the gap between academics and in-country stakeholders and make results more transparent.

Applied simulation modeling for strategic planning for interrupting malaria transmission on Bioko IslandDaniel Citron, *Postdoctoral Fellow*, University of Washington, IHME

While the Bioko Island Malaria Elimination Program has achieved an impressive reduction in malaria prevalence, progress has slowed in recent years. The BIMEP asked us to investigate the potential impact of adding a vaccine to their intervention package. Using data from the BIMEP's Malaria Indicator Surveys, we performed three stages of analysis: mapping PfPR and human travel behaviors, estimating local force of infection and the influence of imported cases, and simulating the vaccine's effectiveness. We found that the continued persistence of malaria on Bioko Island could be attributed to the high volume of imported malaria cases from mainland Africa. We concluded that the vaccine would not be an effective long-term solution and that reducing the importation rate may be a more effective next step for their program.

Health system strengthening in post-conflict and/post-outbreak settings with emphasis on immunizationAdolphus Trokon Clarke, *EPI Manager*, Expanded Programme on Immunization, Ministry of Health, Republic of Liberia

This presentation will focus more on health system strengthening of immunization services in the context of a post-outbreak era. What were the challenges encountered and lessons learned? Also, we will discuss what developing countries need to take away from Liberia's experience.

Mapping malaria for programmatic supportKate Battle, *Senior Postdoctoral Researcher*, Malaria Atlas Project

Until recently, the Malaria Atlas Project (MAP) focussed on generating maps of malaria at global and continental scales using publicly available cross-sectional survey data. With interest from countries and the development of digital platforms routine surveillance data are becoming more readily accessible and reliable. Methods are continually being developed to generate maps using such data. Case surveillance data are more tractable in low endemicity settings and often available at fine spatial and temporal scales. The resulting outputs, informed directly by programmatic data, have been shown to be of use to national control programs in the refining the allocation of resources and control strategies.

2:00-3:30 Measles*Chair: Kevin McCarthy, IDM**Breakout Amy Winter, Johns Hopkins Bloomberg School of Public Health**Juniper**Matt Ferrari, Penn State University**Michael J Mina, Harvard School of Public Health & Medical School**Kurt Frey, IDM***Measles and the canonical path to elimination***Amy Winter, Postdoctoral Fellow, Johns Hopkins Bloomberg School of Public Health*

We find that as countries progress towards measles elimination goals, they undergo predictable changes in the size and frequency of measles outbreaks. A country's position on this 'canonical path' is driven by both measles control activities and demographic factors, which combine to change the effective size of the measles susceptible population, thereby driving the country through theoretically established dynamic regimes. Further, position on the path to elimination provides critical information for guiding vaccination efforts, such as the age profile of susceptibility, that could only otherwise be obtained through costly field studies or sophisticated analysis. Equipped with this information, countries can gain insight into their current and future measles epidemiology, and select appropriate strategies to more quickly achieve elimination goals.

Blood from a stone: Hybrid surveillance to evaluate measles vaccine program performance*Matthew Ferrari, Associate Professor, The Pennsylvania State University*

Evaluation of the performance of measles vaccination programs is challenging because 1) poor access to health services results in significant under-reporting through passive surveillance, 2) a highly sensitive case definition and limited infrastructure for laboratory confirmation results in over-reporting among those recorded within the health system, and 3) administrative estimates of vaccination coverage have historically over-estimated population immunity. While these biases may limit the utility of any metric on its own, we propose that hybrid approaches that combine programmatic and surveillance-based metrics may lead to more robust program evaluation. We illustrate that a hybrid surveillance approach can be used to both prioritize interventions based on relative, rather than absolute, performance and to proactively evaluate the expected benefit of improvements in surveillance itself.

Monday · April 15th

Revealing the consequences of measles infection and control: From individual immune repertoires to population dynamics

Michael Mina, *Assistant Professor*, Harvard School of Public Health / Harvard Medical School

Where measles vaccines are introduced, large and sustained reductions in childhood mortality from all infectious diseases are observed. We find that measles virus deletes the previously acquired immune memory repertoire, leaving hosts with immune-amnesia and susceptible to other infections for years. By preventing measles, vaccination preserves immunity. This talk will discuss the epidemiological and mathematical evidence for these findings and will link these findings to individual level immunological effects of measles infections via comprehensive profiling of the entire antiviral antibody repertoire surrounding clinical measles in children, using extremely-multiplexed antibody detection via phage immunoprecipitation and sequencing.

Maintaining elimination in an environment of persistent importation

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

Local interruption of measles transmission is achievable through high quality immunization campaigns, but the ability of a region to resist the re-introduction of the virus depends on factors such as the growth rate of its susceptible population and frequency of subsequent exposure. This study examines the role of various factors in determining post-exposure transmission dynamics and seeks to identify surveillance methodologies appropriate to preventing a return to endemic transmission.

2:00-3:30 Accelerating calibration and analysis using distributed computing

Breakout *Chair: Benoit Raybaud, IDM*
Madrona Jonathan Russell, *IDM*
 Benoit Raybaud, *IDM*
 Albert Lee, *IDM*

Using software tools to accelerate the calibration of a within-host model of malaria infection and immunity

Jonathan Russell, *Research Scientist*, Institute for Disease Modeling

Mathematical modelling is increasingly used to inform malaria control and elimination policy. Accurately capturing the relationship between exposure, detectability, and infectiousness is essential for model results to be meaningful. We have recently developed an empirical model of within-host asexual parasite dynamics to describe malaria infection and immunity in a computationally efficient way. Through collaboration between research and software teams, we have developed software tools to accelerate model construction, calibration, and analysis given the diversity of reference data sources that inform complex model structures.

Introduction to IDM's server side modeling tools

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

IDM developed a new way for researchers to accelerate their workflows called SSMT (Server-Side Modeling Tools). In this presentation we will give an overview of the system and show ways to leverage its features, enabling users to run complex and resource-intensive workflows quickly and more conveniently than on their own machine.

Spatiotemporal modeling and analysis of malaria barcodes from Senegal

Albert Lee, *Research Scientist*, Institute for Disease Modeling

New genomic surveillance data from Senegal provides an opportunity to study the behavior of endemic malaria in a low-transmission setting. We present spatiotemporal analyses of malaria transmission based on the new data, as well as seasonal dynamics in the complexity of infection. We also report updates to our barcode model and demonstrate the explanatory power of genomic surveillance.

4:00-5:00 Poster session

Larch

Day 2 Overview

8:00-9:00	Registration & Breakfast <i>Auditorium Foyer, Olympic Tower</i>
9:00-10:30 <i>Auditorium</i>	General Session 2: Modeling <i>Chair: Guillaume Chabot-Couture, IDM</i> Niket Thakkar, <i>IDM</i> Amelia Bertozzi-Villa, <i>IDM</i> Sarah Volkman, <i>Harvard T.H. Chan School of Public Health & Broad Institute</i>
10:30-11:00	Break
11:00-12:15 <i>Juniper</i>	Azythromycin <i>Chair: Dennis Chao, IDM</i> Judd Walson, <i>UW</i> Patty Pavlinac, <i>UW</i> Catie Oldenburg, <i>UCSF</i> Christian Bottomley, <i>LSHTM</i> Assaf Oron, <i>IDM</i>
11:00-12:15 <i>Auditorium</i>	Modeling resistance <i>Chair: Prashanth Selvaraj, IDM</i> Nani Mechanun, <i>Center for Development Research</i> Maciej Boni, <i>Penn State University</i> Dan Strickman, <i>BMGF</i> Tamsin Lee, <i>Swiss TPH</i>
11:00-12:15 <i>Laurel</i>	Health economics <i>Chair: Marita Zimmermann, IDM</i> Allison Portnoy, <i>Harvard T.H. Chan School of Public Health</i> Rachel Nugent, <i>RTI International</i> Mercy Mvundura, <i>PATH</i> Carol Levin, <i>UW</i>
11:00-12:15 <i>Madrona</i>	Overview of IDM Modeling Tools Jen Schripsema, <i>IDM</i> Mandy Izzo, <i>IDM</i>
12:15-1:30	Lunch buffet at Eques Restaurant (2nd floor lobby)
1:30-2:30 <i>Auditorium</i>	Student talks <i>Chair: Edward Wenger, IDM</i> Victor Asua, <i>Infectious Diseases Research Collaboration</i> Gonche Danesh, <i>IRD</i> Grace Macklin, <i>LSHTM</i>
2:30-9:00	IDM hosted excursion and dinner

Sessions

9:00-10:30

General Session 2: Modeling

Auditorium

Chair: Guillaume Chabot-Couture, IDM

Niket Thakkar, IDM

Amelia Bertozzi-Villa, IDM

Sarah Volkman, Harvard T.H. Chan School of Public Health & Broad Institute

Measles outbreak prediction with combined mechanistic-machine learning models

Niket Thakkar, *Research Scientist*, Institute for Disease Modeling

Measles remains a major contributor to preventable child mortality, and vaccine dissemination in high burden settings is a pressing global health issue. High spatial resolution outbreak prediction would allow vaccination campaigns to be more targeted and more effective, but data quality and sparsity necessitate the development of novel predictive models. Here, I will show that mechanistic disease models can be used at coarse resolution to predict outbreaks and intervention impacts, and I will demonstrate that vaccination campaign timing can be tuned to optimally interact with local transmission seasonality and recent campaign history. To increase spatial resolution, I will further describe our recent advances in using machine learning methods to combine independent mechanistic disease models. These composite models show promise in predicting district-level measles outbreaks, offering a means to plan targeted vaccination campaigns in general high-burden settings.

A global framework for malaria intervention impact: Merging geospatial and mechanistic modeling

Amelia Bertozzi-Villa, *Postgraduate Research Scientist*, Institute for Disease Modeling, University of Oxford

The push for disease control and elimination has driven the development of both cutting-edge geospatial methods for estimating risk and versatile mechanistic transmission models capable of predicting burden under a range of intervention scenarios. The former provide crucial geographic context but are less causally understood, while the latter are more mechanistically correct but often woefully inaccurate in practice. Using the example of malaria on the African continent, we present a framework for harnessing the strengths of each method to assess current and future intervention impact. Along the way, we hope to show that there is a fruitful and generalizable complementarity between statistical models and our baseline understanding of mechanisms.

Leveraging genetic signals of *plasmodium falciparum* for transmission dynamics and tracking infections

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

Discussion of genetic signatures detected across different levels of malaria transmission and how these are being applied toward decision-making. Focus on experiences in Senegal related to both monitoring transmission dynamics and tracking parasite infection patterns using genetics. Plan to develop comprehensive country-level genetic information about malaria parasite population genetics to understand transmission and tracking for intervention targeting and stratification for malaria elimination efforts.

11:00-12:15	Azythromycin <i>Chair: Dennis Chao, IDM</i>
Breakout	Judd Walson, <i>UW</i>
<i>Juniper</i>	Patricia Pavlinac, <i>UW</i> Catherine Oldenburg, <i>UCSF</i> Christian Bottomley, <i>LSHTM</i> Assaf Oron, <i>IDM</i>

Targeting vulnerable children to optimize mortality reduction

Judd Walson, *Professor, Depts. of Global Health, Medicine (Infectious Disease), Pediatrics and Epidemiology, University of Washington*

Dr. Walson will highlight current trials focusing on identifying and targeting groups of children at highest risk of mortality in low-resource settings. He will provide an overview of efforts of the Childhood Acute Illness and Nutrition Network (CHAIN) to phenotype high-risk groups of children in Africa and Asia and to identify distinct mechanism driven interventions tailored to these populations. He will also discuss the Toto Bora trial, a randomized placebo controlled trial of azithromycin to prevent death and rehospitalization in high-risk children discharged from hospital at multiple sites in Kenya.

Azithromycin to prevent post-discharge morbidity and mortality: The Toto Bora Trial

Patricia Pavlinac, *Assistant Professor, University of Washington*

In this presentation, I will review the burden of childhood morbidity and mortality that occurs in the period following hospital discharge in Sub-Saharan Africa and discuss potential mechanisms of this vulnerability. Then I will introduce the Toto Bora trial which is a double-blind randomized controlled trial assessing whether a 5-course of azithromycin, given at hospital discharge, reduces this risk.

Azithromycin for the prevention of child, infant, and neonatal mortality in Burkina Faso

Catherine Oldenburg, *Assistant Professor, University of California, San Francisco*

The MORDOR study demonstrated a significant reduction in all-cause child mortality in children aged 1–59 months in Niger, Malawi, and Tanzania. The largest reduction in mortality appeared to be in the youngest age group (1–5 months). Ongoing randomized trials in Burkina Faso are evaluating the role of azithromycin administration integrated with early-life well-child healthcare visits (e.g., during vaccination visits) and during the neonatal period. This presentation will describe the methods and rationale for the trials.

Does giving oral azithromycin during labour reduce the risk of neonatal sepsis?

Christian Bottomley, *Associate Professor*, London School of Hygiene & Tropical Medicine

In this presentation I will report on two trials conducted in The Gambia in which oral azithromycin has been given to women in labour. The first trial investigated the impact of this intervention on bacterial carriage in the mother and baby. The second trial, which is ongoing, will assess the impact on neonatal sepsis and mortality.

Demographic Effect Variations in the Mordor trial, and practical implications

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

No information provided.

11:00-12:15**Modeling resistance**

Chair: Prashanth Selvaraj, IDM

Breakout

Nani Mechanun, *Center for Development Research*

Auditorium

Maciej Boni, *Penn State University*

Dan Strickman, *BMGF*

Tamsin Lee, *Swiss TPH*

Exploring methods of malaria vector control in Africa using EMOD

Nawaphan Metchanun, *Junior researcher/doctoral candidate*, Center for Development Research

Female *Anopheles spp.* mosquitoes can transmit *Plasmodium* parasites that cause malaria, a life-threatening infectious disease. The parasites are transmitted to humans through the bites of infected mosquitoes. Despite being preventable and treatable, malaria has devastating impacts on people's health and livelihoods around the world. About 3.2 billion people are at risk of the disease in 97 predominantly tropical countries with an estimated number of more than 198 million cases, even though billions of dollars are spent annually on malaria control and elimination.

This research aims to assess different types of malaria vector control for developing countries by conducting impact and economic evaluation of the methods based on modelling using the Epidemiological MODelling software (EMOD). Since the economic value, outcomes and impacts are crucial indicators of the Global Technical Strategy for Malaria (GTSM) 2016-2030, the research is contributing to achieving the GTSM targets.

Managing antimalarial drug-resistance across high-transmission and low-transmission settings

Maciej Boni, *Associate Professor*, Pennsylvania State University

As long as artemisinin-based therapies continue to be the therapies of choice in malaria-endemic countries, health policy will need to maintain a focus on the emergence and spread of artemisinin-resistant genotypes. Challenges will vary based on whether countries already carry multiple resistant genotypes, whether transmission levels are high or low, whether the health system is flexible enough to alter treatment guidelines in light of new information, and whether drugs are distributed through public or private markets. We highlight some key resistance management decisions that need to be made in each of these contexts, and we make some policy recommendations for the long-term success of drug resistance management in malaria.

Excuses, genetics, and frustration: What does insecticide resistance look like in the field?

Dan Strickman, *Senior Program Officer*, Bill & Melinda Gates Foundation

The biology of insecticide resistance is still a work in progress, both for the scientists studying it and for the mosquitoes. Key questions we'd like to answer remain elusive at a practical level, like the influence of agriculture, the transport of resistance by mosquito movement, and sub-lethal effects on resistant mosquitoes. From an operational standpoint, resistance can erase good efforts, destroy confidence, and provide an excuse for poor technique.

Modelling the spread of drug resistant malaria

Tamsin Lee, *Post doc*, Swiss Tropical and Public Health Institute

It is generally understood that treatment causes drug-resistant malaria. However, the story is more complex than that. Hosts may carry several infections, where drug-sensitive parasitemia multiply quicker than their drug-resistant counterparts. Such within-host mechanisms are included in our Sensitive-Infected-Treated model, thereby quantifying the effect of these mechanisms on drug resistance establishment.

11:00-12:15 Health economics*Chair: Marita Zimmermann, IDM*Breakout Allison Portnoy, *Harvard T.H. Chan School of Public Health*

Laurel

Rachel Nugent, *RTI International*Mercy Mvundura, *PATH*Carol Levin, *UW***Health gains and financial protection from human papillomavirus (HPV) vaccination in Ethiopia**Allison Portnoy, *Doctoral Candidate, Harvard T.H. Chan School of Public Health*

An evaluation of both the health gains and financial protection from routine HPV vaccination is critical to support planned cervical cancer prevention programs in Ethiopia. We used a multiple modeling approach that captured HPV transmission, cervical carcinogenesis, and population demographics to project health and economic outcomes associated with routine HPV vaccination in Ethiopia. To evaluate financial risk protection, we estimated household out-of-pocket (OOP) expenditures averted, catastrophic expenditures averted, and cases of poverty averted by HPV vaccination.

Economic modeling to inform developing country action on non-communicable diseasesRachel Nugent, *Vice President, Global Noncommunicable Diseases, RTI International*

Rachel will present examples of using economic modeling to demonstrate benefits and costs from health intervention and policy changes in developing countries aimed at reducing mortality from non-communicable diseases.

Evaluating the cost effectiveness of self-administered DMPA-SC (Sayana Press) compared to provider administered DMPA-IM in Uganda and Senegal.Mercy Mvundura, *Senior Health Economist, PATH*

The presentation will review the methods and the results of two studies conducted to evaluate the cost effectiveness of self-injection of DMPA-SC compared to provider administration of DMPA-IM. The data for the analysis were collected during research a research setting. The results from the cost effectiveness analyses were used to inform and influence the programmatic implementation the self-injection program.

Tuesday · April 16th**What do we know about the economics of integration and health system strengthening for improving effectiveness and efficiency of health services in limited resource settings?**Carol Levin, *Senior Research Scientist*, University of Washington

This presentation will highlight the role of integration and health system strengthening for improving reach and quality of services in low-and middle-income settings. It will explore available evidence on costs, effectiveness, efficiency and cost-effectiveness of integrating health services (as well as integrating across sectors) to improve health outcomes in primary health care delivery.

1:30-2:30 Overview of IDM Modeling ToolsJen Schripsema, *IDM*Breakout Mandy Izzo, *IDM**Madrona*

This session will provide an overview of IDM's tools used to model epidemiological data and to predict trends in transmission dynamics.

1:30-2:30 Student talks*Chair: Edward Wenger, IDM**Auditorium*Victor Asua, *Infectious Diseases Research Collaboration*Gonche Danesh, *IRD*Grace Macklin, *LSHTM***Changing molecular markers of antimalarial drug sensitivity across Uganda**Victor Asua, *Research Scientist*, Infectious Diseases Research Collaboration

My presentation will focus on spatial and temporal changes in the prevalence of molecular markers of antimalarial drug resistance. Longitudinal molecular data was collected from 10 sites, at 6-month intervals, for 3 time points, representing different malaria transmission epidemiology across Uganda. We aimed to evaluate the evolution of antimalarial drug resistance in line with malaria treatment and prevention practices in Uganda.

Phylogenetics of acute HCV infection in MSMGonché Danesh, *P.h.D Student*, IRD (Institut de Recherche pour le Développement)

Opioid substitution and syringe exchange programs have drastically reduced HCV spread in France but HCV sexual transmission in men having sex with men (MSM) has recently arose as a significant phenomenon. Phylogenetics methods rely on pathogen genetic sequences to approximate a transmission chain via a dated phylogeny. Most of them are limited by the difficulty to compute the function of the likelihood function. The Approximate Bayesian Computation (ABC) method can bypass this problem and perform parameter inference by comparing the simulated data and target data. We used the regression-ABC method to estimate key epidemiological parameters such as the reproduction number (R_0) and the infectious period duration of acute HCV infection (AHI) in MSM.

Modelling mOPV2 campaigns in a post-switch environment

Grace Macklin, *PhD Student*, London School of Hygiene and Tropical Medicine

In April 2016, there was a global withdrawal of type 2 Sabin oral poliovirus vaccine (OPV2), and a stockpile of monovalent OPV2 (mOPV2) was retained for emergency use in case of VDPV2 outbreaks, which could be released under the authorization of the WHO Director-General. Between April 2016-2019, there have been 71 outbreak response campaigns with mOPV2. However, there is now evidence that mOPV2 campaigns are seeding new VDPV events and outbreaks. This presentation aims to assess the persistence and transmission of mOPV2 in the environment after use for outbreak control and estimate the reproductive number of a mOPV2 campaign.

Tuesday · April 16th

Symposium Excursion

IDM hosted tour at the Museum of Pop Culture and Dinner

Please join us for the IDM hosted excursion and dinner. This year's excursion will be held at the iconic Museum of Pop Culture (MoPop). As a guest you'll get to explore exhibits on Seattle's own Pearl Jam and Nirvana as well as take a journey through fantasy, science fiction, and horror with artifacts from iconic television shows and movies. Explore your inner musician in the Sound Lab, a multimedia hands-on attraction where you can explore electric guitars, drums, samplers, mixing consoles, and more.

This year IDM will be hosting featured speaker, Dr. Siddhartha Mukherjee, author of Pulitzer Prize-winning book, *The Emperor of All Maladies*, as well as *The Gene* and *The Laws of Medicine*.

Following the featured speaker, you're cordially invited to join us for an IDM-hosted dinner in the Sky Church area of MoPop. As a guest, you will dine on a unique menu of fresh seasonal ingredients provided by Wolfgang Puck catering. Meal options for those with dietary restrictions will be available.

Transportation will be provided by IDM.

Schedule of Events

2:30: Buses depart from the Hyatt Regency Lobby

3:00: Arrive at MoPop

3:00–5:00: Enjoy the MoPOP

4:45: Auditorium check-in for featured speaker

5:00–5:45: Featured speaker Dr. Siddhartha Mukherjee. Doors close at 5:00pm.

6:00–9:00: Dinner

There will be two buses departing from MoPOP approximately starting at 7:30pm and 8:30pm. Symposium staff will make an announcement during dinner.

Day 3 Overview

8:00-9:00

Registration & Breakfast
Auditorium Foyer, Olympic Tower

9:00-10:30

Auditorium

General Session 3: Informing Policy

Chair: Caitlin Bever, IDM
Abdisalan Noor, *WHO*
Damian Walker, *BMGF*
David Wilson, *The World Bank*

10:30-11:00

Break

11:00-12:15

Juniper

Understanding genomic surveillance data and implications for malaria elimination

Chair: Josh Proctor, IDM
Maxwell Murphey, *UC Berkeley*
Seth Redmond, *Broad Institute/HSPH*
Aimee Taylor, *Harvard T.H. Chan School of Public Health*
Albert Lee, *IDM*

11:00-12:15

Laurel

INFORM

Chair: Andre Lin Ouedraogo, IDM
Abraham Flaxman, *IHME*
Karim Derra, *CRUN-IRSS Nanoro*
Navideh Noori, *IDM*
Qinghua Long, *IDM*

11:00-12:15

Auditorium

Epidemiology

Chairs: Laura Skrip, IDM & Laurent Hébert-Dufresne, University of Vermont
Adia Benton, *Northwestern University*
Sharon Abramowitz, *Independent*
Gerardo Chowell, *Georgia State University*
Laurent Hébert-Dufresne, *University of Vermont*

11:00-12:15

Madrona

Utilizing GPU computational resources for agent-based models

Christopher Lorton, *IDM*

12:15-2:00

Lunch Buffet at Eques Restaurant (2nd Floor Lobby)

2:00-3:30

Juniper

Linking environmental factors to infectious disease and mortality patterns

Chairs: Mollie Van Gordon, IDM & Navideh Noori, IDM
Michael Brauer, *UBC/IHME*
Radina Soebiyanto, *NASA Goddard Space Flight Center*
Pamela Martinez, *Harvard T.H. Chan School of Public Health*
Michele Nguyen, *University of Oxford*

2:00-3:30

Laurel

HIV transmission dynamics in the era of test and treat

Chair: Adam Akullian, IDM
Paul-Marie Grollemund, *Imperial College London*
Will Probert, *University of Oxford*
Hae-Young Kim, *Africa Health Research Institute*
Danae Black, *UW*
Adam Akullian, *IDM*

2:00-3:30

Auditorium

Applications of data science, machine learning, and artificial intelligence in health and development

Chair: Dan Klein, IDM
Uyi Stewart, *BMGF*
Nick Sorros, *Wellcome Trust*
David Wilson, *The World Bank*
Jessica Shearer, *PATH*

3:30-4:00

Auditorium

Symposium Conclusion

Edward Wenger, *IDM*

Sessions

9:00-10:30 General Session 3; Informing Policy

Chair: Caitlin Bever, IDM

Auditorium

Abdisalan Noor, *WHO*

Damian Walker, *BMGF*

David Wilson, *The World Bank*

Estimating the global burden of malaria: Weak data, challenging methods, controversial results, but optimism for the future

Abdisalan Noor, *Team Leader, Surveillance team, Global Malaria Programme, World Health Organization*

Historically, the quality of data in areas with the highest malaria burden has been weak. Therefore, to estimate the burden of malaria globally the WHO has used various methods leading to results that are as controversial as they are informative. As surveillance systems improve, and as estimates become increasingly at odds with national routine data, considerable opportunities have emerged for improving existing methods or developing new ones. However, these national data also suffer from important biases whose influences can be substantial. Here the technical details and challenges of burden estimation methods and a comprehensive plan on the way forward are presented.

Use of economics in data and analytics at BMGF

Damian Walker, *Deputy Director, Data and Analytics, BMGF*

No information provided.

David Wilson, *Program Director, The World Bank*

No information provided.

11:00-12:15 Understanding genomic surveillance data and implications for malaria elimination

Breakout *Chair: Josh Proctor, IDM*

Maxwell Murphey, *UC Berkeley*

Juniper

Seth Redmond, *Broad Institute/HSPH*

Aimee Taylor, *Harvard T.H. Chan School of Public Health*

Albert Lee, *IDM*

Classifying spatial origin of malaria infections using genetic data

Maxwell Murphy, *Graduate Student, UC Berkeley, UCSF*

Classifying malaria cases as imported versus local and determining origin of infection remains an important challenge in elimination settings where, despite thorough case investigation, there continues to be uncertainty about parasite provenance. To help address this challenge, we have applied Gaussian process regression to incorporate spatial information in estimating malaria parasite allele frequencies, providing a formal framework for assigning parasite origin based on a geographically informed model of parasite distribution. Our results demonstrate the advantages of incorporating spatial information into allele frequency estimation, allowing for accurate classification at multiple spatial scales.

Genomic Epidemiology at the Lower Limits of Malaria Transmission

Seth Redmond, *Postdoctoral Associate*, Broad Institute / HSPH

Genomic data has shown its ability to track changes in transmission intensity and prevalence and has a role to play in surveillance of malaria elimination programs. However, this data is less informative as transmission falls and genetic diversity wanes. Using datasets in both Sub-Saharan Africa and the Caribbean, in which outcrossing is reduced to a minimum, we will show how transmission dynamics can still be characterised even at the lower margins of diversity.

Marker requirements for relatedness inference of malaria parasites

Aimee Taylor, *Postdoctoral research fellow*, Harvard T.H. Chan School of Public Health

Relatedness inference is used in malaria epidemiology to study parasite genetic connectivity and selection, to discern domestic versus imported infections, et cetera. We explore marker requirements (numbers of markers and their cardinalities) to infer relatedness with specified error and provide guidelines for prospective studies.

Evaluating genetic epidemiological models in high-dimensional parameter spaces

Albert Lee, *Research Scientist*, Institute for Disease Modeling

Genetic epidemiological models are increasing in predictive and analytical value as more surveys include genomic information about infectious agents. Owing to a high degree of complexity, careful allocation of computational resources is critical for efficiently exploring the parameter space of the genetic models. We describe an iterative and parallelized sampling scheme for evaluating our malaria model via Server-Side Modeling Tools.

11:00-12:15 INFORM

Chair: Andre Lin Quedraogo, IDM

Breakout Abraham Flaxman, IHME

Karim Derra, CRUN-IRSS Nanoro

Laurel Navideh Noori, IDM

Qinghua Long, IDM

Identifying underlying cause-of-death at scale: The verbal autopsy and beyond

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

This presentation will give a recap and status update on a decade of development of the “SmartVA” suite of verbal autopsy tools. It will include the open-source SmartVA-Analyze app that automatically maps from verbal autopsy interviews to underlying cause of death; the Bloomberg Data for Health initiative’s efforts to scale up coverage of vital registration using VA; and, finally, what may happen next with this technology.

Causes of death in rural Africa: Evidence from Nanoro Health and Demographic Surveillance System

Karim Derra, *Junior Research Scientist*, CRUN - IRSS Nanoro (Burkina Faso)

By analysing the disease burden in Nanoro HDSS, the study aims to analyse the double burden of disease in a rural area of sub-Saharan Africa. The verbal autopsy tools are used to collect data.

Spatiotemporal pattern of child mortality in Nanoro HDSS, Burkina Faso

Navideh Noori, *Research Scientist*, Institute for Disease Modeling

We looked at the Nanoro HDSS neonatal mortality as well as mortality among children under 5 to understand and identify any spatiotemporal pattern in data and their potential risk factors.

Overview of the EasyVA platform

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

EasyVA is a web platform allowing clinicians to easily browse verbal autopsy surveys and determine the cause of death of subjects. During this session, we will show a demo of the platform along with a brief overview of the project architecture.

11:00-12:15 Epidemiology

Chairs: Laura Skrip, IDM & Laurent Hébert-Dufresne, University of Vermont

Breakout

Adia Benton, *Northwestern University*

Auditorium

Sharon Abramowitz, *Independent*

Gerardo Chowell, *Georgia State University*

Laurent Hébert-Dufresne, *University of Vermont*

Scenarios, strategies, and structural violence, or what I learned while playing pandemic with first-year students

Adia Benton, *Assistant Professor*, Anthropology and African Studies, Northwestern University

Drawing on ethnographic and textual research about modeling practices and reflections on teaching an undergraduate course about the social lives of epidemics, I examine what can be learned through 'humanizing' and 'politicizing' epidemic scenario- and world-building exercises. Specifically, I underscore lessons learned about how such exercises can help to shape and extend the assumptions, calculations, and interpretations of otherwise socially 'thin' data.

Social and behavioral analysis in Ebola epidemics: Aligning qualitative realities with quantitative analysis

Sharon Abramowitz, *Medical Anthropologist*, Independent

Past and present experiences with Ebola epidemics have taught us that communities, context, and culture are key to understanding outbreak dynamics. However, the integration of this knowledge into the real-time modeling of EVD data remains elusive under outbreak conditions. In this talk, I will address how measuring the effectiveness of public health response measures in real time will require methodological innovation by qualitative researchers, disease modelers, and response actors; serious consideration needs to be given to how epidemiological data, sociometrics, and implementation research can be coordinated to bring new insights to EVD prevention and response efforts. UNICEF C4D's Community Engagement Minimum Standards and Indicators will be highlighted as an example of innovation.

Transmission dynamics and forecasts of the ongoing Ebola outbreak in DRC

Gerardo Chowell, *Professor of Epidemiology and Biostatistics*, Georgia State University

In this talk, I will discuss various mathematical and statistical aspects relating to the real-time analysis of the transmission dynamics and forecasts of the Ebola outbreak in DRC.

Reductions in Ebola virus transmission driven by behavioral interventions in Sierra Leone

Laurent Hébert-Dufresne, *Assistant Professor*, University of Vermont

We present a modeling framework that encapsulates the impact of human behavior on disease spread at two different levels. At the individual level, using contact tracing data to inform models from network theory can help us separate the impact of heterogeneity in human behavior from the inherent stochasticity of disease transmission. At the community level, we aim to parametrize a metapopulation model using behavioral data collected by the Social Mobilisation Action Consortium, a large-scale community engagement partnership that worked in more than 90% of communities across Sierra Leone through 2,466 trained community mobilizers. Using this framework, we revisit the West African Ebola virus epidemic and argue that behavioral change caused a significant fraction of reductions in virus transmission.

11:00-12:15 Utilizing GPU computational resources for agent-based modelsBreakout Christopher Lorton, *IDM**Madrona***GPUs and Disease Modeling**Christopher Lorton, *Managing Principal Software Engineer, Institute for Disease Modeling*

Modern GPUs provide a tremendous amount of computing power without the infrastructure of a high performance computing cluster. GPUs can be used in a variety of ways to assist with modeling diseases. In this presentation we will discuss some particular uses of GPUs for modeling at IDM and cover available tools and approaches for processing data, modeling disease transmission, and analyzing results.

2:00-3:30 Linking environmental factors to infectious disease and mortality patterns

Breakout *Chairs: Mollie Van Gordon, IDM & Navideh Noori, IDM*
 Michael Brauer, *UBC/IHME*
Juniper Radina Soebiyanto, *NASA Goddard Space Flight Center*
 Pamela Martinez, *Harvard T.H. Chan School of Public Health*
 Michele Nguyen, *University of Oxford*

Estimating the burden of disease from environmental risk factorsMichael Brauer, *Professor, The University of British Columbia / Institute for Health Metrics and Evaluation*

The presentation will include an overview of the methodology used to estimate the global burden of disease from environmental risk factors, with an emphasis on ambient and household air pollution and impacts on childhood infectious disease.

Bioclimatic indicators of vector-borne disease riskRadina Soebiyanto, *Research Scientist, Universities Space Research Association / NASA Goddard Space Flight Center*

Epidemics and epizootics of vector-borne diseases (VBDs) are closely associated with fluxes in environmental and climate/weather conditions. We will present our work that illustrates by example how the coupling between climate anomalies serves as a trigger or amplifier of the spatio-temporal outbreak patterns of several VBDs including Rift Valley fever and chikungunya. We will also demonstrate the use of climate observations and forecasts — derived from satellite and in situ measurements — for disease risk mapping, monitoring, and early warning that can aid decision makers in making robust policies for disease preparedness, prevention, and deployment planning.

Climate forcing, environmental factors, and the population dynamics of diarrheal diseases

Pamela Martinez, *Postdoctoral Research Fellow*, Harvard T.H. Chan School of Public Health

Demographic, socioeconomic, and environmental factors have the potential to enhance the sensitivity of infectious disease to climate change. These changes in transmission can result from the formation of reservoirs that promote faster responses to seasonal and inter-annual environmental fluctuations. By looking at the population dynamics of diarrheal diseases, I have explored the role of these external factors, such as environmental drivers and socioeconomic factors, on the temporal and spatial heterogeneity of rotavirus and cholera cases obtained from the Dhaka Hospital, Bangladesh.

A statistical modelling framework for mapping malaria seasonality

Michele Nguyen, *Postdoctoral Researcher*, University of Oxford

Many malaria-endemic areas experience seasonal fluctuations in cases because the mosquito vector's life cycle is dependent on the environment. While most existing maps of malaria seasonality use fixed thresholds of rainfall, temperature, and vegetation indices to find suitable transmission months, we develop a spatiotemporal statistical model for the seasonal patterns derived directly from case data. The methodology is illustrated using health facility data from Madagascar and administrative level data from the Latin America and Caribbean region.

2:00-3:30 HIV transmission dynamics in the era of test and treat

Chair: Adam Akullian, IDM

Breakout Paul-Marie Grollemund, *Imperial College London*

Will Probert, *University of Oxford*

Laurel

Hae-Young Kim, *Africa Health Research Institute*

Danae Black, *UW*

Adam Akullian, *IDM*

Preliminary report of high rates of EXTERNAL (non-domestic) infection sources for newly HIV-1 diagnosed heterosexual men and women in Seattle and King County, USA

Paul-Marie Grollemund, *Research Associate*, Imperial College London

Public Health Seattle & King County (Washington, USA) maintains an HIV viral sequence database containing 12606 partial pol sequences from 15932 HIV-1 infected individuals that live, were diagnosed, or started ART in King County since 1982. From this database, and a [size] set of international sequences added as background, we aim to assess the importance of infections from external sources in comparison to local infections via a phylogenetic analysis. The geographic location of viral lineages were estimated through maximum parsimony ancestral state reconstruction, so that we identified the source locations of 354 distinct chains of transmission that occur in King County. By first focusing on heterosexual individuals infected with a non-B subtype, the estimated crude importation rate was 69% [50%-76%]. Ongoing work aims to adjust for incomplete sampling of the epidemic, and will clarify to what extent the crude estimate is an overestimate.

Quantifying the contribution of different aged men and women to a generalised HIV epidemic

William Probert, *Researcher*, University of Oxford

The HIV epidemic in sub-Saharan Africa is known to be heterogeneous, contributing to the perception that preventative efforts need to be targeted to those at most risk of transmitting or acquiring the virus. Using an individual-based model calibrated to historical prevalence, we quantify the proportion of new infections that arise from men and women of different age groups and the potential impact of suppressing transmissions from each of these groups.

Geographical linkage of HIV transmission in conjugal heterosexual couples in rural KwaZulu-Natal, South Africa

Hae-Young Kim, *Postdoctoral Research Fellow*, Africa Health Research Institute

Using the population-based longitudinal surveillance data from the Africa Health Research Institute, we assessed the geographical linkage of conjugal heterosexual relationships in the surveillance area. We compared the linkage with phylogenetic transmission clusters identified from sequencing samples and examined the potential role of geographical linkage in HIV transmission in this rural hyperendemic setting.

Preventing TB/HIV co-infection among HIV infected adolescents in Kenya

Danae Black, *Research Assistant*, University of Washington

Assessing the use of tuberculosis preventive screening and therapy among HIV-infected adolescents in Kenya.

Aging of the HIV-1 epidemic in sub-Saharan Africa, historical trends and future predictions

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

This talk presents historical data and modeled simulations to suggest a shift in the age distribution of those newly infected and living with HIV both prior to ART scale-up and in the era of universal test and treat.

2:00-3:30 Applications of data science, machine learning, and artificial intelligence in health and development

Breakout *Chair: Dan Klein, IDM*
Uyi Stewart, BMGF
 Auditorium *Nick Sorros, Wellcome Trust*
David Wilson, The World Bank
Jessica Shearer, PATH

From data to decisions: Use cases for artificial intelligence in health and development

Uyi Stewart, *Directory of Global Development Strategy*, Data, and Analytics, Bill & Melinda Gates Foundation

Over the past decade, we have witnessed an unprecedented explosion in data and in the way that analytics is being used to generate insights from such data. For example, in agriculture we used to rely mainly on subjective interpretation of weather or the farmer's almanac to support farmer's productivity. Now, we rely on remote sensing and predictive analytics to forecast yield, crop health, when or what to plant, etc. In healthcare, our polio eradication campaigns used to be targeted uniformly across geographies causing supply chain and coverage estimation nightmares. Now, we rely on analytics to help predict and smartly focus our interventions. This transition from diagnostic to predictive problem solving is happening across research, academic, commercial, and non-governmental global development efforts, albeit with different incentives and underlying assumptions about the Data Value Chain (DVC).

I'll describe my journey from a commercial global innovation lab to the Bill & Melinda Gates Foundation, starting with our work in Africa (Nairobi, Kenya) to set up the first commercial research lab on the continent that is focused on applied and far-reaching exploratory research. I will describe how data and its usage have emerged as one of the most important global public goods at Gates Foundation; in particular, how we are using innovative technologies across the DVC to shape/influence our program strategy teams and the engagement with our partners in pursuit of our core belief that all lives have equal value. In light of these, I will motivate a unifying DVC and global data architecture that will enable data scientists and others from the research, academic, and commercial communities to contribute toward global public good (data science for social good) and help to make tomorrow better than today for billions of people.

Automating the collection of policy impact evidence

Nick Sorros, *Senior Data Scientist*, Wellcome Trust

Scientists produce publications that policymakers read in order to create evidence-based guidelines and reports. But the link from funding scientific research to policy change is not well understood. In Wellcome Data labs, we have created a tool to systematically collect potential evidence of such changes by tracking the citations that openly available policy documents make to scientific publications that we, or other funders, have funded. This is the first step towards a better understanding of this complex process of quantifying policy impact through funding basic science.

Artificial Intelligence and Big Data in Health: Promise, Practice and Policy

David Wilson, *Program Director*, The World Bank

The health sector is more digitized than other sectors, but has not yet fully realized its potential to use big data, AI-enabled analytics and technologies to improve countries' ability to achieve universal health care. In this lightning talk, David will unpack the continuum of AI use cases in health, demonstrated practical obstacles for AI implementation and how to overcome them, additional potential to expand the use of AI to bring concentrate more value to health systems, and the concomitant policy changes that are needed to create an enabling environment in which these innovations can be implemented.

Data for action: rom the front lines of global health

Jessica Shearer, *Acting Director*, PATH

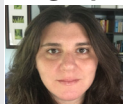
Working in more than 70 countries, PATH is committed to strengthening the skills, tools, and culture needed to use data to improve health. From eliminating malaria to achieving universal immunization coverage, progress towards these goals will be accelerated with data and innovations in analytics, and with an emphasis on data use at the front lines. This presentation will share examples and lessons learned from PATH's use of big data and machine learning.

3:30-4:00 Symposium Conclusion

Edward Wenger, *IDM*

Auditorium

Biographies



Sharon Abramowitz
Medical Anthropologist
Independent
saabramowitz@gmail.com

Sharon Abramowitz is a medical anthropologist who specializes in Ebola, infectious diseases, epidemic preparedness and response, community engagement, and data sharing. Presently, she is consulting on UNICEF's efforts to establish minimum standards for community engagement, and was PI on a Wellcome Trust research study examining data sharing during the West Africa Ebola epidemic and the 2016 Yellow Fever outbreak. She is a leading advocate for the integration of social sciences into epidemic response, and works closely with the World Health Organization, UNICEF, Gates Foundation, Wellcome Trust, USAID, and other partners to identify opportunities for standardizing and accelerating interactions between social science, clinical medicine, and epidemiology in epidemics. She is also an expert on humanitarian intervention, mental health, gender violence, health sector transitions, and post-conflict reconstruction in West Africa. She is the author of *Searching for Normal in the Wake of the Liberian War*, co-editor of the book *Medical Humanitarianism: Ethnographies of Practice*, and numerous publications on the West African Ebola outbreak published in the *Lancet*, *Global Public Health*, *PLOS Neglected Tropical Diseases*, and the *Journal of Infectious Disease*. She is based in Brookline, Massachusetts.



Adam Akullian
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Adam Akullian is a Research Scientist the Institute for Disease Modeling (IDM) and Affiliate Assistant Professor in the Department of Global Health at the University of Washington in Seattle. Adam has a PhD in Epidemiology from the University of Washington and an ScB in Environmental Science from Brown University. As a doctoral candidate, Adam studied the evolutionary ecology and spatial epidemiology of emerging enteric diseases in rural and urban Kenya, as well as the geography of HIV in rural areas of Kenya and Uganda. He is also a recipient of a National Science Foundation (NSF) Graduate Research Fellowship. As a member of IDM's research team, Adam focuses on spatial, mathematical, and epidemiological modeling of HIV in sub-Saharan Africa with the goal of understanding transmission dynamics in high-burden settings.



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Victor Asua is a Research Scientist at Infectious Diseases Research Collaboration, Kampala, Uganda. He obtained his master's degree in Immunology and Clinical Microbiology from Makerere University. Later, he joined Infectious Diseases Research Collaboration as a Junior Scientist. When not busy with research, Victor likes taking road trips to the countryside. He is currently working on antimalarial drug resistance research project under the Program for Resistance, Immunology, Surveillance, and Modulation (PRISM) program in Uganda. You can reach him at victorasua@yahoo.co.uk.



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Kathryn Banke, PhD, is a Program Officer on the Vaccine Development and Surveillance team at the Bill & Melinda Gates Foundation. She oversees the Countrywide Mortality Surveillance for Action (COMSA) grants in Mozambique and Sierra Leone and related investments dedicated to improving the understanding of cause of death among children under five. She has over 20 years of experience as an epidemiologist working in infectious disease surveillance and response, epidemiologic study design and analysis, development and implementation of monitoring and evaluation plans, and survey design and implementation. Previously she led child health research activities, was a monitoring and evaluation advisor for international health projects at Abt Associates, and spent five years working in the Global Immunization Division at the U.S. Centers for Disease Control and Prevention focused on polio eradication and measles elimination. Dr. Banke has a PhD in epidemiology from Emory University and BA in human biology (honors) from Stanford University.



Kate Battle
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Kate Battle is a postdoctoral researcher with the Malaria Atlas Project in Oxford leading the Malaria Eradication Metrics stream of the group. She facilitates technical support to Clinton Health Access Initiative from MAP for countries working towards malaria elimination. Her other work focuses on estimating the global burden of *Plasmodium vivax* malaria.



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Adia Benton is an assistant professor of Anthropology and African Studies at Northwestern University, where she is affiliated with the Science in Human Culture Program. Her first book, *HIV Exceptionalism: Development Through Disease in Sierra Leone*, won the 2017 Rachel Carson Prize, which is awarded by the Society for Social Studies of Science (4S) to the best book in the field of Science and Technology Studies with strong social or political relevance. Her body of work addresses transnational efforts to eliminate health disparities and inequalities, and the role of ideology in global health. In addition to ongoing research on public health responses to epidemics, including the 2013-2016 West African Ebola outbreak, she has conducted research on the growing movement to fully incorporate surgical care into commonsense notions of "global health." Her other writing has touched on the politics of anthropological knowledge in infectious disease outbreak response, racial hierarchies in humanitarianism and development, and techniques of enumeration in gender-based violence programs. She has a PhD in social anthropology from Harvard University, an MPH in international health from the Rollins School of Public Health at Emory University, and an AB in Human Biology from Brown University. She has held a postdoctoral fellowship at Dartmouth College and visiting positions at Oberlin College and in the Department of Global Health and Social Medicine at Harvard Medical School.

Biographies



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Anna Bershteyn heads the HIV and TB research team at the Institute for Disease Modeling. She received her PhD from MIT, where her research focused on adjuvant discovery for new vaccines, especially HIV.



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Amelia Bertozzi-Villa is a Postgraduate Research Scientist at IDM and a PhD candidate with the Malaria Atlas Project at the University of Oxford. She has researched human movement for health-seeking, dynamics of malaria in Southeast Asian settings, interactive data visualization for outbreak scenarios, and serious games for family planning. She holds an MPH from the University of Washington and a Bachelor's from NYU.



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



Samir Bhatt
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Samir Bhatt's interests lie in the development and application of a wide variety of mathematical models to address policy-relevant questions about infectious diseases. His focus is on the spatial modelling of major diseases (malaria, leishmaniasis, HIV, and dengue). In this field he has published the first rigorous estimates of the global distribution and burden of dengue and has led an extensive collaboration with the WHO to determine the patterns and drivers of change in malaria through space and time. His current research agenda involves the development of a new statistical frameworks for mapping using techniques from machine learning and deep learning, the application of Hawkes processes to modelling outbreaks and vector-borne diseases, and a computational platform for mapping HIV in Africa.



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Danae Black is a PhD student in Epidemiology at the University of Washington. Danae received her Master's in Public Health in Global Health Epidemiology from The George Washington University. During her master's level studies, she worked as an assistant study coordinator for the Kenya Medical Research Institute and Centers for Disease Control and Prevention conducting a diagnostic TB trial among children under five. Danae's interests include tuberculosis, global health, and infectious disease epidemiology. Since beginning her training at UW, Danae has also worked with the Strategic Analysis, Research and Training (START) Center conducting technical literature review and analytic support to the Bill and Melinda Gates Foundation and global and public health decision makers.



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Maciej F Boni's academic background is in mathematical epidemiology, mathematical population genetics, individual-based disease transmission models, field epidemiology, phylogenetics, and recombination. His main areas of research are the evolution of antimalarial drug resistance and the dynamics and evolution of influenza virus. Maciej's malaria work has focused on optimal methods of distributing antimalarial drugs to minimize future risks of drug resistance, evaluating risks of drug-resistance emergence during mass drug administration, and planning for the introduction of novel antimalarial compounds. From 2008 to 2016, Maciej's research group was based in Ho Chi Minh City at the Oxford University Clinical Research Unit. In 2016, Maciej joined the Biology Department and the Center for Infectious Disease Dynamics (CIDD) at Pennsylvania State University.



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Christian Bottomley is an Associate Professor in Medical Statistics and Epidemiology at the London School of Tropical Medicine and Hygiene with research interests in epidemiology, statistics, and mathematical modelling. He collaborates with the Medical Research Council Unit in The Gambia, and the KEMRI-Wellcome Trust Research Programme in Kilifi, Kenya on studies evaluating the effectiveness of pneumococcal vaccines and azithromycin in preventing bacterial infections in infants and young children. His methodological research focuses on the development of methods for analysing interrupted time series and mathematical models of pneumococcal transmission.

Biographies



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Michael Brauer is a Professor in the School of Population and Public Health at The University of British Columbia and an Affiliate Professor at the Institute for Health Metrics and Evaluation, where he leads the Environmental Risk Factors team for the Global Burden of Disease. His research focuses on linkages between the built environment and human health, with specific interest in transportation-related and biomass air pollution, the global health impacts of air pollution and the relationships between multiple exposures mediated by urban form and population health. He has participated in monitoring and epidemiological studies throughout the world and served on advisory committees to the World Health Organization, the Climate and Clean Air Coalition, the US National Academies, the Royal Society of Canada, the International Joint Commission and governments in North America and Asia. He is an Associate Editor of Environmental Health Perspectives. His contributions to environmental health have been acknowledged by a number of career achievement and publication awards.



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Ben received his BA (2010) in math from Grinnell College in Iowa. He received his MSc (2014) and PhD (2018) in statistics from Oregon State University where his research extended models for estimating abundances that are imperfectly detected to the application of disease surveillance. He is now in Dr. Leung's lab at the University of Utah as a postdoctoral fellow in data scientist and is working on clinical decision rules for pediatric infectious diarrhea. In his spare time, Ben likes to run, climb, play chess, and watch NBA basketball with his wife.



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Jessie Brown is an Associate at Linksbridge, SPC, an advisory and consulting firm based in Seattle, USA. Linksbridge is a social purpose corporation with expertise in global health, global development, and the humanitarian sector. Since joining Linksbridge three years ago, Jessie has worked with the Bill and Melinda Gates Foundation's TB Delivery Team on areas ranging from the Patient Pathway Analysis to multidrug-resistant TB to TB Drug Development. Jessie holds a Master of Philosophy in Development Studies from the University of Oxford and a Bachelor of Arts in International Studies from the University of Washington.



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Roy Burstein is a recent graduate of the University of Washington's Global Health Metrics and Implementation Science PhD program. He conducted his doctoral research at the Institute for Health Metrics and Evaluation on spatial analysis of child mortality and healthcare utilization. He is currently a Research Scientist at IDM.



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Guillaume Chabot-Couture is Director of Research, Global Development, at the Institute for Disease Modeling. He has a Ph.D. in Applied Physics from Stanford University, where he focused on experimental and theoretical cuprate superconductor research. Guillaume has received two national post-graduate scholarships from the Natural Sciences and Engineering Research Council of Canada. 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, health economics, and weather modeling.



Dennis Chao
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Dennis Chao holds a PhD 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.



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Stewart Chang has a Ph.D. in Bioinformatics from the University of Michigan, where he researched the mathematical modeling of host response to tuberculosis (TB) bacterium. He also has a Bachelor of Arts degree in Biochemistry, as well as Latin, from Rice University. Stewart has over ten years of experience with a variety of computational modeling and analysis techniques, including postdoctoral work at the University of British Columbia (UBC) as well as at the University of Washington, Seattle (UW), where he investigated the mathematical modeling of HIV infection at UBC, and did genomic analysis of influenza-infected and HIV-infected cells at the UW. Stewart also has a strong community focus. Before turning to research, he joined Teach for America and taught math in rural south Louisiana, where he worked with under-resourced communities. As a member of IDM's research team, Stewart is currently developing and parameterizing the IDM model of HIV infection, and is working on the IDM model of TB infection.



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Gerardo Chowell, PhD, is a Second Century Initiative Scholar (2CI) and Professor and Chair of the Department of Population Health Sciences in the School of Public Health at Georgia State University. Before joining Georgia State, Dr. Chowell was a tenured faculty of the School of Human Evolution and Social Change at Arizona State University. He also holds an external affiliation as research associate in the Division of International Epidemiology and Population Studies at the Fogarty International Center, NIH. Dr. Chowell holds a PhD in Biometry from Cornell University. After obtaining his PhD, he was awarded a Director's Funded Postdoctoral Fellowship to support his mathematical modeling research program at the Theoretical Division of Los Alamos National Laboratory.

Dr. Chowell's academic career has primarily focused on the development and calibration of mathematical and computational models of infectious disease transmission to test public health policy. During the 2009 A/H1N1 influenza pandemic he was a consultant for the Mexico Ministry of Health and participated on briefings to the Office of the President of Mexico. Dr. Chowell has published over 180 peer-reviewed articles. His work has appeared in high-impact journals and has been cited numerous times by major media outlets. He serves in the editorial board of several journals including BMC Medicine, Scientific Reports, Epidemics Now, and Mathematical Biosciences and Engineering.



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Daniel Citron received his PhD in physics from Cornell University in 2017, focusing on modeling infectious disease dynamics on heterogeneous contact networks and measuring the development and growth of scientific research communities. Beginning in 2017, he has worked at the Institute for Health Metrics and Evaluation at the University of Washington as a member of the Malaria Elimination Team. His current projects include transmission model development and validation; assisting the Bioko Island Malaria Elimination Program with planning new intervention strategies; and using simulation models to plan cluster randomized trials.



Adolphus Trokon Clarke
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Adolphus is the current Manager for the Expanded Programme on Immunization at the Ministry of Health, Republic of Liberia, where he has devoted about 90 percent of his professional practice to the child survival for more than eight years. He has wide-ranging experience in public health in practice, public health pharmacy, and innovative approaches in improving immunization outcomes. His recent efforts include increasing immunization coverage for the third dose of pentavalent vaccine (Penta 3) from 52 percent to 79 percent, he was very instrumental in working with National Legislature through sustained advocacy to increase the government budgetary allocation for immunization. As a result of this tireless efforts, the Expanded Programme on Immunization national budget increased from US\$ 50,000.00 in 2010 to over US\$ 650,000.00 in 2016 and was successful in establishing the Parliamentary Forum for Immunization at the National Legislature, Republic of Liberia. He was lead architect for the introduction of several new vaccines (PCV, Rota and IPV) into routine immunization including approvals of new vaccines (e.g. MCV2 and HPV) in Liberia.

Adolphus is a frequent speaker and discussant of child health issues and also an instructor at the University of Liberia Department of Chemistry. He lives in Lower Johnsonville, Montserrado County, Republic of Liberia, is interested in learning new things and supporting child health interventions. Adolphus envisage himself as an immunization specialist and wish to continue said through his professional life.



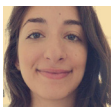
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Justin, an infectious disease epidemiologist, oversees the Clinton Health Access Initiative's operational and technical support to government partners to optimize the impact of national malaria programs, avert disease morbidity and mortality, and eliminate malaria sustainably. CHAI works directly with governmental malaria programs, the private sector, and their partners to build more effective, efficient systems for deploying targeted, tailored prevention and treatment measures guided by enhanced disease intelligence made possible by expanded diagnostic testing. CHAI's malaria program is currently assisting over 20 countries across Latin America, sub-Saharan Africa, and Southeast Asia to strengthen surveillance systems, improve data analytics, streamline operations, enhance strategic planning, target interventions, and mobilize financial resources. Justin earned his doctorate in Epidemiological Science and MPH in International Health from the University of Michigan and studied Molecular, Cellular, and Developmental Biology at Yale University.



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Ruben Conner has worked on data analysis and epidemiology at a variety of NGOs, including IHME, PATH, Medecins Sans Frontieres, and the Gates Foundation. He has lived in in South Sudan, Zambia, Thailand, and India.



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Gonché Danesh is a PhD student in bioinformatics and epidemiology at the IRD in Montpellier, France. She has a Master's degree in Bioinformatics. She works on the Approximate Bayesian Computation (ABC) method for phylodynamic analysis of rapidly evolving virus epidemics such as HIV and HCV. She is currently developing a simulation tool in Rcpp, in order to simulate epidemiological trajectories from any compartmental model, and to simulate sampled transmission trees.

Biographies



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Karim Derra is Demographer with a Mathematician background. He is a Manager of the Nanoro Health and Demographic Surveillance System (HDSS) at the Clinical Research Unit of Nanoro (CRUN), IRSS-DCRO/CNRST, Burkina Faso. His research activities are focused on population and health, particularly on malaria. He has been involved in Epidemiology and Public Health studies. He has good experience on analysis longitudinal data. He will achieve his PhD work, which aims to address a critical issue in malaria control, i.e. developing news tools to accurately assess malaria attributable mortality. He has started publishing papers in International Journal of Epidemiology, Global Health Action, Malaria Journal and Plos One.



Dorothy Echodu
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Dr. Dorothy Echodu is the CEO of Pilgrim Africa, a 501(c)3 engaged in malaria control, operational research and education in Uganda. In the decade she's worked with Pilgrim Africa, she has led and overseen the organization's engagement in malaria. Pilgrim Africa focuses on community-scale field exercises using both tested and novel approaches to comprehensive control in high burden areas, and has a special interest in building innovative local infrastructure for vector control. Aware of the high human and economic toll caused by ongoing tolerance of high morbidity as well as mortality, Pilgrim Africa continually strives for just, economically realistic solutions to the need for more malaria control. Currently, Pilgrim Africa is pleased to partner with Rotary International, Rotarian Malaria Partners, the Bill & Melinda Gates Foundation and President's Malaria Initiative on a multi-year project to bring comprehensive control to a rural, highly endemic region in northeastern Uganda.

Dorothy is also engaged in pedagogy for innovation. Since 2006, Pilgrim Africa has operated a large secondary school in eastern Uganda which specializes in S.T.E.M. disciplines. Dorothy trained as a physical chemist with degrees from Yale (BA) and UW (PhD) and her past work experience includes basic research into HIV-1 RNA, physics education research, and cross-cultural communication of values. She is a Rotarian Malaria Partners Ambassador, a member of the WHO Vector Control Working Group, a board member of Domaine Clarence Dillon, and a vestry member of St. Barnabas Church.



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Matthew Ferrari uses dynamical systems theory to understand the contribution of demographic processes and local and regional variation to the performance of vaccination programs. This work has primarily focused on vaccination programs for measles and rubella; though he has also done evaluations of vaccination programs a range of human and livestock pathogens. In particular, he has worked with national and international actors to develop statistical methodology and evidence-based approaches for program evaluation and decision-making. His work has highlighted the role of seasonal variations in human movement in driving locally erratic, and unstable outbreak dynamics. His work has shown that these seemingly erratic local dynamics are stabilized at the regional scale that modulate the stability of regional persistence of measles and other communicable childhood infections. Large-scale, public health surveillance highlights the need to draw biological inference from systems that are often imperfectly observed because not all individuals are recorded by health systems. He has developed statistical methodology – based on methods in signal processing and hidden Markov models – to formalize inference for partially observed systems. He has formalized these methods to produce annual estimates of the global burden of measles mortality in collaboration with the World Health Organization. He has further combined methods for model-fitting with forward simulation models to allow near-real time analysis of disease surveillance and forecasting to support evaluation of candidate interventions in human and livestock disease settings.



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



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Kurt Frey is a member of the measles team at IDM where he focuses on agent-based simulations of disease transmission, with an emphasis on campaign planning and the elimination threshold. He has a doctorate in Chemical Engineering and a Master of Science in Chemical Engineering Practice from the Massachusetts Institute of Technology, and a Bachelor of Science in Chemical Engineering from the Ohio State University. His previous work at Argonne National Laboratory supported efforts on simulating environmental processes for nuclear waste, both in recycling and disposal.



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Dr. Jennifer Gardy joined the Bill & Melinda Gates Foundation's malaria team as Deputy Director, Surveillance, Data, and Epidemiology in February 2019. Before that, she spent ten years at the BC Centre for Disease Control and the University of British Columbia's School of Population and Public Health, where she held the Canada Research Chair in Public Health Genomics. Her research focused on the use of genomics as a tool to understand pathogen transmission, and incorporated techniques drawn from genomics, bioinformatics, modelling, information visualization, and the social sciences. In 2018, Jennifer was named one of BC's Most Influential Women in STEM by BC Business Magazine, and was named one of the Government of Canada's 20 Women of Impact in STEM. In addition to her science work, Jennifer is also a science communicator, hosting many episodes of science documentary television for Canada's national broadcast, as well as authoring science books for children, including a new book to be released in 2020.



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Paul-Marie Grollemund is a Research Associate in Statistics and Pathogen Phylodynamics at the Department of Mathematics at Imperial College London under the supervision of Oliver Ratmann. He works on HIV transmission and in particular he is focusing on determining the importance of risk factors in transmission network and the proportion of HIV introduction into a population by demographic characteristics.

He did his PhD at IMAG lab of University of Montpellier (France) under the supervision of Christophe Abraham, Pierre Pudlo, and Meili Baragatti.

Biographies



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Kyle earned his PhD in physics at the University of Maryland as a Fellow of the Fannie and John Hertz Foundation with Prof. William Dorland. He was awarded an NSF International Research Fellowship to continue studying plasma physics with Prof. Paolo Ricci in Lausanne, Switzerland at the EPFL. In 2012 he began to study genomic regulation of circadian rhythms in the labs of Prof. Winship Herr at the University of Lausanne and Jacques Rougemont at the EPFL. He was later invited into the lab of Prof. Felix Naef at the EPFL where he helped to mentor Masters and PhD students. Returning to the US in 2016, he studied epidemiological modeling as a postdoc with Dr. Joshua L. Proctor at the Institute for Disease Modeling near Seattle, part of the Global Good initiative of the Bill and Melinda Gates Foundation.



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Haylea Hannah is currently a PhD student in Epidemiology at the University of Washington in Seattle. Haylea earned a Master of Science in Public Health in Epidemiology from Emory University in Atlanta. During her time in Atlanta, Haylea worked on the Domestic TB surveillance team in the Division of TB Elimination at the Centers for Disease Control and Prevention, where she conducted an independent research study analyzing socio-demographic and clinical risk factors associated with TB mortality in the United States. Following her Master's, Haylea completed the CDC/CSTE Applied Epidemiology Fellowship with the Marin County Department of Health and Human Services, where she supported a large TB outbreak investigation, conducted various community-based research projects, and designed routine data collection mechanisms for programs to measure, assess, and evaluate service delivery and health outcomes. Haylea and Dr. Paul Drain collaborated with the Institute for Disease Modeling to assess the population-level impact of integrating diagnostic algorithms for tuberculosis into HIV testing in South Africa, providing key insight into the potential impact of enhanced case finding for TB using various diagnostic algorithms. Haylea is committed to providing research that builds the evidence-base for programs and policies that impact population health.



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



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Laurent Hébert-Dufresne is an Assistant Professor in the Vermont Complex Systems Center with appointments in computer science and mathematics at the University of Vermont. After a PhD in physics focused on network theory, he joined the Santa Fe Institute as a James S. McDonnell postdoctoral fellow, during which he started working in epidemiology and ecology. He then spent a year at the Institute for Disease Modeling, working as a postdoctoral researcher to study the impact of human behavior on emerging infectious diseases.

He now leads the Laboratory for Structure and Dynamics (LSD) at the University of Vermont. Their research tackles any interesting question that depends both on the structure of a system and on the dynamics it supports. Their focus is on network theory, but also general nonlinear dynamics in structured systems. Recent examples of LSD projects include social networks interacting with the spread of diseases and information, the shape of forests coevolving with forest fires, the structure of metabolic networks influencing interactions in microbial communities, and the interplay of commercial honeybees with native bumblebee populations in Vermont.



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



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Hae-Young Kim is a postdoctoral research fellow at the Africa Health Research Institute. She was awarded her PhD in Epidemiology from Johns Hopkins School of Public Health and MPH from Columbia University. Her research interest is to understand epidemiological and behavioral mechanisms to prevent HIV and TB transmission and improve linkage to care among adolescents, pregnant women and marginalized populations.

Biographies



Daniel Klein
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Daniel J. Klein is Sr. Research Manager of the Applied Math Center, a cross-cutting team within IDM that supports modeling and analytics within IDM and on-behalf of IDM's external partners. Since joining IDM in 2010, he has co-lead development of the EMOD-HIV model, published algorithms for stochastic model optimization and calibration, and presented modeling results to international stakeholders. Dr. Klein studied engineering at the Univ. of Wisconsin before earning a PhD in Aeronautics & Astronautics with specialization in control theory from the Univ. of Washington. During 2018, he led various data science and strategy initiatives as a Senior Program Officer in the Global Development Strategy, Data, and Analytics team at the Bill & Melinda Gates Foundation. Prior to joining IDM, Dr. Klein was enjoying the sunshine of Santa Barbara, CA as a postdoctoral scholar with the Center for Control and Dynamical Systems at UCSB.



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Jorge Ledesma earned his Bachelor's in Sociology at the University of Nebraska-Lincoln in 2017. During his undergraduate career, Jorge developed a strong interest in data analytics and statistical computing to understand complex social and health outcomes. His research interests led to an assistantship to conduct a social network analysis among placed-at-risk youth followed by a fellowship at the National Center of Education Statistics to implement mathematical models to estimate global education outcomes.

After graduation, Jorge received a three year post-baccalaureate fellowship at the Institute for Health Metrics and Evaluation (IHME) at the University of Washington. As a fellow, he contributes to the Global Burden of Disease (GBD) study through his responsibilities as the primary modeler of a small interdisciplinary team that aims to estimate the mortality and morbidity of tuberculosis for every country and year. In addition to his position at IHME, his fellowship is complimented with an MPH program in Health Metrics at the University of Washington.



Albert Lee
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Albert Lee is a research scientist at the Institute for Disease Modeling, with a focus on using dynamic evolutionary models to understand malaria genetics. He has a PhD in Physics from Harvard University.



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Tamsin mathematically models what drives resistance to malaria treatment. She has been working at the Swiss Tropical and Public Health Institute, with Prof. Melissa Penny, since January 2018. She recently published work showing that including the in between step of partial resistance, before full resistance, is a key mechanism when modelling the spread of drug resistance throughout a population. A short animation (3:40 min) detailing this is available at TamsinELee.com/videos. Her previous positions include The Mathematical Institute, University of Oxford and The Quantitative and Applied Ecology Group, University of Melbourne.



Carol Levin
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Dr. Carol Levin, both an agricultural and health economist, is an associate professor in the Department of Global Health at the University of Washington. Her research focuses on the costs and cost-effectiveness of introducing and scaling up public health interventions and new technologies related to reproductive, maternal and child health and nutrition interventions, including HIV/AIDS, TB and vaccine preventable diseases. Previously, she provided technical guidance and coordinated the economic analysis for the Disease Control Priorities Third Edition—a nine-volume series aimed at strengthening evidence based priority setting in health and nutrition. Currently, she is the director of the Global Health Cost Consortium to generate improved estimates of costs for HIV and TB for use in planning, budgeting and economic evaluation.

She also conducts research on food security, health and nutrition, with a particular focus on the intersection between agriculture, food systems, and health and nutrition outcomes. She is Director of a new project called 'Strengthening the Economic Evaluation of Multisectoral Nutrition Strategies for Nutrition (SEEMS-Nutrition)'. She is also co-Chair for the Agriculture, Health and Nutrition (AHN) Academy Working Group on Economic Evaluation of Agriculture, Food and Livelihood Strategies for Health and Nutrition.



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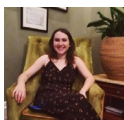
Qinghua has a MS in Public Administration from Illinois Institute of Technology and BS in Science Engineering from Queen Mary, University of London. Qinghua has experience with web applications such as a prosecution system that recorded hunting violations, citation information, and fine amount. As part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



Christopher Lorton
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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.

Biographies



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Grace Macklin is a PhD student on the MRC London Intercollegiate Doctoral Training Partnership Studentships programme at the London School of Hygiene and Tropical Medicine (LSHTM). Based within the Centre for Mathematical Modelling of Infectious Diseases, her research applies statistical and mathematical models to evaluate vaccination strategies against poliomyelitis at the end-stages of eradication. She is a Visiting Research Student at the University of Antwerp, based in the Faculty of Medicine on the Phase I clinical trial of novel oral poliovirus vaccine (nOPV).

Grace Macklin has worked as a consultant for WHO, Polio Eradication in the Research, Policy and Containment Team. In this role, she is responsible for the WHO Registry of vaccine-derived poliovirus in immunodeficient patients. Her previous degrees are BA in Natural Sciences (Pathology), University of Cambridge and MRes Clinical Sciences (Global Health), Liverpool School of Tropical Medicine.



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Niall M. Mangan received the Dual BS degrees in mathematics and physics, with a minor in chemistry, from the Clarkson University, Potsdam, NY, USA, in 2008, and the PhD degree in systems biology from Harvard University, Cambridge, MA, USA, in 2013. She is currently an Assistant Professor of engineering sciences and applied mathematics with Northwestern University, where she works at the interface of mechanistic modeling, machine learning, and statistical inference. Her group applies these methods to biological and materials problems.



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Pamela Martinez is a postdoctoral research fellow at the Harvard T.H. Chan School of Public Health working with Caroline Buckee and Marc Lipsitch in the Department of Epidemiology. She received her PhD in Ecology and Evolution at the University of Chicago in 2017. During her PhD, Pamela conducted research on the interaction of ecological and evolutionary mechanisms driving pathogens diversity and their population structure, under the guidance of Mercedes Pascual. Her current research focuses on the adaptive responses of antigenic loci to selective pressures imposed by the immune system.



Alison Mather
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Alison Mather received a BSc in biomedical toxicology and an MSc in epidemiology from the University of Guelph, Canada. She obtained her PhD from the University of Glasgow, taking an epidemiological and ecological approach to the study of antimicrobial resistant infections. After completing her PhD, she worked in Infection Genomics at the Wellcome Sanger Institute as a postdoctoral fellow and senior staff scientist. Alison subsequently moved to the University of Cambridge for a BBSRC Fellowship. She is now a Research Leader at Quadram Institute Bioscience, Deputy Leader of the Microbes in the Food Chain research theme (department) and a Food Standards Agency Fellow. In 2018 Alison was named one of the Rising Stars in BioBeat's '50 Movers and Shakers in BioBusiness' report. Alison and her colleagues are interested in the application of phylogenetic and statistical tools with whole genome and metagenome sequence data to investigate the ecology, evolution, source attribution, and antimicrobial resistance of bacteria in a One Health framework.



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



Nawaphan Metchanun
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Nawaphan Metchanun is a DAAD scholarship holder and doctoral candidate at the Department of Ecology and Natural Resources Management, Center for Development Research, Germany. Her doctoral research has focused on the methods of vector control in malaria control and elimination in developing countries. Before pursuing her PhD, Nawaphan worked in the pharmaceutical industry mainly overseeing clinical studies. Nawaphan was awarded an MRes in Clinical Research from Faculty of Medicine, Imperial College London, an MBA from the University of Washington where she earned a Certificate in Clinical Trials, and a Bachelor of Pharmacy from Chulalongkorn University.

Biographies



Michael Mina
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Michael Mina, MD, PhD is an Assistant Professor of Epidemiology in the Center for Communicable Disease Dynamics at the Harvard School of Public Health and is an Associate Medical Director of Clinical Microbiology and Virology at Brigham and Women's Hospital and Assistant Professor of Pathology at Harvard Medical School.

After earning his AB at Dartmouth College in physics and engineering, he completed his MD and PhD degrees in the NIH Medical Scientist Training Program at Emory University where he trained under Prof. Keith Klugman to study the impacts of influenza vaccines on pneumococcal bacterial carriage and transmission and subsequently completed his postdoctoral work at Princeton University, under the mentorship of Prof. Bryan Grenfell in the Dept. of Ecology and Evolutionary Biology, where his work described long-lasting immunological sequelae of measles infections that enhance susceptibility to childhood infectious diseases and mortality for years. He then completed his medical residency in clinical pathology at Brigham and Women's Hospital / Harvard Medical School, and a research fellowship in the Dept. of Genetics with Professor Stephen Elledge at HMS.

The Mina lab focuses on the use and development of novel technologies to probe the immunological B cell responses surrounding infections or vaccinations and towards improving understanding of the immunology and epidemiology of heterologous immune protection or disease. His work combines mathematical, statistical and epidemiological models with molecular engineering and biology to leverage novel developments in extremely multiplexed immune profiling for public health surveillance and investigations into host immune-pathogen interactions.



Maxwell Murphy
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Maxwell Murphy is a graduate student in biostatistics at UC Berkeley, working in the lab of Dr. Bryan Greenhouse at UCSF. He is broadly interested in malaria molecular epidemiology, causal inference, machine learning, and reproducible research.



Mercy Mvundura
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Mercy Mvundura, PhD works as a senior health economist with PATH's Devices and Tools program. Dr. Mvundura has experience designing and conducting economic evaluations of health care programs, interventions, and technologies. Her current work involves evaluating the economic and health impact of vaccine supply chain technologies, evaluating the impact of interventions aimed at improving the functioning of immunization programs, and leading and conducting economic evaluations of maternal and child health technologies and reproductive health products. Dr. Mvundura holds a doctorate and masters of economics from Georgia State University and a master of science degree in economics from the University of Zimbabwe. She previously worked for the Centers for Disease Control and Prevention as a Prevention Effectiveness Fellow and prior to that she was an assistant professor of economics at the University of Zimbabwe.



Michele Nguyen
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After completing her PhD in Statistics at Imperial College London in 2017, Michele Nguyen is currently a postdoctoral researcher at the Malaria Atlas Project in the University of Oxford. Her research interest lies in the domain of Spatiotemporal Statistics where models use the characteristics of each location-time observation such as the amount of rainfall or house price as well as the spatiotemporal correlation between the observations. The latter arises by virtue of close proximity in space or time and can be seen to represent factors which we do not have data for; thus mitigating the problem with omitted variables in complex phenomena.

Over the past few years, her work has ranged from theoretical studies on ambit fields, a class of random fields introduced in the context of turbulence, to more application-focused and interdisciplinary work in public health and environmental hazards. Her current research projects include the development of spatiotemporal models for malaria seasonality and forest fire detection.



Abdisalan Noor
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Dr. Abdisalan Noor is Team Leader of the Surveillance, Monitoring and Evaluation Unit at the World Health Organization Global Malaria Programme (GMP) in Geneva, Switzerland.

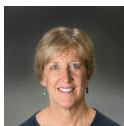
Before joining GMP, Dr. Noor worked for more than 16 years at the Kenya Medical Research Institute/Wellcome Trust Research Programme where he served as a Wellcome Trust Fellow and Director of its Nairobi Programme. He is a Visiting Professor of Malaria Epidemiology at the University of Oxford, UK. His research has focused on measuring access to health care, mapping malaria transmission and at-risk populations, and the coverage and impact of malaria control interventions in Africa. At the GMP, Dr. Noor leads the development of normative guidance, tools and training materials on malaria surveillance and country support to strengthen surveillance systems. He also leads the publication of the World Malaria Report.

Dr. Noor is a Fellow of the African Academy of Sciences (AAS) and the Royal Society of Tropical Medicine and Hygiene (RSTMH). In recognition of his research work in malaria, Dr. Noor was awarded in 2009 the African Union National Scientific Award in Life and Earth Sciences and, in 2016, the Chalmers Medal by Royal Society of Tropical Medicine and Hygiene.



Navideh Noori
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Navideh Noori is a member of Maternal, Newborn and Child Health team (MNCH) at IDM where she works on the spatial and temporal risk factors of child mortality, pregnancy risk stratification, and transmission dynamics of infectious diseases using mathematical, statistical and machine learning models. She was a postdoctoral research associate at the Odum School of Ecology, University of Georgia, Athens, GA, holds a PhD in Forest Hydrology from Auburn University, and a Master of Science in Civil Eng-Water Resource Eng from University of Tehran, Tehran, Iran. Her previous work has included mathematical and computational modeling of disease transmission, and application of statistical inference method and transmission models to infectious disease incidence data. During her PhD, she worked on understanding the dynamics interplay between environmental variations and public health concern, namely flooding and infectious diseases, by applying a combination of hydrologic and hydraulic modeling, machine learning algorithms, field experiments, laboratory work, and statistical modeling.



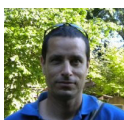
Rachel Nugent
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Rachel Nugent is Vice President for Global Non-communicable Diseases at RTI International. Rachel was Associate Professor in the Department of Global Health at the University of Washington and Director of the Disease Control Priorities Network. She has advised the World Health Organization, the U.S. Government, and non-profit organizations on the economics and policy environment of NCDs. She is a member of WHO's Expert Advisory Panel on Management of Non Communicable Diseases, co-chair of the Coalition on Access to NCD Medicines and Products, and a member of The Lancet Commission on NCDs of the Poorest Billion. She led a Lancet Task Force and Series on NCDs and Economics (2018). She served on the U.S. Institute of Medicine Committee on Economic Evaluation for Investments in Children, Youth, and Families (2015-2016), was co-chair of the IOM Workshop on Country-Level Decision Making for Control of Chronic Diseases (2012), and is currently on the National Academy of Medicine workshop planning committee on Global Obesity. Rachel focuses on using economic analysis for priority-setting in health, and has worked with global and national institutions to increase use of evidence for decision-making. Her recent work includes the costs and cost-effectiveness of HIV and NCD integration, assessing costs and benefits of NCD policies and interventions in multiple countries, and economic impacts of double burden of malnutrition. She received her MPhil and PhD degrees in economics from the George Washington University in Washington, DC, USA.



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Dr. Catherine Oldenburg is an infectious disease epidemiologist with the Proctor Foundation at the University of California, San Francisco. She holds a doctorate in epidemiology with a focus on infectious disease epidemiology from the Harvard T.H. Chan School of Public Health. She has contributed to work focused on the prevention of infectious causes of blindness, antiretroviral strategies for the prevention and treatment of HIV, and antimicrobials for child health. Her current work focuses on the role of azithromycin for the prevention of child mortality in West Africa and for trachoma control in Ethiopia.



Assaf Oron
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Assaf Oron leads IDM's Maternal, Newborn and Child Health (MNCH) team.

Assaf joined IDM in 2017, with diverse experience supporting health-related research as a statistician, and working in science and industry prior to his statistics education (PhD University of Washington). Assaf is currently interested in identifying critical gaps in the intersection between knowledge and implementation, in particular gaps that IDM's quantitative expertise can help close.



Andre Lin Ouedraogo
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André Lin has a PhD 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.



Patricia Pavlinac
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Dr. Pavlinac is an epidemiologist and Assistant Professor in the Department of Global Health at the University of Washington. Dr. Pavlinac also co-directs the Gut Health and Child Survival scientific priority area of the UW Global Center for Integrated Health of Women, Adolescents and Children (Global WACH). Her research aims to identify interventions to halt morbidity and mortality attributed to enteric infectious diseases in children. Dr. Pavlinac has worked in Kenya for the last ten years, including in her current role as project director for two clinical trials testing whether empiric use of a broad-spectrum antibiotic improves post-acute survival in Kenyan children. These trials build on evidence that Kenyan children suffer an elevated risk of mortality and chronic malnutrition after acute infectious illnesses that may be due to inadequately treated or new exposure to bacterial pathogens.



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

Biographies



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Will Probert is a researcher in infectious disease modelling at the University of Oxford working with Professor Christophe Fraser.



Joshua Proctor
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Affiliate Assistant Professor, Applied Mathematics, University of Washington
 Affiliate Assistant Professor, Mechanical Engineering, University of Washington

Joshua Proctor is currently a research manager and senior research scientist at IDM leading the Data, Dynamics and Analytics (DDA) team. DDA is focused on applying modern data science, machine-learning, and statistical techniques to a wide-range of data sources, i.e., surveillance of infectious diseases, household surveys, genome sequencing of viruses or parasites, and demography. We aim to leverage the growing success of these modern analytic and numerical methods to advise on near-term public policy questions facing the global health community. In conjunction, we also identify the short-comings of current methodological approaches and develop novel, principled algorithms to face the challenges of surveillance data.



David Rasmussen
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David Rasmussen joined NC State as an Assistant Professor in the Department of Entomology and Plant Pathology in 2018. Prior to NC State, David did his PhD with Dr. Katia Koelle at Duke University and then a postdoc with Dr. Tanja Stadler at ETH Zurich. During both his PhD and postdoc, he developed phylodynamic methods for tracking the spread of pathogens using genomic sequence data and applied them to study the transmission dynamics of human viruses such as dengue, influenza and HIV. As a member of both the Bioinformatics Research Center and the Emerging Plant Pathogens and Global Food Security cluster at NC State, he plans to continue improving phylodynamic methods for studying human disease as well as agricultural pathogens like plant viruses.



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



Seth Redmond
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Seth Redmond is a postdoctoral associate at the Broad Institute and the Harvard T.H. Chan School of Public Health, specialising in population genetics of infectious disease. His research is focused on the use of high-throughput genetic data in order to understand both vector population structure and pathogen transmission dynamics, encompassing both vector and parasite genetics, and combining studies of structural variants, de novo mutation and IBD haplotype sharing.



Jennifer Ross
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Jennifer Ross, MD, MPH is a physician-researcher and Acting Assistant Professor in the Departments of Global Health and Medicine (Infectious Diseases) at the University of Washington. Her research focuses on modeling approaches to reduce morbidity and mortality in persons with HIV and co-infections. She is principal investigator of a career development (K01) award from the National Institute of Allergy and Infectious Diseases to model prioritized strategies for HIV/ TB prevention in Uganda. She is also a visiting faculty member at the Institute for Health Metrics and Evaluation (IHME), where she leads TB analysis for the Global Fund Prospective Country Evaluation and contributes to the Local and Global Burden of Disease studies.



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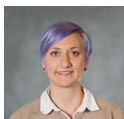
Jon Russell is a Research Scientist at the Institute for Disease Modeling specializing in within-host models of malaria infection and immunity. His work aims to predict the immunological status and parasite burden across individuals in diverse transmission settings using scalable and efficient software tools. Jon grew up in Maine and received his PhD in Biochemistry from Harvard where he studied cell-fate signaling behavior in bacteria.



Marie - Reine I. Rutagwera
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Reine Rutagwera sits at the National Malaria Elimination Centre in Lusaka, Zambia and leads PATH Malaria Control and Elimination Partnership in Africa (MACEPA)'s efforts to optimize and expand community health worker engagement for malaria case management, reactive case detection, and surveillance. She does this in close collaboration with the Ministry of Health and other local partners as part of national efforts to achieve an ambitious elimination agenda. She has a Master's in Public Health and Bachelor of Sciences degree (Microbiology Major) from the University of Zambia.

Biographies



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Jen Schripsema has an MS in User Centered Design and Engineering from the University of Washington and BA in Biology from the Colorado College. She has over a decade of experience working as a science and technical writer covering a diverse range of topics, including chronic health conditions, how to build operating systems for embedded devices, network security, and disease modeling.



Prashanth Selvaraj
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Prashanth Selvaraj has a Ph.D. in Mechanical Engineering from the University of California, Berkeley, and a Master's degree in Fluid Mechanics from Ecole Polytechnique, Paris, France. During his Ph.D., he studied the dynamics of epileptic seizures that form in the human cortex using a physiologically relevant mathematical model of cortical dynamics. Additionally, he proposed the use of optogenetics, which involves light sensitive ion channels expressed by certain cell types in the cortex, to inhibit the spread of seizures before they are fully formed using closed loop control methods. After his Ph.D., Prashanth worked as a postdoctoral researcher at the University of California, San Francisco, as part of the DARPA SUBNETS initiative. He investigated the underlying meso-scale networks in the brain that contribute to neuropsychiatric disorders like PTSD and depression, and worked on a closed loop method of electrical stimulation to disrupt the function of these networks alleviating symptoms of these disorders. As part of the research team at IDM, Prashanth works on calibrating mathematical models of disease spread and control to the dynamics of malaria in different regions around the world.



Adrienne Shapiro
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Adrienne Shapiro, MD, PhD, is an infectious diseases physician and epidemiologist based at the International Clinical Research Center at the University of Washington. Her research has focused on the TB/HIV co-epidemic in resource-limited settings, touching on all aspects of the dual TB/HIV care cascade. She is interested in understanding how using point-of-care tools in resource-limited settings can help health care workers retain patients on the cascade and improve targeted, comprehensive care delivery. Her current projects are focused on reducing the gender gap in HIV testing and treatment in South Africa, optimizing use of novel TB diagnostics for use in low and middle-income settings, and improving TB preventive therapy delivery in high-TB, high-HIV burden settings.



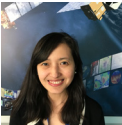
Jessica Shearer
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Jessica Shearer leads PATH's Health Systems Analytics team and is the acting director of PATH's Health Systems Innovation and Delivery program. For over 10 years Jessica has used a range of data and analytic approaches to diagnose and solve complex global health problems, identify what works, and translate data and evidence into action. Jessica's work at PATH is rooted in the belief that for data (or evidence) to be useful, it must be used, and solutions must be designed with the user in mind. Jessica has worked on immunization, maternal, newborn and child health, malaria, HIV, and primary health care issues in multiple countries. She has a PhD in Health Policy.



Laura Skrip
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Laura Skrip completed her MPH in Biostatistics and PhD in Epidemiology of Microbial Diseases at the Yale School of Public Health. She is interested in using quantitative methods to consider the impact of multilevel factors on susceptibility to infectious disease. Her research has involved not only mathematical modeling and statistical analysis but also field work to understand the context of the research and contribute to methods for improved data quality. During the 2014-2015 Ebola outbreak in West Africa, Laura worked with local response leadership to develop and pilot new tools for data collection and dissemination in Montserrado County, Liberia. She subsequently moved to Liberia to serve in a technical assistance and capacity-building role with the newly established National Public Health Institute of Liberia. In that position, Laura worked with a Liberian team on the development of and approval processes for new public health programs at the University of Liberia. As a member of the IDM Epidemiology team, Laura will undertake behavior-epidemiologic transmission modeling with a focus on emerging infectious diseases in humanitarian settings.



Radina Soebiyanto
Research Scientist
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Dr. Soebiyanto is a research scientist with Universities Space Research Association at NASA Goddard Space Flight Center. Her research focuses on understanding the role of climate and environmental factors on infectious diseases transmission, through the use of satellite data and development of mathematical and statistical models. She has developed analytics for chikungunya risk mapping and forecast based on machine learning techniques. Her other works include assessment of climate variability associated with rift valley fever and seasonal influenza. Dr. Soebiyanto obtained her PhD in systems and control engineering from Case Western Reserve University (Cleveland, Ohio). In her study she used complex systems approach with the aid of ordinary differential equations and simulation to understand signaling pathway behavior in cancer with implication for therapeutic biomarker.



Nick Sorros
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Nick Sorros is a Senior Data scientist at Wellcome, responsible for managing a team of data scientists within Data labs. Data labs' vision is to create reusable tools based in data and unify them in products that serve organizations like Wellcome.

Nick has worked as a data scientist in a couple of technology startups before joining Wellcome, such as Conversocial and Seedrs. His academic background is electrical engineering and he has received an MSc in Advanced Computing from Imperial College where he stayed as a research assistant to do work on ways to identify deceptive behavior from video using computer vision.

Biographies



Uyi Stewart
**Directory of Global Development Strategy, Data,
 and Analytics**
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Dr. Uyi Stewart is the director of Global Development Strategy, Data and Analytics at the Bill and Melinda Gates Foundation. His team is responsible for applying innovative technologies such as machine learning, artificial intelligence, etc. to optimize the use of data for decision-making and for delivery effectiveness, as well as leveraging the foundation's data investments to create global public goods.

Prior to joining the Gates foundation in March 2017, Uyi previously spent 13 years with IBM Research where he was promoted to distinguished engineer (one of the firm's highest technical honors) in 2014, and he was also the co-founder and chief scientist of IBM Research – Africa from 2012 – 2016 (the first lab on the continent for conducting applied and far-reaching exploratory research into Africa's grand challenges). Before IBM Research, Uyi held technical leadership positions with AT&T Labs, Call Sciences and Nuance Communications. He was also a lecturer at the University of British Columbia, Vancouver. Uyi holds a PhD in Linguistics with specialization in generative syntax and language/speech interfaces from McGill University, a Master of Philosophy from Cambridge and a Bachelor of Arts (first class honors) from the University of Benin, Nigeria.



Dan Strickman
Senior Program Officer
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Dan Strickman is a senior program officer at the Bill & Melinda Gates Foundation, responsible to the Neglected Tropical Diseases and Malaria Teams for vector control. He works with two other entomologists, including Helen Jamet and Laura Norris to cover everything from surveillance to genetic control to product innovation and development to regulatory reform. Dan has had a career in seven regions of the world during work with Peace Corps, the U.S. Army as an active-duty officer, mosquito abatement, and the US Department of Agriculture. He got his PhD in medical entomology in 1978 from the University of Illinois. He is author on 115 papers, 12 book chapters, and four books.



Aimee Taylor
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Aimee Taylor is a postdoctoral research fellow at the Harvard T.H. Chan School of Public Health working under the mentorship of Caroline Buckee and Daniel Neafsey. Aimee received her PhD from the University of Oxford, joint between the Department of Statistics and the WorldWide Antimalarial Resistance Network, under the supervision of Chris Holmes, Philippe Guérin and Jennifer Flegg. During her doctoral studies, Aimee focused on the development of statistical models to estimate *Plasmodium falciparum* multi-SNP haplotype frequencies, using data collected in highly malaria endemic regions, where multiclonal infections abound. Since completing her doctoral studies, Aimee has studied malaria parasite relatedness to infer connectivity between nearby *P. falciparum* populations in South East Asia and Colombia, and to infer the recurrence states of *P. vivax* recurrent infections.



Niket Thakkar
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Niket Thakkar received his PhD in Applied Mathematics from the University of Washington in March 2017. As a graduate student, he worked on a variety of nanoscale optics problems, using mathematical modeling to guide the design of novel measurement techniques and nanotechnologies. Now at IDM, Niket works on the measles team, creating statistical and machine learning models to support vaccination campaigns and eradication efforts. Outside of research, Niket plays basketball, reads, bikes, and searches for good Mexican food.

<https://nthakkar.github.io/>



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No information provided.



Sarah Volkman
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Sarah Volkman is a Principal Research Scientist at the Harvard T.H. Chan School of Public Health, member of the Broad Institute, and Professor at Simmons University. Dr. Volkman has contributed to the development and utilization of population genetic approaches to understand malaria biology, including identification of genetic variants related to drug resistance, and use of genomics to understand parasite diversity related to malaria transmission. Dr. 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. She received her BS from the University of California, San Diego (cum laude) in 1986 and her Sc.D. from the Division of Biological Sciences at the Harvard T.H. Chan School of Public Health in 1995, and conducted postdoctoral studies with Professor Dyann Wirth and Professor Daniel Hartl at Harvard University. She has received several awards including the Young Investigator Award by the American Society of Tropical Medicine and Hygiene and was a Senior Teaching Fellow at Harvard University. She has served on various advisory boards including the Scientific Advisory Board for the WorldWide Antimalarial Resistance Network (wwARN); EuPathDB Scientific Working Group; and, the Technical Expert Group on malaria drug resistance for the World Health Organization.



Bradley Wagner
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Bradley is an applied mathematician who works on the design and analysis of TB control strategies through the development and application of dynamic models of transmission and pathogenesis. His work focuses on high TB burden countries and deals with HIV coinfection, heterogeneity in biomarkers and risk factors for disease, case detection strategies and diagnostic algorithms, vaccine development and health-systems strengthening.

Biographies



Damian Walker
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Damian Walker is Deputy Director of Data and Analytics, Global Development, and Strategy Planning at the Bill & Melinda Gates Foundation. Damian is a health economist with more than 15 years of experience in international health economics, with a specific focus on the economic evaluation of public health programs in low- and middle-income countries. Prior to the Gates Foundation, Damian was an Associate Professor in the Department of International Health, Bloomberg School of Public Health, Johns Hopkins University. Damian received his PhD in health economics from the London School of Hygiene and Tropical Medicine.



Judd Walson
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Dr. Walson is a Professor at the University of Washington. He completed his training in both Internal Medicine and Pediatrics Residencies at Duke University, a fellowship in Infectious Disease at the University of Washington, and holds a Masters in Public Health from Tufts University. Dr. Walson has extensive experience in the design and implementation of large clinical trials in resource-limited settings. He has worked extensively in Kenya, Ethiopia, Bangladesh, Thailand and Nepal. Dr. Walson is particularly interested in the effects of enteric infection and composition on childhood survival, immunologic function and growth. Dr. Walson is the Principal Investigator of DeWorm3, a large multi-country trial designed to demonstrate the feasibility of interrupting the transmission of soil transmitted helminths. Dr. Walson is also the Co-Director of CHAIN, a large clinical platform in five countries in Africa and Asia designed to evaluate mortality and morbidity among acutely ill children with varying degrees of malnutrition and to develop and test interventions for this high risk population. In addition to his clinical research, Dr. Walson is the Executive Director of the Global Health Strategic Analysis and Research Training Program (START), an innovative collaboration between the Bill & Melinda Gates Foundation and the University of Washington.



Daniel Weiss
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Dr. Daniel J. Weiss is a spatial epidemiologist with the Malaria Atlas Project (MAP) at the University of Oxford. Dan leads the production of MAP's global malaria estimates, which contribute to the World Malaria Report (WHO) and the Global Burden of Disease study (IHME). Dan's methodological expertise lies in the creation of temporally-dynamic geospatial datasets that serve as covariates for disease modeling.



Edward Wenger
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Dr. Edward Wenger directs the IDM global health research program, which includes analyses related to malaria, MNCH, HIV, TB, pneumonia, enteric diseases, and emergent pathogens. His team develops and exercises sophisticated infectious disease models to inform rational, cost-effective intervention campaigns aimed at reducing the burden of disease and achieving eradication.

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



David Wilson
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David Wilson is the World Bank's first Global Lead for Decision and Delivery Science and also Global HIV/AIDS Program Director. He was previously the Bank's Lead Health Specialist focusing on AIDS and the Bank's first Senior Evaluation Specialist working on AIDS. Before joining the Bank, David worked as an academic, development practitioner and global health advisor in Zimbabwe for 20 years. David has published over 100 scientific papers and delivered over 1,000 scientific addresses. He has worked in approximately 50 countries on all continents, including 28 countries in Africa and many fragile and conflict situations in Africa, the Middle East, South Asia and the Pacific.



Amy Winter
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Amy is a postdoctoral fellow in the Department of Epidemiology at Johns Hopkins Bloomberg School of Public Health. She is interested in characterizing and leveraging the complex interaction between human demography and infectious disease dynamics for disease control. Her research focuses on exploring strategies for measles and rubella control and elimination using modeling and serological data.



Marita Zimmermann
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As a health economist an IDM, Marita models the economic effects of infectious disease, vaccination, and health interventions, and assesses value of interventions. Marita's research uses econometric, epidemiologic, and modeling methods to evaluate and increase value in health. Her work aims to inform decision makers how to get the most bang for their healthcare buck. Marita has a PhD in health economics and outcomes research from the University of Washington. She also holds a Master's in Public Health from Brown University and a Bachelor of Science in chemical and biomedical engineering from Carnegie Mellon University. She completed a postdoctoral fellowship with Institute for Clinical and Economic Review, in which she designed and implemented novel cost-effectiveness models for new and existing drugs within selected disease areas, such as multiple sclerosis, blindness, and atopic dermatitis. These models were designed to inform payer or other stakeholder decision making and to influence U.S. policy. Marita has completed many other cost-effectiveness, budget impact, and program evaluation models in both U.S. and global health settings in varying disease areas. She has produced many peer-reviewed publications in journals such as Drug Safety, Journal of AIDS, Journal of the American Pharmacy Association, and American Journal of Public Health.

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IDM DISEASE MODELING SYMPOSIUM

