

Human Behavior And Disease Dynamics

APRIL 24-28, 2023



Speakers

Yeganeh Alimohammadi, Stanford University Taylor Anderson, George Mason University Folashade Agusto, University of Kansas Shweta Bandal, Georgetown University Ana Bento, Rockefeller Foundation & Indiana University Christian Borgs, UC Berkeley Fan Bu, UCLA Lauren Childs, Virginia Tech Jeff Demers, University of Maryland Baltazar Espinoza, University of Virginia Zhilan Feng, Purdue University and NSF Meagan Fitzpatrick, University of Maryland, Baltimore Navid Ghaffazadegan, Virginia Tech University Michelle Girvan, University of Maryland Lou Gross, University of Tennessee Simon Levin, Princeton University Madhav Marathe, University of Virginia Jemal Mohammed-Awel, Morgan State Calistus Ngonghala, University of Florida Sen Pei, Columbia University Chadi Saad-Roy, UC Berkeley Padmanabhan Seshaiyer, George Mason University Joshua Weitz, Georgia Tech Haizhao Yang, University of Maryland Jim Yorke, University of Maryland

Organizers

Abba Gumel, University of Maryland Bill Fagan, University of Maryland

About the Workshop

The novel coronavirus that emerged late in 2019 (COVID-19) has highlighted the importance of incorporating human behavior and socio-economic factors that affect disease risk on the transmission dynamics and control of respiratory pathogens. Several classical epidemiological models that did not explicitly account for these factors generally failed to accurately capture the observed trajectory (thereby failing to make realistic forecasts) of the pandemic. Specifically, classical epidemiological models need to be extended to explicitly account for the impacts of, and the bi-direction feedbacks between, human behavior and socio-economic factors that influence the disease risk choices humans make during outbreaks of respiratory pathogens. This conference brings together a diverse interdisciplinary team of researchers, from mathematics, epidemiology, economics, social science, computer science, statistics, data science and public health, to discuss the state-of-the-art methodologies and theories for realistically incorporating the pertinent human behavior and socio-economic heterogeneities that affect disease risk and transmission dynamics into classical epidemiological models, aimed at enhancing their predictive power. In addition to using behavior theories and observed data to develop behavior-driven mathematical models for the spread of emerging (novel), re-emerging and re-surging respiratory pathogens, the conference will also address the problem of designing realistic models for the spread of new ideas, technologies, information, and misinformation pertaining to (and during) the spread and control of respiratory pathogens. The conference will also celebrate the distinguished career of James Yorke.

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Contents

| Workshop Overview | 5 | | | | | |
|--|----|--|--|--|--|--|
| Workshop Schedule | 6 | | | | | |
| Abstracts of talks | 11 | | | | | |
| Sen Pei | 11 | | | | | |
| Taylor Anderson | 12 | | | | | |
| Folashade Agusto | 13 | | | | | |
| Jim Yorke | 14 | | | | | |
| Jeffery Demers | 15 | | | | | |
| Louis J. Gross | 16 | | | | | |
| Madhav Marathe | 17 | | | | | |
| Meagan Fitzpatrick | 17 | | | | | |
| Omar Saucedo | 18 | | | | | |
| Joshua Weitz | 18 | | | | | |
| Navid Ghaffarzadegan | 19 | | | | | |
| Baltazar Espinoza | 20 | | | | | |
| Haizhao Yang | 21 | | | | | |
| Christian Borgs | 21 | | | | | |
| Michelle Girvan | 22 | | | | | |
| Zhilan Feng | 22 | | | | | |
| Yeganeh Alimohammadi | 23 | | | | | |
| Shweta Bansal | 23 | | | | | |
| Lauren Childs | 24 | | | | | |
| Chadi Saad-Roy | 25 | | | | | |
| Simon Levin | 26 | | | | | |
| Padmanabhan Seshaiver | 27 | | | | | |
| Calistus Ngonghala | 28 | | | | | |
| Jemal Mohammed-Awel | 28 | | | | | |
| Simon Levin | 29 | | | | | |
| The Brin Mathematics Research Center 3 | | | | | | |
| List of Participants | 31 | | | | | |

Schedule at a Glance

| 00.0 | Monday | Tuesday | Wednesday | Thursday | Friday |
|--------|------------------|----------------------------|----------------------|----------------------------|----------------------------|
| \$:00 | | | | | |
| 00.0 | Breakfast | $\operatorname{Breakfast}$ | Breakfast | $\operatorname{Breakfast}$ | Breakfast |
| a.00 | Sen Pei | Louis J. Gross | Navid Ghaffarzadegan | Yeganeh Alimoham- madi | Padmanabhan Se- shaiver |
| 10.00 | | | | | <i>C</i> |
| 00.01 | Taylor Anderson | Madhav Marathe | Baltazar Espinoza | Shweta Bansal | Calistus Ngonghala |
| 11:00 | Coffee Break | Coffee Break | Coffee Break | Coffee Break | Coffee Break |
| 00.61 | Folashade Agusto | Meagan Fitzpatrick | Haizhao Yang | Lauren Childs | Jemal Mohammed- Awel |
| 00.21 | Lunch | Lunch (on your own) | Lunch | Lunch (on your own) | Simon Levin |
| 13:00 | | | | | Lunch |
| 1 1.00 | | | | | |
| 14:00 | Jim Yorke | Omar Saucedo | Christian Borgs | Chadi Saad-Roy | |
| 15:00 | Coffee Break | Coffee Break | Coffee Break | Group Photo | |
| | Jeffery Demers | Joshua Weitz | Michelle Girvan | Simon Levin | |
| 00:0T | | | Zhilan Feng | | |
| 17.00 | | | | High Tea | |

Workshop Overview

The novel coronavirus that emerged late in 2019 (COVID-19) has highlighted the importance of incorporating human behavior and socio-economic factors that affect disease risk on the transmission dynamics and control of respiratory pathogens. Several classical epidemiological models that did not explicitly account for these factors generally failed to accurately capture the observed trajectory (thereby failing to make realistic forecasts) of the pandemic. Specifically, classical epidemiological models need to be extended to explicitly account for the impacts of, and the bi-direction feedbacks between, human behavior and socio-economic factors that influence the disease risk choices humans make during outbreaks of respiratory pathogens. This conference brings together a diverse interdisciplinary team of researchers, from mathematics, epidemiology, economics, social science, computer science, statistics, data science and public health, to discuss the state-of-the-art methodologies and theories for realistically incorporating the pertinent human behavior and socio-economic heterogeneities that affect disease risk and transmission dynamics into classical epidemiological models, aimed at enhancing their predictive power. In addition to using behavior theories and observed data to develop behavior-driven mathematical models for the spread of emerging (novel), re-emerging and re-surging respiratory pathogens, the conference will also address the problem of designing realistic models for the spread of new ideas, technologies, information, and misinformation pertaining to (and during) the spread and control of respiratory pathogens. The conference will also celebrate the distinguished career of James Yorke.

Organizing committee

BILL FAGAN, University of Maryland ABBA GUMEL, University of Maryland

Workshop Schedule

Monday, April 24, 2023

| 8:30 - 8:55 | Breakfast | | |
|---------------|--|--|--|
| 8:55 - 9:00 | DORON LEVY (University of Maryland/Director, Brin MRC) Opening | | |
| 9:00 - 9:45 | SEN PEI (Columbia University) Data-Driven Mathematical Modeling of Respiratory Diseases | | |
| 10:00 - 10:45 | TAYLOR ANDERSON (George Mason University) Spatial Non-Stationarity in Behaviors Protecting Against Infectious Diseases | | |
| 10:45 - 11:15 | Coffee Break | | |
| 11:15 - 12:00 | FOLASHADE AGUSTO (University of Kansas) Modeling the Role of Risky Behavior Among Injection Drug Users on Disease Transmission | | |
| 12:00 - 2:00 | Lunch | | |
| 2:00 - 2:45 | JIM YORKE (University of Maryland) Human Disease, Dynamics and Control, a Journey | | |
| 2:45 - 3:15 | Coffee Break | | |
| 3:15 - 4:00 | JEFFERY DEMERS (University of Maryland) Managing Emerging Epidemics with Limited Testing Resources: COVID-19 and Beyc | | |

TUESDAY, APRIL 25, 2023

8:30 - 9:00 Breakfast

- 9:00 9:45 LOUIS J. GROSS (University of Tennessee) Human Behavior Modeling, the Exposome and Disease Progression
- 10:00 10:45 MADHAV MARATHE (University of Virginia) Digital Twins of US Social Contact Networks and Their Applications to Pandemic Science
- 10:45 11:15 Coffee Break
- 11:15 12:00 MEAGAN FITZPATRICK (University of Maryland School of Medicine) Modeling School-Based Interventions Against COVID-19
- 12:00 2:00 LUNCH (ON YOUR OWN)
- 2:00 2:45 OMAR SAUCEDO (Virginia Tech University) Investigating the Impact of Silent Spreaders in COVID-19
- 2:45 3:15 Coffee Break
- 3:15 4:00 JOSHUA WEITZ (Georgia Tech) Asymptomatic: How Deciphering the Silent Spread of COVID-19 Helps Prepare Us for Pandemics to Come

WEDNESDAY, APRIL 26, 2023

- 8:30 9:00 Breakfast
- 9:00 9:45 NAVID GHAFFARZADEGAN (Virginia Tech University) Incorporating Dynamics of Risk Responsiveness and Human Behavior Change in Epidemic Models
- 10:00 10:45 BALTAZAR ESPINOZA (University of Virginia) Modeling Social Complexity in Epidemiology: Risk Perception and Adaptive Human Behavior
- 10:45 11:15 Coffee Break
- 11:15 12:00 HAIZHAO YANG (University of Maryland) Finite Expression Method for Discovering Physical Laws from Data
- 12:00 2:00 Цинсн
- 2:00 2:50 CHRISTIAN BORGS (UC Berkeley) Is Local Information Enough to Predict an Epidemic?
- 2:45 3:15 Coffee Break
- 3:15 4:00 MICHELLE GIRVAN (University of Maryland) Reservoir Computing for Time Series Prediction with Applications to Disease Dynamics
- 4:00 4:30 ZHILAN FENG (Purdue University and NSF) NSF/Math Bio Funding Opportunities

THURSDAY, APRIL 27, 2023

| 8:30 - | 9:00 | Breakfast |
|--------|------|-----------|
| | | |

- 9:00 9:45 YEGANEH ALIMOHAMMADI (Stanford University) The Efficacy of COVID-19 Testing and Vaccination in Schools
- 10:00 10:45 SHWETA BANSAL (Georgetown University) Unraveling Host Behavioral Heterogeneity for Models of Infectious Disease Dynamics and Control
- 10:45 11:15 Coffee Break
- 11:15 12:00 LAUREN CHILDS (Virginia Tech University) The Role of Interventions in COVID-19 Outbreak Control
- 12:00 2:00 LUNCH (ON YOUR OWN)
- 2:00 2:45 CHADI SAAD-ROY (UC Berkeley) Modelling SARS-CoV-2 Immuno-Epidemiology, Vaccination, and Invasion Dynamics of New Variants
- 2:45 3:15 GROUP РНОТО
- 3:15 4:15 SIMON LEVIN (Princeton University) Distinguished Brin MRC Lecture: The Mathematics of Consilience
- 4:15 4:45 HIGH TEA

FRIDAY, APRIL 28, 2023

- 8:30 9:00 Breakfast
- 9:00 9:45 PADMANABHAN SESHAIYER (George Mason University) Computational Modeling for Understanding the Impact of Social Isolation and Human Behavior on COVID-19 Dynamics
- 10:00 10:45 CALISTUS NGONGHALA (University of Florida) Integrating Human Behavior, Economic Factors, and Infectious Disease Models to Predict Impacts of Disease Dynamics and Control
- 10:45 11:15 Coffee Break
- 11:15 12:00 JEMAL MOHAMMED-AWEL (Morgan State University) Mathematical Assessment of Bednets-Usage Heterogeneity on Malaria Dynamics
- 12:00 12:45 SIMON LEVIN (Princeton University) Challenges to the Classical Theory of Epidemics due to the Social Dimensions
- 12:45 1:15 LUNCH
- 1:15 1:20 Workshop Closing

Abstracts of talks

Data-Driven Mathematical Modeling of Respiratory Diseases

Sen Pei

Columbia University

Monday, April 24, 2023 @ 9:00 AM

In this talk, I will introduce several studies that used human mobility data to simulate transmission dynamics of respiratory diseases. Epidemic models were calibrated to real-world data using data assimilation techniques to generate real-time forecasting and infer key epidemiological parameters. We will further discuss the use of foot-traffic data collected from mobile phones to represent human behavior in disease transmission.

Spatial Non-Stationarity in Behaviors Protecting Against Infectious Diseases

TAYLOR ANDERSON

George Mason University

Monday, April 24, 2023 @ 10:00 AM

ABMs are well-suited for capturing heterogeneous human behaviors, an important underlying driver of disease transmission. Yet, individual health behaviors are highly complex, often influenced by cultural, political, and contextual factors, that are difficult to capture in models of disease spread. One such challenge is accounting for the influence of geographic location on an individual's decision making and how the same determinants of behavior in one location, may not have the same effect in another, also known as spatial non-stationarity. Using COVID-19 as a case study, this talk will explore the idea of spatial heterogeneity and spatial non-stationarity in various behaviors that protect against the transmission of infectious diseases such as following stay-athome guidelines and vaccine uptake and the challenges associated with incorporating spatial nonstationarity into ABMs. Initial results that aim to begin to understand such heterogeneity show that health behaviors can be explained, at least partially, by where people live. Accounting for spatial non-stationarity can help to inform regionally targeted interventions and inclusion into models may be useful.

Modeling the Role of Risky Behavior Among Injection Drug Users on Disease Transmission

FOLASHADE AGUSTO

University of Kansas

Monday, April 24, 2023 @ 11:15 AM

In this seminar, I will present a deterministic model for methicillin-resistant staphylococcus aureus (MRSA) among injection drug users. The model incorporates transmission of the bacteria among non-injection drug users and injection drug users (IDUs) who are both low-and high-risk users. The model also incorporates migratory movement between large metropolitan, suburban, and rural areas.

We use ethogram often used in social sciences to estimate the risk factors distinguishing the non-IDUs from low-risk and high-risk IDUs. Other model parameters were obtained by fitting the model to disease prevalence data from 2008-2013 obtained for non-IDUs from the Agency for Healthcare and Research and Quality (AHRQ), and US Census Bureau 2009-2013 Migration data. We implemented sensitivity analysis to determine the parameters with the most significant impact on the total number of infected individuals; the transmission probability and recovery rates for the subgroup were found to have the highest impact on the number of infected individuals. Furthermore, the sensitivity of the parameters in the different areas was the same when the areas are isolated. When they are connected, the parameters in large-metropolitan areas were more sensitive, and the rural areas were least sensitive.

The result shows that to effectively control the disease across the large-metropolitan, suburban, and rural areas, it is best to focus on managing both behavior and disease in the large-metropolitan area as this has a trickle-down effect on the other areas. Controlling behavior and disease at the same time in all regions will lead to the elimination of the disease.

Human Disease, Dynamics and Control, a Journey

JIM YORKE

University of Maryland

Monday, April 24, 2023 @ 2:00 PM

I will survey my modeling of measles, mumps, chicken pox, polio, gonorrhea, and HIV/AIDS to show how models have yielded important public health insights. And how COVID-19 yields insights important to modelling. All of this work is mostly due to my collaborators. References:

- Recurrent outbreaks of measles, chicken pox, and mumps, I. Seasonal variation in contact rates, and W. London, M.D. and J. A. Yorke, Amer. J. Epidemiology 98 (1973), 453-468.
- Seasonality and the requirements for perpetuation and eradication of viruses in populations, J. A. Yorke, N. Nathanson, G. Pianigiani and J. Martin, Amer. J. Epidemiology 109 (1979), 103-123.
- Gonorrhea Transmission Dynamics and Control, H. W. Hethcote and J. A. Yorke, Springer-Verlag Lecture Notes in Biomathematics #56, 1984.
- HIV Epidemics Driven by Late Disease-Stage Transmission, Brandy L. Rapatski, Frederick Suppe, and James A. Yorke, JAIDS, Journal of Acquired Immune Deficiency Syndromes, 38, 2005, 241-253.
- When the best pandemic models are the simplest, Sana Jahedi and James A. Yorke. Biology 2020, 9, 353;Covid-19 work in progress with Shayak Bhattacharjee

Managing Emerging Epidemics with Limited Testing Resources: COVID-19 and Beyond

JEFFERY DEMERS

University of Maryland

Monday, April 24, 2023 @ 3:15 PM

The emergence and spread of COVID-19 abruptly exposed the world's lack of preparedness for novel disease pandemics. In particular, COVID testing supplies during the initial wave of the pandemic fell well short of the resource levels needed to stymie the outbreak via identification-isolation strategies, and the few tests that were available were reserved for the most severe and vulnerable cases typically found in clinical settings rather than for non-clinical applications like test-tracequarantine programs. It is uncertain if the failure to manage COVID-19 in comparison compared past outbreaks, such as the 2003 SARS-CoV outbreak, for example, has been due to particular biological features of the disease, public policy decisions, or simple random poor luck. To determine how disease biology influences controllability and optimal testing resource allocation strategies, we develop a generalized integro-partial differential equation disease model with resource-limited testing and quarantine controls that can describe a diverse array of diseases such as measles, smallpox, and COVID-19, all under a single analytical framework. We find that no one disease characteristic is sufficient for explaining the controllability of a disease or determining an optimal control strategy. Rather, we find that the compounding influence of multiple plays a key role in determining whether a disease can be controlled with identification-isolation control strategies. In particular, this compounding effect helps explain why the Omicron variant has been especially challenging to manage. Our results help to inform policy makers on controllability expectations and optimal resource allocation strategies applicable to both the current pandemic and the inevitable next novel disease epidemic.

Human Behavior Modeling, the Exposome and Disease Progression

LOUIS J. GROSS

University of Tennessee

Tuesday, April 25, 2023 @ 9:00 AM

The integration of human behavior modeling with classic structured population models for infectious diseases has been ongoing for several decades. Despite the tremendous impact on human health of noncommunicable diseases which make up by far the majority of causes of mortality in much of the world, there has been relatively little connection between human behavior modeling and models in areas such as cancer, heart disease, stroke and other physiologically-connected diseases. Human behavior directly impacts exposure at the individual and population level to known factors which impact noncommunicable disease progression, including diet, activity-level and environmental toxicants. The term used to describe the exposure throughout an individual's lifetime to factors which affect health is the exposome. Much of environmental risk assessment deals with models for the fate and effects of toxicants in the environment, though the magnitude of exposures included in these models doesn't account for social factors which impact behaviors. My objective is to discuss how the various theories derived from social psychology which have been incorporated in human behavior models and linked to climate and infectious disease modeling can provide insights about impacts on the exposome at the individual level, how these may be aggregated at population scale and the implications for disease progression.

Digital Twins of US Social Contact Networks and Their Applications to Pandemic Science

MADHAV MARATHE

University of Virginia

Tuesday, April 25, 2023 @ 10:00 AM

The ongoing COVID-19 serves as a grim reminder of our collective inability to control pandemics. Globalization, anti-microbial resistance, urbanization, climate change, social media and ecological pressures threaten to upend the progress we have made in fighting infectious diseases. Pandemics will happen again: it is not if but when. In this talk, I will describe an approach in data-driven approach to network epidemiology. A critical component of such an approach is the development of national scale digital twins of social contact networks. We describe how such digital twins can be constructed and used to support real-time pandemic science.

Modeling School-Based Interventions Against COVID-19

MEAGAN FITZPATRICK

University of Maryland School of Medicine

Tuesday, April 25, 2023 @ 11:15 AM

The COVID-19 pandemic induced historic educational disruptions. Schools faced substantial challenges in applying infection control principles to their settings. We developed an agent-based model simulating COVID-19 transmission in elementary and high school communities, with the goal of informing COVID-19 mitigation policies for schools in the United States. We evaluated the anticipated impact on outbreak risk and total outbreak size for a range of intervention measures including isolation of symptomatic individuals, quarantine of school-based contacts, reduced class sizes, alternative schedules, asymptomatic screening, and vaccination. We also conducted a costbenefit analysis of various in-school COVID-19 testing programs, considering the counterbalancing costs of childcare for quarantined students. We also identified relationships between community COVID-19 incidence, community vaccination coverage, and expected school-based risk. Our results demonstrated that high levels of community transmission will often lead to outbreaks in school environments, but testing, vaccination, and other in-school mitigation efforts can effectively create safer learning environments and reduce student and teacher absenteeism.

Investigating the Impact of Silent Spreaders in COVID-19

OMAR SAUCEDO

Virginia Tech University

Tuesday, April 25, 2023 @ 2:00 PM

The dynamic nature of the COVID-19 pandemic has demanded a public health response that is constantly evolving due to the novelty of the virus. Many jurisdictions in the United States, Canada, and across the world adopted social distancing efforts and made recommendations for masks to minimize disease spread. Considering these measures, it is important to understand the contributions of subpopulations – such as "silent spreaders" – to disease transmission in order to inform public health strategies. With this in mind, we develop a hybrid stochastic model that includes two classes of individuals: silent spreaders, who neither have symptoms nor disease-induced mortality; and symptomatic spreaders, who experience symptoms and a resultant mortality rate. Using previously established methodologies, we study the role of demographic and environmental variability on COVID-19 dynamics.

Asymptomatic: How Deciphering the Silent Spread of COVID-19 Helps Prepare Us for Pandemics to Come

JOSHUA WEITZ

Georgia Tech

Tuesday, April 25, 2023 @ 3:15 PM

This talk focuses on explaining the governing principles by which behavioral differences associated with asymptomatic vs. symptomatic transmission can lead to a more severe outbreak at the population scale relative to outbreaks in which transmission is tied to severe symptoms. In doing so, I will also identify challenges in developing intervention frameworks required to prepare for pandemics to come.

Incorporating Dynamics of Risk Responsiveness and Human Behavior Change in Epidemic Models

NAVID GHAFFARZADEGAN

Virginia Tech University

Wednesday, April 26, 2023 @ 9:00 AM

While much effort has gone into building predictive models of the COVID-19 pandemic, some have argued that early exponential growth combined with the stochastic nature of epidemics make the long-term prediction of contagion trajectories impossible. We conduct two complementary studies to assess model features supporting better long-term predictions. First, we leverage the diverse models contributing to the CDC repository of COVID-19 USA death projections to identify factors associated with prediction accuracy across different projection horizons. Second, we introduce a very simple model, SEIRb, that incorporates these features, and offers informative predictions for as far as 20-weeks ahead, with accuracy comparable with the best models in the CDC set. We argue that key to the long-term predictive power of multi-wave COVID-19 trajectories is capturing behavioral responses endogenously: balancing feedbacks where the perceived risk of death continuously changes transmission rates through the adoption and relaxation of various Non-Pharmaceutical Interventions.

Modeling Social Complexity in Epidemiology: Risk Perception and Adaptive Human Behavior

BALTAZAR ESPINOZA

University of Virginia

Wednesday, April 26, 2023 @ 10:00 AM

The COVID-19 pandemic highlighted critical factors to be addressed in the modern study of epidemic dynamics: human behavior, economics, biosurveillance, social dynamics and information sharing, are but examples of these. Non-pharmaceutical interventions (NPIs) constitute a suite of front-line behavioral responses, however collective compliance depends on individual level decisions, which may assemble a behavioral immune system at the population scale. Yet, many epidemiological models currently in use do not include a behavioral component, and do not address the potential consequences of individuals' adaptive behavioral responses. The simultaneously evolving processes of individuals making behavioral decisions driven by the epidemic dynamics, that in turn reshape the contagions progression, make of epidemics complex adaptive systems. To study the complex dynamics between behavioral adaptations and the epidemic progression, we use a mechanistic modeling framework that explicitly incorporates the interdependence between the (individual-level) adaptive behavioral choices and the (population-level) progression of the infection process. We found that individuals' risk perceptions in the presence of asymptomatic individuals modulates the final epidemic size. Moreover, under behavioral polarization, privately determined behavioral responses may increase the final size of the epidemic, relative to the homogeneous behavior scenario. Finally, we explored the effect of testing as a potential source of misinformation

about the risk of infection, which may lead to harmful behavioral decisions ultimately increasing

epidemic burden.

Finite Expression Method for Discovering Physical Laws from Data

HAIZHAO YANG

University of Maryland

Wednesday, April 26, 2023 @ 11:15 AM

Machine learning models are currently the tools of choice for uncovering physical laws from data in the era of data science. Although they have shown promising performance in prediction, their descriptions are often too verbose. This talk introduces a new methodology that seeks interpretable learning outcomes in the space of functions with finitely many analytic expressions and, hence, this methodology is named the finite expression method (FEX). It is proved in approximation theory that FEX can avoid the curse of dimensionality in discovering high-dimensional complex systems. As a proof of concept, a deep reinforcement learning method is proposed to implement FEX for learning various PDE systems.

Is Local Information Enough to Predict an Epidemic?

CHRISTIAN BORGS

UC Berkeley

Wednesday, April 26, 2023 @ 2:00 PM

Is local information enough to predict an epidemic?

While simpler models of epidemics assume homogeneous mixing, it is clear that the structure of our social networks is important for the spread of an infection, with degree inhomogeneities and the related notion of super-spreaders being just the obvious reason. This raises the question of whether knowledge of the local structure of a network is enough to predict the probability and size of an epidemic. More precisely, one might wonder whether having access to randomly sampled nodes in the network and their neighborhoods, we can predict that above quantities.

It turns out that in general, the answer to this question is negative, as the example of isolated, large communities show. However, under a suitable assumption on the global structure of the network, the size and probability of an outbreak can be determined from local graph features. The research presented int this talk is joint with Yeganeh Alimohammadi and Amin Saberi.

Reservoir Computing for Time Series Prediction with Applications to Disease Dynamics

MICHELLE GIRVAN

University of Maryland

Wednesday, April 26, 2023 @ 3:15 PM

In recent years, machine learning methods such as deep learning have proven enormously successful for many learning tasks. However, these methods often require huge amounts of training data, which are not available for many applications. In this talk, I will discuss how a reservoir computer (RC) offers key advantages for time series prediction in many applications, with a focus on disease dynamics. An RC - a specific architecture of artificial neural network that offers a "universal" dynamical system - draws on its own internal complex dynamics in order to construct predictions. Like many other machine learning architectures, RCs provide a knowledge-free approach because they forecast purely from past measurements without any specific knowledge of the system dynamics. By building a scheme that judiciously combines the knowledge-free prediction of the RC with a knowledge-based model, we demonstrate a dramatic improvement in forecasting complex dynamics. In addition, we show that we can forecast the dynamics of not only individual time series but also of spatial and networked systems by constructing appropriate parallel RC architectures. Finally, we discuss the utility of RC approaches for forecasting epidemics and demonstrate their effectiveness for predicting COVID-19 dynamics.

NSF/Math Bio Funding Opportunities

ZHILAN FENG

Purdue University and NSF

Wednesday, April 26, 2023 @ 4:00 PM

The Efficacy of COVID-19 Testing and Vaccination in Schools

YEGANEH ALIMOHAMMADI

Stanford University

Thursday, April 27, 2023 @ 9:00 AM

During the COVID-19 pandemic, safety concerns led to widespread closures despite the importance of keeping schools open. Our study investigates how effectively regular testing and vaccination measures can mitigate these concerns and keep children safe in school. Using data from the Los Angeles Unified School District, we found that regular testing was remarkably effective in containing COVID-19, with positivity rates significantly lower than in the entire Los Angeles County. Vaccination also effectively reduced COVID-19 cases among children aged 12-18 and 5-11. Our study revealed a notable association between school socioeconomic status and COVID-19 positivity rates, indicating the need for addressing socioeconomic disparities in COVID-19 prevention efforts.

Unraveling Host Behavioral Heterogeneity for Models of Infectious Disease Dynamics and Control

SHWETA BANSAL

Georgetown University

Thursday, April 27, 2023 @ 10:00 AM

Host behavior remains the single biggest gap in our understanding of infectious disease dynamics for directly-transmitted pathogens, limiting our ability to predict disease emergence, forecast disease spread, and achieve disease elimination. In this talk, I will discuss case studies in which we leverage traditional and novel behavioral data sources with the tools of network science and spatial modeling to inform disease surveillance, disease control, and public health policy.

The Role of Interventions in COVID-19 Outbreak Control

LAUREN CHILDS

Virginia Tech University

Thursday, April 27, 2023 @ 11:15 AM

As COVID-19 is known to be transmitted by non-symptomatic individuals, travel restrictions and social distancing measures were broadly implemented in order to decrease transmission. Alternatives to these restrictive measures, such as testing coupled with quarantine, and the advent of effective vaccines, were used to slow the spread of COVID-19. The latter also led to open questions on how best to build and maintain protection within the population. We developed a suite of ordinary differential equation models to both consider how different testing strategies impact disease spread and how co-variates such as age alter the distribution of immunity. The models also account for changes to infectivity of the virus, such as public health mitigation protocols over time, increases in the transmissibility of variants of concern, changes in compliance to mask wearing and social distancing, and changes in testing rates. We estimated that a large fraction of the population would develop some immunity but it would be insufficient to stave off future resurgence. The timing and severity of such resurgence, however, varies in magnitude based in part on biological and implementation factors such as relaxation of non-pharmaceutical interventions, the rate of waning immunity, the transmissibility of variants of concern, and the protective characteristics of the vaccines. In addition, the role of human behavior needs to be assessed to be able to accurately predict pandemic dynamics and to reduce health and economic impacts.

Modelling SARS-CoV-2 Immuno-Epidemiology, Vaccination, and Invasion Dynamics of New Variants

CHADI SAAD-ROY

UC Berkeley

Thursday, April 27, 2023 @ 2:00 PM

The COVID-19 pandemic is a global emergency with significant morbidity and mortality. In this talk, we summarize recent modeling that investigates SARS-CoV-2 immuno-epidemiology and the impact of vaccination on potential future landscapes of immunity. Through a general framework, we also explore the potential epidemiological and evolutionary considerations of various vaccine dosing regimes, and we then examine the impact of vaccine nationalism. Using a simple model, we examine the invasion dynamics of SARS-CoV-2 variants and the impacts of vaccine breakthrough infections. Finally, we highlight crucial empirical and theoretical gaps that need to be addressed, and conclude with future outlooks.

Distinguished Brin MRC Lecture: The Mathematics of Consilience

SIMON LEVIN

Princeton University

Thursday, April 27, 2023 @ 3:15 PM

In his book, "Consilience: The Unity of Knowledge" the late biologist E.O. Wilson lamented the "fragmentation of knowledge and resulting chaos in philosophy," primarily between the sciences and humanities, which he attributed to "artifacts of scholarship." His concerns and aspirations similarly could have been applied within the disciplines of science, as made clear in Philip Anderson's essay, "More is Different," highlighting the disparities between reductionistic and holistic views of science. Wilson goes on to write that mathematics "because of its effectiveness in the natural sciences seems to point arrowlike toward the goal of objective truth," indeed even referring to Wigner's famous essay "The Unreasonable Effectiveness of Mathematics in the Natural Sciences." But Wilson seems unconvinced, arguing that logical positivism, the notion that the philosophical problems worth studying are just those that are subject to logical analysis, "are more commonly studied in philosophy, as dinosaur fossils are studied in paleontology laboratories, to understand the causes of extinction." I will argue that mathematics has much to offer in providing a unification of the disciplines, drawing on concepts from the subject of complex adaptive systems to relate the reductionistic and holistic approaches, to understand scaling, emergence, pattern formation, critical transitions and, most crucially, the conflicts between the interests of individual agents and the collective good that were central to much of Wilson's own work, and are key to the search for assuring a sustainable planet.

This talk will be in Kirwan 3206.

Computational Modeling for Understanding the Impact of Social Isolation and Human Behavior on COVID-19 Dynamics

PADMANABHAN SESHAIYER

George Mason University

Friday, April 28, 2023 @ 9:00 AM

Social isolation is associated with multiple negative outcomes such as substance use and abuse, domestic violence, and reduced mental and physical health. Many of these outcomes are conditioned on the socioeconomic circumstances of individuals or communities, with rural, low-income, and older communities at elevated risk. However, isolation was always one of first policy actions that was practiced as lockdowns and confinement strategies were implemented worldwide as a common attempt of countries to save lives and mitigate the spread of COVID-19. In this work, we will share some of the models that helped to capture the secondary effects due to social isolation that are often triggered such as domestic violence, human behavior and socio-economic contexts. We will also discuss state-of-the-art the application of neural network methods that are informed by the physics in these models and help to estimate parameters associated with these models. We will share numerical experiments for benchmark problems with both synthetic as well as real data that suggests the importance of such computational approaches that continue to help provide the much-needed insight into understanding spread of infectious diseases.

Integrating Human Behavior, Economic Factors, and Infectious Disease Models to Predict Impacts of Disease Dynamics and Control

CALISTUS NGONGHALA

University of Florida

Friday, April 28, 2023 @ 10:00 AM

A dynamic model framework that incorporates socio-economic and human behavioral approaches into disease epidemiology is presented and analyzed in order to assess the impact of socialdistancing on disease transmission. The model exhibits a variety of dynamical behaviors ranging from globally stable states through bistable states and sustained bounded periodic oscillations. Simulations of the model suggest that the disease under consideration can be contained if a sizable proportion of the population embrace strict social-distancing and that prospects of containing the disease are enhanced by the strength of the economy.

Mathematical Assessment of Bednets-Usage Heterogeneity on Malaria Dynamics

JEMAL MOHAMMED-AWEL

Morgan State University

Friday, April 28, 2023 @ 11:15 AM

The heavy and widespread use of insecticides-based mosquito control, over the last few decades, has resulted in a significant reduction of malaria burden in endemic areas, prompting a renewed quest for malaria eradication. Although most of the gains are attributed to the use of bednets, particularly long-lasting insecticidal nets (LLINs), the significant heterogeneity in bednets usage in endemic areas poses an important challenge to the eradication efforts. In this talk, I will discuss a mathematical modeling framework for assessing the population-level impact of bednets-usage heterogeneity on malaria transmission dynamics and control.

Challenges to the Classical Theory of Epidemics due to the Social Dimensions

SIMON LEVIN

Princeton University

Friday, April 28, 2023 @ 12:00 PM

The standard theory of infectious diseases, tracing back to the work of Kermack and McKendrick nearly a century ago, has been a triumph of mathematical biology, a rare marriage of theory and application. Yet the limitations of its most simple representations, which have always been known, have been laid bare in dealing with COVID-19, sparking a spate of extensions of the basic theory to deal more effectively with aspects of viral evolution, asymptotic stages, heterogeneity of various kinds, the ambiguities of notions of herd immunity, the role of social behaviors and other features. This lecture will address some progress in addressing these, with emphasis on social behaviors, and address the open challenges in expanding the mathematical theory.

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

ALONSO GABRIEL OGUEDA, George Mason University AMIR SAPKOTA, University of Maryland BALTAZAR ESPINOZA, University of Virginia BILL FAGAN, University of Maryland BINOD PANT, University of Maryland CALISTUS NGONGHALA, University of Florida CHADI SAAD-ROY, UC Berkeley CHRISTIAN BORGS, UC Berkeley DAVE LEVEMORE, University of Maryland DORON LEVY, University of Maryland/Director, Brin MRC FOLASHADE AGUSTO, University of Kansas FRANK MCBRIDE, University of Maryland GIULIA PULLANO, Geooge Washington University HAIZHAO YANG, University of Maryland JEFFERY DEMERS, University of Maryland JEMAL MOHAMMED-AWEL, Morgan State University JIM YORKE, University of Maryland JOSHUA WEITZ, Georgia Tech JULIANA TAUBE, Georgetown University LAUREN CHILDS, Virginia Tech University LOUIS J. GROSS, University of Tennessee MADHAV MARATHE, University of Virginia MARRON MCCONNELL, University of Maryland MEAGAN FITZPATRICK, University of Maryland School of Medicine MICHELLE GIRVAN, University of Maryland NAVID GHAFFARZADEGAN, Virginia Tech University **OMAR SAUCEDO**, Virginia Tech University PADMANABHAN SESHAIYER, George Mason University SEN PEI, Columbia University SHWETA BANSAL, Georgetown University SIMON LEVIN, Princeton University SOYOUNG PARK, University of Maryland STEVEN AULT, University of Maryland TAYLOR ANDERSON, George Mason University VINCE LYZINSKI, University of Maryland YEGANEH ALIMOHAMMADI, Stanford University ZHILAN FENG, Purdue University and NSF