Poster Session A

Friday Jan. 3, 7:30PM-9:30PM

A1 - Oscillatory and chaotic synchronization behavior in coupled oscillator systems with higher order interactions, community structure, and phase lags

<u>Sabina Adhikari</u>, University of Colorado at Boulder, Per Sebastian Skardal, Trinity College; Juan G. Restrepo, University of Colorado at Boulder

Despite the prevalence of higher order interactions, phase lags, and community structure in many complex systems, their combined effects in synchronization processes remain unexplored. In this study, we consider coupled oscillator systems with higher order interactions mediated via hyperedges of size 2 (links) and size 3 (triangles), two communities, and identical phase lags between every interacting oscillator group. For some phase lags values, the system exhibits oscillatory and chaotic synchronization behavior, which is not present only when higher order interactions and community structure, or community structure and identical phase lags, are included. Some phase lag values result in almost synchronized and almost in-phase or almost anti-phase communities. For other phase lag values, we observe synchronized states with in-phase, anti-phase and skew phase communities, and incoherent-synchronized states. These results are supported by analytical equations derived using the Ott-Antonsen ansatz and numerical simulations.

A2 - A Mathematical Model for Assessing the Epidemiological Impact of Media Campaigns on HIV Transmission Dynamics

<u>Oluwatosin Babasola</u>, Evans Otieno Omondi, Institute of Mathematical Sciences, Strathmore University, Kenya; Nancy Matendechere Imbusi, School of Mathematics and Acturial Sciences, Technical University of Kenya; Kube Ananda, Department of Mathematics and Actuarial Science, Kenyatta University, Kenya;

This work presents a HIV transmission model that incorporates the influence of media campaigns to explore the relationship between media campaigns and the disease spread. To gain a deeper understanding of the model dynamics, we conduct a thorough bifurcation analysis using centermanifold theory and establish the conditions for the occurrence of a backward bifurcation. We then perform a model simulation, and the results are validated to provide insight into the epidemiological implications of the model and the intricate dynamics involved in HIV transmission. A sensitivity analysis is then performed using the Latin hypercube sampling to demonstrate the significant role of the effective contact rate in driving the proliferation of the HIV epidemic. The analysis suggests that HIV infections can be reduced by increasing awareness through media campaigns, expanding ART treatment, and reducing the contact rate. In general, the work establishes that maintaining media campaign coverage above 55

A3 - Impact of Dual Optical Feedback on the Dynamics of a Photonic Neuron

John Bannon, Whitman College; Eli Main, Whitman College; Thomas Hill, West Valley High School (Spokane); Andrés Aragoneses, Whitman College

In a complex dynamical system, noise, feedback, and external forces shape behavior that can range from regularity to high-dimensional chaos. Multiple feedback sources can significantly alter its dynamics, potentially even suppressing the system's output. This study investigates the impact of competing feedback sources on a stochastic complex dynamical system using a photonic neuron-a diode laser with external optical feedback. By varying the feedback intensities from two external reflectors, we explore how dual feedback influences the system's behavior. Using ordinal analysis and advanced measures of complexity, we quantify the system's dynamics and uncover underlying symmetries. Our findings reveal that the interaction between the two feedback sources induces a more intense deterministic behavior. distinct from the dynamics produced by each feedback source individually. Additionally, clear temporal symmetries emerge across all dynamical regimes. By employing a novel entropy-vector representation, we are able to identify a unique signature that characterizes the system's dynamics.

A4 - Transition to chaos with conical billiards

Lara Braverman, Harvard University; David Nelson, Harvard University

We adapt ideas from geometrical optics and classical billiard dynamics to consider particle trajectories with constant velocity on a cone with specular reflections off an elliptical boundary formed by the intersection with a tilted plane, with tilt angle γ . We explore the dynamics as function of γ and the cone deficit angle χ that controls the sharpness of the apex, where a point source of positive Gaussian curvature is concentrated. We find regions of the (γ, χ) -parameter space where, depending on the initial conditions, either (A) the trajectories sample the cone base and avoid the apex region, (B) sample only a portion of the base region while again avoiding the apex or (C) sample the entire cone more uniformly. The special case of an untilted cone displays only type A trajectories which form a caustic at the distance of closest approach to the apex. However, we observe an intricate transition to chaotic dynamics dominated by Type (C) trajectories for sufficiently strong χ and γ . A Poincare map that summarizes trajectories decomposed into the geodesic segments interrupted by specular reflections provides a powerful method for visualizing the transition to chaos. We then analyze the similarities and differences of the path to chaos for conical billiards with other area preserving conservative maps.

A5 - Constructing a Cerebral Hemodynamics Model within a Data Assimilation Pipeline to Enhance Clinical Decision Support in Neurocritical Care

Jennifer Briggs, University of Colorado Anschutz, Department of Bioengineering; J.N. Stroh - Department of Biomedical Informatics, University of Colorado Anschutz Medical Campus; Brandon Foreman - Department of Neurology and Rehabilitation Medicine, University of Cincinnati; Tellen D. Bennett - Departments of Biomedical Informatics and Pediatrics (Critical Care Medicine), University of Colorado Anschutz Medical Campus; Melike Sirlanci - Department of Biomedical Informatics, University of Colorado Anschutz Medical Campus; Soojin Park - Departments of Neurology and Biomedical Informatics, Columbia University Irving Medical Center; Michael Tymko - Department of Human Health and Nutritional Sciences, University of Guelph; David J. Albers - Departments of Biomedical Informatics and Bioengineering, University of Colorado Anschutz Medical Campus

The brain requires continuous and adequate cerebral blood flow (CBF) to survive. In healthy conditions, CBF is controlled by multiple physiologic mechanisms, collectively known as cerebral vascular tone regulation (CVTR). Brain injuries impact CBF and CVTR mechanisms, thereby impacting patient outcomes. Quantifying CVTR functionality and forecasting CBF could be transformative for clinical decision support by informing personalized therapy to maximize the functional outcome of neurological injury patients.

We constructed and validated a novel model (CVTR model) of cerebral hemodynamics that explicitly includes the action of CVTR mechanisms. We validated the CVTR model against 15 physiological experiments, to show that the model accurately recapitulates data.

We then built this model into a data assimilation framework to estimate parameters (called computational CVTR biomarkers), which are mathematical representations of a patient's CVTR functionality. Using simulated and experimental data, we showed that the CVTR computational biomarkers were uniquely estimable for all patient phenotypes using Markov Chain Monte Carlo (MCMC) optimization.

Using MCMC in an inverse problem framework, we estimated CVTR computational biomarkers for three traumatic brain injury patients. CVTR biomarkers were predictive of patient outcomes and unique from one another. Last, we used these CVTR biomarkers to forecast CBF. The CVTR

model forecast had superior accuracy than the canonical cerebral hemodynamics model or multivariate linear regression.

Clinical decisions are partially based on an understanding of the patient's physiological state. This novel CVTR model built into a data assimilation framework is a first step towards allowing clinicians to forecast CBF, hypothesize CBF responses to intervention, study evolving trends in physiological state, and probe a deeper understanding of the neurovascular system.

A6 - Data-driven model discovery and interpretation for CAR T-cell killing using sparse identification and latent variables

<u>Alex Brummer</u>, College of Charleston; Agata Xella, Moffitt Cancer Center; Ryan Woodall, City of Hope National Medical Center; Vikram Adhikarla, City of Hope National Medical Center; Heyrim Cho, Arizona State University; Margarita Gutova, City of Hope National Medical Center; Christine E. Brown, City of Hope National Medical Center; Russell C. Rockne, City of Hope National Medical Center; Whitney Kitchen, College of Charleston

In the development of cell-based cancer therapies, guantitative mathematical models of cellular interactions are instrumental in understanding treatment efficacy. Efforts to validate and interpret mathematical models of cancer cell growth and death hinge first on proposing a precise mathematical model, then analyzing experimental data in the context of the chosen model. In this work, we present the first application of the sparse identification of non-linear dynamics (SINDy) algorithm to a real biological system in order discover cell-cell interaction dynamics in in vitro experimental data, using chimeric antigen receptor (CAR) T-cells and patient-derived glioblastoma cells. By combining the techniques of latent variable analysis and SINDy, we infer key aspects of the interaction dynamics of CAR T-cell populations and cancer. Importantly, we show how the model terms can be interpreted biologically in relation to different CAR T-cell functional responses, single or double CAR T-cell-cancer cell binding models, and density-dependent growth dynamics in either of the CAR T-cell or cancer cell populations. We show how this data-driven model-discovery based approach provides unique insight into CAR T-cell dynamics when compared to an established model-first approach. These results demonstrate the potential for SINDy to improve the implementation and efficacy of CAR T-cell therapy in the clinic through an improved understanding of CAR T-cell dynamics. In closing, we present extensions of this work to spatial systems involving chemical reactions with known reaction kinetics as part of a broader effort toward model discovery of spatially dependent cellular interactions.

A7 - Dynamic Health Monitoring: Predicting COVID-19 with Wearable Sensor Data and catch-22 Features

<u>Paul Buttkus</u>, Technische Universität Dresden - SynoSys; Dirk Brockmann, Technische Universität Dresden In the initial stages of a pandemic, controlling infectious disease spread is crucial. The rapid, global transmission of COVID-19 underscored the urgent need for tools that detect early signs of infection to contain outbreaks before they escalate.

Recent studies have shown that physiological changes—such as increased resting heart rate, prolonged sleep, and reduced physical activity—often occur shortly after COVID-19 infection. When tracked by wearable sensors, these signals, analyzed through time series, offer a real-time perspective on infection dynamics. Combining wearable sensor data with machine learning, we aim to classify infection status, harnessing physiological trends that emerge dynamically in large, uncontrolled environments.

Using data from the Corona Data Donation Project, which provides resting heart rate, step count, and sleep duration time series from over 120,000 voluntary participants in uncontrolled, real-world settings, we developed a Logistic Regression model to classify COVID-19 test results [1]. This model achieved a Receiver Operating Characteristic Area Under the Curve (ROC AUC) of 0.58, with a precision of 0.26 and recall of 0.54. Employing the catch22 (22 CAnonical Time-series Characteristics) feature set allowed for interpretable feature extraction, enabling a detailed analysis of specific physiological shifts that distinguish COVID-19positive individuals.

This study demonstrates the feasibility of predicting infectious disease status using wearable sensor data from large, uncontrolled cohorts. Our findings underscore the potential for wearable-based prediction models to enhance public health tools, offering timely insights into disease dynamics in natural, everyday environments.

[1] https://corona-datenspende.github.io/en/

A8 - The Spatiotemporal Dynamics of P. mirabilis Swarm Cycling

Morgan Byers, University of Colorado at Boulder; Eliotte Garling, Department of Plant and Microbial Biology, University of California, Berkeley; Elizabeth Bradley, University of Colorado - Boulder and The Santa Fe Institute; Karine A. Gibbs, Department of Plant and Microbial Biology, University of California, Berkeley; James D. Meiss, University of Colorado at Boulder

Proteus mirabilis, a bacterium that naturally occurs in the gut, can traverse catheters and cause urinary tract infections. This migration, termed swarming, encompasses a dynamic developmental cycle in which populations oscillate between two primary states: (1) little-to-no movement with closely packed short cells and (2) micron-scale movement of short and dramatically elongated cells. As cells move, the colony migrates; its leading edge expands outward in a non-uniform way. We use computational geometry and computational topology to identify, characterize, and track the resulting structures in microscope photographs of *Proteus* colonies. Since these cells communicate by touching one another, adjacency is a particularly salient property. Density

of the cells is also important, as is their alignment. Using these and other quantities, we can identify important features like the fractal dimension of the leading edge of a swarm, the local and global connectedness of the cells, and the alignment in different regions of the swarm. These results empower biologists with the ability to characterize mesoscale behaviors, such as disentangling the role of cellcell communication in collective migration, which is a step towards a better understanding of how *P. mirabilis* causes disease.

A9 - Synaptic reorganization of plastic neuronal networks during (de)synchronization.

Kanishk Chauhan, Stanford University; Alexander B. Neiman, Department of Physics and Astronomy, Ohio University; Peter A. Tass, Professor, Department of Neurosurgery, Stanford University

Abnormal synchronization of neurons may underlie neurological disorders like Parkinson's disease and epilepsy, necessitating the need for therapeutic stimulation protocols to desynchronize neurons and restore normalcy. We leverage the plastic nature of neuronal networks and model those using leaky integrate-and fire neurons with spike-timingdependent plasticity for synaptic weight change and structural plasticity for rewiring of the network. We study the reorganization of synaptic contacts and simultaneous change in neuronal activity as a network (de)synchronizes and investigate the efficacy of a variant of Coordinated Reset stimulation to counter synchrony. We show that different levels of synchrony and desynchrony emerge depending upon initial connectivity. The synaptic reorganization enhances synchrony. Preferential removal of weaker contacts may cause enhanced synchrony with significantly fewer contacts. The numbers of incoming and outgoing contacts of neurons depend on their firing rate. The degree-frequency and degreedegree correlations, and a mixture of degree assortativity emerge in synchronized state. We then show that networks evolving with structural plasticity require a higher level of stimulus intensity to transition from synchronized to desynchronized states.

A10 - All Spectral Instabilities of Stokes Waves

Ryan Creedon, Brown University; Bernard Deconinck, University of Washington

Abstract: In 1847, George Stokes derived asymptotic expansions for the small-amplitude, periodic traveling-wave solutions of the full water wave equations. In the years since his work, much has been studied about these waves, including their instabilities. Among the foundational results concerning the stability of Stokes waves was discovered in the 1960s by Benjamin, Whitham, and Lighthill, who independently showed via formal methods that Stokes waves are modulationally unstable in sufficiently deep water. Since their pioneering work, other instabilities, now dubbed the highfrequency instabilities, have come to light. In this poster, we characterize both the modulational and high-frequency instabilities of small-amplitude Stokes waves by obtaining explicit, asymptotic expansions for their growth rates as a function of the amplitude of the wave. For the first time, we are able to compare the growth rates of all instabilities of Stokes waves via analytical methods. We find that Stokes waves are, in fact, unstable in all depths, contrary to the popular perception that Stokes waves are stable in sufficiently shallow water.

A11 - Chaotic Structure in the Non-extracted Region of a Rotation Potential Mixer

<u>Tomas Dabove</u>, University of Colorado at Boulder; Roseanna M. Neupauer, University of Colorado at Boulder

The rotating potential mixer (RPM) has been proposed as a method for enhancing mixing and reaction during insitu remediation of a contaminated groundwater aquifer, in which a chemical or biological amendment is emplaced within a contaminant plume to react with and degrade the contaminant in situ. The RPM is created by installing an even number of wells at uniformly spaced intervals along a circle surrounding the contaminant plume. A well pair consisting of two wells on opposite sides of the circle is operated as a dipole for a fixed amount of time. Then the dipole is rotated through a specified angle to another well pair. The rotation continues until the dipole returns to the original well pair, concluding one cycle of the RPM. Prior studies have shown that when the RPM operates for many cycles, the extraction and reinjection of fluid creates a pattern of elliptic islands within a chaotic sea; thus, the originally isolated contaminant and amendment plumes are intermixed, promoting degradation of the contaminant. However, regulatory requirements prohibit the reinjection of contaminated groundwater, so the RPM must be designed such that the contaminant and amendments plumes remain within the non-extracted portion of the circular region contained by the wells. This study investigated the chaotic structure of the non-extracted region and found that it has a KAM (Kolmogorov-Arnold-Moser) tori at its core, centered around a period-one elliptic point. Outside of the KAM tori, the remaining space of the non-extracted region is filled with a presumably infinite number of invariant tori. Fluid parcels exhibit substantial stretching along these tori; thus, even if the contaminant and amendment plumes of an in-situ groundwater remediation system remain inside the non-extracted region of the RPM, significant elongation of the plume interface will occur, leading to substantial enhancement of contaminant degradation reactions.

A12 - The Effects of Bromide and Sulfuric Acid Concentrations on Propagating BZ wave patterns

<u>Neil Divins</u>, Elizabethtown College; Desmond Yengi, Elizabethtown College

The Belousov-Zhabotinsky (BZ) reaction involves the oxidation of an organic substrate by bromate ions in an acidic

solution in the presence of a metal ion catalyst like ferroin, cerium (iv), and manganese(ii). Spontaneous propagating wave patterns are observed when the right BZ solution mixture is placed in a guasi-two-dimensional medium. The observation of propagating wave patterns is due to metal catalysts undergoing continuous oxidation-reduction cycles that alternate colors. The BZ reaction system serves as a model that provided essential contributions to our understanding of the principles of self-organization, reaction-diffusion dynamics, and the emergence of complex spatiotemporal patterns. Variations in the BZ reaction mixture affect oscillation and wave patterns. In this work, we report our investigations into the effects of bromide and sulfuric acid concentrations on spontaneously propagating wave patterns in the BZ reaction system conducted at room temperature. The average wave velocity, wavelength, and period measurements show dependence on concentration. The wave patterns transition from target wave patterns to spiral wave patterns, and the average wave velocities increase with decreasing bromide and increasing sulfuric acid concentrations. The wavelength and period increase with increasing bromide concentration and decreasing sulfuric acid concentration. The findings from our work advance insights into how varying concentrations influence reaction-diffusion wave behavior.

A13 - Boundary layer heterogeneities can enhance scroll wave stability

<u>Sebastian Echeverria-Alar</u>, University of California, San Diego; Wouter-Jan Rappel, University of California, San Diego

Spatiotemporal dynamics, such as turbulence in active matter, oscillations in chemical reactions, and disorganization of electrical waves in cardiac tissue, pose significant challenges in many physical and biological systems. A key question in these contexts is how to control such complex dynamics, which is particularly relevant in the framework of cardiac dynamics where scroll wave dynamics may cause life-threatening arrhythmias. We explore how boundary layer heterogeneities affect the scroll wave dynamics in a semidiscrete electrophysiological model. Using numerical simulations, we show that reducing the coupling strength near the boundaries of thin tissues results in a decrease of the angular frequency of the scroll wave. Furthermore, we demonstrate that the introduction of the boundary layer heterogeneity can prevent a meandering instability of scroll waves. We address the suppression of the meandering bifurcation by weakly nonlinear analysis. Finally, we derive a simplified model that only considers activation in the boundary layer and in one bulk tissue slice, and show that this model is able to capture the numerically observed stabilization of scroll waves and their reduction in frequency. We discuss the extension of our results in terms of controlling more complicated spatiotemporal dynamics such as scroll wave break-up. Our findings suggest a novel approach to controlling arrhythmias with minimal tissue intervention, which can be essential for treating patients with tachycardia and fibrillation.

A14 - Can Steady Helical Flow in Porous Media Generate Chaotic Advection?

Brittany Fager, University of Colorado Denver; Madeline Manfre Sarno, Colorado Department of Public Health and Environment; Roseanna M. Neupauer, University of Colorado Boulder; David C. Mays, University of Colorado Denver

Chaotic advection provides an opportunity to enhance chemical reactions in porous media where laminar flow prevents the turbulence that drives mixing in most engineered reactors. To date, most research on chaotic advection in porous media has focused on unsteady two-dimensional (2D) flow, for example by engineered injection and extraction. In this work, we explore chaotic advection in steady 3D flows, using an engineered pattern of hydraulic conductivity designed to generate helical flow. Numerical simulations indicate that this hydraulic conductivity pattern promotes plume splitting, especially in intersections of overlapping high conductivity zones, with more splitting occurring in more upstream intersections. Here we analyze particle tracking results using tools from complex systems science such as Lyapunov exponents and Poincaré sections. This analysis is intended to promote deeper understanding of steady 3D flows that are potentially valuable in environmental and industrial applications such as groundwater remediation.

A15 - Chaos Analysis of a New 3D Finance System and Generalized Synchronization for n-Dimension

Muhammad Fiaz, Independent Researcher

The article in hand is the study of complex features like Zero Hopf Bifurcation, Chaos and Synchronization of integer and fractional order version of a new 3D finance system. Trusted tools of averaging theory and active control method are utilized for investigation of Zero Hopf bifurcation and synchronization respectively for both versions of the system. Novelty of the paper is to find the answer of a question that is it possible to find a chaotic system which can be synchronized with any other of the same dimension? Based on different examples we categorically develop a theory that if a couple of master and slave chaotic dynamical system is synchronized by selecting a suitable gain matrix with special conditions then the master system is synchronized with any chaotic dynamical system of the same dimension. With the help of this study we developed generalized theorems for synchronization of n-dimension dynamical systems for integer as well as fractional versions. We proposed that this investigation will contribute a lot to control dynamical systems, shorten the required criteria to synchronize the system under consideration with any other chaotic system of the same dimension and ultimately will minimize the cost. Chaotic properties of fractional version of the new finance system are also analyzed at fractional order q = 0.87. Simulations results, where required, also provided for authenticity of analytical study.

A16 - The origin of the nucleation of frictional ruptures and earthquakes

Jay Fineberg, The Hebrew University of Jerusalem

Frictional motion is mediated by rapidly propagating ruptures that detach the ensemble of contacts that form the frictional interface that separates contacting bodies. These ruptures are akin to shear cracks. When this process takes place within natural faults, these rapid ruptures are essentially earthquakes. While fracture mechanics describe the rapid motion of these singular objects, the nucleation process that creates them is not understood. Here, by extending fracture mechanics to explicitly incorporate finite interface widths (that are generally ignored), we fully describe the nucleation process. We show, experimentally and theoretically, that slow steady creep ensues at a well-defined stress threshold. Moreover, as slowly creeping patches approach the interface width, a topological transition takes place in which these creeping patches smoothly transition to the rapid fracture that is described by classical fracture mechanics. Besides its obvious relevance to fracture and material strength (integrity), this new picture of rupture nucleation dynamics is directly relevant to earthquake nucleation dynamics; slow, aseismic rupture must always precede rapid seismic rupture (so long as the initial defect within the interface is localized in both spatial dimensions). The theory may provide a new framework to understand how and when earthquakes nucleate.

A17 - Entropy, Cross Entropy, and Data Assimilation

Andrew Fraser, FraserPhysics

I use estimates of cross entropy, $h_{\phi,\theta}$, to compare the fidelity of a few data assimilation techniques, eg, hidden Markov models, extended Kalman filters, and particle filters, for modeling time series from simulations of the Lorenz system.

If the set of probability functions $\{P_{Y[0:t]|\phi} \forall t \in Z+\}$ characterizes a *true* stochastic process, then for sequences y[0:t] drawn from the process the estimates,

$$\hat{h}(\phi, y[0:t]) \equiv -\frac{1}{t} \log \left(P(y[0:t]|\phi) \right),$$

almost surely converge to the entropy rate h_{ϕ} .

Similarly, for a different set of probability functions $\{P_{Y[0:t]|\theta} \forall t \in Z+\}$ and sequences y[0:t] drawn from the true process characterized by ϕ , the estimates,

$$\hat{h}(\theta, y[0:t]) \equiv -\frac{1}{t} \log \left(P(y[0:t]|\theta) \right), \tag{1}$$

almost surely converge to the cross entropy rate,

$$h_{\phi,\theta} \equiv \lim_{t \to \infty} -\frac{1}{t} \mathbb{E}_{\phi} \log \left(P(Y[0:t]) \right)$$

I use various data simulation techniques to obtain probability functions P_{θ} , and use (1) to estimate their cross entropies $h_{\phi,\theta}$.

The true entropy is a lower bound on the cross entropy, $h_{\phi} \leq h_{\phi,\theta}$, and I use Benettin's procedure for calculating Lyapunov exponents numerically to estimate h_{ϕ} . Then I use the difference, $h_{\phi,\theta} - h_{\phi}$ to quantify fidelity.

While these are old ideas, years of improving hardware and software tools have made desktop implementations feasible. I talk about those improvements and quantitative characterizations of that progress.

A18 - Incorporating physiological constraints in estimates of insulin secretion rate

<u>Justin Garrish</u>, Colorado School of Mines; Christine L. Chan, CU Anschutz Medical Campus; Douglas Nychka, Colorado School of Mines; Cecilia Diniz Behn, Colorado School of Mines

Features of insulin secretion rate (ISR) during an oral glucose tolerance test (OGTT) provide insight into an individual's metabolic health, and specifically, beta-cell function. However, during an OGTT, we cannot measure ISR directly. We propose a Bayesian hierarchical model (BHM) that incorporates physiological constraints to precisely infer continuous ISR profiles from discrete C-peptide data. We take C-peptide as the output of a common C-peptide dynamics model with ISR as a forcing function, and the logarithm of ISR as a Gaussian process with a quadratic mean trend. The quadratic component captures the overall rise and fall generally observed in ISR during an OGTT, and the exponential form of ISR precludes non-positive values across the distribution of ISR profiles. Positivity propagates through to the posterior distribution obtained in inversion. Further, the method furnishes a linear approximation of the non-linear transformation from log-ISR to C-peptide that adheres to the constraints. Results obtained from the logtransformed model correlate well with the purely Gaussian model, however, the log-transformed model yields more precise estimates, characterized by narrower credible envelopes. In this presentation, we develop the BHM, outline the inversion and uncertainty quantification methods, and compare the ISR results obtained from the log-transformed and purely Gaussian models on a set of OGTT data from youth participants with and without cystic fibrosis.

A19 - Consensus on Higher Order Networks

Joe Geisz, Colorado State University

We discuss mathematical models of consensus on networks, at three levels of complexity. First, graphs as models for networks are explained and a model for consensus on a graph is derived using the graph Laplacian. Next, the idea of higher-order networks is introduced, and simplicial homology using real coefficients is used to define the Hodge Laplacian. These tools allow the consensus model to be applied on edges and higher order connections. Finally, simplicial sheaves are explored as a model for higher-dimensional state spaces. A toy model of birds coming to consensus while flocking is discussed as an example of consensus on a sheaf.

A20 - Acoustic control of nonspherical shape oscillations in bubbles using Koopman LQR

<u>Andrew Gibson</u>, University of Colorado Colorado Springs; Xin (Cindy) Yee, University of Colorado Colorado Springs

In recent decades, data science has yielded powerful new tools for the study of dynamical systems. These tools have proven able to solve traditionally intractable problems and are being understood through more modern mathematical perspectives. One such perspective is the Koopman operator theory. This theory enables the identification of nonlinear dynamical systems using linear Koopman observables of the dynamic system.

As a result, the Koopman framework has opened the door to applying classical linear theories of estimation and control to strongly nonlinear systems. Although the framework began in fluids, it has since spurred advances in many subjects, from neuroscience to traffic control, energy systems to epidemiology, robotics and even pure mathematics.

In this work, we apply Koopman theory and a classical linear quadratic regulator (KLQR) to acoustically drive gas bubbles in liquid water. These results have applications in industry and biomedicine, such as abrasive cleaning, ultrasound imaging and gene therapy. In our study, we control nonspherical shape oscillations of bubbles through their radial mode using the Reddy & Szeri model. In this model, the radial dynamics are governed by balancing internal and external pressures, surface tension, viscosity, compressibility effects and far-field acoustic pressure. The shape modes come from a decomposition into spherical harmonics using Legendre polynomials and behave as parametrically-driven damped harmonic oscillators whose coefficients are complicated nonlinear functions of the radial mode. We show that we can achieve complex control objectives using the datadriven Koopman linear quadratic regulator controller.

A21 - Inaccuracy of the variance evolution associated with discrete covariance propagation

Shay Gilpin, University of Arizona; Tomoko Matsuo, Smead Aerospace Engineering Sciences, University of Colorado, Boulder, and Department of Applied Mathematics, University of Colorado, Boulder; Stephen E. Cohn, Global Modeling and Assimilation Office, NASA Goddard Space Flight Center, Greenbelt, Maryland

The propagation of the estimation error covariance is an important aspect of the statistical estimation of dynamical systems, such as data assimilation. Conventional propagation methods often employ the same discrete dynamical model used to evolve the state estimate to also propagate an approximation of the error covariance. Such approximate evolution schemes for the covariance imply an approximate evolution of the error variance along the covariance diagonal. For continuum states governed by the advection equation and related hyperbolic differential equations, we show that the discrete variance evolution implied by the usual discrete covariance propagation $M(MP)^T$, with M a typical discrete propagator for the state dynamics, is surprisingly inaccurate, more so than traditional error analysis would suggest. The underlying cause is the continuum covariance dynamics, which admits two solutions along its covariance diagonal: the first being the continuum variance dynamics, and the second solution being the dynamics of the continuous spectrum of the covariance operator. The latter solution makes its presence known as correlation lengths approach grid scale, which occurs naturally in shear flow, for example. Through extensive error analysis, we show that conventional discrete variance propagation derived from $M(MP)^T$ gives rise to error terms that depend on the ratio of the grid scale to the correlation length. As this ratio approaches unity, these error terms alter the continuum dynamics being approximated along the covariance diagonal, producing diagonals that hardly resemble the continuum variance dynamics nor the continuous spectrum dynamics. We verify our analytical results and illustrate the corresponding degree of inaccuracy through one-dimensional examples. The analytical results and insights gained from this work may help explain the surprisingly inaccurate variance evolution often observed in the chemical constituent data assimilation community.

A22 - Structural identifiability of weak-form ODE systems

<u>Nora Heitzman-Breen</u>, University of Colorado at Boulder; David Bortz, University of Colorado at Boulder

Compartmental modeling of biological systems provides insights into biological interactions and mechanisms not easily observed in vivo. Accurate and robust parameter estimation is critical to studying such biological problems. A common approach to parameter estimation is nonlinear least squares using a forward solver. However, as model size and noise in data increase these methods become computationally expensive to maintain accuracy in parameter estimates. The recently proposed Weak-form Estimation of Nonlinear Dynamics (WENDy) method is more accurate, robust to noise, and computationally efficient than forward solverbased approaches (even for higher dimensional systems). This method involves using carefully chosen test functions to convert the strong form representation of a model to its weak form, and estimating parameters by solving an equation error-based generalized least squares problem.

A23 - The Effects of Bromate and Sulfuric Acid Concentrations on BZ Propagating Wave Patterns

Andrew Hoch, Elizabethtown College; Desmond Yengi, Elizabethtown College

Oscillations and wave patterns are ubiquitous in biological systems, and they might be central to biological activities like circadian rhythms, cell division, and signal transduction processes. For instance, the intricate spatiotemporal distribution of the oscillatory signals in cardiac pacemaker cells is responsible for the heart's rhythmic beating. The wave patterns and self-organization observed in some of these biological systems closely resemble those in the Belousov-Zhabotinsky (BZ) reaction system. Therefore, the BZ reaction system can serve as a model for studying the dynamical behaviors of biological and chemical systems. The BZ reaction is an auto-catalytic oscillatory reaction that consists of bromate, bromide, organic substrate, sulfuric acid, and metal catalyst reagents that undergo a cyclic reduction-oxidation reaction. Variations in the BZ reaction mixture affect oscillation and wave patterns. Here, we report our experimental investigations into the effects of varying sulfuric acid and bromate concentrations on spontaneously propagating wave patterns in the BZ reaction system conducted at room temperature. Our measurement found that increasing bromate and sulfuric acid concentrations increase wave velocities and decrease wavelength and period. These findings advance our understanding of how altering chemical concentrations affect wave dynamics.

A24 - CardioCare Quest: Integrating Mathematical Models for Culturally Sensitive Hypertension Management

<u>Tochukwu Ikwunne</u>, Northern Arizona University; Jared Duval, Northern Arizona University

Hypertension impacts 35.9The core of CardioCare Quest is its modular mini-games, which target key behavioral aspects of hypertension management, such as healthy eating, physical activity, medication adherence, and blood pressure monitoring. A key mathematical feature is the use of a Markov Decision Process (MDP) to model behavior changes over time. Each user's health journey is represented as a state, with transitions determined by actions (e.g., medication adherence or exercise) and probabilities informed by real-time gameplay data. A Markov Decision Process (MDP) is defined mathematically as a tuple (S, A, P, R, γ) , where: 1. States (S): The set of possible states representing the user's current health and engagement. S = s1, s2, ..., sn, where each s_i captures variables like blood pressure, medication adherence, or game engagement level. 2. Actions (AAA): The set of actions the user can take. A = a1, a2, ..., am, e.g., playing a mini-game, logging a meal, or recording a blood pressure reading. 3. Transition Probability (PPP): The probability of transitioning from one state to another given an action. P(s'|s, a), where $s' \in S$ is the next state, $s \in S$ is the current state, and $a \in A$ is the action taken. This satisfies the condition: $\sum P(s'|s, a) = 1$, $\forall s \in S, a \in A$. 4. Reward Function (RRR): The immediate reward received for taking an action in a given state. R(s,a), where $R:S \times A \rightarrow R$, quantifies the benefit of specific actions.

A25 - Spatial spread of epidemic in a system of weakly connected networks

Evgeniy Khain, Oakland University

A metapopulation consists of a group of spatially distanced subpopulations, each occupying a separate patch. It is usually assumed that each localized patch is well-mixed. In this talk, we will discuss the spread of an epidemic in a system of weakly connected patches, where the disease dynamics of each patch occurs on a network. The SIR dynamics in a single patch is governed by the rate of disease transmission, the disease duration, and the node degree distribution of a network. Monte-Carlo simulations of the model reveal the phenomenon of spatial disease propagation. The speed of front propagation and its dependence on the single patch parameters and on the strength of interaction between the patches was determined analytically, and a good agreement with simulation results was observed [1]. Next, we will discuss front propagation in case of an Allee effect, where the effective transmission rate depends on the fraction of infected, and the state of no epidemic is linearly stable. We discovered [2] a novel phenomenon of front stoppage: in some regime of parameters, the front solution ceases to exist, and the propagating pulse of infection decays despite the initial outbreak.

[1]. E. Khain and M. Iyengar, Phys. Rev. E 107, 034309 (2023). [2]. E. Khain, Phys. Rev. E 107, 064303 (2023).

A26 - Neural Network Two-Sample Testing: Detecting Distribution Differences

<u>Khurana Varun</u>, Brown University; Alex Cloninger (UCSD), Xiuyuan Cheng (Duke University)

We construct and analyze a neural network two-sample test to determine whether two datasets came from the same distribution (null hypothesis) or not (alternative hypothesis). We perform time-analysis on a neural tangent kernel (NTK) two-sample test. In particular, we derive the theoretical minimum training time needed to ensure the NTK two-sample test detects a deviation-level between the datasets. Similarly, we derive the theoretical maximum training time before the NTK two-sample test detects a deviation-level. By approximating the neural network dynamics with the NTK dynamics, we extend this time-analysis to the realistic neural network two-sample test generated from time-varying training dynamics and finite training samples. A similar extension is done for the neural network two-sample test generated from time-varying training dynamics but trained on the population. To give statistical guarantees, we show that the statistical power associated with the neural network twosample test goes to 1 as the neural network training samples and test evaluation samples go to infinity. Additionally, we prove that the training times needed to detect the same deviation-level in the null and alternative hypothesis scenarios are well-separated. Finally, we run some experiments showcasing a two-layer neural network two-sample test on a hard two-sample test problem and plot a heatmap of the statistical power of the two-sample test in relation to training time and network complexity.

A27 - Logical Extrapolation for Mazes with Recurrent and Implicit Networks

Brandon Knutson, Colorado School of Mines (CSM); Amandin Chyba Rabeendran, NYU; Michael Ivanitskiy, CSM; Jordan Pettyjohn, CSM; Cecilia Diniz-Behn, CSM; Samy Wu Fung, CSM; Daniel McKenzie,CSM

Recent work has suggested that certain neural network architectures-particularly recurrent neural networks (RNNs) and implicit neural networks (INNs) are capable of logical extrapolation. That is, one may train such a network on easy instances of a specific task and then apply it successfully to more difficult instances of the same task. In this paper, we revisit this idea and show that (i) The capacity for extrapolation is less robust than previously suggested. Specifically, in the context of a maze-solving task, we show that while INNs (and some RNNs) are capable of generalizing to larger maze instances, they fail to generalize along axes of difficulty other than maze size. (ii) Models that are explicitly trained to converge to a fixed point (e.g. the INN we test) are likely to do so when extrapolating, while models that are not (e.g. the RNN we test) may exhibit more exotic limiting behaviour such as limit cycles, even when they correctly solve the problem. Our results suggest that (i) further study into why such networks extrapolate easily along certain axes of difficulty yet struggle with others is necessary, and (ii) analyzing the dynamics of extrapolation may yield insights into designing more efficient and interpretable logical extrapolators.

A28 - Predicting High-Dimensional Chaotic Time Series by Employing Hybridized Local State Reservoir Computing

Daniel Köglmayr, DLR KI-Sicherheit; Tamon Nakano, Deutsches Zentrum Für Luft und Raumfahrt (DLR); Dennis Duncan, Ludwig-Maximilians-Universität München (LMU); Fabian Fischbach (DLR); Alexander Haluszczynski (LMU); Michael Klatt (DLR); Haochun Ma (LMU); Davide Prosperino (LMU); Christoph Räth (DLR, LMU)

Reservoir Computing (RC) has been shown to be one of the most promising methods for the prediction of chaotic spatiotemporal systems.

Recently it has been demonstrated that by combining knowledge-based models (KBMs) with fully data-driven RC, prediction performance exceeding both methods can be achieved [1].

Additionally, this approach is compatible with a parallel prediction scheme based on local states, making forecasting of high-dimensional chaotic spatiotemporal systems of arbitrarily large extent possible [2].

We demonstrate this using three of the most common RC techniques, namely classical RC, Next Generation RC (NGRC), and Minimal RC (MRC), as well as three hybrid methods: input hybrid (IH), output hybrid (OH), and full hybrid (FH). A find that NGRC and MRC yield equivalent

prediction performance with up to two orders of magnitude less computing time and training data than classical RC [3].

Furthermore, our implementation of these techniques in the publicly available software package "SCAN" (Software for Chaos Analysis using Networks) enables the processing of generalized system topologies. We discuss different examples for the prediction of spatially extended systems, whether on a two-dimensional plane or a network (e.g. power grid data), and outline possible applications [4].

[1]: Pathak et al. "Hybrid Forecasting of Chaotic Processes: Using Machine Learning in Conjunction with a Knowledge-Based Model." (Chaos, 2018)

[2]: Pathak et al. "Model-Free Prediction of Large Spatiotemporally Chaotic Systems from Data: A Reservoir Computing Approach." (PRL, 2018)

[3]: Nakano et al. "Predicting Two-Dimensional Spatiotemporal Chaotic Patterns with Optimized High-Dimensional Hybrid Reservoir Computing." (In preparation, 2024)

[4]: Baur et al. "SCAN: A Versatile Implementation of Reservoir Computing Methods." (In preparation, 2024)

A29 - Quantifying Causal Dynamics of Mouse EEG in Sleep States Using Symbolic Transfer Entropy

Kazuki Koyama, Rikkyo University; Masanori Sakaguchi, University of Tsukuba; Takaaki Ohnishi, Rikkyo University.

Transfer Entropy (TE) is a powerful tool derived from information theory, used to quantify causal relationships in high-dimensional time series data. Extensively applied to physiological signals such as EEG, PSG, and fMRI, TE provides insights into temporal causality by assessing entropybased interactions between paired signals. In this study, we employ Symbolic Transfer Entropy (STE), a non-parametric extension of TE that enhances computational efficiency and noise robustness by transforming signal values into ranked symbols. We apply STE to phase-space-embedded EEG data, $\{\mathbf{x}_1, \mathbf{x}_2, \dots\}$, recorded from mice, using an optimal embedding dimension of 5 determined based on permutation entropy in previous studies. STE is calculated by analyzing pairs of vectors \mathbf{x}_i and their lagged vectors $\mathbf{x}_{i+\Delta}$, to probe causal dynamics. To compute STE, we need to set 2parameters, the time delay and Δ .

For each 4-second epoch, we categorize sleep states into Rapid Eye Movement (REM) and non-REM and further divide wakefulness into states of high- and low-amplitude theta waves. Our results demonstrate that STE distributions vary significantly across these states, with notable differentiation observed as delay times changes. Tuning the parameters allows for the successful classification of REM, non-REM, and high- and low-amplitude theta wave. Statistical validation using the Kolmogorov-Smirnov test (p < 0.05) confirms significant distinctions in STE distributions, particularly at a time delay of 78 ms and $\Delta = 87$ ms. These findings underscore the utility of STE in distinguishing sleep and wake states, offering insights into the causal structure of brain

activity across different phases of rest and activity.

A30 - Self-consistent approach for synchronization in networks with higher-order interactions

Chanin Kumpeerakij, University of Colorado at Boulder; Juan G. Restrepo, University of Colorado at Boulder

We study synchronization on networks with higher-order interactions, i.e., networks where multiple oscillators can interact simultaneously. Recent studies have examined the effects of structured higher-order interactions on the collective behavior of coupled phase oscillators, often relying on mean-field approximations that may not capture the complexities of real-world systems. In this work, we develop a formalism to study synchronization on arbitrary network structures by extending the original self-consistent analysis of Kuramoto to networks with higher-order interactions. In contrast to mean-field methods, this approach enables us to characterize the order parameter in networks with arbitrary structure. We obtain a set of coupled nonlinear equations for the network's local order parameters. From these equations we obtain conditions for bistability between the synchronized and incoherent states in terms of spectral properties of the network and the structure of the higher-order interactions. These conditions generalize recent results that are given in terms of moments of the network's degree distribution. Finally, we validate our results with numerical simulations of the coupled oscillator system.

A31 - Optimal ambition in business, politics and life

Ekaterina Landgren, University of Colorado at Boulder; Ryan Langendorf, University of Colorado at Boulder; Matthew G. Burgess, University of Wyoming

How high should an innovator, entrepreneur, or activist reach? When should we be satisfied and when should we look for greener pastures? When is the perfect the enemy of the good? This type of question arises in many different contexts, including business, politics, resource exploitation, and many aspects of our personal lives. Empirical research across diverse domains supports the intuition that people maximize their benefits, on average, by aiming for above-average achievement, but that aiming too high carries costs. Here, we mathematically formalize this intuition. We model a search for strategies, having uncertain rewards, over a fixed time period. The agent knows the statistical distribution of rewards across strategies. At each time step, the agent either is satisfied and sticks with their current strategy or continues searching. We prove that the agent's optimal satisfaction threshold is both finite and strictly larger than the mean of available rewards. Compared to the optimal threshold, being too ambitious has a higher expected cost than being too cautious, implying that uncertainty over the reward distribution should motivate caution. The optimal threshold becomes larger if the search time is longer, if the reward distribution is left skewed, or if the reward landscape is rugged (compared to smooth). When the agents compare their performance to that of others, the optimal threshold is lower when the agents engage in upward social comparison rather than peer-to-peer comparison. We discuss how these insights can be applied in diverse domains.

A32 - Reconstructing networks from simple and complex contagions

Nicholas Landry, University of Virginia; Will Thompson, University of Vermont; Laurent Hébert-Dufresne, University of Vermont; Jean-Gabriel Young, University of Vermont

Network reconstruction is the problem of inferring a network of contacts from temporal observations of an individual's dynamical status. This problem has been extensively studied for simple dynamics generated by models such as the Susceptible-Infectious-Susceptible or Ising models, for instance, but little is known about reconstruction from more complicated dynamical processes. Here, we study how a dynamic's complexity affects the problem. We inspect "simple" contagions, spread independently by infected contacts-the classical epidemiological picture-and "complex" contagions where interactions between infected contacts are needed for infections to occur-a class of models primarily used to describe the adoption of behaviors or opinions. We break this strict dichotomy and introduce a nonparametric neighborhood-based susceptible-infectedsusceptible (SIS) model that can express the classical SIS model and the threshold model as special cases. We fit the model with an efficient Gibbs algorithm that simultaneously reconstructs a network of contacts and the dynamical rules-the specific contagion function-from time series data. Using generative network models as representatives of empirical network structure, we show that simple and complex contagions learn different types of network structures differently.

A33 - Understanding Conversation Dynamics through the Lens of Intersectionality and Underrepresentation

Olga Lew-Kiedrowska, Northwestern University; Richard J. Wiener, Research Corporation for Science Advancement; Andrew L. Feig, Research Corporation for Science Advancement; Ruoming Gong, Northwestern University; Daniel M. Abrams, Northwestern University

Collaboration is crucial to the advancement of science, driving progress and innovation. We have previously developed a simple ordinary differential equation model for predicting new collaborations, inspired by the physics of catalysis. The model uses the interaction patterns of scientists at conferences to predict the probability of their forming a team (to apply for seed funding) at the end of the conference. That model makes a simplifying assumption of equal participation in conversations, which is a poor approximation of reality. We now attempt to improve on that assumption by analyzing recorded group conversations and modeling the conversation dynamics that take place. We examine turntaking, interruptions, and speaking time distributions among participants through the perspectives of intersectionality and underrepresentation. We also investigate other factors, such as homophily, that might play a role in team formation. We find that, in general, these scientific conversations show far less evidence of bias than has been reported in prior work.

A34 - Gait Classification of C. elegans Locomotion

Jenny Magnes, Vassar College; Raffaella F. Zanetti, Vassar College; Katherine Canavan, Vassar College; Susannah G. Zhang, Vassar College

Dynamic diffraction (DOD) is a form of microscopy that allows the dynamic tracking of plasticity in a 3D locomotory pattern and condense that pattern into a 1D time series. DOD is capable of capturing the locomotion of a nematode while swimming freely, allowing the locomotion of the worm to more closely mimic natural behavior than in some other laboratory environments. Diffraction covers the dynamics on multiple length scales. This work introduces a multichannel method to measure the dynamic complexity of microscopic organisms. We show that parameters associated with chaos, such as the largest Lyapunov exponent (LLE), the mean frequency, mutual information (MI), and the embedding dimension, may be associated with various gaits. These chaotic markers may be an indication of a neuronal switch in the head oscillator governing the locomotion of the nematode

A35 - Decay Rates of Neutral Multispecies Plasmas

Grace Mattingly, Colorado School of Mines; Steve Pankavich, Colorado School of Mines; Jonathan Ben-Artzi, Cardiff University

Collisionless plasmas arise within a variety of settings, from magnetically confined plasmas in laboratories to space plasmas in planetary magnetospheres and solar winds. The fundamental electrostatic model that describes such phenomena is a system of nonlinear PDEs known as the Vlasov-Poisson (VP) system. After providing some background information concerning VP, recent results regarding the largetime behavior of solutions will be introduced. These results establish a variety of limiting self-similar behaviors for the associated charge density and electric field with time decay rates up to any integer order. This behavior is physically attributed to the degree of charge cancellation amongst moments of different particle species within neutral plasmas.

A36 - Multipartite Entanglement Routing as a Hypergraph Immersion Problem

Xiangyi Meng, Rensselaer Polytechnic Institute; Yu Tian, Nordita; Yuefei Liu, KTH Royal Institute of Technology

Quantum networks rely on entanglement, a unique quantum resource, to connect nodes. Multipartite entanglement, linking multiple nodes simultaneously, is a higher-order correlation that offers advantages over simpler, pairwise connections. However, creating reliable, large-scale multipartite entanglement requires entanglement routing, a process that combines local, short-distance connections into a longdistance connection, which can be considered as a transformation of network topology. In this work, we investigate which network topologies are achievable through such transformations, given an initial topology. We establish a mathematical correspondence between entanglement routing and the concept of hypergraph immersion, allowing us to determine which network transformations are feasible. This provides crucial insights for designing and controlling complex quantum networks. [https://arxiv.org/abs/2406.13452]

A37 - Discovering Closed-Form Weather Models from Data

<u>Seth Minor</u>, University of Colorado at Boulder; Vanja Dukic, University of Colorado at Boulder; David Bortz, University of Colorado at Boulder

The multiscale and turbulent nature of Earth's atmosphere has historically rendered accurate weather modeling a hard problem. Recently, there has been an explosion of interest surrounding data-driven approaches to weather modeling (e.g., GraphCast), which in many cases boast both improved forecasting accuracy and computational efficiency when compared to traditional numerical methods. However, many of the new data-driven approaches employ highly parameterized neural networks, which often result in uninterpretable models and limited gains in scientific understanding. In this talk, we cover a research direction that addresses the interpretability problem in data-driven weather modeling. In particular, we describe an approach for explicitly discovering the governing PDEs symbolically, thus identifying mathematical models with direct physical meaning. In particular, we use a weak-form sparse regression algorithm, the Weak Sparse Identification of Nonlinear Dynamics (WSINDy), to learn effective models from simulated and assimilated weather data.

A38 - An Evolutionary algorithm for inferring differential equations from data

<u>Garrett Mitchener</u>, College of Charleston; Alex Brummer, College of Charleston; Whitney Kitchen, College of Charleston; Aidan Riordan, College of Charleston

Consider the challenge of inferring equations of motion for a physical system from measurements. Symbolic regression (SR) is a family of techniques that address this problem. A search process generates algebraic expressions. An optimization process steers the search toward expressions with low prediction error that may yield insights into an underlying physical process.

This project focuses on a new evolutionary SR algorithm called Jessamine. Each genome consists of instructions applied to input variables, scratch variables, scalar parameters, and output variables z_n . It specifies a function from a state array of z's and t's at one time step to its value at the next. Ridge regression applied to the z's from the final time step

yields a prediction \hat{y} . An optimization routine adjusts the parameters to minimize the prediction error. A selectionmutation process modifies a population of genomes through reproduction, mutation, and recombination, favoring those that yield good predictions.

As a test case, a trajectory of the Brusselator dynamical system was computed,

$$u' = u^2 v + 2 - 8.2u, v' = -u^2 v + 7.2u$$

Given samples of (u, v), Jessamine recovers both ODEs exactly up to rounding errors.

The Brusselator can be spatially extended,

$$u_t = u^2 v + 2 - 6.4u + \frac{3}{10}u_{xx}, v_t = -u^2 v + 5.4u + \frac{3}{80}v_{xx}$$

Sample points near a sharp increase in u do not satisfy the PDE to acceptable accuracy. If such points are filtered out, the Jessamine system can recover the PDEs up to rounding errors.

For a greater challenge, an oscillating chemical system was run in a dish under a camera. When this data is put through Jessamine or other SR packages, the resulting expressions include unnecessary terms that probably reflect numerical and measurement errors rather than the underlying dynamics. An ongoing project is to identify ways to improve the symbolic results using lessons learned from the spatial Brusselator test case.

A39 - A Network Diffusion Model of Urban Development and Inequality

Ashley Peake, Massachusetts Institute of Technology; Peko Hosoi, Massachusetts Institute of Technology

Wealth inequality between the richest and poorest U.S. Americans has continued to increase over the last several decades. In designing intervention strategies to address this growing social problem, it is useful to recognize that there is a distinct geographic structure to the distribution of wealth. Within a city, neighborhoods tend to cluster into wealthier "nice" parts of town and poorer "bad" parts of town, often limiting the upward mobility of residents in "bad neighborhoods." To better understand and address this phenomenon, we build a dynamical model to study the geospatial patterns of urban development and inequality. Specifically, we model the flow of wealth in an urban area as a diffusive process on a network. Using this model, we characterize the effects of investment and other development strategies on the distribution of wealth and economic opportunities within a city. Furthermore, we link these effects to changes in rent prices and racial distributions to study the process of gentrification. We test our model using data from the National Historic GIS. Ultimately, our model shows that combatting wealth inequality must involve a fundamental shift in how and where money is invested.

A40 - Flash Synchronization of Fireflies with Information Disparities

Nicholas Barendregt, BioFrontiers Institute, University of Colorado Boulder; Orit Peleg, BioFrontiers Institute, University of Colorado Boulder

To achieve collective goals, groups of agents must develop effective methods of communication to share information and preferences with other agents. While these interactions are fundamental to any complex system's dynamics, how such communication strategies adapt to the group interaction structure remains an open scientific question. In this work, we study how communication adapts to network topology by using fireflies as a model system, a well-documented organism with visually identifiable communication signals that can be well-approximated as stochastic oscillators. We model information flow through a network of fireflies based on experiments we performed that had both known information input (in the form of a programmed LED) and known network topology (in the form of visual barriers between fireflies). Through this work, we find that information reaches individuals that cannot directly observe the source via conduit agents, and that this information flow scales in a predictable way as the network topology is altered. Our work demonstrates how group communication strategies adapt to environmental features and give rise to the complex dynamics we can observe in nature.

A41 - Adaptations and mechanical memory in honeybee swarms in response to temperature changes

Danielle Chase, University of Colorado at Boulder; Nina van Hoorn, Skidmore College; Andrew Swanson, University of Colorado, Boulder; Jenn Kaphammer, University of Colorado, Boulder; Daniel Moran, University of Colorado, Boulder and Community College of Aurora; Caitleen Reyes, Indiana University; Olga Shishkov, University of Colorado, Boulder; Pedro Albuquerque Lemos, University of Colorado, Boulder; Orit Peleg, University of Colorado, Boulder

Honeybee swarms, consisting of a queen bee and thousands of workers, hang suspended from structures in nature for periods ranging from hours to several days while searching for a new hive. During this time, the swarm is subject to dynamic environmental forces including wind, rain, and temperature fluctuations. Individual bees respond to local cues, such as pheromones, tension in bee-bee bonds, and environmental factors, by making topological and geometric changes to their connections with neighboring bees. These modifications in bee-bee connections give rise to both local and global changes in the swarm's network architecture and morphology, which, in turn, modify the microenvironment within the swarm, driving a continual cycle of adaptation and self-optimization of the physical network to buffer the swarm against environmental perturbations. Using X-ray computed tomography as a lens into the swarm, we characterize the evolution of the swarm's structure in response to ambient temperature fluctuations. We find that thermally-

induced mechanical memory in the swarm leads to hysteresis and distinct morphological adaptations during heating and cooling. Additionally, we explore the trade-offs faced by both individual bees and the swarm as a whole while optimizing competing biological objectives, such as maintaining mechanical stability, thermoregulation, and cohesion.

