IDM ANNUAL SYMPOSIUM

May 22–24, 2023
Bill & Melinda Gates Foundation
Conference Center

IDM

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Welcome

On behalf of the entire team at the Institute for Disease Modeling at the Bill & Melinda Gates Foundation, I want to welcome you all to our 2023 Annual IDM Symposium. After a pause over the past few years due to COVID and a shorter introductory meeting last fall, we are delighted to move back to our annual cadence for this convening.

IDM is now an embedded research institute within the Global Health division of the Bill & Melinda Gates Foundation, made up of researchers, engineers, and other team members who all work together to support global efforts focused on achieving permanent improvements in health, eradicating certain infectious diseases, advancing child and maternal health, improving primary health care, and advancing progress on other key health and development goals.

Our theme for this year is 'Frontiers in Modeling' and it is truly an exciting time to be exploring key topics in health and development through the lens of modeling. The last few years have underscored the importance of partnerships for disease modeling; the critical nature of data and data strategies; and, most importantly, the role of innovation in pushing the field forward. Our hope is that this Symposium provides opportunities to reconnect and to build new partnerships as well within and across topic areas.

Our speakers and sessions provide an opportunity to look at modeling across disease and health areas, and to hear from a diverse set of researchers and policymakers using data and modeling to drive decision-making across their communities.

This Symposium provides an opportunity to reunite as a community, to discuss lessons learned over the past few years and learn from each other, and to dive into important and timely topics such as the ethical use of AI and LLMs for scientific research, as well as thematic sessions on enteric infections, environmental surveillance, women's health, vulnerability and resilience, malaria, and health system strengthening. Each of these topics underscores how *essential* collaboration is for achieving lasting progress in global health.

Thank you for joining us, we are delighted you are here!

Philip Welkhoff
Director, Malaria / Institute for Disease Modeling
Bill & Melinda Gates Foundation

Monday, May 22: Overview

7:30–9:30 am	Registration and breakfast The Lakes Rooms	
9:30–9:45 am	Opening remarks The Lakes Rooms *Philip Welkhoff*	
9:45–10:45 am	Opening plenary panel: Data ethics & AI The Lakes Rooms	Page 5
10:45–11:00 am	Break	
11:00 am– 12:15 pm	Session 1: Interactive session on data ethics & AI The Lakes Rooms	Page 5
12:15–1:30 pm	Lunch	
1:30–3:00 pm	Session 2: Applied perspectives on AI & large language models The Lakes Rooms	Page 5
3:00–3:15 pm	Break	
3:15–5:00 pm	Poster session The Lakes Rooms	
5:00–6:00 pm	Happy hour Atrium	

Monday, May 22: Sessions

| 9:45–10:45 am | Data ethics & AI
The Lakes Rooms |

Join scholars working at the leading edge of the ethical, environmental, social, and political dimensions of data and AI for a discussion on navigating an AI future through the lens of equity.

- *Kate Crawford, Atlas AI / ea@katecrawford.net*
- *Nathaniel Raymond, Yale University, Data Ethics / nathaniel.raymond@yale.edu*
- *Jer Thorp, Living in Data / jer@ocr.nyc*

| 11:00 am–
12:15 pm | Interactive session on data ethics & AI
The Lakes Rooms |

This 75-minute interactive session will focus on introducing several popular AI tools, trying them in real-time, and discussing the promise and challenges of applying these AI tools in global health contexts. For this session, we will be highlighting advances in AI image generation using MidJourney, language and chat using ChatGPT, and software programming support using CoPilot and ChatGPT.

- *Jenn Gardy, BMGF*
- *Christopher Lorton, IDM*
- *Josh Proctor, IDM*

| 1:30–3:00 pm | Applied perspectives on AI & large language models
The Lakes Rooms |

The history and capabilities of generative models, with an eye towards their applications in health and to help improve accessibility
Sasha Luccioni, Hugging Faces / sasha.luccioni@huggingface.co

AI sustainability, ethics, and transparency, a deep dive into the training corpus
Jesse Dodge Allen Institute for AI / jessed@allenai.org

AI frontiers in healthcare, emerging topics and relevance for low and middle income countries
Kommy Weldemariam, IBM Research / komminist@gmail.com

Tuesday, May 23: Overview

7:15–8:15 am	**Breakfast**
8:15–8:45 am	**Opening plenary:** **Incorporating inequity aversion into disease modeling** Lake Union *Anna Bershteyn*
8:45–9:00 am	**Break**
9:00–10:30 am	**Session 1**

10:30–11:00 am	**Break**
11:00 am– 12:30 pm	**Session 2**

12:30–1:45 pm	**Lunch & Learn** Shilshole From modeled evidence to policy decision-making—Key takeaways from four countries
1:45–3:15 pm	**Session 3**

3:30–4:30 pm	**Keynote speaker** Camano Island / Whidbey Island *Dr. Robert Ballard, President of Ocean Exploration Trust &* *National Geographic Explorer*

4:30–5:15 pm	**Transition to the waterfront** Transportation departs from the Museum of Pop Culture driveway (across the street from the conference center)
5:15–6:30 pm	**Reception** Seattle Aquarium pier
6:30–9:30 pm	**Dinner** Seattle Aquarium

Tuesday, May 23: Sessions

9:00–10:30 am	**Modeling infection inequity from local to global levels** Lake Union *Facilitator: Jon Zelner, University of Michigan School of Public Health*

Moving beyond the equal opportunity infector: Making equity a first-class concern of transmission modeling
Jon Zelner, University of Michigan School of Public Health / jzelner@umich.edu

In this talk, I will show how some of the implicit assumptions of epidemic models used for pandemic preparedness and response result in tools that obscure infection inequity by default. Specifically, I will show how many models implicitly encode the idea of an 'equal opportunity infector' in which pathogen and host biology are assumed to be the key determinants of infection, with the structural determinants of inequity a subsidiary concern. I will then outline an alternative framework that places socio-structural inequity equity as a central concern of epidemiological models and show how this change of focus may impact our choice of outcome measures, statistical models, and data sources. I will conclude with a brief review of positive advancements in the area of equity-oriented infectious disease modeling using examples from my own research as well as others working both inside and outside the field of epidemiology and infectious disease ecology.

Risk inequality metrics in population health and disease
Gabriela Gomes, University of Strathclyde / gabriela.gomes@strath.ac.uk

Abstract: Global stakeholders including the World Health Organization rely on predictive models for developing strategies and setting targets for disease control programs. Failure to account for variation in individual risk leads to substantial biases that impair data interpretation and policy decisions. Anticipated impediments to estimating heterogeneity for each parameter are discouraging despite considerable technical progress in recent years. Here we identify acquisition of infection as the single process where heterogeneity most fundamentally impacts model outputs, due to selection imposed by variable forces of infection. We introduce concrete metrics of risk inequality, demonstrate their utility in mathematical models, and pack the information into practical risk inequality coefficients that can be calculated and reported by national disease control programs for use in policy development and modeling.

Regional level drivers of microbial transmission in northwestern coastal Ecuador: characterizing the landscape, bioscape and socioscape

Joe Eisenberg, University of Michigan / jnse@umich.edu

Understanding the spatial dynamics of infectious disease transmission is crucial in evaluating how environmental change and specifically climate change will impact the emergence and spread of infectious diseases. Often neglected in these frameworks is how social structure at multiple scales and its interplay with landscape and biological factors influences transmission. We have been studying the environmental determinant of both enteric and vectorborne pathogens in northwestern Ecuador for over 2 decades, a region that has been experiencing rapid environmental change. Borrowing from metapopulation theory, I will present a framework to characterize infectious disease transmission dynamics in a network of patches that describe environmental, social, and biological dynamic processes at multiple scales. These dynamic processes are heterogeneous and interconnected to varying degrees.
The relative contribution of intra- and inter-location human and pathogen movements depends on key geolocatable characteristics that we categorize as landscapes (e.g., weather, structural and surface features), bioscapes (e.g., mosquito behavior and human immunity), and socioscapes (e.g., movement, social networks). To illustrate the power of this framework, I will provide examples in our field site in Ecuador and elsewhere that highlight each of these "scapes" with a focus on how social structure through social cohesion can be a major driver of for waterborne and vectorborne transmission.

Understanding the role of health disparities & environmental racism in infectious disease dynamics

Micaela Martinez, WE ACT for Environmental Justice / micaela.martinez@weact.org

My talk will cover the landscape of health disparities and Environmental and structural racism in US. I will discuss ways in which structural racism impacts disease transmission and pathology, with recommendations for how cumulative impacts and environmental exposures can be considered in models, particularly spatial and metapopulation models.

9:00–10:30 am	**Enterics and the environment** Lake Washington *Facilitator: Jillian Gauld, IDM*

Real-time sewage surveillance for SARS-CoV-2 in Dhaka, Bangladesh versus clinical COVID-19 surveillance: a longitudinal environmental surveillance study (December, 2019–December, 2021)

Isobel Blake, Imperial College London / isobel.blake@imperial.ac.uk

Clinical surveillance for COVID-19 has typically been challenging in lower-middle-income settings. From December, 2019, to December, 2021, we implemented environmental surveillance in a converging informal sewage network in Dhaka, Bangladesh, to investigate SARS-CoV-2 transmission across different income levels of the city compared with clinical surveillance.

We analysed 2073 sewage samples, collected weekly from 37 sites, and 648 days of case data from eight wards with varying socioeconomic statuses.

SARS-CoV-2 was consistently detected across all wards (low, middle, and high income) despite large differences in reported clinical cases and periods of no cases. The majority of COVID-19 cases (55·1%) were reported from Ward 19, a high-income area with high levels of clinical testing (70 times the number of tests per 100 000 individuals compared with Ward 5 [low-income] in November, 2021), despite containing only 19·4% of the study population. Conversely, a similar quantity of SARS-CoV-2 was detected in sewage across different income levels (median difference in high-income vs low-income areas: 0·23 log10 viral copies + 1). The correlation between the mean sewage viral load and the log10 clinical cases increased with time (r=0·90 in July–December, 2021 and r=0·59 in July–December, 2020). Before major waves of infection, viral load quantity in sewage samples increased 1–2 weeks before the clinical cases.

This study demonstrates the utility and importance of environmental surveillance for SARS-CoV-2 in a lower-middle-income country. Environmental surveillance provides an early warning of increases in transmission and reveals evidence of persistent circulation in poorer areas where access to clinical testing is limited.

Wash, sanitation and hygiene (WASH) in low-income settings

Andrew Bouwer, University of Michigan / brouweaf@umich.edu

Recent large-scale trials have revealed that interventions improving water, sanitation, and hygiene (WASH) in low-income settings may not confer the expected health gains for young children; evidence-based guidance is needed to inform programs and future studies. We developed a mechanistic infectious disease transmission model to account for transmission across multiple

environmental pathways, multiple interventions (water (W), sanitation (S), hygiene (H), nutrition (N)) applied individually and in combination, adherence to interventions, and the impact of individuals not enrolled in the study. Leveraging a set of mechanistic parameter combinations fit to the WASH Benefits Bangladesh trial (n=17,187 individuals) using a Bayesian sampling approach, we simulated trial outcomes under counterfactual scenarios to estimate how changes in intervention completeness, coverage, fidelity and adherence, and efficacy, as well as baseline WASH conditions and disease burden, impacted intervention effectiveness. Increasing community coverage was associated with the greatest impact on intervention effectiveness (e.g., 26.9% and 52.7% median increases in effectiveness in the WSH and WSHN intervention arms when increasing coverage to 20%). The effect of community coverage on effectiveness depended on intervention completeness, i.e., the fraction of transmission that was along pathways modified by the interventions. Intervention effectiveness was reduced in counterfactual simulations with lower levels of preexisting WASH conditions or increased baseline disease burden. Individual interventions had complementary but not synergistic effects when combined. Next-generation WASH programs must address coverage and completeness and account for the fact that effect of individual-level WASH improvements will be blunted the further the community is from achieving herd protection.

Typhoid control and elimination efforts in Samoa in the shadow of COVID-19
Mike Levine & Mike Sikorski, University of Maryland School of Medicine

Dr. Branko Cvjetanovic, an epidemiologist at the World Health Organization (WHO) and colleagues, devised the first computer model of endemic typhoid to assess the relative benefits derived from vaccinating a population (with the best vaccine of the era), improving water supplies and sanitation, or both. Data they used to prepare their model derived from endemic typhoid on the island nation of Samoa, in Oceania. Crude typhoid incidence at that time was 72 cases/105/year. In 2013 the WHO and the government of Samoa invited Prof. MM Levine to visit the island nation to assess the current endemic situation and design a possible Typhoid Fever Control Program. A proposed control program was accepted by the government and in 2018 feasibility funding for a Preparatory Phase of the Samoa Typhoid Fever Control Program (STFCP) was provided by the Bill & Melinda Gates Foundation. One of the early partners was the Institute of Disease Modeling. Three Phases were envisioned for the STFCP: 1) a Preparatory Phase during which the clinical microbiology infrastructure and ability to perform epidemiologic investigations was strengthened, the baseline burden of endemic Samoa typhoid was documented and described by person, place and time, and genomic analyses of Samoan strains was undertaken; 2) an Attack Phase with the main proposed intervention being vaccination of all

Samoans 1-45 years of age with Typbar TCV Vi conjugate vaccine (and possible targeted WASH improvements where a need was identified and resources were available); 3) and a Consolidation Phase that aimed, once typhoid control was achieved (defined as <5 cases/105/year), to identify the chronic typhoid carriers (mainly adults >45 years of age with gallbladder disease) who constitute the long-term reservoir of the pathogen and to offer them treatment and prospective monitoring.

Samoa has two main populated islands, Upolu (smaller in size but where 78% of the population resides) and larger Savaii where 22% of Samoans reside. Surveillance data has revealed no seasonality of typhoid in Samoa. Pre-Attack Phase incidence was relatively low in children 0-4 years of age, peaked in school age children (5-19 years) and working age adults (20-45 years), and dropped markedly in persons >50 years of age. There have been no enteric fevers due to S. Paratyphi A, all S. Typhi isolates are pan-susceptible to clinically-relevant antibiotics, and whole genome sequencing has revealed a unique Samoan S. Typhi genotype. A stockpile of Typbar TCV vaccine sufficient for all Samoans 1-45 years of age arrived in Samoa in Q1 2020 for vaccination campaigns that were planned to commence in Q2 and Q3 of 2020. These plans were drastically altered by the COVID-19 pandemic. Samoa, with few resources to grapple with the COVID-19 waves occurring elsewhere in Oceania and in Asia, went into self-quarantine in Q2 2020, virtually cutting itself off from the world. This resulted in a severe economic recession. During lockdowns typhoid cases fell. The inaugural vaccination campaign with Typbar TCV finally proceeded in August 2021 in schoolchildren in the Apia Urban Area with good coverage (84%) and an Adverse Events Following Immunization (AEFI) survey showing that the vaccine was well tolerated. Subsequently, COVID-19 outbreaks in Samoa and diversion of vaccination team resources from typhoid vaccination to COVID-19 vaccinations repetitively hampered the STFCP's Attack Phase. Routine immunization of infants and toddlers with Typbar TCV when they received MMR vaccine was minimally impacted by the COVID-19 vaccination campaigns. Despite the diversions and interruptions of the Attack Phase due to COVID-19, in two of three key age groups very substantial progress has been made towards control of typhoid (defined as <5 cases/105/year) and even towards elimination (0 cases/105/year in the 0-4 years age group). This is exemplified by analysis of data from Upolu where most Typbar TCV vaccination intervention has occurred. Much has been learned. Most typhoid occurs in specific "hot spots". Going forward, our strategy will focus on interventions in these hotspots. These will include targeted vaccinations and systematic surveys to detect chronic typhoid carriers and offer them treatment. These interventions are feasible in Samoa.

Experiences of wastewater surveillance in LMIC
Farah Qamar, Aga Khan University

I will present our experience of environmental sewage surveillance on enteric pathogens from Karachi. The talk will focus on challenges in establishing environmental sewage surveillance in LMIC. The challenges of blue line tracing, sampling, population assessment and laboratory challenges will be discussed briefly. Issues in site validation and comparison of various lab methods will be described. The challenges in validating the selected sites and isues in data analysis, particularly linking the clinical case data with pathogens identified in sewage.

9:00–10:30am   **COVID-19: Methodologies and healthcare policy**
Greenlake
Facilitator: Dan Klein, IDM

Are alternative modalities of COVID-19 testing worth it? The societal costs of pharmacy based and contact testing of COVID-cases vs. health-centre based testing
Lucky Ngwira, Health Economics Policy Unit & Malawi-Liverpool-Wellcome Trust / Lngwira@mlw.mw

Background: The standard COVID-19 testing in most low- and middle-income countries (LMICs) has been in hospitals for only severe cases due to constrained health budgets. However, the associated costs of accessing health care facilities makes it difficult for patients to seek care. Alternative modalities of COVID-19 testing including pharmacy-based, drug vendors and self-testing of contacts of COVID-19 cases might potentially reach more under-served populations. Evidence in this regard is limited in LMICs, and many countries are still waiting for more evidence before promoting alternative testing modalities. This paper assesses and compares the costs of testing in different scenarios.

Methods: The 3ACP is a multi-country study taking place in primary health care facilities, private pharmacies, drug vendors, and secondary distribution of self-test kits to COVID-19 cases' contacts. Provider costs will include the cost of buying and delivering test kits and/or testing services including trainings. For clients, economic costs will estimate time spent on COVID-19 testing, including opportunity cost of testing, and assessing the test results, distribution of test kits as well as the cost of any third-party time spent in accompanying the user for testing.

Expected outcomes and policy implications: The major outcomes will be the cost per COVID-19 test and the cost per positive COVID-19 case identified by alternative modalities, which will be compared with the costs for facility-based testing. It is hypothesized that COVID-19 testing through pharmacies and secondary distribution of test kits may allow to identify more cases at a lower cost than facility-based testing, ultimately provide to be cost-effective for providing testing as it cuts down on provider and client related costs. Combined with research on acceptability and the profile of the people accessing the tests for each testing modality, our work may also help inform discussions on the most cost-effective ways of reaching populations rarely presenting at health centres. The results are expected to better inform policy for decision making in these settings.

Advancing simulation methodology for identifying optimal healthcare policy during COVID-19 pandemic
Serin Lee, University of Washington / serinlee@uw.edu

"The COVID-19 pandemic has posed unprecedented challenges around the world. Modelling studies such as agent-based models and compartmental models have provided valuable insights to policymakers. We discuss our research on optimal COVID-19 policy identification, and optimal resource allocation for vaccine campaigns under opinion dynamics using simulation and optimization approaches.

We developed a large-scale agent-based simulation to evaluate public health interventions for COVID-19 pandemic scenarios in a large urban area (King County, WA). The effects of non-pharmaceutical interventions (NPIs) and vaccination are explored under various virus scenarios. With enhanced immune protection from a pan-coronavirus vaccine, the most optimistic periodic vaccination rate reduces average total deaths by 44.6% compared to the most pessimistic periodic vaccination rate. A strict threshold NPI policy reduces average total deaths by 71.3% compared to an open society, while a moderate NPI policy results in a 33.6% reduction. Our results demonstrate the importance of dynamic NPIs and periodic vaccination under highly contagious virus strains.

To address vaccine hesitancy, we developed a compartmental model that considers opinion behavior dynamics and disease transmission, calibrated to Clark County, WA. We explore budget allocations for vaccine promotion campaigns among different age and geographic groups. We present early results using a global optimization approach.

Overall, our research aims to advance simulation methodology in policy decision-making, allowing healthcare policymakers to consider the impact of dynamic human behavior and social networks on policy outcomes while utilizing time and computational resources efficiently.

Wastewater sequencing analyses uncover pathogen evolution and spread

Joshua Levy, The Scripps Research Institute, USA / jolevy@scripps.edu

The COVID-19 pandemic has illustrated the importance of early pathogen and variant monitoring to the effectiveness of public health interventions. However, inferring pathogen and variant prevalence by clinical testing is infeasible at scale, especially in areas with limited resources, testing participation, or sequencing capacity. For SARS-CoV-2, RNA concentration in wastewater successfully tracks regional infection dynamics and provides less biased abundance estimates than clinical testing. Analysis of sequencing of viruses in wastewater has the potential to improve community prevalence estimates and detect emerging variants. Here, we describe Freyja, a computational tool for analyzing virus mixtures that enables researchers to perform robust, real-time wastewater pathogen surveillance. We show that Freyja can resolve virus lineage abundances from wastewater sequencing, enabling detection of SARS-CoV-2 variants of concern weeks earlier via wastewater as well as multiple instances of virus spread not captured by clinical genomic surveillance. These findings are reproduced at partner sites across the globe including in South Africa, Malawi, and Bangladesh. We further demonstrate the use of Freyja for identifying possible high-fitness and immune-escape mutants and their precursors, and how this may be used to inform our understanding of emergence of variants of concern. Overall, the Freyja toolset enables interpretable and reproducible wastewater genomic surveillance analyses, is easily deployed, and is naturally generalized to other pathogens.

The use of preference modelling for understanding COVID-19 vaccine hesitancy

Michael Strauss, University of KwaZulu-Natal / straussm@ukzn.ac.za

COVID-19 vaccination uptake in South Africa remains low particularly among young people aged 18-34 (just 40% by March 2023). This is despite a national vaccination programme which has been widely and easily accessible to the adult population since August 2021 – both in and outside of formal healthcare settings.

To understand the drivers of vaccine hesitancy, we conducted a discrete choice experiment among 390 staff and students from the University of KwaZulu-Natal in Durban, which modelled preferences in relation to vaccine characteristics (effectiveness, origin, number of doses, frequency of boosters) and service delivery models (location, waiting time, incentives). Mixed effects logistic regression and latent class models were used for analysis.

Results showed that vaccine effectiveness was the strongest driver of preferences, with the number of doses, and the frequency of boosters being significant drivers of choice regarding vaccination. Waiting time and the possibility of a financial incentive for vaccination were also significant in participants' preference structures. A latent class analysis showed that preferences were broadly grouped among 1) participants who would likely vaccinate in the future; 2) those who would not vaccinate under any circumstances; and 3) those who were hesitant, but whose choices are influenced by vaccine characteristics and service delivery models.

These findings were used to develop the Trust-Risk framework, a conceptual model of vaccine hesitancy based on risk perceptions and levels of trust in vaccines. The framework suggests entry points for addressing vaccine hesitancy, which are valuable for the continued scale-up of COVID-19 vaccines and future vaccination programmes.

9:00–10:30 am   **Coming up short: Delivering on the promises of primary healthcare systems**
Elliot Bay
Facilitator: Brittany Hagedorn, IDM

Scaling up human resources for health in rural India to achieve health-related SDGs: projections of personnel and costs for 2030

Siddhesh Zadey, Association for Socially Applicable Research (ASAR) / sidzadey@asarforindia.org

We projected deficits in the human resources for health (HRH) for India's rural public health system, estimated the required growth to achieve the SDG 2030 target, and calculated costs for the required scale-up.

Average annual percent change (AAPC) for essential HRH (doctors, nurses, and midwives) at rural primary and community health centers for 2009-19 from Rural Health Statistics were analyzed using JoinPoint (piecewise linear) regression. Projections for 2020–2030 were created using AAPCs assuming an exponential growth rate. The 2030 projected deficits (absolute differences) were assessed w.r.t WHO acute threshold (22.8 per 10,000 people), SDG Index threshold (44.5), and Govt. of India (GoI) SDG target (55.5). The statistical average salary for an HRH bundle was calculated using National Health Mission deployment data. Costs for recruiting and retaining HRH were calculated assuming a 1% increase in salary allowance each year after recruitment. During 2009–19, AAPC was 2.59% (95%CI: 0.93-4.28). The national density was 8.85 in 2019. It is projected to reach 11.47 in 2030. National deficits will be 0.47, 1.39, and 1.83 million HRH as per WHO acute, SDG Index, and GoI target thresholds, respectively. The corresponding growth rates for target achievement should be 8.84%, 15.66%, and 17.91%. The corresponding scaleup costs would be $18.68, $48.91, and $63.61 billion. Essential HRH in India's rural public healthcare is

deficient with low growth. Policymakers should adopt an incremental salary model to improve HRH retention.

Using conditional prediction to translate the measurement of a complex theoretical model into interpretable results
Valentina Martufi, CIDACS-Fiocruz/BA / valentina.martufi@fiocruz.br

Introduction: Under-5 mortality is affected by a range of determinants, including access to and quality of health services. Specifically, Primary Health Care (PHC) plays a significant role in preventing a portion of these deaths. However, PHC is a complex intervention: its quality is not easily measurable as a single exposure, given its multiple components. Employing different statistical approaches allows the measurement of the effect of a complex intervention such as PHC on under-5 mortality.

Objective: To predict under-5 mortality related to a complex theoretical model of PHC, providing interpretable results for the formulation of recommendations.

Methodology: Under-5 mortality rates were conditionally predicted by fitting generalized linear models with a probit link function. Over 600 scenarios were established according to our model of PHC determinants of under-5 mortality, using different combinations of percentiles for components measured with Bayesian Confirmatory Factor Analysis.

Results: This approach allowed us to predict under-5 mortality rates when Building Blocks of our PHC model (Planning and Organization, Infrastructure, Workforce, General Supplies and Referral and Regulation) improved in quality individually, ceteris paribus. Furthermore, this conditional prediction approach allowed us to elaborate two extreme scenarios that provided an estimation of the effect of an improvement across all Building Blocks at once.

Discussion: The development of this innovative approach allowed us to uncover a new finding—the potential impact on under-5 mortality of improving the quality of Planning and Organization of PHC services—, as well as substantiate the idea that "PHC is greater than the sum of its parts".

Estimating human resources for health workload at the primary health care level using the PACE-HRH model in Ethiopia
Meghan Arakelian, Vital Wave / meghan.arakelian@vitalwave.com

Using a bottom-up, time accounting tool, IDM's Population-Aware Capacity Estimator on Human Resources for Health, Vital Wave and MERQ are modeling prospective and evolving demands for Health Extension Program (HEP) services in Ethiopia over the next 15 years and forecasting health worker effort required to meet them. Importantly, the model and forecasting will account

for variability in needs and demand across Ethiopia's diverse regions and populations. Bridging the gap from theory to practice, Vital Wave and MERQ will fuel the model with up-to-date inputs collected through rigorous time and motion studies across disparate geographic areas and populations. This will include data on the workload of various health post staff, including Health Extension Workers, midwives, and nurses. Data collected will include localized detail such as time required per task, relevant population coverage, incidence rate in the population, local insights on seasonality, and skillset required for delivery. The work will inform systemic, data-driven changes to primary health care (PHC) programming and the introduction of workload management tools. In the short term, activities conducted by Vital Wave and MERQ will help build knowledge and capacity, through active engagement with the Ethiopian Ministry of Health and health system staff to test the model and its prospective integration into HEP and other PHC program decisions. At the time of the IDM Symposium, Vital Wave and MERQ are expected to be in the midst of the first round of data collection and can present on the research approach and tools developed to fuel the model.

Applying the Community Health Worker Coverage and Capacity Tool for time-use modeling to improve planning for human resources for health
Melanie Morrow, ICF / melanie.morrow@icf.com

Community health workers (CHWs) are critical human resources for health, especially in health systems in lower- and middle-income countries. However, when policy recommendations exceed what is feasible to implement, CHWs are overstretched by the volume of activities, implementation strength is diluted, and programs fail to produce promised outcomes. To counteract this, we developed a time-use modeling tool—the CHW Coverage and Capacity (C3) Tool, used with several government partners in Africa to address common policy questions related to CHW needs, coverage, and time optimization.

In Zanzibar, the C3 Tool was used to update the national community health strategy to include community health volunteers (CHVs) for the first time and determine how many CHVs were needed. The tool projected that 2,200 CHVs could achieve approximately 90% coverage of all defined services. Based on these figures, Zanzibar updated its national community health strategy, which officially launched in February 2020.

Translating analysis into decision making depends not only on the programmatic will and motivation of governments but also on finding opportune timing for when policy and program processes allow for optimization of CHW investments.

The proposed presentation would draw heavily on the following paper, though could be shaped to suit session interests and desired format accordingly:

Morrow M, Sarriot E, Nelson AR, et al. Applying the Community Health Worker Coverage and Capacity Tool for time-use modeling for program planning in Rwanda and Zanzibar. Glob Health Sci Pract. 2021;9(Suppl 1):S65-S78. https://doi.org/10.9745/GHSP-D-20-00324"

Use of HrH modelling to explore implications of CHWs administering vaccines

Tafwirapo Chihana, VillageReach / tschihana@gmail.com

With chronic health worker shortages and stagnating routine immunization rates globally, new strategies are needed to increase vaccination coverage and equity. Leveraging community health workers (CHWs) as vaccinators is a promising approach that may help countries maximize their health workforce, increase vaccination coverage, reach more zero-dose children, and offer relief to other strained cadres of health workers, such as nurses. Our rapid review showed that of the 75 countries with a CHW program, only 20 leveraged CHWs to administer vaccines. Although current documentation suggests that the use of CHWs as vaccinators is a successful model for routine immunization, a significant amount research is needed to quantify its efficacy, cost-effectiveness, and HrH implications.

What would happen if a national health system were to task-shift the responsibility of routine vaccination to CHWs? This change in approach would have significant effects on health system client loads, immunization coverage/reach, staffing, costs, and task-delegation. There is an opportunity to apply existing HrH models, such as the PACE HrH model, to explore how leveraging CHWs to vaccinate in new settings might help to save time, money, increase vaccination coverage, and illuminate wider implications for the health workforce.

Given that currently no global guidance exists on how to successfully leverage CHWs to vaccinate, the evidence generated from HrH modelling are needed to fill the evidence gap and shape global guidance, as well as for advocacy purposes to inform countries who are considering task-shifting vaccination responsibilities to CHWs.

| 9:00–10:30 am | Invited software demonstrations
Portage Bay |

Epistemix: Platform to build agent-based models that generate actionable insights
John Cordier

ClinEpiDB: An open-access data exploratory data analysis platform
Dan Beiting, Danica Helb, Dan Roos

| 11:00 am–
12:30 pm | Beyond pharma: Big ideas to reach elimination in TB and other diseases
Lake Union
Facilitator: Stewart Chang, IDM |

Impact of interventions for tuberculosis prevention and care in South Africa—A systematic review of mathematical modelling studies
Lauren Brown, SACEMA / laurenbrown@sun.ac.za

Substantial additional efforts are needed to prevent, find and successfully treat tuberculosis (TB) in South Africa. In the past decade, an increasing body of mathematical modelling research has investigated the population-level impact of TB prevention and care interventions. To date, this evidence has not been assessed in the South African context. We searched PubMed, Web of Science, and Scopus databases for studies that used transmission-dynamic models of TB in South Africa and reported on at least one of the End TB Strategy targets at population-level. We described study populations, type of interventions and their target groups, estimates of impact and other key findings. For studies of country-level interventions, we estimated average annual percentage declines (AAPDs) in TB incidence and mortality attributable to the intervention. Among 29 studies that met our inclusion criteria, the highest impact was estimated for interventions of TB vaccination, preventive therapy and ART scale up among PLHIV. Only one study focused on reducing catastrophic costs due to TB. For preventive interventions, average annual percentage declines in TB incidence varied between 0.06% and 7.07%, and for interventions along the TB care cascade between 0.05% and 3.27%. Higher impact estimated for preventive interventions highlights the need to invest in TB prevention in South Africa. However, study heterogeneity and inconsistent baseline scenarios limit the ability to compare impact estimates between studies. Combinations rather than single interventions are likely needed to reach the End TB Strategy targets in South Africa.

Modelling the social determinants of TB to inform a better TB response model
Delia Boccia, World Health Organization / bocciad@who.int

Tuberculosis (TB) is a disease and also a manifestation of profound unbalances in the society. These inequalities are still the major drivers of the TB epidemic and the main barriers to its end. The WHO multisectoral accountability framework (MAF-TB) acknowledges this and claims for a more holistic response to TB based on the synergistic effect of biomedical and social protection strategies. In 2018 the Bill & Melinda Gates Foundation sponsored the S-PROTECT Modelling Consortium. S-PROTECT aimed to develop a mathematical model able to capture the influence of social determinants and social protection on the epidemiology and control of TB. By developing a generalisable modelling framework, S-PROTECT proved that achieving its goal was complex but doable. However, it also showed the existence of important methodological and conceptual gaps, including the lack of good quality and harmonised data on social determinants of TB, the need to move beyond the current social epidemiological model explaining TB inequalities through income, housing and nutrition to encompass more complex social determinants of TB including gender, climate change, social exclusion and injustice. This talk will discuss how the research road map drawn by S-PROTECT has moved forward, what gaps persist, what evidence have been generated and how the policy environment has changed since the inception of this first mathematical modelling effort. The talk will conclude by illustrating how progress in the mathematical modelling of the social determinants of TB will be crucial to inform an improved and more equitable TB response model based on "cash & care".

Part 1—The potential impact of novel tuberculosis vaccines on health equity and financial protection in low- and middle-income countries
Richard White, London School of Hygiene and Tropical Medicine / richard.white@lshtm.ac.uk

Integrating retrospective impact evaluations with microsimulation models to forecast the effects of social protection interventions
Davide Rasella, Institute of Collective Health, Federal University of Bahia, Brazil / davide.rasella@gmail.com

The COVID-19 pandemic caused the most significant setback to global poverty in decades, exacerbated by climate shocks among the world's biggest food producers, and by the negative impact of the Russian-Ukraine war on food and energy prices. These multiple crises contributed to slowing down the progress for the achievement of the Sustainable Development Goals (SDGs), halting or—in most countries—even reversing years of progress in poverty reduction.

There have been repeated calls to expand social protection interventions to the new poor as a potential mitigation policy, arguing that they have a larger impact on income growth compared to other interventions, and they are a far more effective mechanism for supporting vulnerable groups. We developed a series of studies estimating the effects of poverty on infectious (HIV/AIDS, TB) and non-infectious diseases and health conditions (including child and adult morbidity and mortality), using big longitudinal data from Brazil and other Latin American Countries. Through quasi-experimental impact evaluation designs, we assessed the effects of poverty-reduction policies during the last decades in the same countries and health outcomes. Subsequently, we integrated all datasets and parameter estimates from the retrospective studies with dynamic microsimulation models, forecasting potential evolutions of the current global crisis and evaluating the mitigation effects of alternative policy responses, ranging from an expansion of social assistance to cover all the newly poor individuals, to the implementation of fiscal austerity measures that would reduce social assistance coverage. We then compared policy scenarios in terms of incidence and mortality rate ratios, and number of potentially averted cases and deaths over the forecasted period.

11:00 am–   **Polio**
12:30 pm   Lake Washington
            Facilitator: Hil Lyons, IDM

Potential impact of wild poliovirus 1 introduction into South Africa
Zinhle Mthombothi, SACEMA / zinhlem@sun.ac.za

Polio is a highly contagious, life-threatening infectious disease. Although the last case of polio in South Africa (SA) was reported in 1989, Mozambique and Malawi have reported 9 cases of wild poliovirus type 1 (WPV1) in the past 2 years, suggesting there may be ongoing transmission in the region. We developed an age-structured compartmental model to examine the potential magnitude of poliovirus outbreaks following the successful introduction of WPV1 in SA The model is run separately for each of SA's 52 districts, based on the population's age structure and estimated immunity profile.

Our model suggests that successful introductions of WPV1 could lead to large outbreaks in some districts, even with reactive vaccination campaigns. Specifically, Ehlanzeni District Municipality and the City of Johannesburg Metropolitan Municipality could each have over 300 cases of acute flaccid paralysis (AFP). In contrast, Namakwa and Lejweleputswa District Municipalities are each expected to have no cases of AFP. Our model suggests that preemptive catchup campaigns targeting 70% coverage of under-15-year-olds

in areas where vaccination coverage is low could substantially reduce potential outbreak size.

Estimating immunity against wild poliovirus type 1 in South Africa

Jeremy Bingham, SACEMA / jeremyb@sun.ac.za

Quantifying immunity to poliovirus serotypes in the South African population is valuable to inform public health resource allocation, particularly in the context of recent and ongoing outbreaks in the region. We present district-level estimates, in five-year age bands, of humoral and mucosal immunity to wild poliovirus type 1 (WPV1) for each of South Africa's 52 districts. The estimates integrate data on annual doses of Oral Poliovirus Vaccine (OPV) and Inactivated Poliovirus Vaccine (IPV) administered at the district level between 2009 and mid-2022, live births in these years, population sizes, and a nationally representative serosurvey of young children conducted in 1995. We use a combination of bootstrapping and proxy measures where data on doses administered are incomplete. We simulate distribution of vaccine doses to the eligible population and then estimate immunity levels by birth year, assuming a per-dose efficacy of 76% for OPV and n-dose efficacies for people who received 1–4 IPV doses.

Mucosal immunity levels for people born between the 1995 serosurvey and 2009 are extrapolated for each realization by fitting a straight line from the survey-estimated immunity level to the level estimated based on 2009 data.

Our results highlight that immunity against WPV1 is highly heterogenous across districts, and the estimates are a key input for our poliovirus transmission model.

Our approach allows immunity estimation from imperfect data, is applicable to other poliovirus serotypes, and can be easily adapted to similar data-poor settings for other diseases.

A framework to assess poliovirus elimination from clinical and environmental surveillance data

Kathleen O'Reilly, London School of Hygiene and Tropical Medicine / kathleen.oreilly@lshtm.ac.uk

The pillars of surveillance for poliovirus; acute flaccid paralysis (AFP) and environmental sampling (ES), have been essential in detecting poliomyelitis cases and poliovirus detections in endemic and outbreak settings. As polio incidence edges towards elimination, it is becoming increasingly important to both monitor detections and assess the evidence of absence. Well-tested approaches for assessing elimination are limited, so we provide a statistical framework to do this and a corresponding critique. We start with a positive null hypothesis that poliovirus is present in a population (eg., Pakistan and Afghanistan), and the aim of the analysis is to disprove this hypothesis using data. To do this, we assume that poliovirus is present at a low (pre-determined) value, and ask what the probability of detection is given the surveillance data. Each mode of surveillance (in this case AFP and ES) are described using surveillance trees to define the sensitivity of surveillance. These estimates are combined within a statistical model to return a probability that Pakistan and Afghanistan are infection free for each month of surveillance data with negative samples, and these estimates accrue in time to provide monthly estimates of elimination. We compare model estimates to a simple mathematical model of polio to establish the sensitivity of elimination estimates, and apply the model to recent surveillance data from Pakistan and Afghanistan. As the modelling progresses the outputs will become increasingly useful for other aspects of polio epidemiology, such as validating the absence of circulating vaccine-derived polioviruses.

Health benefits, risks, and costs of polio vaccination strategies against wild poliomyelitis under limited resources: a modelling study

Megan Auzenbergs, London School of Hygiene and Tropical Medicine / megan.auzenbergs@lshtm.ac.uk

Polio eradication was threatened in 2022 by importation of wild poliovirus serotype 1 (WPV1) into Malawi and international spread, the first cases outside of endemic countries in over five years. Preventing importations and spread of WPV1 is important, but recent financial constraints limit preventive supplementary immunisation activities (pSIAs).

We developed a mathematical model of polio transmission dynamics to evaluate the risk of poliovirus importations, probability of an outbreak and the costs of vaccination strategies. Across varying levels of routine immunisation (RI) coverage, we explore four strategies: RI only, RI plus annual pSIAs, RI plus biannual pSIAs, and RI plus outbreak-response SIAs (oSIAs).

Annual pSIAs had higher costs but lower probability of outbreaks: under our model assumptions, annual pSIAs reduced outbreak probability over a 5-year period below 80% when RI coverage ≥50%. Biannual pSIAs cost less and avert more outbreaks than oSIAs or RI alone, but RI coverage ≥65% was required to achieve equivalent outbreak risk. oSIAs had lower costs than pSIAs, but RI coverage of at least 75% was required to achieve equivalent outbreak risk.

pSIA prioritisation must balance outbreak risk against implementation costs, ideally favouring the smallest manageable outbreak risk for elimination. We infer from our analysis that few short-term costs exist due to RI immunity, but long-term risks accumulate and can result in considerable size outbreaks and potential for international spread. We do not consider the costs of further

delaying the eradication timeline or societal implications of outbreaks on polio eradication, both of which emphasise the need for pSIAs, even when outbreak risks are small.

11:00 am –
12:30 pm

COVID-19: Understanding epidemics & addressing issues in equity
Greenlake
Facilitator: Cliff Kerr, IDM

Retrospective analysis of equity-based optimization for COVID-19 vaccine allocation
Laura Matrajt, FHCRC / laurama@fredhutch.org

Background: Despite the development of safe and effective vaccines and antiviral treatments against COVID-19, marginalized racial/ethnic groups in the United States (US) continue to be disproportionally burdened by COVID-19. Methods: We constructed an age- and race-stratified mathematical model of SARS-CoV-2 transmission and vaccination, fitted to data from Oregon in January 2021. We used counterfactual scenarios to determine the optimal use of limited amounts of vaccine over 4 months with the goal of minimizing 1) number of deaths or years of life lost (YLL), 2) inequity between race groups, or 3) a combination of both.

Results: We found that limited vaccine supply (enough to cover 10% of the population), there is a trade-off between minimizing mortality or minimizing inequity. For minimizing mortality, it is optimal to allocate vaccine to the oldest age group, irrespective of race. To minimize inequity, vaccine was first allocated to marginalized young- and middle-aged groups. However, this strategy incurred in more deaths, including in these groups. When minimizing both deaths and inequity, the optimal vaccination strategy achieved a significant reduction in inequity while preserving most of the reduction in mortality. Once vaccine supply was enough to cover 20% of the population, our results suggest that it is possible to minimize both mortality and inequity at the same time, protecting marginalized communities and the oldest populations first.

Conclusions: With low vaccine supply, there is a trade-off between being more equitable and protecting overall mortality. This is true because COVID-19 related mortality is concentrated in the oldest populations. This trade-off quickly disappears when more vaccine is available.

Calculating the impact of single individuals on population-scale epidemic outcomes.
Joel Miller, La Trobe University / joel.c.miller@gmail.com

Many policy responses to infectious diseases involve behavior changes, either by encouragement or through restriction. Often these are associated with penalties/rewards to produce behavior change. When designing a policy, ethical considerations suggest that the penalties/rewards for an action should be proportional to the harm/benefit to others resulting from that action. In this talk, I will explore the expected impact on the final size of an epidemic of a single individual changing behavior as well as the combined impact of a group. Due to the convex it's of the final size relation, the marginal benefit of an individual changing behavior to prevent transmission is increased if others are also taking actions to prevent transmission, this benefit is largest with the reproduction number is close to 1.

Heterogenous effects of COVID-19 on labour market outcomes in Malawi
Norah Mwase, Malawi Liverpool Wellcome Programme / norahmwase@gmail.com

This paper investigates the disproportionate effects that the COVID-19 pandemic has on different groups of workers in the labour market in Malawi. We disaggregate the workers by gender, age, level of education and sector of employment and apply survival analysis to assess survival and hazard rates. Using monthly panel data from the Malawi High-Frequency Phone Survey on COVID-19 (HFPS COVID-19) collected between May 2020 and April 2021, we show that the COVID-19 pandemic has affected different labour market participants differently. Specifically, there is a high risk of job loss for women, those with low or no education, those working in the education, and retail and wholesale sectors, and those who tested positive for COVID-19. These results can assist in targeting appropriate groups with COVID-19 response interventions especially women; who are a key to a stronger and quick economic recovery.

A challenge: Understand and predict the course of COVID-19 epidemic in Poland. Opportunities and obstacles.
Franciszek Rakowski, ICM, University of Warsaw / rakowski@icm.edu.pl

A detailed and geo-referential Agent-Based ICM UW Model for predicting and elucidating the course of the Covid-19 epidemic in Poland will be presented. It is a full population model suitable for studying many possible scenarios resulting from application of various types of NPI's. The model was operationally running since the very beginning of the epidemic in Poland, being one of the principal analytical systems supporting the decision makers of all levels in Poland and elucidating the epidemic processes to the public.

In the lecture I will talk also about the course of the epidemic in Poland as it is expressed in numbers, and as it should be interpreted by scientific knowledge. I will point out the difficulties in building the comprehensive picture of the epidemic course and the role of the mathematical and formal models of epidemic in explaining and forecasting the epidemic spread. I will discuss the problem of limitations imposed on the model by the lack of data, and the consequences of accepted "modus operandi" in which practical usefulness and operational mode overtake scientific precision.

The model and observation data describing the epidemic in Poland will be compared with the data from other EU countries. A special focus will be put on the causes of excess deaths observed during pandemic months.

Since the ICM UW Model played an important public role, I will briefly discuss the challenges related to the communication of the quantitative results in understandable and credible way.

Secondary attack rates and determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) household transmission in Pakistan: a case-ascertained prospective, longitudinal study

Mashal Amin, The Aga Khan University / mashal.amin@aku.edu

Households are considered ideal settings for studying the transmission dynamics of an infectious disease. A prospective study was conducted, based on the World Health Organization FFX protocol from October 2020 to January 2021. Household contacts of laboratory-confirmed index cases of SARS CoV-2 were followed up for their symptomatic history, nasal swabs for RT-PCR and blood samples for anti-SARS CoV-2 antibodies were collected at enrollment and days 7, 14, and 28. We estimated the secondary attack rate (SAR), effective reproduction number (Re), and determinants of secondary infection among susceptible household contacts using multivariable logistic regression. We enrolled 77 index cases and their 543 contacts. Out of these, 252 contacts were susceptible at the time of enrollment. There were 77 household clusters, out of which, transmission took place in 20 (25.9%) giving rise to 34 cases. The acquired secondary attack rate (SAR) was rate 14.0% (95% CI 9.0–18.0). The average effective reproduction number (Re) was 0.44 (95% CI 0.33–0.60). Reported symptoms of nausea and vomiting (OR, 7.9; 95% CI, 1.4–45.5) and fatigue (OR, 9.3; 95% CI, 3.8–22.7) were associated with SARS-CoV-2 transmission. We observed low SARS-CoV-2 transmission in the backdrop of high seroprevalence among households in Karachi, Pakistan. Symptomatic history influences infection transmission.

| 11:00 am – 12:30 pm | **Quantifying the "softer side" of effective health systems: Is it a bad idea?** Elliot Bay *Facilitator: Brittany Hagedorn, IDM* |

CIDACS Primary Health Care (CIDACS-PHC) Cohort: An innovative approach to link real-world data with health facilities surveys to evaluate how PHC components affect Under-5 mortality in Brazil.

Elzo Pereira Pinto Junior, Centro de Integração de Dados e Conhecimentos para Saúde/Fiocruz / elzo.junior@fiocruz.br

Using real-world data to evaluate how different interventions impact health outcomes increases the potential to understand complex phenomena and guide public policy. Under-5 mortality (U5M) is an outcome with multicausal determinants, including Primary Health Care (PHC) access and quality. Robust evidence demonstrates how increased PHC access improves child health outcomes. However, there is a lack of evidence regarding the quality of PHC components and how they influence U5M. Taking advantage of Brazil's extensive data ecosystem, we used data from the Health Information Systems, alongside databases of Social Protection Policies beneficiaries and linked this information to a national survey of PHC facilities to estimate the quality of care received by children of program beneficiaries, and the resulting probability of U5M. This resulted in the creation of a retrospective cohort of 143,070 Brazilian children, accompanied from birth to the completion of 5 years-of-age. At the individual level, this cohort provides socioeconomic, maternal, and child characteristics information. In addition, we linked each child to information regarding different PHC components, classified as Building Blocks (Reference and Regulation, Planning and Organization, Facility Infrastructure, General Supplies, and Workforce) and Clusters of Services (Antenatal Care, Child Care, and Immunization), considering at which PHC facility beneficiaries fulfilled their conditional transfer requirements. The construction of this cohort, alongside the application of sophisticated statistical methods to create the PHC components (Latent Class Analysis, Bayesian Confirmatory Factorial Analysis) and to assess their influence on U5M (Multilevel Bayesian Path Analysis, Conditional Prediction) amplify the potential to evaluate complex interventions such as PHC.

Targeted scale-up and interventions to improve Availability, Accessibility, Acceptability and Quality of Human Resources for Health in India
Sweta Dubey, Association for Socially Applicable Research (ASAR) India / swedu25@gmail.com

Background: WHO recommends improvement in four human resources for health (HRH) dimensions—Availability, Accessibility, Acceptability, Quality (AAAQ). These HRH dimensions remain understudied in India.

Methods: We formulated four deficit indices to measure AAAQ dimensions. Availability deficit (AvD) measured deficit of available HRH against contextually relevant requirement thresholds, accessibility deficit (AsD) measured deficit of HRH present in rural areas relative to urban counterparts, acceptability deficit (ApD) measured the imbalance of female HRH personnel relative to males, and quality deficit (QD) measured deficit of qualified HRH relative to the total. Deficit values were calculated for six HRH cadres over four decades i.e. 1981–2011 at national-level. Data sources included Census, National Sample Survey rounds, and High-Level Expert Group report 2012. Deficit values for 2021 and 2031 were extrapolated using average decadal change in deficit indices between 1981–2011. Further, number of excess HRH needed to have zero AAAQ deficit by 2031 was calculated.

Results: AAAQ indices will show deficit for majority of HRH cadres in 2031 except for AvD of doctors, indigenous practitioners, and auxiliary nurse-midwives (ANMs), AsD of ANMs, and ApD of nurses. Pharmacists and nurses will require highest scale-up to reduce AvD to zero in 2031. Doctors and nurses must be scaled up the most in rural areas (for zero AsD). Priority scale-up of female doctors and pharmacists is needed for zero ApD. ANMs and nurses should be the priority for quality-related interventions.

Conclusion: Targeted investments on scale-up based on cadre-specific needs will ensure HRH development across all dimensions by 2031.

11:00 am – 12:30 pm	IDM software demonstrations Portage Bay

Introduction to the SAE Dashboard
David Kong, IDM / david.kong@gatesfoundation.org

MosquitoDB: A comprehensive electronically-based entomological surveillance system for the control and elimination of mosquito-borne diseases
Jamese Silayo Michael, Ifakara Health Institute, University of Dar es Salaam

1:45 – 3:15 pm	**Beyond pharma 2: Turning nutrition and determinants into interventions for TB** Lake Union *Facilitator: Stewart Chang, IDM*

Part 2—The potential impact of novel tuberculosis vaccines on health equity and financial protection in low- and middle-income countries
Richard White, London School of Hygiene and Tropical Medicine

The TB vaccine we already have: Addressing undernutrition to end TB
Natasha Hochberg, Boston University School of Medicine / nhochberg@gmail.com

Undernutrition is the leading risk factor for TB globally. Indeed, one in five cases of TB worldwide are attributable to undernutrition. Not only does undernutrition increase the risk of TB, it also increases risk of mortality and morbidity. Despite the enormous impact of undernutrition, it remains at the periphery of the global response to TB and few interventions have targeted this widespread risk factor. In this talk, we will define the scale of the problem, review the evidence linking undernutrition to TB. Further, we will discuss how mathematical modeling couples with clinical studies can propel policy change.

Meals as medicines: A new model for TB elimination
Pranay Sinha / psinha@bu.edu

One in 5 tuberculosis (TB) cases worldwide is attributable to undernutrition. Poor nutritional status is the leading cause of acquired immunodeficiency worldwide. While the link between undernutrition and TB has been long-recognized, many questions remain to be answered about the impact of undernutrition, the benefits of nutritional support, and the cost-effectiveness of various nutritional interventions. This talk will identify some critical knowledge

gaps at the intersection of undernutrition and tuberculosis. Several of these gaps can be addressed through mathematical modeling coupled with strategically designed clinical studies. Doing so expeditiously can propel policy change and accelerated global TB elimination efforts.

Action on social determinants and undernutrition in communities and patients: A key intervention for TB Elimination
Anurag Bhargava, Yenepoya Medical College / anuragb17@gmail.com

Social determinants are integral to causation of TB and its outcomes. They were once considered central to TB care and prevention but were rendered invisible after the advent of effective chemotherapy and vaccines as a panacea for TB control. Undernutrition is a key determinant of immune function in patients and populations and was once considered central to TB care and prevention. However, for the past 60 years, it was neither appropriately assessed, researched or addressed in strategies for TB control.

This talk will draw upon the experience and research of the authors over the past more than 2 decades that led to the recognition of undernutrition in patients as a key risk factor for the continued high TB mortality in India, undernutrition in communities as the major driver of the TB epidemic in India and globally, and lessons in TB control from the pre-chemotherapy era that suggested a major role for adequate nutrition in TB control. We will describe briefly why the WHO methodology for estimation of PAF for TB related to undernutrition needs modification. Finally, the talk will describe the RATIONS trial, a recent cluster-randomized trial of nutritional support implemented with the National TB Elimination Programme among poor communities in eastern India that aims at significant reductions of TB incidence and improved TB outcomes.

In conclusion, we shall draw attention to the need for a more comprehensive and accurate map of actionable factors(beyond diagnostics, drugs and vaccines) for improving TB care and prevention on the path to TB elimination.

1:45–3:15 pm   **Under 5 mortality**
Lake Washington
Facilitator: Dennis Chao, IDM

Parsing the impact of Child Growth Failure on morbidity and mortality: an analysis of the Global Burden of Disease Study 2021
Bobby Reiner, University of Washington / bcreiner@uw.edu

Quantifying the burden of Child Growth Failure (CGF) requires both an understanding of how many children have what level of severity for CGF

indicators (stunting, wasting, underweight) as well as estimates of the increased relative risk for those children for associated disease outcomes. Over the past 4 years, researchers within IHME have worked to fundamentally reframe both the processes used for estimating the distribution of mild, moderate, and severe growth failure as well as use newly available data sources to re-estimate the increased relative risks for children with CGF associated with poor health outcomes. Using these newly available data sources we are able to separate the impact of CGF on morbidity from the impact of CGF on mortality, as well as identify non-negligible impacts of CGF on malaria outcomes (a risk-outcome pair previously not included in the GBD). Our results confirm that the risk of death for those impacted by CGF is substantially higher than the risk of disease, and have far reaching consequences for how treatment for CGF should be targeted as well as how interventions should be evaluated.

Individual-based simulation for evaluating intravenous iron use in antenatal and postpartum populations
Sylvia Lutze, IHME / lutzes@uw.edu

Supporting maternal and neonatal health is important for communities and individuals worldwide. While there has been significant progress in recent years, there is still opportunity for improvements, including providing antenatal and postpartum intravenous (IV) iron, which has been shown to improve pregnancy and birth outcomes. However, the population-level impact of IV iron is subject to regional differences such as eligible population size, which can alter the potential impact and costs. Simulation models can include these regional differences, making them ideal to support planning and implementation strategies. We explored the impact of IV iron using a discrete-time, individual-based simulation platform called Vivarium, which utilizes Monte Carlo uncertainty and is calibrated to match Global Burden of Disease (GBD) study estimates. Our simulation linked maternal-child dyads, allowing for paired effects of antenatal interventions on mothers and infants. Results from the maternal simulation served as inputs to a separate child simulation, allowing for differential time-step durations between the respective populations, increasing run-time efficiency. Our simulation also utilized parameter uncertainty estimated by GBD and a novel approach to common random numbers. With this model structure, we found that adding antenatal and postpartum IV iron compared to a scaled-up oral iron would avert 1.4 million and 1.1 million DALYs annually in South Asia and Sub-Saharan Africa respectively. Our simulation platform Vivarium supported our IV iron simulation structure to produce robust estimates of the impact of MNCH interventions.

Prioritisation of diarrhoea treatment interventions for the under-five population based on district-level treatment gaps in India

Vidhi Wadhwani, Association for Socially Applicable Research (ASAR), India / sidzadey@asaforindia.org

Background: Diarrhoea is the third most common cause of under-five mortality in India. ORS and Zinc can reduce diarrhoea morbidity and mortality. However, district-level utilisation of Zinc and ORS in under-five diarrhoea patients have not been measured.

Methods: We used India's National Family Health Survey 5 (NFHS-5) to calculate the district-level percentage of under-five children with diarrhoea who did not receive ORS and Zinc and labeled them as 'ORS treatment gap (TG)', and 'Zinc TG', respectively. We developed six priority rank categories based on ORS and Zinc TGs and classified districts, accordingly. For e.g. districts with ORS TG of >50% and Zinc TG of >50% were assigned first priority rank and those with ORS TG of <35% and Zinc TG of <35% were assigned the last (sixth) priority rank. Districts with first priority rank signify the highest need for diarrhoea care intervention and vice versa.

Results: Anantapur district of Andhra Pradesh showed the highest ORS TG (81.2% TG). Kishanganj district of Bihar showed the highest Zinc TG (95.8%). The top-five districts requiring first-priority diarrhoea care intervention were located in Jharkhand (Deoghar, Dhanbad, Garwha) and Uttar Pradesh (Mathura, Muzaffarnagar). The bottom-five districts with the lowest priority for intervention included Ratlam in Madhya Pradesh, Rajsamand in Rajasthan, South East Delhi, Kodagaon in Chhattisgarh, and Kupwara in Jammu and Kashmir.

Conclusion: District-wise priority-based targeted interventions will ensure early care to the neediest population, will allow focused investments, and solve the problem of diarrhoea TG in a logical stepwise manner."

Hospitalizations due to diarrhea in the under-five population in India: District-level analysis.

Divya Shrinivas, Association for Socially Applicable Research (ASAR), India / sidzadey@asarforindia.org

Background: Diarrhea is a common cause of under-five mortality in India with a national prevalence of 7.3%. Approximately, 60% of under-five children with diarrhea are hospitalized. However, wide district-level variations exist in diarrhea hospitalizations.

Methods: We obtained number of under-five children with diarrhea and number of under-five children with diarrhea who were hospitalized for the years 2017–18, 2018–19, and 2019–20 using the Health Management Information System (HMIS), India. The district-level percentage of under-five children with diarrhea undergoing hospitalization (or diarrhea hospitalization rates) was calculated using this data. We evaluated the national-level longitudinal changes in the diarrhea hospitalization rate from 2017 to 2020 and identified states and districts with the highest and lowest diarrhea hospitalization rate for 2019–20.

Results: The under-five diarrhea hospitalization rate showed a 2% decline between 2017 to 2020. For years 2019–2020, the states with the highest hospitalization rates were Maharashtra and Jharkhand while Arunachal Pradesh and Gujarat were the states with the lowest hospitalization rates. Aurangabad, Akola, Buldhana, and Parbhani districts from Maharashtra, and Pithoragarh district from Uttarakhand were top-five districts in terms of under-five diarrhea hospitalization rates (>85% each). Umaria district (Madhya Pradesh), Bharuch (Gujarat), Thanjavur (Tamil Nadu), Lower Dibang Valley and Tirap districts (Arunachal Pradesh) were the bottom-five districts with lowest diarrhea hospitalization rates (<1% each).

Conclusion: The hospitalization rate for diarrhea varies widely across states and districts. This variation needs to be studied to divert resources to districts with more inpatient load as well as to study the causes of such inpatient burden.

1:45–3:15 pm   **Model calibration**
                   Greenlake
                   Facilitator: Jamie Cohen, IDM

Inferring the natural history of HPV from global cancer registries: A multi-country calibration exercise

Robyn Stuart, IDM and the Bill & Melinda Gates Foundation

The primary goal of this work is to determine how much of the variation in the distribution of cervical cancer burden across 30 countries in Sub-Saharan Africa can be explained by differences in demographic and behavioral factors alone, and how much would appear to be attributable to underlying differences in host immune responses and thus reflected in different natural history parameters.

Calibrating complex models using emulation and history matching: the hmer package

Andy Iskauskas, Durham University / andrew.iskauskas@durham.ac.uk

Complex epidemiological models are prevalent in a wide range of applications to understand the transmission dynamics and natural history of a disease, and to assess the potential effects of vaccine and intervention strategies.

Calibrating such a model to data, however, can be difficult: these models often have large numbers of input parameters and are computationally expensive to run, making a systematic exploration of the parameter space infeasible. Furthermore, for stochastic models, the variability of output at a parameter set can confound attempts to perform robust calibration.

The application of emulation and history matching can surmount these problems. We may efficiently explore the parameter space and determine underlying dynamics via the use of statistical surrogates (emulators). The history matching framework allows us to find all parameter sets that could give rise to observed reality robustly, taking into account any and all uncertainties in the system. The underlying stochasticity of a model, and any potential multistate behaviour, can also be elegantly encompassed in the framework. I will discuss the theoretical underpinning of emulation and history matching by demonstration, using our hmer package. The examples used to demonstrate the techniques and software will be linked to real-world calibration problems regarding models of TB, Covid, and HPV.

Understanding the key determinants of an HPV therapeutic vaccine: A modeling analysis
Jamie Cohen, IDM / jamie.cohen@gatesfoundation.org

Despite incredibly effective tools to prevent HPV infection and treat precancerous lesions, the scale-up of existing interventions in most low and middle-income countries has been slow, leaving a residual burden of invasive cervical cancer that will persist for decades. An HPV therapeutic vaccine may overcome some of the scalability and infrastructure challenges of traditional screening and treatment programs, though its potential public health value depends upon its characteristics, delivery strategy, and the underlying natural history on which it would act. This work highlights the importance of the underlying natural history assumptions in mathematical models and the need to explicitly account for parametric uncertainty.

Universal or targeted HIV prevention for HIV-1 in Africa? Evidence from phylogenetic studies and modelling.
Christophe Fraser, University of Oxford / christophe.fraser@bdi.ox.ac.uk

HIV incidence is decreasing in sub-Saharan Africa (SSA), but not as fast as expected given progress made to reach the UNAIDS treatment targets. This suggests that a substantial fraction of new infections is coming from virally unsuppressed persons with disproportionately high risk of onward transmission compared to the general HIV positive population.

Highly effective biomedical prevention interventions such as oral and long-acting PrEP are most feasible when focused on relatively small and defined groups of people at high risk of transmission Phylogenetic and clustering approaches have been used to identify the demographic and behavioural characteristics of these groups and, in the Global North, to focus prevention efforts on fast-growing clusters identified in near-real time.

When analysing HIV genomic PANGEA datasets from Zambia, Botswana and Uganda and comparing them with a European and a UK dataset, we find an absence of large clusters in the sub-Saharan African epidemics while controlling for sampling fraction. The observed cluster distributions and are in line with predictions from the PopART IBM model calibrated to the Zambian epidemic, and somewhat lower than predictions from EMOD calibrated to eSwatini.

The absence of large clusters makes it less likely that a substantial proportion of new infections is driven by a small key population, but it does not exclude the existence of high-risk groups. It does suggest however that focussing on small demographic groups for prevention efforts is likely to have a smaller effect on population-wide incidence than cluster-busting approaches currently being deployed in European and North American settings.

1:45–3:15 pm   **Measles**
Elliot Bay
Facilitator: Kevin McCarthy, IDM

SCOptimal vaccination policy: Theory and application to measles and rubella in China
John Glasser, Centers for Disease Control and Prevention / Jglasser@cdc.gov

Measles and rubella are rash illnesses that typically afflicted young children in the pre-vaccination era, but rubella usually is mild while measles may be severe. Because child deaths to which measles contributes often have other proximate causes, measles mortality is under-ascertained. Rubella during the first trimester invariably causes miscarriages, stillbirths and, among livebirths, congenital rubella syndrome, an array of afflictions that often co-occur. As childhood vaccines commonly include antigens to the viruses causing both diseases, vaccination programs must be designed to prevent measles among young children and rubella among young women. By virtue of increasingly effective routine vaccination, together with targeted supplemental immunization activities (SIAs), health authorities in the PRC have reduced the burden of both diseases. To assist in devising strategies for accelerating elimination, we evaluated gradients of effective reproduction numbers derived from meta-population models with respect to immunization rates. Within regions, gradients identify provinces where vaccination would reduce the

effective reproduction number the most. And within provinces, they identify age classes where vaccination would be most effective. Measles' gradient is more heterogeneous than rubella's, but indicates that vaccinating adults is optimal. Simulations corroborate this, but indicate that a catch-up campaign among adolescent schoolchildren would accelerate elimination nonetheless. Moreover, this strategy is optimal for rubella. Thus, using MR or MMR vaccine in SIAs during the first months of several consecutive school years would both accelerate measles elimination and avert impending outbreaks of rubella that, because of the immune profile in China, would greatly increase the incidence of CRS.

Optimal timing regularly outperforms higher coverage in prophylactic measles SIAs

Katherine Rosenfeld, IDM / krosenf@gmail.com

Measles SIAs have provided doses to millions of children. However, they can be costly and coverage metrics as high as 95% are commonly sought. Consequently, there can sometimes be a fine balance between doing something well enough and at the right time. In the context of endemic measles transmission this tradeoff is not a subtle one. We demonstrate this in a generalized context as well as Pakistan exemplar. Additionally, this discussion serves as an introduction to some of the work at IDM to support decision making and policy

Modeling the spread of rubella disease using a stochastic delay dynamic system

Getachew Teshome Tilahun, Haramaya University, Ethiopia / gmgech@gmail.com

Rubella is a highly contagious and serious human viral disease that affects everyone in the world, especially when pregnant women are infected with the rubella virus and their newborns inherit Congenital Rubella Syndrome. In this study, deterministic, delay, stochastic, and stochastic-delay mathematical models of the dynamics of rubella were formulated and analyzed by dividing the total population into six classes, namely: S(t) susceptible, V(t) vaccinated first, P(t) protected, who received the second vaccination dose and developed active immunity for the rest of their lives, E(t) exposed, I(t) infected, and R(t) recovered. The deterministic model was expanded to a delay mathematical model that included past behavior because it did not account for the disease's incubation period. Neither the deterministic nor the delay mathematical models of the dynamics of rubella disease could explain the effects of environmental factors such as temperature changes, so the model was extended to stochastic and stochastic-delay mathematical models, where the total population is divided into five classes. The qualitative behavior of the models of all approaches is analyzed, and the result of the

model analysis reveals that the basic reproductive number in the delay case is less than that of deterministic as well as stochastic models. Also, the basic reproductive number for stochastic delay is smaller than others due to time delay and stochastic disturbances. Some values for the parameters were taken from relevant published articles and others. Numerical simulations were performed to investigate the effects of the basic parameters, and the results of the simulations were displayed graphically using MATLAB 2020a computer software. Simulation results suggest that reducing contact, exposure, and vertical transmission rates and increasing time delays and first and second dose vaccination rates play a role in minimizing the spread of rubella.

Calculating the optimal age to recommend measles vaccination in endemic populations

Elizabeth Goult, Max Planck Institute for Infection Biology / goult@mpiib-berlin.mpg.de

To reduce measles burden, and take steps towards elimination, measles vaccines must be used as effectively as possible. The vaccine effectiveness of measles containing vaccines (MCVs) increases with vaccination age. Hence, the recommended vaccination age should trade-off between vaccinating too early—risking vaccine failure—and vaccinating too late—risking infants contracting measles before vaccination.

Here, we propose a method to calculate the optimal age to recommend vaccination. First, we constructed a model of measles transmission and vaccination in endemic settings, incorporating realistic models of age-specific MCV vaccine effectiveness, and MCV-delay from the recommended age. Then, we simulated measles incidence for different recommended vaccination ages, looking at different social contact patterns, MCV coverages, and transmission settings.

We were able to identify the optimal age to recommend measles vaccination in all simulated scenarios. The optimal age was affected most by MCV coverage and transmission setting, with older optimal ages in high-coverage low-transmission settings, and younger optimal ages in low-coverage high-transmission settings. Differences in social contact patterns were also influential on the optimal recommended vaccination age, with South Africa's contact patterns resulting in the lowest optimal vaccination ages, and China's contact patterns resulting in the oldest optimal ages.

The heterogeneity in optimal vaccination ages reflect the need for recommended vaccination ages to reflect the population-specific measles epidemiology. Application of our proposed method to calculate a population specific recommended MCV age could lead to reduced measles cases, taking steps along the road to measles elimination."

Sub-national level analysis of measles prevalence in India
Rama Pal, Indian Institute of Technology Bombay / ramapal@iitb.ac.in

India is committed to eliminate measles by 2023. However, given the recent outbreaks in various parts of India, this goal is far from realistic. To formulate a reasonable policy action, sub-national level differences in the prevalence of measles cases has to be considered. The government policy document identifies four priority states, Uttar Pradesh, Bihar, Arunachal Pradesh and Maharashtra, based on size and repeated occurrence of measles outbreak. Again all the districts of these states do not face the same level of risk. We analyze the monthly pattern of measles cases using HMIS district level dataset for April'13-March'20. Based on this analysis the high priority districts in each of the four states have been identified. For each district we have focused on the TSIR model proposed by Thakkar et al.(2018) for the estimation of the susceptible and infected population and the reporting rate of the disease. We have used these estimates to predict the trajectory of the susceptible and infected population for the next twenty years in these high burden districts. We also compare the cost-effectiveness of various SIA scenarios to provide policy recommendations for reducing measles cases across these districts.

1:45 – 3:15 pm   **Applied math & software**
                    Portage Bay
                    Facilitator: TBD

Accelerating malaria prevention through modeling-informed product selection and design: Eradication thresholds in deterministic models with an application to Human Papillomavirus (HPV) Types 6 and 11.
Cody Palmer, Merck and Co., Inc / cody.palmer@merck.com

As coordinated disease control efforts expand across the globe, the possibility of achieving eradication of various infectious agents increases. Correspondingly, the role of modeling in informing strategy and eradication timing has expanded. Stochastic models have generally been considered the ideal tool for these kinds of problems, but deterministic compartmental models (DCMs) have been used in this context due to their relative conceptual and computational simplicity. However, these models can never achieve a measurement of zero, and so a small positive threshold is generally chosen as a proxy for eradication or cessation of transmission. No standard threshold has been adopted for eradication modeling.

In this talk, we will review the various thresholds that have been used in the literature for this purpose. We will then investigate a conservative threshold based on Markov's Inequality: For $0<p<1$, if a DCM estimates an upper bound of p on the expected number of infectious individuals, then the probability of eradication is at least 1-p. The theoretical limitations of this threshold will be discussed, but even with these limitations, this threshold represents a non-arbitrary choice for eradication modeling with deterministic compartmental models.

Also, we will examine the performance of this threshold in several illustrative examples using mathematical analysis and IDM's Compartmental Modeling System. We also apply this to a large DCM of HPV vaccination in the United States and investigate the impact of HPV vaccination on the eradication of HPV6 and HPV11, the causative agent for 95% of cases of juvenile onset recurrent respiratory papillomatosis.

Estimating the population-level impact of vaccines using counterfactual prediction with LASSO regression
Anabelle Wong, Max Planck Institute for Infection Biology / wong@mpiib-berlin.mpg.de

Background: Vaccine impact estimation is challenging for two reasons. First, population-level vaccine impact involves indirect protection for the unvaccinated (i.e., herd immunity), which cannot be easily assessed in conventional randomized controlled trials. Second, one needs to compare the observed disease burden to a counterfactual (i.e., what would have been without the vaccine policy) to estimate the vaccine impact but it is difficult to obtain the counterfactual – intuitive methods use the same population in the pre-vaccine era as the comparator but confounders can limit the validity of such methods.

Methods & Results: Addressing these challenges, we present a new approach: using a machine learning algorithm, LASSO regression, to predict the counterfactual outcome for vaccine impact inference. We designed a simulation study to test the performance of LASSO regression and commonly used methods, including interrupted time series (ITS), by comparing their ability to estimate the pre-specified impact of the pneumococcal conjugate vaccines (PCVs), and found that LASSO regression achieved accurate and precise estimation with high coverage while ITS estimates were biased. Then we applied LASSO regression to published pneumonia hospitalization data from Chile, Ecuador, Mexico, and the US and found that it yielded similar estimates to the established method, synthetic control using Bayesian variable selection (SC).

Conclusion: The LASSO method is accurate, easily implementable and interpretable. In complement to existing methods like SC, LASSO can be used to study the population-level impact of PCVs and other vaccines.

Demonstrating multi-country calibration of a tuberculosis model using new history matching and emulation package—hmer

Danny Scarponi, London School of Hygiene and Tropical Medicine / danny.scarponi@lshtm.ac.uk

Infectious disease models are widely used by epidemiologists to improve the understanding of transmission dynamics and disease natural history, and to predict the possible effects of interventions. As the complexity of such models increases, however, it becomes increasingly challenging to robustly calibrate them to empirical data. History matching with emulation is a calibration method that has been successfully applied to such models, but has not been widely used in epidemiology partly due to the lack of available software. To address this issue, we developed a new, user-friendly R package hmer to simply and efficiently perform history matching with emulation. In this presentation, we demonstrate the first use of hmer for calibrating a complex deterministic model for the country-level implementation of tuberculosis vaccines to 115 low- and middle-income countries. The model was fit to 9–13 target measures, by varying 19–22 input parameters. Overall, 105 countries were successfully calibrated. Among the remaining countries, hmer visualisation tools, combined with derivative emulation methods, provided strong evidence that the models were misspecified and could not be calibrated to the target ranges. This work shows that hmer can be used to simply and rapidly calibrate a complex model to data from over 100 countries, making it a useful addition to the epidemiologist's calibration tool-kit.

Project PreFac: Using satellite imagery, non-traditional data and machine learning to identify health facilities

Victoria Gammino, The MITRE Corp / vgammino@mitre.org

No single, geo-referenced database of public health facilities for sub-Saharan Africa exists, constraining humanitarian missions, health program efficiencies and development efforts. Well-known, open crowd-sourced georeferenced datasets tend to be biased towards larger facilities leaving rural dispensaries underrepresented, and legacy and obsolete data can introduce significant error for end-users and modelers. We developed a process to evaluate and test non-traditional data (NTD) to inform model development for building identification and trained a model to detect public health facilities in Nigeria using NTD, building-footprint datasets and satellite imagery. NTD included two sources of telemetry data generated by health programs during the course of routine activities pertaining to disease surveillance and vaccine delivery. A "ground-truthed" health facility building which was also intersected by two independent telemetry sources was defined as the gold standard. Machine learning models characterized the gold standard facilities to assign probabilities to all buildings not intersected by telemetry sources. Models had an area under the curve of between 0.89-0.90 in the test sets. The geographic features that were most important in predicting if a building was a health care facility was building footprint area and vertices; building density; and distance to artificial surface area, schools, and secondary/tertiary roads. Models performed better in rural, Northern regions of Nigeria, but had consistent performance between primary and secondary/tertiary facilities. This model assigns a building footprint with a probability of being a health facility. Our test-verified algorithm to predict health facility locations offers a significant pathway towards completion of national health facility registries.

Wednesday, May 24: Overview

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8:00–9:00 am	Opening session: Development of modeling centers in Africa Lake Union	Page 46
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	Introducing the Africa CDC Continental Framework for Strengthening Mortality Surveillance Systems: Current and future agendas Greenlake	Page 53
	Malaria modeling for sub-national tailoring Elliot Bay	Page 57
	IDM software demonstration: Introduction to PACE-HRH Portage Bay	
10:45–11:00 am	Break	
11:00 am–12:30 pm	Session 2	
	Family planning & fertility Lake Union	Page 60
	Gender disparities & comorbidities HIV infection Lake Washington	Page 61
	Verbal autopsy IT tools: Software developers and modelers come together to accelerate certification of cause of death in LMICs Greenlake	Page 64
	Malaria modeling for next generation interventions Elliot Bay	Page 66
12:30–1:45 pm	Lunch	
1:45–3:15 pm	Session 3	
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3:15–3:30 pm	Break	
3:30–5:00 pm	Session 4: Closing panel: Gender intentional research & data Camano Island / Whidbey Island	Page 79
5:00–5:15 pm	Break	
5:15–5:45 pm	Closing remarks *Philip Welkhoff*	

Wednesday, May 24: Sessions

8:00–9:00 am   **Development of modeling centers in Africa**
Lake Union

Infectious disease mathematical modeling: an Africa-based training to support evidence-based policies
Sylvia Ofori, Harvard T.H. Chan School of Public Health / sylviaofori@hsph.harvard.edu

Background: The use of mathematical modeling of infectious diseases in policymaking is a pressing challenge, especially in Africa, due to its complexity, the lack of enough local expertise in modeling, and the high burden of infectious diseases. Therefore, there is the need to build the capacity to use findings from mathematical modeling studies to inform policy. Through a University of Global Health Equity (Rwanda)-Harvard (USA) partnership, we are implementing a mathematical modeling training program targeted at public health professionals who lead infectious disease research and program implementation in Africa.

Methods: The training uses a deliverable-driven and learning-by-doing model, adapted from previously successfully implemented Intermediate Operational Training Courses. The training consists of two in-person sessions and a practicum session with intensive mentorship. At the end of the training, the trainees will develop a policy brief to support the dissemination of the results of their modeling projects.

Results: Ten trainees were selected for the course: six from Rwanda, two from Kenya, and two from Uganda, with inputs from an advisory committee. Seven trainees work with government institutions, one from an academic organization, and two from NGOs. At the end of the first session in March 2023, trainees developed their compartmental model structures suitable to answer policy questions across four infectious diseases of public health concern.

Conclusions: Mathematical modeling training programs for public health professionals in Africa can be an effective tool for timely policy implementation, research capacity building, and increased research expertise in Africa.

Strengthening capacity in meaningful modeling of infectious disease dynamics: insights from the International Clinics on Infectious Disease Dynamics and Data Program
Juliet Pulliam, SACEMA, Stellenbosch University / pulliam@sun.ac.za

For more than a decade, the International Clinics on Infectious Disease Dynamics and Data (ICI3D) Program has delivered training in infectious disease modeling to hundreds of under-served students, mainly from the Global South. Our current workshops have achieved success through a project-driven approach to learning modeling skills. We emphasize connecting participants across disciplines and countries, both during and after workshops. Many program alumni have grown into independent researchers, including some who helped guide COVID-19 responses in their home countries.

In a recent faculty retreat, we reflected on the lessons of the past decade and laid out plans for the next decade of work. In this talk, we share those lessons, highlight necessary ingredients to grow future capacity, and discuss our own plans for contributing to that future.

Key lessons include the importance of meeting people where they are, the value of repeated interactions with participants, and the need to embed short courses in a larger professional development plan. Future capacity development requires an ecosystem of both educational opportunities and institutional structures that promote long-term growth. Within such an ecosystem, short courses, such as those offered by ICI3D, play a key role of providing both intensive training and cross-fertilization of ideas and approaches from different groups. As we look to our own future, we are focused on bringing on previous generations of participants as future leaders of the ICI3D Program and expanding our efforts to incubate new programs as needs change with new discoveries, approaches, and challenges.

Utilizing mathematical modeling to contain disease outbreaks in Malawi: Emergence of Malawi Centre of Epidemiological and Mathematical Analysis (MACEMA)
Nicholas Adam, MACEMA

Recent infectious diseases outbreaks have been bigger and wider in scope. African health systems already resource constrained are caught unaware oftentimes. For example, we cannot predict when an outbreak would occur or end, there is no proper disease surveillance systems, inefficient public health policies and shortage of modelling capacity. Malawi Centre of Epidemiological and Mathematical Analysis (MACEMA) aims at using mathematical and statistical techniques to improving health in Malawi and beyond by developing surveillance systems that would be able to detect diarrhoeal outbreaks when some thresholds have been reached, and spatially map both diarrhoeal and malaria cases within a defined small area in real time.

Through use of built mathematical model, we aim to use the already captured data about diarrhoea and malaria to learn from the past. We intend to use android phones with built in questionnaire that would be given to the health surveillance personnel at community level to be fed into the model about their dairy data captured during their routine work. Wherever they note a case of

either malaria or diarrhoea, they would follow-up with the patient to point the location using customized google maps in the phones and get location about their community or village, and phone numbers if available. The georeferenced points would be fed into the model and show the exact locations of where disease outbreak was likely. The mobile numbers would be used to trace the locations of the persons as they migrate from one place to another.

We expect to have (1) improved contact tracing and (2) tailored interventions at community levels. We believe that through trainings, mentorship, collaboration with relevant stakeholders, this is achievable. The good, up and running surveillance system that provide warnings about the outbreak would help the stakeholders (3) prepare in advance, understand the routine and areas of focus on containing the outbreaks. Not only that but also (4) prepare the health personnel with knowledge on outbreak containment, as well as (5) get good quality data for future forecasts of pandemics.

9:15–10:45 am   **Maternal, neonatal, and child health**
Lake Union
Facilitator: Anu Mishra, IDM

Building and strengthening the MNCH evidence base
The broad nature of the maternal and child health and well-being field necessitates a strong evidence base that provides stakeholders, policymakers, and researchers a critical view of where progress is needed and where there is potential for change. This session showcases research in maternal, newborn, and child health by providing a more in-depth understanding of the current state and levers for impact, through a data, modeling, and health systems strengthening lens.

Intimate partner violence and malnutrition among women of reproductive age in West Africa: A geostatistical analysis
Ezra Gayawan, Federal University of Technology / egayawan@futa.edu.ng

Women in most sub-Saharan African countries suffer from intimate partner violence (IPV), which greatly affects their health, wellbeing and nutritional intake. We used a geostatistical technique to jointly explore the association between IPV and undernutrition across smaller geographical settings in ten Western Africa countries. Inference was based on a Bayesian approach that relies to Markov chain Monte Carlo simulation. The findings demonstrate spatial clustering in the likelihood of experiencing IPV and being underweight. The clusterings are somewhat similar when each of physical and emotional violence are combined with underweight. The findings provide insight into the location-specific variations that can aid targeted interventions.

Strengthening maternal and women's health systems
Salome Maswime, University of Capetown / salome.maswime@uct.ac.za

No information provided.

Postpartum hemorrhage detection and treatment care pathways and identifying interventions: A decision tree model
Chris Troeger, BMGF / chris.troeger@gatesfoundation.org

Postpartum hemorrhage (PPH) is the leading cause of maternal mortality. Despite effective first response and emergency treatments, PPH is often undiagnosed or untreated and subsequently it was responsible for nearly 40,000 deaths among women in South Asia (SA) and sub-Saharan Africa (SSA) in 2019. Existing or novel intervention strategies should be informed by an understanding of which level of a PPH care cascade PPH burden occurs. We built a decision tree model to segment the population of women who develop PPH into different stages of a care pathway including women at high risk of PPH (moderate/severe anemia or delivery by C-section), delivery location (home, low-level facility, high-level facility with emergency obstetric care), diagnosis and treatment of PPH, and fatal and non-fatal disease burden. The model was used to test counterfactual scenarios such as scale-up of intervention strategies including forecasts to 2040. The model includes uncertainty in the inputs and is calibrated to estimates from the Global Burden of Disease Study 2019. We estimated that approximately 65% of cases and 80% of PPH deaths in SA and SSA were untreated. Deaths due to PPH were forecasted to decline to 23,000 in 2040 in the absence of interventions but improving early detection and first response treatments (uterotonics, massage, tranexamic acid) could avert about 5,300 (95% CI: 3,600–7,800) deaths in 2019 and more than 500,000 (95% CI: 280,000–694,000) cumulative DALYs from 2025–2040. Our results emphasize the avertable burden of undiagnosed PPH and suggest several potential points for intervention on the PPH care pathway.

Systematic estimates of cause-specific mortality for neonates, children and adolescents under 20 in Africa for 2000–2021
Jamie Perin, Johns Hopkins University / jperin@jhu.edu

In the Africa region, there are not generally direct measures of the causes of mortality among neonates or children under 20. However, there are mortality data from Africa in the public health literature, as well as from sample registration systems. Systematic reviews were conducted for neonates and children in five age groups, and separately by sex in the oldest age group, to identify all available cause-specific mortality data meeting minimum criteria in low and middle income countries world wide, including the Africa region. Cause-specific mortality data were modelled by age group (and by sex for older

children) using a Bayesian framework for comprehensive covariate selection in a multinomial setting. Model parameters were used to project cause-specific mortality by country and age, which were combined with WHO-estimated mortality for measles, tuberculosis, and crisis-related mortality for years 2000 to 2021. Systematic reviews identified over 400 studies from Africa reporting cause-specific mortality. The resulting modelled estimates indicate that acute respiratory infection (ARI) is the number one cause of death among children under 5 in the Africa region in 2021 (at 12.5, 11.8, and 10.1 per 1000 live births), and that malaria is the number one cause of death in children and adolescents 5–19, followed by diarrhoeal diseases and injuries (at 0.8, 0.6, and 0.5 deaths per 1000). These estimates can inform policy initiatives and health programs in Africa both regionally and in specific countries. These estimates have limitations and would benefit from additional high quality mortality data from Africa.

Simulation-based estimates and projections of global, regional and country-level maternal mortality by cause

Zach Ward, Harvard T.H. Chan School of Public Health / zward@hsph.harvard.edu

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9:15–10:45 am   **Modeling HIV prevention policies**
Lake Washington
Facilitator: Josh Herbeck, IDM

Adherence to the Dual Prevention Pill for HIV and Contraception: Identifying thresholds for net benefit and cost-savings using mathematical modeling.

Masabho Peter Milali, Grossman School of Medicine / masabho.milali@nyulangone.org

Women in sub-Saharan Africa experience the world's highest rates of unintended pregnancy and HIV infection. The Dual Prevention Pill (DPP) under development for HIV prevention and contraception, could help address these dual health risks. We adapted EMOD-HIV and evaluated the cost-effectiveness, net benefit, net harm, and cost-savings of the DPP among different user populations and adherence levels in South Africa and western Kenya. We focused on the primary DPP user population of current oral contraceptive (OC) users aged 25–49, as well as adolescent girls and young women (AGYW) aged 15–24, female sex workers, and women in serodiscordant relationships. For each population and adherence level, ranging from 5% to 95% (with 10% interval), we estimated the disability-adjusted life-years (DALYs) averted, as well as the incremental cost of using DPP in comparison to oral contraceptive use alone (with 90% adherence) over a 30-year time horizon and 3% annual

discount rate in 2021 USD. We find that providing DPP to OC users in South Africa and western Kenya would be harmful if adherence rates drop below 30% and 73%, respectively. While DPP would provide benefits at an additional cost, it would not become cost-saving for OC users in both countries. However, DPP would be net beneficial with adherence rates as low as 5% and 7%, and it would be cost-saving with adherence rates of 81% and 85%, respectively, among serodiscordant couples in both countries. In South Africa, DPP would be cost-saving even with adherence as low as 23% among female sex workers.

Community scale-up of oral HIV PrEP in Western Kenya: a health and economic modeling analysis

Rachel Wittenauer, University of Washington / rwitten1@uw.edu

Background: The Kenya Ministry of Health's strategic plan to combat HIV includes expansion of oral PrEP access via differentiated service delivery channels (e.g., community pharmacies). Understanding the relative benefit of prioritizing different subgroups for PrEP can inform demand generation strategies to optimize PrEP scale-up.

Objective: Evaluate the cost-effectiveness of community-based oral PrEP scale-up comparing multiple implementation scenarios.

Methods: We parameterized EMOD-HIV (IDM, Gates Foundation) to simulate increasingly broad PrEP coverage scenarios: 1) current PrEP coverage (counterfactual), 2) current coverage + female sex workers and serodiscordant couples, 3) scenario 2 + individuals with ≥2 concurrent partners 4) scenario 3 + higher coverage of adolescent girls and young women, 5) scenario 3 + men and women aged 18-45 years. Primary cost data were derived from pharmacy-based PrEP trials in Kenya and published literature. We calculated the incremental cost-effectiveness ratio (ICER) in 2021 USD/DALY averted and assumed a willingness to pay threshold of $1,000/DALY averted. We conducted the analysis from both the payer and societal perspective over a 20-year time horizon using a 3% discount rate.

Results: The scenario targeting the narrowest group of individuals (scenario 1) was cost-saving from the societal perspective. ICERs became increasingly higher with broader coverage. For all scenarios, PrEP scale-up was more cost-effective when considering the societal perspective than only the payer perspective. These results can inform priority-setting for PrEP expansion programs.

Comparison of HIV self-test distribution modalities to reduce HIV transmission and burden in western Kenya: a mathematical modeling study
Hae-Young Kim, Grossman School of Medicine / hae-young.kim@nyulangone.org

Introduction: HIV self-testing (HIVST) is an effective and acceptable method of HIV diagnosis. In this study, we compared the impact of different HIVST distribution modalities on population-level HIV outcomes in western Kenya.

Methods: We used EMOD, an agent-based network transmission model, and simulated three HIVST distribution modalities: 1) secondary distribution to male partners via women who attend ANC visits ("ANC"); 2) secondary distribution to partners of index patients newly diagnosed with HIV at health facilities ("index"); and 3) distribution to patients who attend outpatient clinics ("outpatient"). We projected the number of HIV tests, infections, deaths, and disability-adjusted life-years (DALYs) by HIVST distribution modalities, compared to the standard of care (SoC).

Results: Over the 30-year period (2022–2052), the maximum demand for HIVST was 11.4 million tests for ANC, 15.8 million for index, and 37.8 million outpatient testing. Meeting demand for each modality could increase annual testing rates by up to 12% (n= 1,767,386) with ANC, 20% (n= 1,872,266) with index, or 42% (n=2,224,939) with outpatient HIVST, compared to SoC (n=1,566,364). The number of HIVST needed per additional HIV infection averted was 100 with ANC, 63 with index, and 91 with outpatient HIVST. The number of HIVST needed per additional HIV-related deaths averted was 236 with ANC, 138 index, and 156 with outpatient HIVST.

Conclusion: Secondary distribution to partners of index patients could prevent the most HIV infections and HIV-related deaths, while outpatient HIVST could prevent the most infections and deaths if demands were met. HIVST can be an important strategy to improve uptake of testing and long-term population health effects.

Universal or targeted HIV prevention for HIV-1 in Africa? Evidence from phylogenetic studies and modelling.
Christophe Fraser, University of Oxford / christophe.fraser@bdi.ox.ac.uk

HIV incidence is decreasing in sub-Saharan Africa (SSA), but not as fast as expected given progress made to reach the UNAIDS treatment targets. This suggests that a substantial fraction of new infections is coming from virally unsuppressed persons with disproportionately high risk of onward transmission compared to the general HIV positive population.

Highly effective biomedical prevention interventions such as oral and long-acting PrEP are most feasible when focused on relatively small and defined groups of people at high risk of transmission Phylogenetic and clustering approaches have been used to identify the demographic and behavioural characteristics of these groups and, in the Global North, to focus prevention efforts on fast-growing clusters identified in near-real time.

When analysing HIV genomic PANGEA datasets from Zambia, Botswana and Uganda and comparing them with a European and a UK dataset, we find an absence of large clusters in the sub-Saharan African epidemics while controlling for sampling fraction. The observed cluster distributions and are in line with predictions from the PopART IBM model calibrated to the Zambian epidemic, and somewhat lower than predictions from EMOD calibrated to eSwatini.

The absence of large clusters makes it less likely that a substantial proportion of new infections is driven by a small key population, but it does not exclude the existence of high-risk groups. It does suggest however that focussing on small demographic groups for prevention efforts is likely to have a smaller effect on population-wide incidence than cluster-busting approaches currently being deployed in European and North American settings.

9:15 – 10:45 am   **Introducing the Africa CDC Continental Framework for Strengthening Mortality Surveillance Systems: Current and future agendas**
Greenlake
Facilitators: Erin Nichols, CDC / Andre Lin Ouedraogo, IDM

Introducing the Continental Framework for Strengthening Mortality Surveillance Systems in Africa
Emily Barigye Atuheire, Africa Centres for Disease Control and Prevention / Atuheiree@africa-union.org

Introduction: Accurate and timely information about the number and causes of death enables countries to formulate right policies, effectively plan and implement interventions to reduce preventable deaths and improve health outcomes. In Africa, the availability of data and timley information on deaths and their causes is a challenge, especially observed during COVID-19 pandemic. Most African countries have weak civil registration systems and lack nationwide death recording systems. Further, many African countries have several fragemented and siloed mortality data sources that collect data on disease specific and population specific topics such as the maternal perinatal death surveillance and reaponse (MPDSR), cancer registries, etc. These fragmented systems do not often feed into a central repository at the national

level. Thus producing valid and timely national and sub national data remains a significant challenge.

Rationale: In September 2022, Africa CDC launched the continental framework (CF) for strengthening mortality surveillance systems in Africa. The main objective of the framework is to provides guidance on how to harmonise, standardise and integrate mortality data into national repositories in alignment with international standards.

Scope: The CF draws from both global and regional policies and agendas to propose a coordinated and integrated approach for streamlining mortality data reporting in African countries. It is intended to help countries to develop and enhance holistic mortality surveillance systems that generate information for public health programming and policies while supporting official registration of these events. Further, it is aimed at increasing the availability of high-quality and timely mortality data that can be used for public health action across the African continent. Finally, it serves as a catalyst for countries to work towards achieving regional and global development goals.

Target Audience: The framework is intended to be used by relevant policy makers and programme implementers in the health sector, their counterparts in the civil registration and vital statistics sector, development and implementing partners and civil society organizations.

COVID-19 mortality surveillance in the community — Lusaka, Zambia, 2021
Priscilla Kapombe, Ministry of Health Zambia / priscillakapombe@gmail.com

COVID-19 deaths likely exceeded the number captured in official statistics in Zambia because of limited testing and incomplete death registration. SARS-CoV-2 testing among deceased persons can provide insight into knowledge gaps about mortality from the virus. We described a COVID-19 mortality sentinel surveillance system in Lusaka, Zambia.

We analyzed SARS-CoV-2 test results among deceased persons at the University Teaching Hospital (UTH) in Lusaka, Zambia, where >90% of deceased persons who die in the community are taken. There, trained surveillance officers perform a verbal autopsy (VA) with relatives using a questionnaire about the circumstances proximal to death. A probable underlying cause of death (UCOD) is assigned based on VA responses. During January-August 2021, deceased persons at UTH morgue were tested for SARS CoV-2 using polymerase chain reaction and rapid diagnostic tests, subject to testing supplies availability. We analyzed the UCODs and other factors based on COVID-19 results.

Of 6,926 deceased persons undergoing VA, 3,826 (55.2%) were tested for SARS-CoV-2 postmortem. Of these, 154 (4.0%) tested SARS-CoV-2 positive, with;

152 of these (98.7%) died in June and July 2021, which was during the Delta wave (postmortem positivity during June-July: 10.7%). Deceased persons testing SARS-CoV-2 positive were older than those testing negative but the difference in HIV positivity was not statistically significant (Table). Most (79.2%) persons testing positive reportedly had ≥1 classic COVID-19 symptom and most (76.0%) were reportedly tested for COVID-19 prior to death. Among persons testing SARS CoV-2 positive, the most common UCODs were respiratory tract infections (24.0%), acute cardiac disease (16.9%), other cardiac diseases (14.3%), and stroke (7.1%).

A notable portion of deaths in the community tested SARS-CoV-2 positive during the Delta wave in Zambia. Most persons testing positive postmortem displayed classic symptoms and were tested before dying in the community, potentially indicating strained medical services during waves. In addition, the high proportion of cardiac disease and stroke among deceased persons testing SARS-CoV-2 positive might reflect the hypercoagulable state during severe COVID-19. Preventive measures, early supportive treatment, and availability of therapeutics like antivirals could avert future mortality. Mortality surveillance during outbreaks can provide useful information to inform public health and clinical care.

Sample Registration System as a strategy for immediate and long-term availability of representative mortality data in Mozambique
Celso Monjane, National Institute of Health, Mozambique / celso.monjane@ins.gov.mz

Mozambique launched in 2017 the Countrywide Mortality Surveillance for Action (COMSA) also known as Community Observation System for Health and Vital Events (SIS-COVE) to generate annually-updated mortality rates, causes and determinants of deaths at national and provincial levels. SIS-COVE is a sample registration system with representativeness at national and provincial level that collect data on pregnancies, births, and deaths, with cause of death assessment using updated WHO forms to implement verbal and social autopsies using mobile technology for real time data collection.

With its potential, SIS-COVE shown its power in supporting the integrated disease surveillance, the civil registration and vital statistics (CRVS) system, the COVID response and recently the outbreak of cholera in Mozambique, where using SIS-COVE was possible to identify excess mortality in a short time and identify diarrhea as the main cause of death in a remote community. An ongoing CRVS pilot in Inhambane province to assess the community workers willingness to fill-out the CR forms has shown that the SIS-COVE increased by 26% the births registration and the community workers can correctly fill-out the CR forms. Current interoperability with CRVS platform and HMIS to

support civil registration and improve access to data at district and provincial level is also running.

SIS-COVE is the best immediate and long-term strategy to ensure the availability of representative data for CRVS and a strong data repository to improve mortality and causes of death estimations to fill data gaps in Mozambique.

Integration of mortality surveillance systems into CRVS in Rwanda
Godfrey Ngoboka, Ministry of Health, Rwanda / gngoboka@dataforhealth.org

Introduction: Timely and accurate mortality data are important for monitoring health interventions and responding to health threats and epidemics. Rwanda had multiple fragmented mortality surveillance systems for the collection of mortality data to address public health issues. In 2020, the government decided to integrate the health sector with the civil registration authority to ensure real-time, continuous, and accurate mortality and causes of death information. This paper presents the experiences and best practices in establishing integrated MS systems with the CRVS system in Rwanda.

Approach: In 2020, the government of Rwanda approved the regulations that allow the health sector to timely notify and register deaths and causes of death (COD) in the digital CRVS system for deaths that occurred in the facility within 30 days of occurrence and deaths that occurred outside health facilities into the lowest level of administration at the Cell level. The verbal autopsy (VA) is integrated with the routine CRVS system to improve reporting of COD data for community deaths. The amendment of the regulations has led to an increase in registration coverage from 446 to 3,220 registration points across the country. The health sector adopted the international form of MCCD in all public and private hospitals in Rwanda to improve the reporting of COD information for public health decision-making.

Results: The enablers for the integration of MS systems with the CRVS were: 1) a situational assessment and process mapping to check the country readiness; 2) a review of the relevant legal framework to unlock the bottlenecks and set the ground for the integrated systems; 3) data standardization across all MS systems, and 4) engaging all relevant CRVS stakeholders to understand their needs, 5) CRVS Governance and coordination, 6) availability of high penetration of internet services at the national level, and 7) the commitment of partners in supporting the integrated MS systems with CRVS.

Conclusions: Integrating MS systems with the CRVS system is a key undertaking for the routine collection of nationally representative mortality statistics and COD information for evidence-based decision-making. While a systematic review of the existing mortality reporting systems provided critical information in the design of national MS systems.

Scoping review of digital tools for mortality surveillance in sub-Saharan Africa
Malick Kante, Johns Hopkins University / akante1@jhu.edu

Sub-Saharan Africa (SSA) is the region of the world with the highest rates of mortality. However, most of these deaths are not registered, and little is known about what caused them. This situation underscores an assessment of the existing tools needed to build well-functioning, digitized, systems that collect data on death and cause-of-death. To better understand the use and the feature of digital tools for a digital mortality surveillance system (MMS), we conducted a) a landscape and scoping review of platforms and digital tools at the global and selected country levels, b) a literature review focused on published articles on 2005–2022 and c) 82 key informant interviews with global and country stakeholders.

Our results depicted 10 MMS that are currently being implemented in selected countries, with different levels of maturity and experience in the use of digital solutions. Within countries, capacity to develop interoperable and scalable systems, interoperability between existing systems and tools were limited. Yet, the surveyed institutions expressed their interests in obtaining reliable and timely representative national and subnational data for monitoring mortality and their causes, although recognizing financial support could a major constraining factor.

This assessment illuminates the core functions of digital tools that can be optimized for MSS, built up from existing country digital solutions and surveillance systems, and linked and interoperable with civil registration and vital statistics systems (CRVS). Other functions include improvements in data standards, quality, security, and governance. A central data depository with the skilled personnel should also be considered.

9:15–10:45 am   **Malaria modeling for sub-national tailoring**
Elliot Bay
Facilitator: Amelia Bertozzi-Villa, IDM

Developing a critical mass of data scientists and mathematical modelers to support National Malaria Control/Elimination Programs
Samson Kiware, Ifakara Health Institute, Dar es salaam, Tanzania / skiware@ihi.or.tz

National Malaria Control Programs (NMCPs) in sub-Saharan Africa increasingly recognize the value of modeling for decision making. However, efforts to integrate modeling into routine planning and decision-making are hampered by a lack of sufficient modeling expertise in most malaria-endemic countries

in Africa. We highlight initiatives implemented to develop a critical mass of data scientists and mathematical modelers in Tanzania — that can be attached or easily accessible to NMCP to provide the required technical support. We present specific examples of the capacity strengthening initiatives and technical support provided to NMCPs. Initiatives that may be adapted in other malaria endemic countries to strengthen the required capacity.

Modeling to support decisions about the geographic and demographic extensions of seasonal malaria chemoprevention in Benin
Jeanne Lemant, Swiss Tropical and Public Health Institute, University of Basel / jeanne.lemant@swistph.ch

Seasonal malaria chemoprevention (SMC) in Benin targeted more than 400 000 children under 5 in the northern departments of Alibori and Atacora in 2021. The Benin National Malaria Control Program (NMCP) recently considered an extension of SMC, either demographically to children aged 5 to 10 in the same departments, or geographically to children under 5 in new departments. As neither extension had been tested before, the NMCP turned to modeling to estimate their impact. The model OpenMalaria was calibrated to represent the history of malaria interventions, the transmission risk, and the population age structure in Benin. The already planned future interventions were simulated together with the two extensions of SMC. The model predicted that the demographic extension of SMC could avert on average 4.6 severe cases per 1000 targeted children between 2024 and 2026, and the geographic extension between 13 and 14.3, depending on the targeted department. To be less cost-effective than the demographic extension, the geographic extension should thus be three times more expensive, when 2021 costs indicate it would cost only 40% more. Numbers of severe cases averted per targeted child were similar between operational zones of departments considered for the geographic extension, probably due to similar transmission risks. These findings led to recommend targeting highly populated zones in priority, as SMC in the three most populated zones could avert as many severe cases as in the six other zones. Modeling allowed not only to choose the geographic over demographic extension, but also to quantify their comparative impact.

Use of mathematical modeling to inform insecticide-Treated bednet distribution campaigns in Haiti
Billy Bauzile, Swiss Tropical and Public Health Institute / billy.bauzile@swisstph.ch

Haiti has made significant progress towards malaria elimination. In 2021, the number of presumed and confirmed malaria were 10642, down from over 84153 in 2010. As cases have fallen, they have become increasingly concentrated; thus, interventions such as insecticide treated bednets should be strategically targeted to reach maximal epidemiological impact.

In order to identify the optimal set of communes in which bednet distribution would result in the most cases averted through the once-every-three years distribution campaign, we use a metapopulation model that was fitted on historical reported cases between 2014 and 2021 and on spatial data estimates from the Malaria Atlas Project. The model includes past bednet distributions, case management indicators and human inter-commune mobility as informed by mobile phone data. Several versions of the model are compared to evaluate the sensitivity to the input data. The fitted model was used to identify the communes in which the intervention would have the most impact at the national scale. The model ranked 125 communes, of which we selected the top 25 given the diminishing benefit of each additional commune and the defined number of bednets the country would receive. The selected communes accounted for 82% of observed cases in 2021.

As this model combines the effects of connectivity, past interventions and local trends in transmission intensity, it provides a useful additional piece of information in prioritized communes for interventions such as LLIN distributions and communication campaign aiming at increasing bednet usage. The results provided insights about the impact of the targeted communes at the national scale and identified communes to be targeted with communication campaign. Finally, this calibrated model provides an additional tool to support routine campaign planning including the 2023–2026 Global Fund application.

Analyzing malaria in Indian states and modeling future trends
Usha Ananthakumar, SJMSOM, IIT Bombay / usha@som.iitb.ac.in

Malaria is a major public health problem in India that places a significant burden on the population and the health care system. This study utilizes data from the period of 1997–2022 to examine the incidence of malaria and associated mortality across different states in India. While there has been an overall decline in the prevalence of malaria cases during this period, the decline has not been uniform across all states. States which significantly impact the national malaria figures are identified, and comparative analyses of regional demography and climatic conditions are performed. This is done using EMOD, an agent-based stochastic disease modeling tool that is used to simulate the dynamics of malaria and a variety of other diseases. Furthermore, current demographic and environmental trends for these states, combined with our knowledge of malaria pertaining to its incubation, larval habitat, migration, immunity, infectivity, and parasite dynamics, are used as input to EMOD to model future trends. The results could provide valuable insights for policymakers and health officials in India to better target their intervention strategies and resources towards reducing the burden of malaria in the country.

Mathematically modelling the impact of case management at border areas on malaria transmission in the MOSASWA region
Vusi Mpendulo Magagula, University of Cape Town / mggvus002@myuct.ac.za

Eswatini and South Africa are in the path of malaria elimination but however, they share borders with Mozambique who has a high incident rate of malaria. Studies conducted show that most of the malaria cases recorded in both South Africa and Eswatini are imported cases from Mozambique. For these countries to attain their goal of malaria elimination, they need to prioritize case management at border areas as their main strategy of malaria elimination. Will the use of rapid antigen tests at the border gate areas accelerate the elimination of malaria in the MOSASWA region? What impact will border management have on the malaria transmission in these countries? A Nonlinear stochastic ordinary differential equation model is used to simulate the impact of case management at border areas on malaria transmission in the MOSASWA region which consists of eastern Eswatini, the southern Mozambican provinces of Maputo, Gaza and Inhambane, and the north-eastern districts of the South African provinces of KwaZulu-Natal, Mpumalanga, and Limpopo. The results show us that malaria transmission can be reduced significantly if rapid antigen tests are conducted at the borders in the MOSASWA region. The results show us that malaria cannot be eliminated by this intervention but can reduce the malaria burden significantly in Eswatini and South Africa endemic regions. Case management at border areas is a vital strategy for malaria elimination in South Africa and Eswatini. However, malaria cannot be eliminated and hence this intervention combined with other interventions can contribute towards malaria elimination in the region.

| 11:00 am – 12:30 pm | **Family planning & fertility**
 Lake Union
 Facilitator: Marita Zimmermann, IDM |

Exploring vulnerability and family planning
This session brings together experts in family planning and empowerment to examine vulnerability components and their influence on family planning and contraceptive use. Vulnerability has a profound interaction with family planning, as vulnerable women tend to experience more unintended pregnancies as well as adverse pregnancy and birth outcomes. Vulnerability may be experienced due to social inequities, lack of autonomy, or young age, among other factors. In this session, we explore how women in these vulnerable populations use family planning. Better understanding of contraceptives use among these groups of women may allow us to better target interventions to increase access to those who need it most.

Associations between light-touch enhancements and postpartum family planning take-up among young first time mothers in Tanzania: a quantitative analysis
Jennifer Seager, George Washington University / jseager@email.gwu.edu

No information provided.

Measuring inequity in family planning using Bayesian hierarchical sparse regression models
Leontine Alkema, University of Massachusetts Amherst / lalkema@umass.edu

No information provided.

Recent work: Demographic analysis (with Jamaica) on fertility among wealthier women in SSA; Using modern contraception while wanting a child. What does "overmet" mean for the human rights-based approach in Burkina Faso? A 2018 PMA2020 data analysis.
Moussa Lonkila Zan, ISSP / lonkilazan@yahoo.fr

No information provided.

| 11:00 am – 12:30 pm | **Gender disparities & comorbidities HIV infection**
 Lake Washington
 Facilitator: Adam Akullian, IDM |

Modeling the co-occurrence of HIV and Depression to Evaluate the Impact of Mental Health Care on HIV Outcomes
Daniel Citron, NYU Grossman School of Medicine / daniel.citron@nyulangone.org

Common mental disorders, such as anxiety and depression, are a leading cause of morbidity in sub-Saharan Africa (SSA). Depression in particular is highly prevalent among people living with HIV (PLHIV), and the two conditions are known to interact in complex and bidirectional ways. Individuals with depression are more likely to engage in risky sexual behaviors, putting them at a higher risk of HIV acquisition. Furthermore, depression can disrupt the HIV care cascade, resulting in worse health outcomes. On the other hand, successful HIV treatment can improve depressive symptoms. Treatments for depression such as interpersonal therapy are promising in SSA, and present an opportunity to both treat depression and improve HIV care outcomes.

We have developed a mechanistic model of the co-occurrence of HIV and depression to simulate the population dynamics of both conditions and evaluate how treating depression may improve HIV outcomes. The model is based on EMOD-HIV, an agent-based model of HIV transmission in Kenya, and

also includes a model of depression which accounts for incidence, recovery, remission and treatment history. We have conducted a systematic review to quantify how depression interacts with HIV risk, treatment initiation, and treatment outcomes. Each of these interactions has been incorporated into EMOD-HIV to model to complex interactions between the two health conditions.

Our modeling results suggest that treating depression leads to better overall HIV outcomes, reducing HIV incidence and improving treatment efficacy among PLHIV. This project demonstrates the utility of EMOD-HIV's agent-based modeling framework for investigating interactions between infectious and non-communicable diseases.

Translating community-level HIV prophylactic drug concentration into epidemic impact in western Kenya: mathematical modeling analysis of the Monitoring PrEP in Young Adult women (MPYA) study.
David Kaftan, NYU Grossman School of Medicine / david.kaftan@nyulangone.org

Women in sub-Saharan Africa have experienced the majority of global HIV infections, but their adherence to oral pre-exposure prophylaxis (PrEP) is variable. The Monitoring PrEP in Young Adult women (MPYA) study offered PrEP to 18–24-year-old women in the Nyanza region of western Kenya and measured PrEP drug concentrations in dried blood spots (DBS) and self-reported sexual behavior. We modeled (1) PrEP effectiveness in MPYA, given measured adherence and its alignment with risk, (2) coverage of the MPYA intervention required to reduce incidence to <0.1% per person-year by 2040 in Nyanza, and (3) drug concentrations that would indicate Nyanza is on track to <0.1% incidence.

We calculated MPYA PrEP effectiveness by age and number of sexual partners by translating DBS concentrations of tenofovir diphosphate (TFV-DP) into incidence reductions using previously analyzed pooled randomized controlled women's PrEP trials. Using the agent-based model EMOD-HIV, we simulated MPYA reaching different proportions of young women in Nyanza. Reversing the PrEP concentration-to-efficacy calculation, we estimated drug concentrations associated with <0.1% incidence by 2040. In sensitivity analysis, we altered the concentration-efficacy relationship to assume no PrEP efficacy at DBS concentrations <400 fmol TFV-DP per punch.

The MPYA intervention cut incidence 33% among those enrolled. MPYA would need to reach ≥35% of young women to reduce incidence in Nyanza to <0.1% by 2040. This would translate into 18% of young women having ≥400 fmol tenofovir per DBS punch. Results were not sensitive to effectiveness of low DBS PrEP concentrations.

PrEP can significantly reduce HIV incidence among young women in Nyanza. Because low-adherence PrEP use makes little impact, adherence monitoring is needed to assess population-level protection.

Enhanced cervical cancer and HIV interventions reduce the disproportionate burden of cervical cancer cases among women living with HIV: A modeling analysis
Darcy Rao, BMGF / darcy.rao@gatesfoundation.org

No information provided.

Growing gender disparities in HIV infection in Uganda: sources and policy implications
Kate Grabowski, Johns Hopkins University / mgrabow2@jhu.edu

HIV incidence in Africa has historically been concentrated among girls and women 15–24 years, but as new cases decline with HIV interventions, population-level infection dynamics may shift by age and gender. Here, we integrated population-based surveillance and longitudinal deep-sequence viral phylogenetics to assess how HIV incidence and the population groups driving transmission have evolved over a 15-year period from 2003 to 2018 in Uganda. Viral suppression increased more rapidly in women, resulting in 1.5–2-fold higher virus suppression rates in women with HIV by 2018 across age groups. Incidence declined more slowly in women than men, increasing pre-existing gender disparities in HIV transmission. Age-specific transmission flows shifted, with the contribution of flows to girls and women aged 15–24 years from older men declining by approximately one third and the contribution of flows to women aged 25–34 years from men aged 0-6 years older doubling from 2003 to 2018. We estimate closing the gender gap in viral suppression could have reduced HIV incidence in women by half in 2018 and ended gender disparities in incidence. This study suggests male-targeted HIV programs aimed at closing the emerging gender gap in population-level HIV suppression rates are critical to reduce incidence in women, close gender disparities in infection burden, address stigma associated with gender inequities in HIV infection, and improve male health in Africa.

11:00 am –
12:30 pm

Verbal autopsy IT tools: Software developers and modelers come together to accelerate certification of cause of death in LMICs
Greenlake
Facilitators: Andre Lin Ouedraogo, IDM / Isaac Lyatuu, Ifakara Health Institute

Solution in Scarcity: Verbal autopsy and verbal autopsy manager (VMan), tools to increase coverage and availability of cause of death information in resource-poor settings: A case of Iringa Region in Tanzania
Isaac Lyatuu, Ifakara Health Institute / ilyatuu@ihi.or.tz

Knowledge on what do people die from and circumstances leading to death is an important information to public health surveillance, disease monitoring and health planning. Such information can inform interventions, decision-making processes, contribute to policy formulation and add to improve the quality of life, guide investment projects and contribute to achieving sustainable development. Despite such potential, most places in LMIC including Tanzania lack such information. Over 70% of deaths in Tanzania are not reported in civil registration and vital statistics and/or misses cause of death. Most of these deaths occur outside health facilities, in community settings where there exist no medical professional or mechanism to ascertain cause of death. On the other hand, verbal autopsy is a method for determining probable cause of death where there is no formal medical record or death certificate is not available. VA involve interviewing deceased' next of kin to gather information on symptoms, signs and circumstances of death. Such information is then processed by trained clinicians or computational methods to assign probable cause of death. Here we present how verbal autopsy and verbal autopsy manager (VMan) has been implemented in the Iringa region in Tanzania to resulted into increasing coverage and availability of COD information in the Iringa region Tanzania.

Intro to EasyVA
David Kong, IDM / david.kong@gatesfoundation.org

The Easy Verbal Autopsy, or EasyVA, platform is a user-friendly, web-based interface enabling clinicians and algorithm-based applications to accelerate certification of cause of death.

Here we will demonstrate the utility of EasyVA, user roles, the cause of death (CoD) workflow, data submission and export, and explain the VA algorithm tools it supports.

Users will also learn about the architecture of EasyVA for future collaboration and expansion. There will be additional live demos for hands-on use of the tool

Towards robust and generalizable cause-of-death assignment algorithms using verbal autopsies
Richard Zehang Li, University of California, Santa Cruz / lizehang@ucsc.edu

Abstract: Verbal autopsy (VA) is a survey-based tool for assigning a cause to deaths when traditional autopsy and cause certification are not available. It has been routinely used for mortality surveillance in low-resource settings. In the last decade, several statistical and machine learning methods for inferring cause of death using VA data have been developed. We will discuss a new class of statistical methods to assign causes of death and estimate population-level cause-specific mortality fractions, accounting for potential dataset shift across different populations. We will demonstrate that our model tackles the important issue of generalizability in VA algorithms and show improved assignment accuracy for out-of-domain cause-of-death classifications. We will also discuss the challenges using reference deaths data subject to non-ignorable selection mechanisms for training VA algorithms.

Correcting for verbal autopsy misclassification bias in cause-specific mortality estimates
Abhi Datta, Johns Hopkins University / abhidatta@jhu.edu

Verbal autopsies (VA) are extensively used to determine cause-of-death (COD) in many low and middle income countries. However, COD determination from VA can be inaccurate. Computer-coded-verbal-autopsy (CCVA) algorithms used for this task are imperfect and misclassify COD for a large proportion of deaths. If not accounted for, this misclassification leads to biased estimates of cause-specific mortality fractions (CSMF), a critical piece in health-policy making. We discuss how to estimate and use CCVA misclassification rates to calibrate raw VA-based CSMF estimates to account for the misclassification bias in Bayesian hierarchical model. We review the current practices and issues with raw COD predictions from CCVA algorithms and provide a complete primer on how to use the VA calibration approach with the calibratedVA software to correct for verbal autopsy misclassification bias in cause-specific mortality estimates. We use calibratedVA to obtain CSMF for child (1–59 months) and neonatal deaths using VA data from the Countrywide Mortality Surveillance for Action Mozambique (COMSA) project in Mozambique.

11:00 am –
12:30 pm

Malaria modeling for next generation interventions
Elliot Bay
Facilitator: Caitlin Bever, IDM

Modelling the innovative 1,7—malaria reactive community-based testing and response (1,7 mRCTR) strategy.

Victoria James Githu, Ifakara Health Institute / vjames@ihi.or.tz

As the World Health Organization emphasizes the importance of transforming the malaria surveillance response strategy as a core intervention through its T3 (Test-Treat-Track) initiative, a pilot study in Tanzania on the adoption of the '1-3-7' China's individual-based model strategy resulted into a 1,7—malaria reactive community-based testing and response (1,7-mRCTR) strategy to fit to Tanzanian transmission setting. 1,7-mRCTR has proved to reduce the odds of malaria infection by 66% and prevalence declined by 81% in a pilot study in Rufiji, Tanzania. Scaling up of this strategy requires proper planning; hence this study proposes to use the OpenMalaria simulation platform to predict scenarios for successful implementation of 1,7-mRCTR in different malaria transmission settings to maximizing its impact. The achievements of this study are firstly, to determine the frequency required to implement 1,7 mRCTR approach at different baseline points to attain different malaria reduction targets; secondly, to obtain the minimum coverage required to attain specific targets; and thirdly to evaluate optimal malaria control interventions (i.e. Long Lasting Insecticide Nets (LLIN), indoor residual spraying (IRS), mass drug administration (MDA) and larva source management (LSM)) in combination with the 1,7 mRCTR approach that can be used to achieve malaria reduction and/or elimination in different epidemiological settings. Finally, we will use this analysis to build a computational tool (R-shiny app) to predict strategies (frequency to implement 1,7 mRCTR and coverage to target) at different malaria transmission settings required to attain malaria reduction targets to be used by decision makers for scaling up 1,7 mRTCR strategy.

Mixtures for insecticide resistance management: exploring dosage, cross resistance, and pre-existing resistance.

Neil Hobbs, Liverpool School of Tropical Medicine / neil.hobbs@lstmed.ac.uk

Next generation mixture long-lasting insecticide treated bednets (LLINs) are currently outperforming standard pyrethroid only LLINs in field trials. Although these mixture nets are currently mix a pyrethroid and a novel insecticide. Mixtures have frequently come out as the best performing IRM strategy, with the important prerequisites of limited resistance to both insecticides being deployed at full-dose, minimal resistance and no cross resistance between the insecticides.

Using a dynamic model assuming polygenic resistance, we first compare mixture deployments versus monotherapy deployments across a range of initial pyrethroid resistances and mixture dosages, and across a wide biological parameter space. Second, we explore the impact of cross resistance on mixtures versus monotherapy rotations to slow the rate of evolution of insecticide resistance. We evaluate IRM strategies on their effectiveness of slowing the evolution of resistance.

We find full-dose mixtures are most beneficial from an IRM perspective when there is limited resistance to either insecticide, with this benefit falling as resistance increases. Half-dose mixtures can lead to higher levels of resistance than if the equivalent insecticides were deployed as monotherapies in rotation, especially in the presence of cross resistance. Deploying novel insecticides in mixture with pyrethroids is a viable IRM strategy and prolongs the effectiveness of the novel longer than deploying the novel insecticide as a monotherapy. How this translates to longer term disease control is unclear.

Pharmacological modelling of malaria drug treatment and evaluation of drug efficacy trials

Ian Hastings, Liverpool School of Tropical Medicine / ian.hastings@lstmed.ac.uk

Malaria parasites in a patient treated by an antimalarial drug typically decline to sub-patent levels within 48 hours and, if not completely cleared by the drug, reappear as a patent infection up to several weeks later. This long period of sub-patency is caused by the drugs' long half-lives supressing parasite growth. We have been developing and applying pharmacological modelling to infer these sub-patent dynamics. A problem in drug trials is that if a malaria infection occurs 2 to 6 week post-treatment, it is difficult to tell whether it is a drug failure, or is a new infection acquired during follow-up. Molecular analysis of the infection at treatment and at re-appearance can, in principle, distinguish drug failures from new infections. However, the genotyping methods routinely used in the field are insensitive and our pharmacological/genotyping modelling suggests that current analytic methods probably miss around half of the drug failures i.e. that failure rates in high transmission areas are probably twice that estimated by current WHO-recommended methodology. This is important given current concerns about the spread of antimalarial drug resistance in Africa and the analyses recommend and suggest improved methods of surveillance.

More details in: Hastings, I. M. and I. Felger (2022). ""WHO antimalarial trial guidelines: good science, bad news?"" Trends in Parasitology 38(November): 933-941. DOI 10.1016/j.pt.2022.08.005

Application of Vector Control Optimization Model (VCOM) on eave ribbons for malaria vector control in Kilombero Valley, Tanzania

Ismail Nambunga, Ifakara Health Institute / inambunga@ihi.or.tz

Despite significant progress against malaria, the use of insecticide-treated nets (ITNs) and indoor residual spraying (IRS), are becoming increasingly vulnerable due to insecticide resistance and outdoor biting by mosquitoes. Further progress is required to identify the supplementary tools to combine effectively with ITNs to reduce mosquito exposure. Using the Kilombero Valley as a case study, the Vector Control Optimization Model (VCOM) was adapted and extended to simulate the impact of adding eave ribbons treated with spatial repellent (ER) with ITN. Simulation was conducted to assess the impact of varying coverage of ER on the entomological inoculation rates (EIR) generated by two common vectors, Anopheles arabiensis and Anopheles funestus. Finally, the impact of introducing ER on the combined EIR from An. arabiensis and An. funestus was assessed to identify scenarios in which values fell below 1; the likely threshold required for malaria interruption. ER was predicted to substantially reduce the EIR when combined with 80% ITN coverage. However, the nature of the impact varied notably between vector species. ER was predicted to have a much larger effect on An. funestus than An. arabiensis. Additionally, in the situation where EIR from both An. arabiensis and An. funestus was combined, substantial coverage of ER was predicted to lower EIR to below one. Despite the significant impact of ER in one of the two vectors (An. funestus or An. arabiensis), this intervention is insufficient to reduce the EIR to below one in settings like Kilombero Valley where both species contribute to malaria transmission.

Accelerating malaria prevention through modeling-informed product selection and design: insights from vaccines, monoclonal antibodies, and chemoprevention drugs

Lydia Braunack-Mayer, Swiss Tropical and Public Health Institute / lydia.braunack-mayer@swisstph.ch

Malaria remains a critical global health challenge, with a looming threat of both drug and insecticide resistance. We urgently need new interventions to bring malaria burden back on track and, yet, product development remains slow and costly. Our integrated disease-modelling framework is addressing this challenge to accelerate the development of new malaria therapeutics: malaria vaccines, monoclonal antibodies, and chemoprevention drugs. For these interventions, the interplay between a product's mechanism-of-action, pharmacokinetic/pharmacodynamic properties, and deployment will strongly influence impact on individual- and population-level outcomes. To best use R&D, we must understand the influence of these product characteristics early in clinical development. We are using individual-based models that incorporate detailed intervention models, spanning large parameter spaces, to link product characteristics to public health impact, enabling funders, regulators, and product developers to focus resources on the candidates most likely to have a marked impact on malaria prevention. We present applications of this individual-based modelling framework to small molecule chemoprevention drugs, next-generation vaccines, and monoclonal antibodies. For small molecule drugs, results show that selecting candidates based on their duration of protection and ease of administration, rather than on treatment efficacy, can maximize malaria burden reduction in children. For vaccines, we identified a potential for improved first-generation products to provide protection cross multiple malaria seasons. For all three prevention tools, our work underscores the importance of understanding of the standard-of-care and generating early clinical evidence on product mechanism of action, pharmacokinetics, and pharmacodynamics for accurate predictions of impact.

1:45–3:15pm   **Family planning & fertility 2**
Lake Union
Facilitator: Michelle O'Brien, IDM

New perspectives on family planning metrics & measurement
Development and refinement of family planning metrics and measurement has stagnated over the last few decades. Researchers and policy-makers alike continue to use heavily critiqued indicators to describe progress (or lack thereof) toward ensuring equitable and voluntary access to safe and effective family planning. This session explores new perspectives on metrics and measurement in an effort to challenge mainstream thinking in the field, with three innovative new approaches to understanding women's sexual and reproductive health rights, family planning needs and preferences, and lived experiences at the facility level.

Taking the population control out of family planning measurement: The case of unmet need
Leigh Senderowicz, University of Wisconsin-Madison

No information provided.

Estimating the effect of facility-level characteristics on contraceptive use discontinuation rates.
Lucas Godoy Garraza, University of Massachusetts Amherst

No information provided.

New SRHR index to measure social norms in the World Values Survey
Signe Svallfors, Stanford University & Karin Barge, Karolinska Institutet

No information provided.

1:45–3:15 pm   ### Neglected tropical diseases: Screening & assessment to improve intervention impact
Lake Washington
Facilitator: Jamie Cohen, IDM

Heterogeneity in network structure changes the dominant transmission mode of an infectious disease
Pratyush Kollepara, La Trobe University / P.Kollepara@latrobe.edu.au

Several recent emerging diseases have exhibited both sexual and non-sexual transmission modes (Ebola, Zika and mpox). In the recent mpox outbreaks, transmission through sexual contacts appears to be the dominant mode of transmission. Motivated by this, we use an SIR-like model, to argue that an initially dominant sexual transmission mode can be overtaken by casual transmission at later stages, even if the basic casual reproduction number is less than one. Our results highlight the risk of intervention designs which are informed only by the early dynamics of the disease.

Inferring the spatial distribution of visceral leishmaniasis burden in India: the impact of targeted surveillance and considerations for the near- and post-elimination strategy
Emily Nightingale, London School of Hygiene and Tropical Medicine / emily.nightingale@lshtm.ac.uk

Visceral leishmaniasis (VL) is a debilitating and—without treatment—highly fatal disease which burdens impoverished communities in north-eastern India. Control and ultimately elimination of VL depends heavily on prompt case detection, with delays contributing to persistence of transmission and the risk of resurgence in a population with likely waning immunity. However, the constraints of an NTD elimination setting inevitably demand a reduction in the intensity of surveillance in order for the programme to be sustainable in the long-term. An understanding of patterns in disease burden at a fine geographic scale could inform optimal and efficient use of available resources and guide case detection activities, improving promptness of detection in a way that is sustainable from pre- to post-elimination.

This presentation discusses two complementary pieces of work, analysing variation in both individually-reported diagnosis delays and cumulative incidence at a fine spatial resolution (village) across the entire endemic state of Bihar, using geostatistical modelling approaches and statistical downscaling. Conclusions are drawn as to what actionable inference can be gained from routinely-collected data at this late stage, considering potential biases introduced by targeted surveillance as individual cases become sparser and more difficult to detect, and assessing the added value of resource-intensive surveillance at village level compared to a broader administrative level.

Applications and use-cases of HPVSim (an agent-based model of HPV transmission and cervical cancer disease)
Jahanara Rahemtulla / jrahem@mit.edu

Cervical cancer is the fourth most common cancer among women globally. Over ninety percent of deaths due to cervical cancer occur in low to middle income countries (GLOBOCAN estimates). There is extensive research and knowledge on how to treat, screen and prevent cervical cancer. Unfortunately however, in low resource settings, many women do not and/or cannot access adequate treatment and screening. IDM has created an open source, mechanistic stochastic agent-based model called HPVSim, which can be used to analyze the outcome and effectiveness of various screening, prevention and treatment strategies. In the lightening talk, I will discuss the use of HPV Sim in determining optimal prevention and screening programs. Specifically, I review the results of multiple simulations that focus on vaccine uptake, screening likelihood as well as loss to follow up (for treatment) ratios. The presentation will then provide insights based on screening and prevention policies based on projected outcomes (i.e. age standardized cervical cancer incidence rates, cancer mortality and HPV prevalence). The analysis using HPV Sim, also serves as a use case for understanding how the tool or other mathematical models might be used by external users and researchers.

Cost-effectiveness of colorectal cancer screening in different health subsectors of Argentina
SANTIAGO HASDEU, RedArets (Argentine Public Network of Health Technology Assessment) / hasdeusanti@gmail.com

INTRODUCTION: Colorectal cancer (CRC) is one of the main causes of mortality in adults. In Argentina it is the second among tumors, and there are differences between province mortality rates. CRC screening is underutilized in Argentina, where there is an important fragmentation of the health care system into multiple subsectors. OBJECTIVES: To assess the cost-effectiveness (CE) of different screening strategies based on annual immunochemical fecal occult blood test (IFOBT) followed by confirmatory colonoscopy for different health subsectors of Argentina. METHODS: A Markov model was developed, which allowed to compare three different strategies: screening population aged 50 to 74 years, screening population aged 50 to 64 years, and no screening. The

model was populated with demographic, epidemiological, clinical practice and cost data from each health subsector.

RESULTS: Important differences in costs and clinical variability were found among health subsectors of Argentina. Screening the population aged 50 to 74 years showed a slightly higher incremental CE ratio than screening the population aged 50 to 64, with values lower than per capita gross regional product. This result was robust in the sensitivity analysis. CONCLUSIONS: The compared results from seven regional health subsectors in Argentina, with their differences in epidemiology, organization, installed capacity and resources, as well as clinical variability and differences in costs, are robust in showing that CRC screening remains cost-effective under different scenarios. In order to analyse the CE in Argentina, it is necessary to take into account the local context of different health subsectors.

1:45 – 3:15 pm   **Verbal autopsy data collection and epidemiology of certified causes of death in SSA and South Asia**
Greenlake
Facilitators: Andre Lin Ouedraogo, IDM /
Samantha Dolan, BMGF

Monitoring excess mortality during the COVID-19 pandemic in Karachi, Pakistan, through burial site surveillance and GIS mapping
Abdul Momin Kazi, Aga Khan University, Department of Paediatrics /
momin.kazi@aku.edu

Pakistan's poor system of registering deaths and determining their causes highlights the need for precise documentation of excess fatalities during pandemic. Accurate data on deaths is vital to monitor the pandemic's progress and evaluate the efficiency of measures such as lockdowns, social distancing, and vaccinations. In this study, we utilized burial site surveillance to collect data from 177 graveyards and morgues in Karachi, Pakistan, both retrospectively and prospectively. By using GIS mapping, we located burial sites in 7 districts of Karachi and created density maps to visualize excess mortality. Our findings revealed that total deaths captured were (N=137,393) from 2019–2022. In addition a sub-sample of 26,237 mortalities from 21 graveyards spanning 2016–2018 is also being captured and the work is in progress. In addition, 1612 deaths were attributable to COVID-19. Karachi Central had the highest mortality proportion among the seven districts of Karachi. Further GIS mapping and data visualization demonstrated a surge in fatalities between May–June 2020, after which it began to decline, reaching its lowest point in July 2020. Another peak in mortality rate was observed in August 2021, followed by a decrease in September 2021. These findings suggest that the COVID-19 pandemic has

had a profound impact on mortality rates in Karachi, with distinct waves of increased mortality observed over time. Overall, the use of geospatial analysis provides valuable insights into the distribution of mortality rates, allowing for targeted interventions to mitigate the impact of the pandemic.

Estimating excess mortality during COVID-19 pandemic in Bangladesh — findings from a household survey in a rural sub-district
Aniqa Tasnim Hossain, International Centre for Diarrhoeal Disease Research,
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Background: COVID-19 has caused over six million deaths worldwide. Policymakers need reliable estimates of mortality, but deaths due to COVID-19 have been heavily underreported in many countries. This study aims to estimate excess mortality, risk factors, and leading causes of death during the first year of the pandemic in Bangladesh.

Methods: In February 2021 we conducted household surveys in Sitakundu, a subdistrict of Chattogram, and analyzed deaths occurring between January 2018 and December 2020. Cause of death was assigned using the InterVA-5 model. Excess mortality was measured using proportional all-cause excess mortality score. Segmented regression with Poisson distribution was performed to evaluate change in mortality rate by age, sex, education, and socioeconomic status (SES).

Findings: A total of 1748 deaths were recorded, including 1411 people ≥40 years. Compared to 2018–2019, 54% excess mortality was observed in 2020. Leading causes of death in 2020 included cardiac disease (18%), stroke (16%), acute respiratory infection (9%). and epilepsy (9%), similar to previous years, but mortality rates for each were higher in 2020. Older age, less education, and lower SES groups had higher mortality rates in 2020 compared to pre-pandemic years.

Interpretation: Although our results suggest deaths attributed to COVID-19 have been underreported, main leading causes of deaths were similar in 2020 compared to pre-pandemic. Special measures should be taken to identify patients at higher risk of death due to co-morbid COVID-19 infection. These findings also highlight the need to address inequities in social determinants of health that increase risk of death from COVID-19.

Certification of medical causes of death by verbal autopsy in rural Burkina Faso: a comparative approach between physicians and algorithms through the easyVA platform.

Vincent J. Lamien, Clinical Research Unit of Nanoro / dofindoubel@gmail.com

Backgrounds: The purpose of our work was to study the methods of certification of medical causes of death in the health district of Nanoro in Burkina between January 2014 and November 2016 through the electronic platform easyVA.

Methods: We conducted a descriptive cross-sectional survey that focused on deaths registered between January 2014 and November 2016 for which verbal autopsy (VA) data had already been collected and integrated on the easyVA platform by the Clinical Research Unit of Nanoro (CRUN). These VAs were then read by 33 physicians and by the InterVA and InsilicoVA algorithms. The causes of death thus generated by the two algorithms were finally compared with those determined by the physicians.

Results: Of the 1424 deaths to which physicians and both algorithms assigned causes, communicable diseases were the leading cause of death in the population (40.1%, 571/1424) with malaria at the top of the list (33.8%, 193/571). Non-communicable diseases claimed the lives of 24.9% of the population (355/1424), with cardiovascular diseases being the leading cause (31.0%, 110/355). External causes accounted for 6.0% (85/1424) of deaths, with drowning predominating (21.2%, 18/25). Eight (08) similar causes of death were identified by the physicians and the two algorithms in determining the top 10 causes of death in the population. InterVA-physician and InsilicoVA-physician agreements were 66.3% and 51.8% respectively.

Conclusion: EasyVA is a tool that facilitates the reading of VAs. The InterVA and InsilicoVA algorithms should be used in addition to the physician certification method which remains the ideal model.

Improving mortality data for national and subnational decision making in Ethiopia

Awoke Misganaw, IHME/EPHI / awoket@uw.edu

Background: Evidence on cause of death and premature mortality from any cause is vital for national and subnational decision making, to understand disparities in the availability and accessibility of health care and health resource allocation across regions and chartered cities. This analysis investigates the levels of causes of mortality across Ethiopia.

Methods: EPHI and IHME collaborative subnational burden of disease analysis in the GBD 2019 study used all accessible mortality and causes of death data to calculate cause of death and premature mortality for nine regions and two chartered cities in Ethiopia.

Results: Overall, 559,997 (95% UI: 506,117–621,976) deaths occurred in Ethiopia in 2019. Age-standardized death rate due to communicable, maternal, neonatal and nutritional diseases and disorders (CMNND), non-communicable disease (NCDs), and injuries were 368.6 (329.7–413.5), 553.4 (501.9–604.9), and 71.6 (61.1–82.7) per 100,000 populations respectively in 2019. Neonatal disorders (including preterm birth, sepsis, and encephalopathy), diarrheal diseases, lower respiratory infections, tuberculosis, stroke, and HIV/AIDS featured among the five leading specific causes of age-standardized YLL rates in all regions with different ranking orders. HIV/AIDS was the leading cause of age-standardized YLL rates in Addis Ababa and Gambella, causing respectively 4,381.9 (3,213.4–5,800.0) and 4,584.1 (2,776.2–7,087.1) YLL per 100,000 population in 2019. Tuberculosis was the leading cause of YLL in the Afar region, with YLL rates of 4,224.4 (3,303.1–5,286.2) per 100,000 populations in 2019.

Conclusion: These findings could support disease prevention strategies and treatment priorities, essential health service package implementation, national insurance package and health in all policy developments as well as increasing national budget allocations for health. However, there is a need to improve mortality data to decrease big uncertainties around the estimates for better national and subnational decision making in Ethiopia.

1:45 – 3:15 pm   **Arboviruses and vector-borne diseases**
Elliot Bay
Facilitator: Kate Battle, IDM

Human movement and environmental barriers shape the emergence of dengue

Vinyas Harish, University of Toronto / v.harish@mail.utoronto.ca

Understanding how emerging infectious diseases spread within and between countries is essential to contain future pandemics. Spread to new areas requires connectivity between one or more infected sources and a suitable local environment, but how these two factors interact at different stages of disease emergence remains largely unknown. Further, no analytical framework exists to examine their roles. Here we develop a new dynamic modelling approach for infectious diseases that explicitly models both human mobility and environmental suitability interactions and use it to better understand recently observed (1995–2019) patterns as well as predict past unobserved (1983–2000) and future (2020–2039) spread of dengue in Mexico and Brazil.

We find that these models can accurately reconstruct long-term spread pathways, determine historical origins, identify specific routes and modes of invasion, and generalise to other settings. Compared to previous estimates, our work suggests the rate of future expansion in the 2020s and 2030s may be underestimated, with the last southern Brazilian major cities predicted to be invaded by 2030 and invasion of Mexico City in the late 2030s. Our results have immediate practical applications for forecasting and containing the spread of dengue and emergence of new serotypes at a time when new vaccines and mosquito control tools are becoming available at scale. Given current and future trends in human mobility, climate, and zoonotic spillover, understanding the interplay between connectivity and environmental suitability will be increasingly necessary to contain emerging and re-emerging pathogens.

Statistical power analysis framework to design robust vector control experiments in semi-field systems

Andrea Kipingu, University of Glasgow/Ifakara Health Institute / a.kipingu.1@research.gla.ac.uk

Background: Semi-field experiments are a very good first way of understanding the impacts of potential new vector controls before field trials. However, the design of the semi-field experiment is critically important to ensure the outcomes are measurable and robust. One of the best ways to assess this is by power analysis. A framework was developed to determine the required number of semi-field chambers and sampling frequency and size to achieve sufficient power for evaluating the impact of single and combined interventions.

Methods: By analysing 1000 simulated data sets per scenario with generalized linear mixed-effects models, the power was estimated for various experimental designs, including short (24h) vs long-term (3 months) experiments and single vs combined application of LLIN and LLIN-PPF. Appropriate power was considered when the proportion of simulations where the null hypothesis was rejected was >80%.

Results: Although power increased with an increasing number of chambers and sampling size, the number of chambers and variance between chambers were the dominant factor determining power relative to all other design choices. Intervention effect size significantly affects power, therefore, choosing this parameter value carefully is crucial for realistic power estimates. The higher the effect sizes, the higher power to quantify LLIN-PPF interaction with minimal resources. The high variance between chambers decreased power, highlighting the importance of making conditions similar among chambers, e.g., by rotating treatments and samplers.

Conclusion: A generic statistical power analysis framework developed may be adapted to design robust vector control experiments in semi-field settings.

Exploring the impact of temperature on the efficacy of replacing the wild Aedes aegypti population by Wolbachia-carrying one

Claudia Pio Ferreira, Unesp, Brazil / claudia.pio@unesp.br

In this talk, I will present and discuss the results obtained by a non-autonomous time-delayed differential system, which was proposed to reproduce the dynamics of both Wolbachia-infected and non-infected mosquito populations in several scenarios that differ by daily environment temperature, the bacterial strain that promotes the infection on mosquitoes, and the release guidelines of infected mosquitoes. The numerical results show that: (i) multiple releases were more efficient than a single one, (ii) when the mosquito population is high is the best moment to implement the releasing of infected mosquitoes, (iii) strains that produce both high levels of cytoplasmic incompatibility and maternal inheritance boost the efficacy of the technique, (iv) high temperature can jeopardize the efficacy of the technique.

Climate change impacts on Zika and dengue risk: projections using a temperature-dependent basic reproduction number

Hannah Van Wyk, University of Michigan School of Public Health Department of Epidemiology / hcvw@umich.edu

Recent work characterizing the temperature dependencies of the basic reproduction number $\mathscr{R}_0$ for vectorborne disease highlights how climate change may impact geographic spread. Of particular importance is understanding how arboviruses might be affected by changing temperature. We applied a temperature-dependent $\mathscr{R}_0(T)$ to characterize Zika (and, for comparison, dengue) transmission potential under future climate change scenarios in four cities in Brazil. The $\mathscr{R}_0(T)$ for Zika and dengue were derived from a compartmental transmission model. We obtained historical temperature data for the years 2015–2019 and projections for 2045–2049 by fitting cubic spline interpolations to simulated atmospheric data under four climate change severity scenarios. We applied this approach to four Brazilian cities: Manaus, Recife, Rio de Janeiro, and São Paulo. We calculated seasonal $\mathscr{R}_0(T)$ for each city and climate change scenario for both diseases. Our model predicts that the $\mathscr{R}_0(T)$ for Zika peaks at 2.7 around 30° Celsius while for dengue it peaks at 6.8 around 31°. We predict that, regardless of the specific climate change scenario, there will be an increase in arbovirus disease pressure in Brazil. For Manaus, we predict that the annual $\mathscr{R}_0$ range will increase from 2.1–2.5, to 2.3–2.7, for Recife from 0.4–1.9 to 0.6–2.3, for Rio de Janeiro from 0–1.9 to 0–2.3, and for São Paulo from 0–0.3 to 0–0.7. As temperatures increase, there will be increasing epidemic potential, especially in regions where transmission is currently marginal. Surveillance systems should be implemented and sustained for early detection.

Investigating the impact of larviciding as a supplementary malaria vector control tool in rural south eastern Tanzania: A simulation study
Gloria Salome, Ifakara Health Institute / gshirima@ihi.or.tz

Even after a huge reduction of malaria burden due to the massive use of insecticide-treated nets (ITNs) and indoor residual spraying, transmission continues in most of sub-Saharan Africa. Larviciding is an intervention that controls mosquitoes in the larval stage and has shown a positive contribution in vector control to be considered as a supplementary tool. This study shows an impact assessment of larviciding using a mathematical model, based on Rufiji district. The Vector Control Optimization Model was adapted and simulated with 80% ITN coverage as a baseline. To evaluate the effect of larviciding on the mortality rate of An. gambiae, mature and immature mosquitoes were collected in two phases, before (2016–2017) and after (2019–2021) larviciding application. The entomological inoculation rates (EIR), reproduction number and biting rate were used as the primary outcome measures. In the simulation of 1 year, larviciding was predicted to reduce EIR by 76.43% and mosquito biting rate (approximately 60%) relative to the scenario without larviciding. Sensitivity analysis over a range of likely values for the biting rate and mosquito lifespan shows comparable the estimated impact between scenarios. This indicates that the predicted impact is robust to uncertainty in model parameters and assumptions. The application of larviciding has practical challenges, hardship in attaining high coverage but gives an assurance to vector control especially targeting the spreading An. Stephensi. This study supports larviciding as a successful strategy that policymakers and public health professionals, like the NMCP, may use to control malaria vectors based on WHO application recommendations.

Investigating the impact of irrigation on malaria vector larval habitats and transmission using a hydrology-based model
Ai-Ling Jiang, University of California, Irvine / jiangal@uci.edu

A combination of accelerated population growth and severe droughts has created pressure on food security and driven the development of irrigation schemes across sub-Saharan Africa. Irrigation has been associated with an increase in malaria risk, but it remains a challenge to understand the underlying mechanism and develop countermeasures to mitigate its impact. While helpful in investigating transmission dynamics, malaria models cannot be applied directly in regions with irrigation as they typically rely only on rainfall as a source of water to quantify larval habitats. By coupling a hydrologic model with an agent-based malaria model for a sugarcane plantation site in Arjo, Ethiopia, we demonstrated how incorporating hydrologic processes to estimate larval habitats can affect malaria transmission. Using the coupled model, we then examined the impact of an existing irrigation scheme on transmission dynamics. The inclusion of hydrologic processes increased the variability of larval habitats by around two-fold and resulted in reduction in malaria transmission by 60%. Irrigation increased all habitat types in the dry season by up to 7.4 times and converted temporary and semi-permanent habitats to permanent habitats in the rainy season, which grew by about 24%. Malaria transmission was sustained all-year round and intensified during the primary transmission season, with the peak shifted forward by around one month. Lastly, we demonstrated how habitat heterogeneity could affect the spatiotemporal dynamics of malaria transmission. These findings help larval source management as a supplementary malaria vector control tool to identify transmission hotspots and prioritize resources for malaria elimination planning.

3:30 – 5:00 pm   **Closing panel: Gender intentional research & data**
Camano Island / Whidbey Island

- *Sonalde Desai, University of Maryland and National Council of Applied Economic Research, New Delhi*
- *Diva Dhar, BMGF*
- *Naa Dodoo, African Institute for Development Policy*
- *Luisa Flor, Institute for Health Metrics and Evaluation*
- *Sylvia Muyingo, African Population and Health Research Center*

Conference Center Map

Main Level

The Lakes Rooms

Lake Union

Lake Washington

Green Lake

Elliott Bay

Portage Bay

Shilshole Bay

Business Center

Conference Center Registration Desk

Lower Level

Bainbridge Island

San Juan Island

Lopez Island

Orcas Island

Shaw Island

Camano Island

Whidbey Island

Fox Island

Maury Island

Vashon Island

Wellness Room