WORKSHOP ON RECENT TOPICS IN DYNAMICAL SYSTEMS MEMORIAL IN HONOR OF PROFESSOR SHUI-NEE CHOW

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Georgia Institute of Technology, Atlanta, GA

Is there a Sturmian theory for nonlocal equations?

Peter Bates
Michigan State University

Abstract. In 1836 Sturm published two papers in Liouville's J. Math. Pures et Appl. giving his famous comparison and Oscillation theorems. In it's simplest form, the one that I will focus on is:

Theorem Let $p(x) > q(x)$, let u be a nontrivial solution to $u" + p(x)u = 0$ on $[a, b]$ and let v be a nontrivial solution to $v" + q(x)v = 0$ on $[a, b]$ with $v(a) = v(b) = 0$. Then u has at least one zero in (a, b).

Now let J be nonnegative, with unit integral, and with positive second moment, c_J. Let $J_\epsilon(x) = J(x/\epsilon)/\epsilon$ and let $L_\epsilon w = [J_eps * w - w]/\epsilon^2$ for $w \in H^2$. One can show that in a weak sense,$\lim_{\epsilon \to 0} L_\epsilon w = c_J w"/2$. It is natural, therefore, to ask if the above theorem holds when the second derivative is replaced by L_ϵ, at least for ϵ sufficiently small. Some preliminary results with Guangyu Zhao will be presented.

Stability for the logarithmic Hardy-Littlewood-Sobolev Inequality with application to the Keller-Segel equation

Eric Carlen
Rutgers University

Abstract. We apply a duality method to prove an optimal stability theorem for the logarithmic Hardy-Littlewood-Sobolev inequality, and we apply it to the estimation of the rate of approach to equilibrium for the critical mass Keller-Segel system.

In memory of Shui-Nee: from my first seminar talk to my latest paper

Bo Deng
University of Nebraska–Lincoln

Abstract. Shui-Nee's impact on my research career has been long-lasting. His first seminar-talk assignment for me led to a serendipitous solution to the Markus-Yamabee conjecture, and his joint work with Mallet-Paret and Yorke on locating all zeros of polynomials inspired a homotopy method to train AI models error-free.

Following the Footsteps of the Unbounded Perturbation of Exponential Dichotomy: Lessons from Dr. Shui-Nee Chow

Hugo Leiva
Yachay-Tech University (Ecuador)

Abstract. In this heartfelt presentation, I've shared experiences from my time as a doctoral student under the guidance of the inspiring Dr. Shui-Nee Chow. Together, we delved into solving challenging mathematical problems, specifically focusing on the unbounded perturbation of exponential dichotomy for evolution equations. Within a memorable anecdote, I grappled with the enigma of perturbing the system with an unbounded linear operator, pushing the boundaries of my knowledge and abilities.

The narrative unfolds with Dr. Chow's resolute response: "Find the metric." After a night of intense research, I uncovered a perturbation principles in the works of Dunford and Schwartz, along with a key metric in Hile and Philips. These findings not only unraveled the puzzle but also shaped a paper that I proudly presented to Dr. Chow.

Calculus of score functions dedicated to Prof. Shui-Nee Chow

Wuchen Li
University of South Carolina

Abstract. We provide a Lyapunov convergence analysis for time-inhomogeneous variable coefficient stochastic differential equations (SDEs). Three typical examples include overdamped, irreversible drift, and underdamped Langevin dynamics. We first formula the probability transition equation of Langevin dynamics as a modified gradient flow of the Kullback-Leibler divergence in the probability space with respect to time-dependent optimal transport metrics. This formulation contains both gradient and non-gradient directions depending on a class of time-dependent target distribution. We then select a time-dependent relative Fisher information functional as a Lyapunov functional. We develop a time-dependent Hessian matrix condition, which guarantees the convergence of the probability density function of the SDE. We verify the proposed conditions for several time-inhomogeneous Langevin dynamics. For the overdamped Langevin dynamics, we prove the $O(t^{-1/2})$ convergence in L^1 distance for the simulated annealing dynamics with a strongly convex potential function. For the irreversible drift Langevin dynamics, we prove an improved convergence towards the target distribution in an asymptotic regime. We also verify the convergence condition for the underdamped Langevin dynamics. Numerical examples demonstrate the convergence results for the time-dependent Langevin dynamics.

Data-driven Fokker-Planck equation solvers

Yao Li
University of Massachusetts Amherst

Abstract. The Fokker-Planck equation describes the time evolution of probability density function of stochastic differential equations. Numerically solving Fokker-Planck equation in higher dimension is known to be challenging. In this talk, I will briefly summarize my recent progress in solving Fokker-Planck equations in both low and high dimensions. The main idea is to utilize Monte Carlo simulation data to "guide" the solver. I will also discuss possible extensions in solving quasi-potential functions and eigenfunctions.

Interplay between permanent charge and boundary conditions on ionic flow

Weishi Liu
University of Kansas

Abstract. Permanent charge (mathematical model for protein structure) is the most important structure of an ion channel which, together with boundary conditions, control specifics of ionic flows through the ion channel. In this talk, we will report our studies toward an understanding of effects of interplays between permanent charge and boundary conditions on ionic flow via a quasi-one-dimensional Poisson-Nernst-Planck (PNP) model.

For ionic mixtures with one cation (positively charged) species and one anion (negatively charged) species, a rich behavior of permanent charge effects has been revealed from rigorous analyses based on a geometric framework for PNP and from numerical simulations guided by the analytical results. For ionic mixtures with three ion species: two cations and one anion, richer behavior is expected and our preliminary analysis and case studies identify, in concrete manner, a number of these, including some surprising ones.

On invariant measures for delay equations with stochastic negative feedback

Sjoerd Verduyn Lunel

Utrecht University

Abstract. In this talk we present recent results regarding the existence of invariant probability measures for delay equations with stochastic negative feedback. We will consider the setting that the underlying deterministic delay equation is given by a monotone feedback system, i.e.,

$$\frac{dx}{dt}(t) = -\gamma x(t) + f(x(t-1)), \tag{1}$$

where $\gamma \geq 0$ and f is a differentiable real function with negative derivative.

In general, additive noise destroys all dynamical properties of the underlying dynamical system, and therefore we are motivated to study a class of stochastic perturbations that preserve some of the dynamical properties of monotone feedback systems. We will prove the existence of (nontrivial) invariant probability distribution in a setting relevant in applications. The applications include Nicholson blowflies equation, the Mackey-Glass equation, and Wright's equation. In this talk we will use Wright's equation to illustrate our main results.

This is joint work with Mark van de Bosch and Onno van Gaans.

The Uniform Shape of Slowly Oscillating Solutions of Delay-Differential Equations

John Mallet-Paret
Brown University

Abstract. We study singularly perturbed delay-differential equations of Mackey-Glass type, in which (among other conditions) negative feedback and instability of the origin are assumed. We show that slowly oscillating solutions (which are not necessarily periodic) assume a uniform square-wave shape as the singular parameter approaches zero.

This result was established for periodic solutions with period approaching 2 over thirty years ago; here we extend it to general slowly oscillating solutions. This entails using new techniques to obtain uniform estimates on the shape of such solutions which are independent of the period.

Identifying Nonlinear Dynamics from Sparse Data

Konstantin Mischaikow
Rutgers University

Abstract. There are a variety of statistical techniques that identify explicit models, e.g. differential equations or maps, from time series. Typically, these explicit models are then used to predict dynamics. However, bifurcation theory tells us that dynamics

can be extremely sensitive to the choice of model. and hence to small errors in data. This suggests a potential inherent instability in this data analysis pipeline: small errors in data can lead to slightly different models which in turn can produce different dynamics.

We propose a novel method, combining Conley theory and Gaussian Process surrogate modeling with uncertainty quantification, through which it is possible to characterize local and global dynamics, e.g., existence of fixed points, periodic orbits, connecting orbits, bistability, and chaotic dynamics, and to provide lower bounds on the confidence that this characterization of the dynamics is correct. Furthermore, numerical experiments indicate that it is possible to identify nontrivial dynamics with high confidence with surprisingly small data sets.

Traveling Waves and Spreading Speeds in Chemotaxis Models with a Logistic Source

Wenxian Shen
Auburn University

Abstract. Propagation phenomena exist in a large number of mathematical models in the fields of population biology, population genetics, material sciences, and other research areas. This talk is concerned with propagation phenomena in chemotaxis models with a logistic source. Such models are used to describe the movements of biological species or living organisms in response to certain chemicals in their environments. In particular, I will discuss spatial spreading speeds and traveling wave solutions in such models. Special attention will be given to the combined effect of the chemotaxis sensitivity and the logistic damping on the spreading speeds/minimal wave speed.

The Mathematics behind Precision Nutrition

Diana Thomas
West Point

Abstract. Nutrition is at the epicenter of human health and disease. However, our current “one size fits all” approach to clinical nutrition is failing a large segment of the population. Individual factors including genetics, metabolism, physiology, microbiome, behavior, the built and contextual environment all underlie the inherent variability in response to diets. Exciting new research shows that machine learning algorithms can integrate this complex information and predict how someone responds to a given diet. If validated, this innovative approach will provide a radical change in the delivery of personalized nutrition prescriptions to promote health and treat chronic diseases in all people. The goal of the Nutrition for Precision Health (NPH)

research study, where I serve as a PI for an AI Center, is to study a large and diverse group of American adults and to use machine learning and artificial intelligence models to understand the individual responses to foods and dietary patterns. As part of this study, we are measuring response to meals by glucose concentration curves generated after consuming a provided meal. Investigators in the field of obesity, nutrition, and diabetes have typically collapsed the post-prandial curve to a single value using either the area under the curve (AUC) or the incremental area under the curve (iAUC), which is the area between the curve and fasting glucose concentrations. In this presentation, I will show that calculus-based curve properties beyond AUC, such as the number of critical points, optimal values, inflection points, maximum rate of incline or decline, can 1) discriminate between healthy and at-risk populations and 2) predict onset of type 2 diabetes in previously non-diabetic patients. As key part of this presentation I will be sharing the data science research journey behind working with clinical investigators, pre-processing messy human subject data, asking the right questions that can transform human health, and developing end-user tools to clinically deploy mathematical models.

Reduced Order Modeling for Particle Filtering

Erik S. Van Vleck
University of Kansas

Abstract. Particle filters (PFs) are employed in data assimilation (DA) contexts to combine models and observational data and make improved predictions together with measures of uncertainty. PFs play an important role especially when (in space and time) there are non-Gaussian, multi-modal posterior distributions. However, PF techniques generally suffer from a curse of dimensionality and performance tends to degrade, e.g., due to particle collapse, in the presence of high dimensional models and data. In this talk we outline a reduced order modeling approach based upon frequent (in time) updates and sparse mode selection. Numerical results using a popular PF variant, the so-called optimal proposal PF, illustrate the effectiveness of these techniques on a Lorenz '96 model and a slow/fast, ocean/atmosphere model.

Generative Adversarial Nets (GAN)

Yang Wang
Hong Kong University of Science and Technology

Abstract. Generative Adversarial Nets (GAN) have been one of the most exciting developments in machine learning and AI. In this talk I will give an introduction to GAN, and discuss the difficulty of training a GAN. I'll propose a framework to learn deep generative models via Variational Gradient Flow (Vgrow) on probability

measure spaces. Connections of our proposed VGrow method with other popular methods, such as VAE, GAN and flow-based methods, have been established in this framework, gaining new insights of deep generative learning.

Mathematics in action: from pandemic to drug discovery

Guo-Wei Wei
Michigan State University

Abstract. Mathematics underpins fundamental theories in physics such as quantum mechanics, general relativity, and quantum field theory. Nonetheless, its success in modern biology, namely cellular biology, molecular biology, chemical biology, genomics, and genetics, has been quite limited. Artificial intelligence (AI) has fundamentally changed the landscape of science, engineering, and technology in the past decade and holds a great future for discovering the rules of life. However, AI-based biological discovery encounters challenges arising from the intricate complexity, high dimensionality, nonlinearity, and multiscale biological systems. We tackle these challenges by a mathematical AI paradigm. We have introduced persistent cohomology, persistent spectral graphs, persistent path Laplacians, persistent sheaf Laplacians, and evolutionary de Rham-Hodge theory to significantly enhance AI's ability to tackle biological challenges. Using our mathematical AI approaches, my team has been the top winner in D3R Grand Challenges, a worldwide annual competition series in computer-aided drug design and discovery for years. By further integrating mathematical AI with millions of genomes isolated from patients, we discovered the mechanisms of SARS-CoV-2 evolution and accurately forecast emerging dominant SARS-CoV-2 variants months in advance. This work was supported in part by NIH grants R01GM126189, R01AI164266, and R35GM148196, National Science Foundation grants DMS2052983, DMS-1761320, and IIS-1900473, NASA grant 80NSSC21M0023, MSU Foundation, Bristol-Myers Squibb 65109, and Pfizer.

Response Solutions in Forced Nonlinear Oscillators

Yingfei Yi
University of Alberta & Jilin University

Abstract. For a quasi-periodically forced differential equation, response solutions are quasi-periodic ones whose frequency vector coincides with that of the forcing function and they are known to play a fundamental role in the harmonic and synchronizing behaviors of quasi-periodically forced oscillators. These solutions are well-understood in quasi-periodically perturbed nonlinear oscillators either in the presence of large damping or in the non-degenerate cases with small or free damping. This

talk will present some recent results on the existence of responsive solutions in degenerate, quasi-periodically forced nonlinear oscillators with small or free damping. The cases with singular or noise perturbations will also be discussed.

Temporal Clusters Prefer to be Equally Distributed - an example from the Yeast Cell Cycle

Jan Rombouts, Kiattisak Prathom, Todd Young*
Ohio University

Abstract. Synchrony, the phenomenon where components of a system experience events in unison, seems to be common in many systems. Relatedly, Temporal Clustering or Phase Synchrony, is where sub-groups (or cohorts) of components synchronize among themselves, but are out of phase with other cohorts.

In bioreactor experiments on yeast metabolic oscillations we discovered a case where a culture of yeast exhibits temporal clustering in which two groups progress through their cell cycles in anti-phase. In these experiments the cell cycle clusters and oscillations in the metabolism are seen to be tightly linked.

The discovery raises a number of mathematical questions such as: ‘What accounts for the difference between a system that synchronizes and one that forms clusters?’, ‘What determines the number of clusters that appear?’, and ‘How do individual cells distribute among clusters?’.

In this talk we will focus on the last question using a biologically motivated nonlinear model. We observe in numerical simulations of the model that the clusters tend very strongly toward having nearly equal numbers of cells. This is consistent with the available experimental data. We study the case of two unequal clusters analytically and conclude that solutions with two unequal clusters are locally asymptotically stable in the clustered subspace, but, local asymptotic stability of unbalanced clusters in the full phase space depends delicately on details of the model. However, global dynamics reveal a more robust picture. If clusters become unbalanced, the influence of the larger cluster can radically shift the ‘basins of attraction’ of individual clusters, making it more likely for an unclustered cell to join a smaller cluster. We propose that this points to a general principle: systems that form temporal clusters via non-local coupling tend to form nearly equal clusters.

Solving puzzles with friends, a retrospective

James Yorke
University of Maryland

Abstract.