Mathematics of Malaria Transmission Dynamics

November 13-17, 2023

About the Workshop

This workshop brings together a multidisciplinary team of researchers (including mathematicians, modelers, entomologists, ecologists and epidemiologists) to discuss recent results and challenges associated with modeling the impacts of climate change and insecticide resistance on malaria vector and disease.

Organizers

Lauren Childs, Virginia Tech

Abba Gumel, University of Maryland

Jemal Mohammed-Awel, Morgan State University

Speakers

Folashade Agusto, Kansas University

Etienne Bilgo, IRSS-DRO and Muraz Center

Jackson Champer, Peking University

Jaline Gerardin, Northwestern University

Katharine Gurski, Howard University

Juan Gutierrez, University of Texas at San Antonio

Megan Greischar, Cornell University

Mallory Harris, Stanford University

Neil Hobbs, Swiss Tropical and Public Health Institute

Xi Huo, University of Miami

Shirley Luckhart, University of Idaho

Hassen Mamo, University of Addis Ababa

Nicole Mideo, University of Toronto

Calistus Ngonghala, University of Florida

Krijn Paaijmans, Arizona State University

Zhuolin Qu, University of Texas at San Antonio

Jordan Pellett, University of Tennessee

Michael Robert, Virginia Tech

Omar Saucedo, Virginia Tech

Miranda Teboh-Ewungkem, Government

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DEPARTMENT OF
MATHEMATICS

Contents

Schedule at a Glance

Time	Monday	Tuesday	Wednesday	Thursday	Friday
8:00					
9:00	Breakfast	Breakfast	Breakfast	Breakfast	Breakfast
	Krijn Paaijmans	Mallory Harris	Megan Greischar	Jackson Champer	Omar Saucedo
10:00					
11:00	Xi Huo	Folashade Agusto	Nicole Mideo	Zhuolin Qu	Katharine Gurski
	Coffee Break	Coffee Break	Coffee Break	Coffee Break	Coffee Break
12:00	Calistus Ngonghala	Jaline Gerardin	Jordan Pellett	Yuan Allegretti	Miranda Teboh-Ewungkem
13:00	Lunch	Lunch	Lunch and sightseeing (on your own)	Lunch	Lunch (on your own)
14:00					
15:00	Neil Hobbs	Shirley Luckhart		Etienne Bilgo	
	Coffee Break	Coffee Break		Coffee Break	
16:00	Hassen Mamo	Michael Robert		Juan Gutierrez	
17:00	High Tea & Photo				

Workshop Overview

Malaria, a parasitic disease spread between humans via the bite of infected adult female Anopheles mosquitoes, is one of the deadliest infectious diseases of mankind. The widespread and large-scale use of chemical insecticides in malaria-endemic areas has resulted in a dramatic reduction in malaria burden, prompting a renewed quest for malaria eradication. Unfortunately, the eradication effort faces numerous challenges, including widespread insecticide resistance, anthropogenic climate change (global warming significantly affects the lifecycle of the malaria vector and the parasite), human mobility, land use changes etc. This workshop brings together a multidisciplinary team of researchers (including mathematicians, modelers, entomologists, ecologists, and epidemiologists) to discuss recent results and challenges associated with modeling the impacts of climate change and insecticide resistance on malaria vector and disease. Some of the specific topics to be discussed include:

1. Genomic-epidemiology modeling framework for the population abundance of the malaria vector

2. Formulating and fitting models for malaria spread that incorporate climate change and insecticide resistance. Modeling impacts of climate change on the global distribution of malaria mosquitoes and disease burden.

3. Optimal deployment of insecticide-based resources (long-lasting insecticidal nets, indoor residual spraying etc.)

4. Biological methods of vector control: gene-drive based approaches (CRISPR-Cas9, release of transgenic mosquitoes, sterile insect technology and Wolbachia-based control).

5. Emergence and evolution of parasite drug resistance and impact on malaria spread. Quantifying the impacts of immunity and parasite diversity on drug resistance evolution

Organizing committee

LAUREN CHILDS, Virginia Tech University

ABBA GUMEL, University of Maryland

JEMAL MOHAMMED-AWEL, Morgen State University

Workshop Schedule

Monday, November 13, 2023

8:30 - 9:00   Breakfast

9:00 - 9:15   Doron Levy (University of Maryland/Director, Brin MRC). *Opening*

9:15 - 10:00   Krijn Paaijmans (Arizona State University)
                   Understanding mosquito population dynamics in spatially heterogeneous and temporally stochastic environments

10:00 - 10:15   Break

10:15 - 11:00   Xi Huo (University of Miami)
                   Vector-borne disease outbreak prevention: linking mosquito trap data to mathematical models

11:00 - 11:30   Coffee Break

11:30 - 12:15   Calistus Ngonghala (University of Florida)
                   Assessing the impact of insecticide-treated nets in the face of insecticide resistance on malaria control

12:15 - 2:15   Lunch

2:15 - 3:00   Neil Hobbs (Swiss Tropical and Public Health Institute
                                & Liverpool School of Tropical Medicine)
                   Insecticide Resistance Management (IRM) for Disease Vectors: Insights from Mathematical Modelling

3:00 - 3:30   Coffee Break

3:30 - 4:15   Hassen Mamo (University of Addis Ababa)
                   Malaria Vector Insecticide Resistance in Ethiopia

4:15 - 5:00   High Tea & Photo

Tuesday, November 14, 2023

8:45 - 9:15   Breakfast

9:15 - 10:00   Mallory Harris (Stanford University)
Testing the Temperature Dependence of Mosquito-Borne Disease Transmission

10:00 - 10:15   Break

10:15 - 11:00   Folashade Agusto (Kansas University)
Optimal Control of Malaria Transmission Across Sub-Sahara Africa Temperature Gradient

11:00 - 11:30   Coffee Break

11:30 - 12:15   Jaline Gerardin (Northwestern University)
Application of malaria transmission modeling to vector control policy in Guinea

12:15 - 2:15   Lunch

2:15 - 3:00   Shirley Luckhart (University of Idaho)
Impacts on malaria transmission of altered biogenic amine levels in Anopheles mosquitoes: evidence from empirical studies

3:00 - 3:30   Coffee Break

3:30 - 4:15   Michael Robert (Virginia Tech)
Impacts on malaria transmission of altered biogenic amine levels in Anopheles mosquitoes: insights from a mathematical model

5:00 - 6:00   Transportation to Dinner

6:00 - 8:00   Conference Dinner

WEDNESDAY, NOVEMBER 15, 2023

8:45 - 9:15   BREAKFAST

9:15 - 10:00   MEGAN GREISCHAR (Cornell University)
Developmental synchrony and extraordinary multiplication rates in malaria infections

10:00 - 10:15   BREAK

10:15 - 11:00   NICOLE MIDEO (University of Toronto)
Optimal cues for transmission investment

11:00 - 11:30   COFFEE BREAK

11:30 - 12:15   JORDAN PELLETT (University of Tennessee)
A within-host model for the pharmacokinetics and pharmacodynamics of malaria

12:15 - 5:00   LUNCH AND SIGHTSEEING (ON YOUR OWN)

Thursday, November 16, 2023

8:45 - 9:15   Breakfast

9:15 - 10:00   Jackson Champer (Peking University)
Modeling assessment of population suppression and modification using gene drive

10:00 - 10:15   Break

10:15 - 11:00   Zhuolin Qu (University of Texas at San Antonio)
Multistage Spatial Model for Informing Release of Wolbachia-Infected Mosquitoes as Disease Control

11:00 - 11:30   Coffee Break

11:30 - 12:15   Yuan Allegretti (Berkeley University and Peking University, China)
Application of a Simulation-Based Deep Learning Framework for Modeling CRISPR Gene Drives Mosquitos for Malaria Suppression

12:15 - 2:15   Lunch

2:15 - 3:00   Etienne Bilgo (IRSS-DRO and Muraz Center)
Modeling Malaria Control with Transgenic Fungi in Burkina Faso

3:00 - 3:30   Coffee Break

3:30 - 4:15   Juan Gutierrez (University of Texas at San Antonio)
Multi-scale Models of Malaria

Friday, November 17, 2023

8:45 - 9:15   Breakfast

9:15 - 10:00   Omar Saucedo (Virginia Tech)
                 The Role of Human Movement on the Spread of Malaria

10:00 - 10:15   Break

10:15 - 11:00   Katharine Gurski (Howard University)
                 An Application of a malaria model with non-exponential waiting times: the impact on treatment outcomes

11:00 - 11:30   Coffee Break

11:30 - 12:15   Miranda Teboh-Ewungkem (Government)
                 Using Mathematics to Understand the Complexities that Enable a Successful Malaria Transmission in a Human-Mosquito Built Environment

12:15 - 12:30   Workshop Closing

12:30 - 2:00   Lunch (on your own)

Abstracts of talks

Understanding mosquito population dynamics in spatially heterogeneous and temporally stochastic environments

Krijn Paaijmans

Arizona State University

Monday, November 13, 2023 @ 9:15 AM

The impact of global warming is expected to be particularly severe on ectothermic animals, especially those that live near their physiological limits for temperature. This includes many tropical and desert mosquito species. Long-standing theoretical predictions, some accompanied by experimental data, indicate that global warming will decrease their diversity and shift their geographic species distribution. However, current predictions are (i) too often based on macroclimate data, ignoring the actual environmental conditions experienced by mosquitoes, (ii) do not consider the concept of thermoregulation, and (iii) do not fully explore the impact of stochastic, extreme weather events. I will discuss (our) ongoing research aimed to better understand the impact of global warming on vectors and disease, including the challenges we face in closing those research gaps.

Vector-borne disease outbreak prevention: linking mosquito trap data to mathematical models

Xi Huo

University of Miami

Monday, November 13, 2023 @ 10:15 AM

Aedes aegypti is responsible for a few arbovirus transmissions. In this talk, I will present how we connect differential equation parameters with the mosquito trap data collected from 2017 to 2019. We specifically will talk about parameter identifiability and model comparison problems we encountered during our fitting. The model is then used to compare the Ae. aegypti population and evaluate the impact of rainfall intensity in different urban built environments. Our results show that rainfall affects the breeding sites and the abundance of Ae. aegypti more significantly in tourist areas than in residential places. In addition, we apply the model to quantitatively assess the effectiveness of vector control strategies in Miami-Dade County in South Florida, USA.

Assessing the impact of insecticide-treated nets in the face of insecticide resistance on malaria control

Calistus Ngonghala

University of Florida

Monday, November 13, 2023 @ 11:30 AM

Malaria remains a global health and economic threat, with insecticide-treated nets (ITNs) being a valuable tool for disease control in endemic areas. However, challenges such as mosquito resistance to insecticides, decay in ITN efficacy, and net attrition reduce their effectiveness. This study proposes mathematical models incorporating asymptomatic infectious individuals, insecticide resistance, and ITN decay. Analytical and numerical analyses reveal crucial parameters influencing disease control measures. The study emphasizes the importance of considering asymptomatic cases and ITN efficacy decay, underlining the significance of timely replacements and innovative ITN designs, particularly those addressing insecticide resistance. Piperonyl butoxide (PBO) ITNs prove superior in malaria control, showcasing potential for enhanced malaria control through the widespread adoption of high-quality ITNs, especially when coupled with appropriate lifespan management.

Insecticide Resistance Management (IRM) for Disease Vectors: Insights from Mathematical Modelling

Neil Hobbs

Swiss Tropical and Public Health Institute & Liverpool School of Tropical Medicine

Monday, November 13, 2023 @ 2:15 PM

The widespread use of insecticides for vector control has led to the inevitable rise of insecticide resistance. With new insecticides soon to reach the market, there is a need to evaluate how best to deploy insecticides in order to maximize their operational lifespan. Evaluating insecticide resistance management (IRM) strategies in trials is complex due to the need for long study durations and replication across multiple eco-epidemiological settings. The use of mathematical modelling to evaluate IRM strategies is there required. Generally, models evaluating IRM strategies for public health deployment of insecticides assume resistance to be a monogenic trait. We present a methodology for dynamically calculating the level of selection in mosquito populations. The model allows for the inclusion of parameters frequently highlighted as an issue for IRM namely cross resistance, insecticide decay and insecticide dosing. Using models which assume a polygenic basis of resistance, we the effectiveness of multiple different IRM strategies including mixtures, micro-mosaics (household level mosaics) and combinations of bednets and indoor residual spraying across a range of biological and operational scenarios. In this talk we present the results from these scenarios and discuss the IRM implications.

Malaria Vector Insecticide Resistance in Ethiopia

Hassen Mamo

University of Addis Ababa

Monday, November 13, 2023 @ 3:30 PM

Ethiopia has set an ambitious goal of eliminating malaria in certain low-transmission settings by 2030. However, the massive deployment of the core insecticide-based vector control tools, insecticide residual spray (IRS) and long-lasting insecticidal nets (LLIN), has resulted in insecticide resistance. Particularly, Anopheles arabiensis, the major malaria vector in Ethiopia, has developed resistance against insecticides belonging to all four chemical classes approved for IRS/LLIN use, including DDT (organochlorine), malathion (organophosphate), bendiocarb and propoxur (carbamates) and alpha-cypermethrin, cyfuthrin, deltamethrin, etofenprox, lambda-cyhalothrin and permethrin (pyrethroids). Complicating the matter further, the newly reported hitherto Asian urban malaria vector from Ethiopia, Anopheles stephensi, is widely spreading in the country and is also reported to be insecticide-resistant. Effective close surveillance is vital to understanding the intensity and distribution of nationwide mosquito insecticide resistance, mathematically predicting and managing the threat, and achieving malaria elimination. On the other hand, the real impact of insecticide resistance on malaria control/elimination in light of mosquito fitness cost requires comprehensive modelling. Without these and related imperative information, defining the micro-epidemiology of malaria elimination and undertaking targeted interventions is easier said than done. This paper is aimed at reviewing the current mosquito insecticide resistance status in Ethiopia and its implications for malaria transmission dynamics.

Testing the Temperature Dependence of Mosquito-Borne Disease Transmission

Mallory Harris

Stanford University

Tuesday, November 14, 2023 @ 9:15 AM

The mosquito vectors for diseases like malaria are highly temperature-sensitive, suggesting that disease burden may shift considerably due to anthropogenic climate change. Mathematical models using experimental data on mosquito traits predict a nonlinear relationship between transmission intensity and temperature. Malaria transmission is expected to peak at an optimal temperature of 25C, suggesting that transmission risk will increase with warming in some temperate regions but decline in warmer areas where temperatures begin to exceed the thermal optimum. However, relative risk based on vector biology may not necessarily correspond directly to human cases, morbidity, and mortality. I will provide examples of how different quantitative approaches, including meta-analysis, mechanistic modeling, and causal inference, have been applied to epidemiological data at scales ranging from municipal to global to characterize the relationship between temperature and vector-borne disease. These studies generally validate expectations based on vector biology, in addition to revealing how covariates like precipitation and vector control may moderate the effects of temperature on disease. I will also discuss how these estimates may be applied to attribute the contribution of climate change to recent disease burden and to project how vector-borne disease incidence will change under different climate change scenarios.

Optimal Control of Malaria Transmission Across Sub-Sahara Africa Temperature Gradient

Folashade Agusto

Kansas University

Tuesday, November 14, 2023 @ 10:15 AM

In this seminar, I will present the results obtained from investigating the optimal control strategies for malaria in the presence of temperature variation using a temperature dependent malaria model. A 2015 study by Agusto et al. [1] identified the suitable temperature ranges for mosquitoes in four different geographical regions of Sub-Saharan Africa as [22.61oC - 28.58oC] in West African cities, [16.68oC -27.92oC] in Central African cities, [19.04oC - 26.75oC] in East African cities, and [16.66oC - 25.32oC] in Southern Africa. The optimal control strategies in these temperature ranges suggest on average a high usage of both larviciding and adulticiding followed by a moderate usage of personal protection such as insecticide treated bednet. The average optimal bednet usage mimics the trajectory of the mosquitoes as the mosquitoes respond to temperature variations. These results triggered the investigation of the impact of insecticide resistance mosquitoes on disease burden in the face of temperature variations. The results indicate that optimal bednet usage on average is higher in the presence of insecticide resistance mosquitoes. Furthermore, on average bednet usage increases as temperature increases to the optimal temperature suitable for mosquitoes and it decreases thereafter, a pattern similar to earlier results involving insecticide sensitive mosquitoes. References: [1] Agusto, F.B., Gumel, A.B., & Parham, P. E. (2015). Qualitative assessment of the role of temperature variations on malaria transmission dynamics. Journal of Biological Systems, 23(04), 1550030.

Application of malaria transmission modeling to vector control policy in Guinea

JALINE GERARDIN

Northwestern University

Tuesday, November 14, 2023 @ 11:30 AM

In the last five years, progress against malaria in the highest-burden countries has stalled or reversed. Resources for adequately controlling malaria remain insufficient in many countries. In response, malaria programs are increasingly using data-driven approaches to target intervention planning to the local context. Our group has been supporting these efforts alongside WHO by developing mathematical models that countries can use to compare the epidemiological impact of candidate intervention plans and to obtain realistic predictions of their plan's impact. I present our modeling approach for Guinea and demonstrate how modeling has been used to predict the impact of standard and next-generation bednets to support Guinea's funding request for the Global Fund.

Impacts on malaria transmission of altered biogenic amine levels in Anopheles mosquitoes: evidence from empirical studies

Shirley Luckhart

University of Idaho

Tuesday, November 14, 2023 @ 2:15 PM

Malaria is caused by Plasmodium species that are transmitted to humans by Anopheles mosquitoes. Interactions between Plasmodium and its mosquito host are often complex and can be influenced by a myriad of factors. In this talk, we describe empirical studies showing that malaria-induced allergic inflammation controls parasite transmission from humans to mosquitoes, biology that could inform novel strategies for malaria control. Specifically, severe malaria can be associated with 10-fold higher histamine and 10-fold lower serotonin levels in human blood compared to healthy individuals. These biogenic amines are important insect neuromodulators and their presence in blood makes them available to mosquitoes. Experimentally, we showed that provisioning female Anopheles stephensi with malaria-associated levels of histamine and serotonin, compared to provisioning healthy control levels, resulted in complex effects on reproduction and behavior. Female mosquitoes treated with the malaria-associated combination also exhibited enhanced flight behavior and object inspection relative to controls. Notably, mosquitoes treated with the malaria-associated combination exhibited higher mean malaria oocysts and sporozoite infection relative to mosquitoes treated with the healthy combination. In a follow-up talk, Michael Robert will discuss the potential impacts of our results on population level transmission as studied with a model.

Impacts on malaria transmission of altered biogenic amine levels in Anopheles mosquitoes: insights from a mathematical model

Michael Robert

Virginia Tech

Tuesday, November 14, 2023 @ 3:30 PM

Empirical studies revealed that altered biogenic amine levels impact the biology and behavior of Anopheles mosquitoes that ingest them in bloodmeals, but it remains to be seen what role these changes may have on mosquito population dynamics and malaria transmission. We developed a stage-structured discrete time mathematical model of mosquito population dynamics coupled with population-level malaria transmission dynamics to investigate how these altered biogenic amine levels may play a role in the malaria transmission cycle. We incorporated demographic, behavioral, and parasite reproduction data into the model and explored scenarios that consider different possible concentrations of histamine and serotonin in bloodmeals and the effects thereof by studying impacts on mosquito population size and malaria incidence and prevalence. We explore different possible extensions of the model and discuss our findings in the context of malaria control as well as future experimental work. This is a joint work with Shirley Luckhart

Developmental synchrony and extraordinary multiplication rates in malaria infections

Megan Greischar

Cornell University

Wednesday, November 15, 2023 @ 9:15 AM

Parasite multiplication rates underpin many aspects of within host dynamics, such as the likelihood of evolving traits of concern like drug resistance. Thus, the ability to accurately estimate parasite multiplication rates is required to understand the role of natural immunity and assess the efficacy of interventions like vaccination and drug therapies. We have recently shown that estimated parasite multiplication rates can be severely biased upwards—exceeding true values by orders of magnitude—when certain phases of development are more difficult to sample than others and when the development of parasites that make up an infection is synchronized, both features of malaria infections that may be common in other pathogenic organisms. In human malaria parasites (Plasmodium falciparum), parasite-occupied red blood cells are difficult to sample in the latter portion of parasite development, so that changing parasite age distributions generate spuriously large estimates of multiplication rates. Two key questions arise from that finding: (1) what aspects of parasite biology generate spuriously large estimates of population growth rates, rather than underestimates? (2) in other pathogenic organisms with different biology and developmental rhythms, to what extent (and in which direction) are estimates of multiplication rates likely to be biased? Understanding and accounting for the processes that lead to biased multiplication rate estimates will inform predictions regarding parasite evolution in response to intervention. This is joint work with Lauren Childs.

Optimal cues for transmission investment

Nicole Mideo

University of Toronto

Wednesday, November 15, 2023 @ 10:15 AM

Like all sexually-reproducing organisms, malaria parasites face a trade-off in allocating resources between growth and reproduction, since a given infected red blood cell can either produce more merozoites (akin to "growth" of the infection) or a transmissible gametocyte (akin to "reproducing" an infection). Relative investment in transmission varies with parasite genotype, across hosts, and even over the course of infection. Previous theory identified optimal investment strategies under different within-host conditions, treating transmission investment as a function of time. Here, using mechanistic models, we instead define parasite strategies as functions of within-host environmental cues to ask what cues should parasites use to determine transmission investment and how do different choices impact infection outcomes?

A within-host model for the pharmacokinetics and pharmacodynamics of malaria

Jordan Pellett

University of Tennessee

Wednesday, November 15, 2023 @ 11:30 AM

Malaria is a significant public health concern, especially as the increasing presence of drug resistance creates challenges for control efforts. Over the last several decades, mathematical modeling has been used to gain insight into the within-host dynamics of malaria parasites. Within the human host, the parasite undergoes several life stages, including an asexual replication stage associated with the onset of symptoms, and a sexual stage of parasites (the gametocytes) which can be transmitted to mosquitoes. Of particular importance is the incorporation of pharmacokinetics and pharmacodynamics to better understand how different actions of treatment on malaria parasites impact gametocyte levels and the potential to select for drug-resistant parasites. In this talk we discuss a within-host model that incorporates anti-malarial treatment and explore the impact of different dosing regimes and drug actions on parasite load and probability of forward transmission.

Modeling assessment of population suppression and modification using gene drive

Jackson Champer

Peking University

Thursday, November 16, 2023 @ 9:15 AM

Gene drive alleles bias inheritance in the favor, allowing them to quickly spread throughout a population. They could combat malaria by rapidly spreading a cargo gene that blocks pathogen transmission, or they could directly suppress vector populations. However, computational analysis using individual-based models predicts that suppression drives may not succeed in spatially structured natural populations due to the "chasing" phenomenon that causes chaotic, long-term persistence of both drive and wild-type alleles. We assessed this for Anopheles mosquitoes with existing suppression drives, and we also found that competing species can reduce this effect, albeit at the cost of increased rate of drive loss. Another major challenge is confinement of a gene drive to a target population. We have modeled and constructed new "toxin-antidote" drives that are also simpler to construct than more well-known homing drives. This highly efficient class of drives could allow modification or suppression to be confined, allowing flexible use of gene drives in the future.

Multistage Spatial Model for Informing Release of Wolbachia-Infected Mosquitoes as Disease Control

Zhuolin Qu

University of Texas at San Antonio

Thursday, November 16, 2023 @ 10:15 AM

Wolbachia is a natural bacterium that can infect Aedes mosquitoes and block the transmission of mosquito-borne diseases, including dengue fever, Zika, and chikungunya. Field trials have been conducted worldwide to suppress local epidemics. We present a new partial differential equation model for the spread of Wolbachia infection in mosquitoes. The model accounts for both the complex Wolbachia vertical transmission cycle and detailed life stages in the mosquitoes, and it also incorporates the spatial heterogeneity created by mosquito dispersion in the two-dimensional release domain. Field trials and previous modeling studies have shown that the fraction of infection among mosquitoes must exceed a threshold level for the infection to persist. We use the spatial model to identify a threshold condition for having a self-sustainable Wolbachia infection in the field. When above this threshold, the model gives rise to a spatial wave of Wolbachia infection. We quantify how the threshold condition and invasion velocity depend on the diffusion process and other model parameters, and we study different intervention scenarios to inform the efficient releases.

Application of a Simulation-Based Deep Learning Framework for Modeling CRISPR Gene Drives Mosquitos for Malaria Suppression

Yuan Allegretti

Berkeley University and Peking University, China

Thursday, November 16, 2023 @ 11:30 AM

Engineered CRISPR gene drives are a promising new strategy for fighting malaria and other vector-borne diseases, made possible by genome engineering with the CRISPR-Cas9 system. One useful approach to predict the outcome of a gene drive mosquito release is individual-based modeling, which can be spatially explicit and allows flexible parameters for drive efficiency, mosquito ecology, and malaria transmission. However, the computational demand of this type of model significantly increases when including a larger number of parameters. Thus, we built a simulation-based deep-learning model to comprehensively understand the effects of parameters on mosquito suppression and malaria prevalence among the human population. This model offered a high level of granularity in the estimation of the impacts of gene drive and ecological factors on malaria and vectors. The results suggest that reducing the embryo resistance cut rate, functional resistance forming rate and increasing the drive conversion rate plays the major role in mosquito suppression and related phenomena, greater than expected compared to simple panmictic simulations. We also observed that the parameter space for eliminating malaria was larger than that for mosquito suppression, suggesting that even a considerably imperfect drive may still successfully accomplish its objective. This study shows the potential application of deep learning for simulating potential interventions on vector-borne diseases.

Modeling Malaria Control with Transgenic Fungi in Burkina Faso

Etienne Bilgo

IRSS-DRO and Muraz Center

Thursday, November 16, 2023 @ 2:15 PM

Malaria, a critical public health challenge in Burkina Faso, has necessitated the exploration of innovative vector control measures. The development of transgenic entomopathogenic fungi, specifically Metarhizium pingshaense, designed to target and kill malaria vectors, presents a promising intervention. This study employs mathematical modeling to assess the potential impact of deploying this transgenic fungus on the malaria transmission dynamics within Burkina Faso. A compartmental model, incorporating mosquito lifecycle stages and the interaction of mosquitoes with the transgenic Metarhizium pingshaense, will be developed. The model parameters will be calibrated using laboratory, semi field and limited field data, factoring in the efficacy of fungal infection and consequential mosquito mortality and pre-lethal effects. We will simulate various scenarios reflecting different coverage rates of fungal application and evaluating their potential in reducing the Anopheles mosquito population, and by extension, malaria transmission. Our results would suggest that a well-strategized deployment of transgenic Metarhizium pingshaense can substantially curtail mosquito survival, fecundity and other fitness parameters, pivotal for disrupting malaria transmission. The effectiveness of the intervention could markedly enhanced when combined with other control measures like insecticide-treated nets. Furthermore, the model will certainly underscore the importance of understanding local environmental conditions, ensuring the persistence and effectiveness of the fungi. In conclusion, the mathematical modeling of transgenic Metarhizium pingshaense deployment would highlight its potential as a formidable tool in Burkina Faso's arsenal against malaria, offering a sustainable solution to counteract the rising tide of insecticide resistance.

Multi-scale Models of Malaria

JUAN GUTIERREZ

University of Texas at San Antonio

Thursday, November 16, 2023 @ 3:30 PM

Multi-scale mathematical models have emerged as potent tools in understanding the complex dynamics of malaria transmission. Such models can be constructed in two primary ways. First, a single integrated model can be developed that encompasses one or more scales directly, from the molecular interactions of the parasite with its human and mosquito hosts, up to the population dynamics of disease spread. This approach offers the advantage of a unified framework that can capture direct interactions between different scales. However, it often faces challenges related to computational complexity and the integration of disparate data types. Alternatively, one can build a collection of models, each dedicated to a specific scale, and then link these models to address overarching questions that span multiple scales. This modular approach facilitates focused refinement at each scale and can be computationally more manageable. However, ensuring consistent and meaningful communication between the individual scale models can be intricate. In this talk, we will discuss both methodologies, with their respective advantages and drawbacks, and how they have provided valuable insights into malaria dynamics, highlighting the versatility and adaptability of multi-scale modeling techniques.

The Role of Human Movement on the Spread of Malaria

OMAR SAUCEDO

Virginia Tech

Friday, November 17, 2023 @ 9:15 AM

Mosquitos are known for being a source of infectious diseases and are a cause of great concern within the public health community. As traveling has become more accessible, diseases such as malaria have surfaced in areas in which it has not been previously detected. Additionally, factors such as mobility patterns, environmental changes, and local transmission characteristics play an important part in the disease dynamics. Thus, a better sense of mosquito-borne diseases is needed to determine the best course of action to undertake this serious threat. In this presentation, we will explore how epidemiological and ecological features influence mosquito-borne diseases via a multi-patch compartmental model. The objective of this talk is to present the analytical tools and methodology to help understand how human mobility and regional attributes combine to impact disease dynamics.

An Application of a malaria model with non-exponential waiting times: the impact on treatment outcomes

Katharine Gurski

Howard University

Friday, November 17, 2023 @ 10:15 AM

Most epidemiological models for malaria assume exponentially distributed residence times in disease stages to simplify the model formulation and analysis. However, these models do not allow for accurate description of the interaction between drug concentration and parasite load within humans and mosquitos. To improve this, we formulated a model by considering arbitrarily distributed sojourn for various disease stages. When the general distributions were replaced by gamma distributions fit to data, the system of integral equations can be reduced to a system of ODEs, which has some non-trivial characteristics which are only captured by non-exponential distributions for disease stages. We incorporate data for asexual parasite and gametocyte levels, drug concentrations, and recorded patient recovery times to the malaria model with gamma distributed infection and treatment stages. The goals are to study effects of timing of treatment, the impact of asymptomatic population, and the treatment drug with dosing protocol.

Using Mathematics to Understand the Complexities that Enable a Successful Malaria Transmission in a Human-Mosquito Built Environment

Miranda Teboh-Ewungkem

Government

Friday, November 17, 2023 @ 11:30 AM

Human malaria is caused by Plasmodium falciparum parasites and transmitted from one human to another by female Anopheles mosquitoes. Part of the parasite's life cycle resides in humans and the other part in female mosquitoes. Transmission of the parasite from an infectious human to a susceptible feeding mosquito is plausible when the mosquito successfully draws blood from the infectious human, with success if the drawn blood meal contains the transmissible parasite forms (gametocytes) from humans to mosquitoes. On the other hand, transmission from an infectious mosquito to a susceptible human is plausible following a successful feeding encounter between the mosquito and the human, with success if the feeding encounter results in the injection of the transmissible parasite forms (sporozoites) from mosquitoes to humans. Notably, the process is not always successful; the quest to draw blood is costly and may fail resulting in the mosquito's demise. Moreover, even when blood is successfully drawn from a human, parasite transmission may fail. In fact, a successful parasite transmission, and hence malaria transmission, requires two sequentially distinct successful feeding episodes by a susceptible feeding mosquito, the first from an infected human with the transmissible parasite forms followed by one from a susceptible human, with the parasite being in its transmissible state in the feeding mosquito at the latter feeding. Thus humans, parasites and female mosquitoes must interact synergistically in order for the transmission cycle to be successfully completed. The bottlenecks involved illuminate how the human-mosquito interaction enhances the parasites' exploitation of the evolutionary and reproductive needs of mosquitoes to ensure the parasites success and survivability. Therefore, understanding this complex process, viewed from the lens of transmitting mosquitoes, also driven by their evolutionary need to survive, is essential. This is situated in a built environment that showcases fluctuations in temperature which affect various aspects in the malaria problem. In this talk, I will illustrate the role of mathematics in aiding our understanding of the malaria problem.

The Brin Mathematics Research Center

The Brin Mathematics Research Center is a research center that sponsors activity in all areas of pure and applied mathematics and statistics. The Brin MRC was funded in 2022 through a generous gift from the Brin Family. The Brin MRC is part of the Department of Mathematics at the University of Maryland, College Park.

Activities sponsored by the Brin MRC include long programs, conferences and workshops, special lecture series, and summer schools. The Brin MRC provides ample opportunities for short-term and long-term visitors that are interested in interacting with the faculty at the University of Maryland and in experiencing the metropolitan Washington DC area.

The mission of the Brin MRC is to promote excellence in mathematical sciences. The Brin MRC is home to educational and research activities in all areas of mathematics. The Brin MRC provides opportunities to the global mathematical community to interact with researchers at the University of Maryland. The center allows the University of Maryland to expand and showcase its mathematics and statistics research excellence nationally and internationally.

List of Participants

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