CCSS 2022 Abstracts

WEDNESDAY, AUGUST 10TH

Morning Session

Chair: Nicholas Landry, University of Vermont

Bounded-confidence models of opinion dynamics on networks
9:00 AM - 10:00 AM (Invited)
Heather Zinn Brooks, Harvey Mudd College

To better understand the spread of online content and its consequences on public opinion, policy, and voting, mathematical modeling of opinion dynamics is becoming an increasingly popular field of study. In this talk, I will introduce you to a class of models of opinion dynamics on networks called bounded-confidence models. These relatively simple models can produce delightfully complicated dynamics and provide a rich source of study for the interplay between dynamics and structure. I will discuss some novel twists on bounded-confidence models that my collaborators and I have been developing, including one or more of the following: information cascades, bifurcations in "smoothed" bounded-confidence models, and extensions to hypergraphs.

Simulating the spread of an emerging multihost pathogen in a novel wildlife reservoir
10:30 AM - 10:50 AM (Contributed)
Aniruddha Belsare, Emory University

Using an agent-based modeling approach that incorporates within-host infection and immunity dynamics, age- and sex-dependent sociality, seasonality, and harvest, I am investigating the factors that drive the spread, persistence, and evolution of SARS-CoV-2 in white-tailed deer populations.

Asymmetric coupling optimizes interconnected consensus systems
10:50 AM - 11:10 AM (Contributed)
Dane Taylor, University at Buffalo, SUNY

Networks are often interconnected with one system wielding greater influence over another, yet we lack basic insights for how such an asymmetry affects collective dynamics. This is particularly important for group decision making within social networks supported by AI agents, which we model as coupled consensus systems. We show that coupling asymmetry can monotonically increase/decrease the convergence rate of consensus or give rise to different types of optima that maximally accelerate consensus. For the coupling of faster and slower systems, we identify a bifurcation: if their timescales are very dissimilar, then the optimal asymmetry involves the faster system "dominating" the slower one; otherwise, they are optimized with an intermediate amount of asymmetry, and it is less clear which system should be more influential. Our findings support the design of human-AI decision systems and asymmetrically coupled networks, more broadly.

Unrepresentative Outcomes in a Model of Voter Turnout
11:20 AM - 11:40 AM (Contributed)
Ekaterina Landgren, Cornell University

Voter models can provide insight into voter behavior and help forecast elections. Many popular voter models are based on opinion dynamics. However, patterns in voter turnout can affect election outcomes and distort representation of opinions. Furthermore, voter turnout varies highly depending on type, place, and size of elections. In our agent-based model, we take voter turnout into account by making a distinction between voter opinion and the act of voting. We assign an opinion to each node, which represents a potential voter. The potential voters make a decision to vote or not based on their local network information. We explore a variety of network structures and node distributions and find that certain structures and parameter regimes favor undemocratic outcomes where a minority faction wins, especially when the local opinion distribution is not representative of the global opinion.

Modeling Misinformation Discourse and Influence on Social Media using Agent-Based Modeling
11:40 AM - 12:00 PM (Contributed)
Hong Qu, Northeastern University

Monitoring the diffusion of misinformation on social media in real-time requires new approaches for modeling the behavior of the accounts who share content. We propose a novel process for tracking the path of retweets to identify purveyors of misinformation. Three insights inform this model: 1) social media content update frequently, hence we must use temporal rather than static networks; 2) shared social media posts contain the entire original content and cascade forward as out-degree edges in directed graphs; 3) whereas centrality typically represents influence as positive authority but neglects to account for negative misinformation, we propose assigning fakeness and credibility values for posts and agents respectively on a diverging scale between -1 to 1 to modulate whether downstream agents will or won't share particular posts. To evaluate this model, we designed a two-step agent-based simulation: in the first step, we generated a 500 node network for 50 messages to diffuse; in the second step, we simulate a random walker to iteratively explore the graph seeking the most influential agents by snowball sampling for the highest out-degree nodes. Additionally, we conducted an empirical experiment to identify anti-vaccination influencers on Twitter to validate the efficacy of this process. Results demonstrate that this approach for graph exploration successfully identifies and ranks influencers in synthetic networks as well as in a real-world retweet network.

Afternoon Session

Chair: Dan Larremore, University of Colorado Boulder

Complex contagions and hybrid phase transitions
2:00 PM - 3:00 PM (Invited)
Joel Miller, La Trobe University

A complex contagion is an infectious process in which individuals may require multiple transmissions before changing state. These are used to model behaviours if an individual only adopts a particular behaviour after perceiving a consensus among others. We may think of individuals as beginning inactive and becoming active once they are contacted by a sufficient number of active partners. These have been studied in a number of cases, but analytic models for the dynamic spread of complex contagions are typically complex. Here we study the dynamics of the Watts threshold model (WTM) assuming that transmission occurs in continuous time as a Poisson process, or in discrete time where individuals transmit to all partners in the time step following their infection. We adapt techniques developed for infectious disease modelling to develop an analyse analytic models for the dynamics of the WTM in configuration model networks and a class of random clustered (triangle-based) networks. The resulting model is relatively simple and compact. We use it to gain insights into the dynamics of the contagion. Taking the infinite population limit, we derive conditions under which cascades happen with an arbitrarily small initial proportion active, confirming a hypothesis of Watts for this case. We also observe hybrid phase transitions when cascades are not possible for small initial conditions, but occur for large enough initial conditions. We derive sufficient conditions for this hybrid phase transition to occur. We show that in many cases, if the hybrid phase transition occurs, then all individuals eventually become active. Finally, we discuss the role clustering plays in facilitating or impeding the spread and find that the hypothesis of Watts that was confirmed in configuration model networks does not hold in general. This approach allows us to unify many existing disparate observations and derive new results.

Methods for Determining Subsets of High Impact, Probabilistically Dependent Medical Conditions Represented in a Directed Graph
3:30 PM - 3:50 PM (Contributed)
Hunter Rehm, University of Vermont

One of the longest standing questions in network theory is how a component influences other parts in the system, and how that role is affected when restricting the navigation through the network. The Katz score, one of many centrality measures created for this purpose, takes into account all possible walks through the network, penalizing each additional step in a walk by a scalar called the Katz parameter. This centrality measure often covers an infinite number of walks with infinite length. In this paper we identify the maximum path length which has influence on the Katz score. We ultimately provide guidance when deciding which Katz parameter to use as it depends on the path length of interest. We show how changing the Katz parameter affects the ranking of the vertices in some synthetic graphs as well as NASA's expert informed network of medical dependencies called the Susceptibility Inference Network (SIN).

The Role of Masks in Mitigating Viral Spread on Networks
3:50 PM - 4:10 PM (Contributed)
Yurun Tian, Carnegie Mellon University

Mask-wearing has been an important measure in curbing the spread of the virus during the COVID-19 pandemic. While it is well-known that masks qualitatively mitigate viral spread by limiting the transmission of respiratory droplets, many important questions about the quantitative impact of masks remain open. In this work, we provide comprehensive quantitative analysis of the impact of mask-wearing where people can wear one of several types of masks with different levels of protection, or wear no mask. Typically, the protection provided by a mask is characterized in terms of its inward and outward efficiency. The former is the probability that respiratory droplets will pass from the outside layer of the mask to the inside, while the latter gives the probability that respiratory droplets will pass from the inside layer of the mask to the outside. The transmission probability from a type-i mask-wearing individual to a type-j mask-wearing individual is thus given by $\mathbf{T}_{ij} := \epsilon_{out,i}\epsilon_{in,j}T$, where $\epsilon_{out,i}$ is the outward efficiency of a type-i mask, $\epsilon_{in,j}$ is the inward efficiency of a type-j mask, and T is the baseline transmissibility of the virus, i.e., the probability of transmission in the presence of no masks. We derive analytical results for three important quantities: the probability of emergence, the epidemic threshold (i.e., the basic reproductive number R0) and the expected epidemic size. Leveraging our analytical results, we also seek to answer an important question as to whether masks with high outward efficiency or high inward efficiency are most effective in mitigating a viral spread. Interestingly, we find that different mask allocation strategies work best at different stages of the propagation process. Simulation result shows that the probability of emergence decreases while the total epidemic size increases as the proportion of the outward-good mask wearers in the population grows. Put differently, outward-good masks are more helpful in terminating the spreading process before the emergence of the pandemic, while it is the inward-good masks that are most essential in reducing the total fraction of the infected population given that the epidemic has already emerged. More generally, we show that at the early stages of a spreading process, a source-control oriented strategy is crucial to preventing the epidemic to emerge. On the other hand, if an epidemic has already emerged, it becomes most effective to implement a strategy focusing on individuals' self protection to limit the final epidemic size. We believe that this result has implications that go beyond the impact of masks can be applied to other pandemic mitigation strategies including prioritization of vaccines, social distancing measures, and other non-pharmaceutical interventions.

THURSDAY, AUGUST 11TH

Morning Session

Chair: Joan Ponce, UCLA

Linking viral kinetics with disease transmission and control
9:00 AM - 10:00 AM (Invited)
Stephen Kissler, Harvard University

The detectability, contagiousness, and clinical course of acute infections all depend on viral load. Viral load can vary immensely across individuals and over time. However, standard disease transmission models overlook much of this complexity, treating infection and infectiousness as a binary state. In our recent work, we study the impact of viral kinetics on disease transmission. I will introduce a statistical framework for inferring key components of SARS-CoV-2 viral trajectories. Using this framework, I will discuss how an understanding of viral kinetics assists with the detection and diagnosis of infection, informs outbreak control, and illuminates important elements of the immune response. I will conclude with a look forward at the role viral kinetic studies may play in the control of acute respiratory viruses and infectious diseases more broadly.

Estimating the Mitigation Potential of Screening Programs for Infectious Diseases
10:20 AM - 11:20 AM (Invited)
Dan Larremore, University of Colorado Boulder

The premise of screening programs for infectious diseases is that screening tests taken on the individual level have effects on population transmission. How can we estimate those effects? What data or assumptions are needed to do so effectively? And, how can estimates be integrated into typical SIR-family transmission models? In this talk, I'll introduce the idea of test effectiveness, TE, a quantity that can be calculated from information about testing, within-host kinetics, and how individuals behave after receiving a positive diagnosis. Using examples of SARS-CoV-2, RSV, and influenza, we'll explore the factors that affect TE, and show how one can integrate testing into SIR-family models without directly simulating within-host kinetics, screening programs, and behavioral responses. Joint work with Casey E. Middleton.

Dynamics on Simplicial Complexes using the Generalized Hodge Laplacian
11:40 AM - 12:00 PM (Contributed)
Cameron Ziegler, University at Buffalo, SUNY

Simplicial complexes provide us with a way to generalize graphs into higher-dimensions. We can study dynamics, such as opinion dynamics or contagion spread, on simplicial complexes instead of on graphs. Consensus dynamics applied to simplicial complexes will converge to a certain subspace dependent on the homology of the complex. These dynamics are based on the Hodge Laplacian, a matrix obtained from the connections of nodes through simplicies of multiple dimensions. In addition, we can weight the higher- and lower-dimensional components of the Hodge Laplacians to optimize the convergence rate of these dynamics.

Afternoon Session

Chair: Heather Zinn Brooks, Harvey Mudd College

Harder, better, faster, stronger cascades – or simply larger?
2:00 PM - 2:20 PM (Contributed)
Jonas Juul, Cornell University

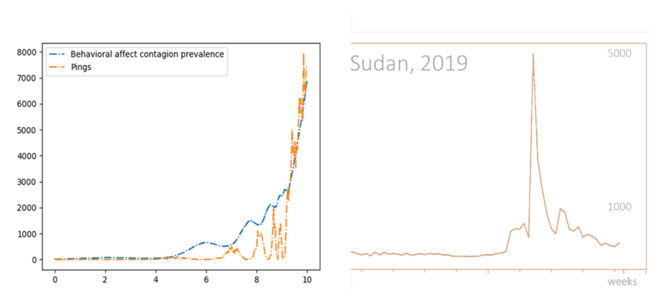
Do some types of online content spread faster or further than others? In recent years, many studies have sought answers to such questions by comparing statistical properties of network paths taken by different kinds of content diffusing online. Here we demonstrate the importance of controlling for correlations in the statistical properties being compared. In particular, we show that previously reported structural differences between diffusion paths of false and true news on Twitter disappear when comparing only cascades of the same size; differences between diffusion paths of images, videos, news, and petitions persist. Paired with a theoretical analysis of diffusion processes, our results suggest that in order to limit the spread of false news it is enough to focus on reducing the mean "infectiousness" of the information. Joint work with Johan Ugander.

Log-periodic Power Laws in Behavioral Synchronization

2:20 PM - 2:40 PM (Contributed)

T. Martin Smyth, United States Department of Defense, Washington, DC **Joseph Finn**, IMC Trading, Chicago, IL **Cody Buntain**, University of Maryland College of Information Studies, College Park, MD **Jason J. Jones**, Stony Brook University Institute for Advanced Computational Science, Stony Brook, NY

This research seeks to emulate the dynamics driving a characteristic signal in the time series of aggregate social media platform activity observed during mass mobilization events; it draws on prior work that describes the application of Log-Periodic Power Law Singularity (LPPLS) models to financial market contagions [1]. Information behavioral contagions propagate freely on social media follower networks. However, the effect of inhomogeneities in the substrate graph morphology is that the contagion-spreading parameter β varies in time. We take the manifestation of an LPPLS waveform in the contagion prevalence as given; we model the contagion-spreading rate parameter β as varying log periodically in time and propagate the simulated contagion process on toroidal grid lattices, which we expand exponentially in time. We find that doing so yields simulated activity time series resembling empirical observations for real-world mass mobilization events (Fig. 1).



[1] Sornette D, Johansen A and Bouchaud J-P (1996). "Stock Market Crashes, Precursors and Replicas." Journal de Physique I, EDP Sciences, 6(1), 167–175.

The coevolution of alcohol use and social networks of college students

2:40 PM - 3:00 PM (Contributed)

Alice Schwarze, Dartmouth College

Recent findings in behavioral research indicate a complex interplay between a student's alcohol consumption, intended change to alcohol consumption, and their social networks. Guided by evidence from a recent study involving ecological momentary assessment (EMA) of college students, we develop a mathematical model of the coevolution of students' social networks, drinking behavior, and intention to change. The 2-variable co-evolving weighted network model leads to a "consensus" alcohol consumption in the asymptotic limit on each connected component. We identify the transition between a parameter regime in which one observes a long transient period with a connected network with consensus alcohol consumption and a parameter regime with a short transient period that leads to an asymptotically fragmented network in which students in different connected components can have different drinking behaviors. Our model facilitates the theoretical and computational exploration of interventions (such as mindfulness training or perspective taking) and heterogeny in students' decision-making (such as decisions to decrease ties with the most- or least-drinking friends). We anticipate that our model can provide a theoretical and computational framework for developing successful personalized interventions that can help students develop responsible and healthy drinking behaviors.

FRIDAY, AUGUST 12TH

Morning Session

Chair: Joel Miller, La Trobe University

The importance of heterogeneity and adaptivity of human behavior for epidemic models

9:00 AM - 10:00 AM (Invited)

Laurent Hébert-Dufresne, University of Vermont

Modern epidemic models have a long history going back almost a hundred years to the seminal work of William O. Kermack and Anderson G. McKendrick at the end of the 1920s. Their models were meant to provide a theoretical understanding of epidemic dynamics, and not necessarily to contribute to epidemic forecasting and public health policies as is now common practice for the work they inspired. In this lecture, I will review the impacts of one key assumption made by Kermack and McKendrick regarding homogeneous, random, and static human behavior. To relax this assumption we will then rely on mathematical tools from network science as well as data on human mobility. The implications of these new tools will be discussed in the context of past and current epidemics. As we will see, failure to account for the heterogeneity and adaptiveness of human behavior affects epidemic forecasting as well as our basic understanding of epidemic dynamics.

Weighted Belief Networks Unify Simple and Complex Contagion
10:30 AM - 10:50 AM (Contributed)
Rachith Aiyappa, Indiana University Bloomington

From the spreading of infectious diseases to the diffusion of behaviors, and beliefs, contagion is one of the most fundamental dynamical processes in social systems. It drives challenges like the prevalence of false information. The dynamics of contagion fall into two classes—simple and complex. Simple is when each exposure results in an adoption probability independent of past exposures (SIR) while complex is when the adoption probability is no longer independent but reinforced with the increasing number of exposures (threshold models). Although many theories and models have been proposed to understand the cognitive mechanisms of diffusion of human beliefs and behaviors, integrating them with social contagion theory is still in its infancy. For instance, it is well known that humans strive for the internal coherence of beliefs but it is rarely studied in the context of social networks. On the other hand, social contagion models often ignore cognitive mechanisms and assume dynamics rather than allowing them to emerge from underlying cognitive mechanisms. This is particularly troubling given that a single social system can exhibit a spectrum of contagion dynamics—from simple to complex—simultaneously. This raises the question—can there be a unifying cognitive model giving rise to both simple and complex contagion dynamics? We show that our weighted belief dynamics model can unify internal coherence with social contagion theory and exhibits both simple and complex contagion dynamics. Building on a recent work that models the internal belief system as an undirected, unweighted network where nodes represent concepts and binary edges represent beliefs, we show that introducing the belief strength to the model allows both simple and complex contagion dynamics to emerge from belief interactions. We model the force toward internal coherence based on the energy of an individual. The lower the energy is, the more stable such an individual is. Social communication is modeled as a process of transmitting a belief from one individual to another. At each time step, an individual communicates a belief, from their internal belief system. Their neighbor, in response to this, updates their internal belief based on a Gaussian distribution whose mean is governed by social influence and the cognitive bias of the individual to be an internally coherent state. We demonstrate that both simple and complex contagion dynamics can indeed emerge from our model. When there is a stabilizing contagion that stabilizes unstable belief systems, we observe the simple contagion dynamics; when a new stable belief system competes with an already established stable belief system, the dynamics manifest itself as a complex contagion. This finding is reinforced by the observation of optimal modularity, a counter-intuitive phenomenon occurs with complex contagion.

A Simplicial Threshold Model for Higher-order Cascades
10:50 AM - 11:10 AM (Contributed)
Bengier Ülgen Kılıç, University at Buffalo, SUNY

The spread of contagions, information, and epidemics across spatially embedded social networks often exhibit two competing spreading mechanisms, local wavefront propagation (WFP) and nonlocal appearance of new clusters (ANC), which occur due to the presence of both short- and long-range edges. At the same time, persons' behaviors can be influenced by their relationships with individuals as well as groups, and there is a lack of models and theory for higher-order cascades in which spreading is mediated by dyadic, triadic and higher-order interactions. Thus motivated, we extend the Watts threshold model for social contagions by introducing a simplicial threshold model (STM) for cascades over simplicial complexes in which k-simplices encode relationships between k+1 actors. We find that higher-order interactions and thresholding cooperatively guide cascades along multidimensional geometrical channels in a simplicial complex. We support our findings with bifurcation theory to predict wavefront speeds and cluster appearance rates. Time permitting, I will discuss the use of latent geometry and topological data analysis (TDA) tools to provide complementary data-driven perspectives. Our framework and findings show that the dynamical/structural interplay of higher-order nonlinearity and the multidimensional geometry of simplicial complexes is a fruitful direction for uncovering the multiscale mechanisms that orchestrate higher-order cascades within social systems and other complex networks. Joint work with Dane Taylor

Modelling the spread of mutations in multilayer contact networks
11:20 AM - 11:40 AM (Contributed)
Mansi Sood, Carnegie Mellon University

We develop epidemiological models that account for variability in transmission risks associated with the emergence of new variants and changes in the contact network structure under policy interventions. Our recent work proposes a modeling framework that accounts for the multi-layer structure typical of human contact networks. Specifically, we assume that the risk of transmission depends not only on the type of strain carried by an infective individual but also on the nature of links used to infect their neighbors. For characterizing epidemic outbreaks caused by mutating pathogens over multi-layer contact networks, we derive the probability of emergence of an epidemic, the expected fraction of individuals infected with each strain, and the phase transition point at which an epidemic emerges.

Social influence and political mobilization: Evidence from two randomized, controlled experiments in US elections
11:40 AM - 12:00 PM (Contributed)
Jason Jones, Stony Brook University

TBA

Afternoon Session

Chair: Alice Schwarze, Dartmouth College

From models to public policies: challenges and opportunities in modeling infectious disease threats
2:00 PM - 3:00 PM (Invited)
Jessica Davis, Northeastern University

The increase in data availability and computational power relating to human mobility and contact patterns have led to the construction of epidemic models that can capture the diverse and heterogeneous nature of complex socio-technical systems. The COVID-19 pandemic has fundamentally challenged how these models are used for forecasting and scenario planning to inform policy and intervention strategies. In this talk I will discuss how we use the Global Epidemic and Mobility model (GLEAM) to respond to the COVID-19 pandemic in real time. I will review how our lab's research evolved with the pandemic's trajectory: from estimating the onset of cryptic transmission of SARS-CoV-2 in January 2020 to modeling emerging SARS-CoV-2 variants throughout 2022.

Effects of Group-Individual interaction in a Generalized Voter Model with Hyperedge Opinions
3:00 PM - 3:20 PM (Contributed)
Corbit Sampson, University of Colorado Boulder

The study of opinion dynamics provides useful insight into the large-scale trends in opinion formation and acts as a platform for rich dynamical behavior. In recent years there has been an increased interest in the effects of multi-agent interaction on models of opinion dynamics. When individuals participate in group interactions there may be a tendency for the group to come to some level of agreement, forming a group opinion. Here we propose a new model that allows for the formation of group opinion without spontaneous consensus in the group, leading to the possibility of group-individual agreement and opposition. Particularly, we consider a hypergraph generalization of a non-linear voter model where we allow nodes and hyperedges to each have opinions drawn from a binary set, nodal opinions are updated probabilistically via a response function which depends on the average neighbor opinion and all hyperedge opinions which the node participates in. Hyperedge opinions are updated similarly based on all participating nodes and their own opinion. This model produces regions of bistability with both group-individual agreement and opposition as stable behavior. Further the model contains regions of oscillatory behavior driven by the random formation of contrarians. Our model can act as a testbed to study the interplay between individual and group opinions.