Kolmogorov-Arnold Attention

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TBA

Kernel Density Estimation in Spatial Ecology

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Kernel Density Estimation (KDE) is a cornerstone technique in statistics for estimating a probability density function when its parameterized form is unknown. KDE is widely used in spatial ecology for calculating animal home ranges and species distributions where the assumptions behind conventional KDE are often pushed beyond their limits. In this seminar I will present over a decade of research that now allows for accurate kernel density estimates to be computed from irregularly sampled times-series data that are sampled from heterogeneous populations.

Application of Physics-Informed Neural Networks with Topological Validation on Gene Regulatory Networks

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Gene regulatory networks (GRNs) modern cellular behavior through activating and suppressing interactions. I present a physics informed neural network (PINN) that couples ODE based GRN representations with data to infer, predict, and control dynamics. The method estimates key regulatory parameters, including Hill and piecewise linear Ramp steepness, via a loss that enforces data fit and equation fidelity. Accuracy is improved with Fourier, radial basis function, and B spline features, plus learned embedding. PINN inferences are compared with DSGRN's global dynamical predictions, clarifying when step function abstractions hold and guiding model selection and control.

Finite-Dimensional Reduction of Dissipative Evolution Equations

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One of the central problems in the study of dissipative systems governed by PDEs is whether their long-term dynamics are effectively finite-dimensional and can be captured by a system of ODEs. To address this issue, Foias, Sell, and Temam introduced the concept of inertial manifolds, namely, finite-dimensional, Lipschitz-continuous, invariant manifolds that attract all trajectories of the associated dynamical system exponentially fast. The existence of an inertial manifold for an infinite-dimensional evolution equation provides the strongest analytical reduction of such a system to a finite-dimensional one. For example, reaction-diffusion equations are known to possess inertial manifolds. However, it remains an open question whether the Navier–Stokes equations admit an inertial manifold. In this talk, I will survey this topic and discuss the existence of inertial manifolds for certain regularized versions of the Navier–Stokes equations. Interestingly, this topic is related to number-theoretical results on large gaps between sums of squares.

Bayesian Spatiotemporal Modeling of Sparse Count Processes: From Deer Mouse Traps (NEON) to Imaging-Derived Landslides (Oregon)

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Many population and event-monitoring systems produce sparse spatiotemporal count data with three recurring features: (i) many zeros (rarity and imperfect detection), (ii) overdispersion and bursty extremes, and (iii) spatial and temporal dependence driven by shared environments and episodic shocks. This talk presents a Bayesian modeling framework designed to deliver interpretable inference and stable computation for such data, illustrated through two case studies that share the same statistical structure but arise from different scientific workflows.

First, using National Ecological Observatory Network (NEON) deer mouse (Peromyscus maniculatus) trap data across the contiguous United States (2013–2022), we model trap-level counts as a function of precipitation and temperature covariates with climate-informed regional effects and interactions. Seasonal dynamics are captured by a Gaussian process prior on month effects,

enabling smooth, repeating annual patterns while allowing region-specific temporal shifts. We highlight posterior findings that quantify how precipitation and temperature associate with population variability across regions, including behavior in an “extreme” high-count subset of traps.

Second, motivated by imaging and remote sensing pipelines that yield regional event catalogs, we consider Oregon county–year landslide counts and develop a Bayesian zero-inflated negative binomial model that separates structural-zero risk from intensity when events occur. Spatiotemporal dependence is modeled via Gaussian process random effects, and efficient posterior computation is enabled by Pólya–Gamma augmentation. We discuss practical identifiability and numerical issues that arise in spatiotemporal GP count models (variance confounding, rank deficiency from indicator designs, ill-conditioned kernels), and present stabilizing strategies including a noisy-GP signal-to-noise reparameterization and contrast-coded designs.

Finally, we outline ongoing work that replaces discrete-time temporal random effects with continuous-time stochastic differential equation (SDE) dynamics to better represent irregular sampling, unit-specific temporal trajectories, and mechanistic time scales. Overall, the talk emphasizes a reusable Bayesian template for population-style counts that integrates covariates, interpretable spatiotemporal random effects, scalable computation, and uncertainty quantification.

Improving Statistical Methods for Wildlife Corridor Estimation

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Habitat connectivity is essential to conserving biodiversity, by allowing animals to search across landscapes for resources and mates. This is particularly important for migration and dispersal, which can be impeded by human activities that degrade and fragment habitats. To maintain connectivity, it is imperative that we identify wildlife corridors—areas where animals traverse frequently to move between suitable environments. Traditionally, connectivity has been modeled via two main methods: resistance circuit models and Brownian bridges. However, these methods do not target a “well-calibrated” probabilistic corridor distribution—i.e., where 95% of animals pass through the 95% cross-section. We have developed a new statistical method for corridor estimation, using cross-sectional kernel density estimation (KDE) to model corridors as “range distributions” from animal tracking data. We define the corridor by the distribution of repeated passages between two areas in a landscape. To ensure that this method is robust and offers improvements, we conducted a comparative sensitivity analysis across parameters that impact performance, such as sampling frequency and passage count, using GPS-tracked mule deer (*Odocoileus hemionus*) and jaguars (*Panthera onca*). We found that cross-sectional KDE is insensitive to the sampling frequency and produces consistent distribution estimates regardless of the location-recording in-

terval, thus demonstrating that our method provides more rigorous estimates of corridor space needed by migrating animals even with few tracking points available. Our research, implemented in the `ctmm` R package, contributes a novel statistical tool that ecologists can directly apply to conservation management, through designating new wildlife corridors and evaluating the impact of existing ones.

Fidelity Preserving Phenomenon Under Mixed Unitary Quantum Channels

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Correlations between quantum states are important resources in quantum information theory. In this talk, I will introduce the scenario when fidelity between quantum states could be perfectly preserved under mixed unitary quantum channels. The ability for such a quantum channel to preserve fidelity highly depends on its local operations and the correlation between original quantum system and the environment. A nice example would be the generalized dephasing channel, which exemplifies that phenomenon.

Recent Developments in Modeling HIV Infection and Treatment

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HIV infection remains a significant global public health challenge. While combination antiretroviral therapy can effectively suppress viral replication, complete eradication of the virus remains elusive. Mathematical models, integrated with experimental and clinical data, provide a quantitative framework for understanding HIV dynamics, treatment effects, and immune responses. Yet several key questions remain: Are some drug classes more effective than others in specific settings? Does treatment intensification provide measurable benefits? What mechanisms contribute to multiple infections? And beyond latent infection, what additional sources might sustain viral persistence during long-term therapy? In this talk, I will highlight recent developments in HIV modeling that address these questions and discuss their implications for HIV treatment and management.

Asymptotic Profiles of Basic Reproduction Number for Epidemic Spreading in Heterogeneous Environment

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The effect of diffusion rates on the basic reproduction number of a general compartmental reaction-diffusion epidemic model in a heterogeneous environment is considered. It is shown that when the diffusion rates tend to zero, the limit of the basic reproduction number is the maximum value of the local reproduction number on the spatial domain. On the other hand, when the diffusion rates tend to infinity, the basic reproduction number tends to the spectral radius of the average next generation matrix. These asymptotic limits of basic reproduction number hold for a class of general spatially heterogeneous compartmental epidemic models, and they are applied to a wide variety of examples. Related results for patch epidemic models will also be discussed.

Quantifying the Impact of Partial Immunity on Disease Endemicity

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The basic reproduction number of an epidemiological model, $\mathcal{R}_0$, is a well-established threshold parameter that determines the persistence of a disease, but it alone cannot reliably quantify other characteristics of an outbreak, like long-term disease prevalence or endemicity. In this talk, we present a standard-incidence SIR model incorporating partial immunity, prove the existence, uniqueness, and stability of the disease-free and endemic equilibria, and show that the endemicity of the outbreak depends on critically on the interaction between between the degree of partial immunity and $\mathcal{R}_0$. This analysis motivates the definition of a reinfection reproduction number, $\mathcal{R}_0^s$, which characterizes disease persistence in the recovered population and accurately delineates between parameter regimes with high and low endemicity. We conclude by discussing the biological significance of $\mathcal{R}_0^s$, particularly in quantifying the interplay between susceptibility and immunity in shaping epidemic outcomes.

Dynamics of Cascading Failures in Biological Networks

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Understanding the structural differences in gene networks under different physiological conditions is crucial for elucidating the mechanisms of complex traits and diseases. In this study, we propose a modeling-based structural analysis method (MSAM) to quantify gene network structures for three species. Using a betweenness centrality-based cascading failure simulation, we show that the AFS curves of the experimental group (EG) and control group (CG) differ significantly across all thresholds. Genes responsible for these structural differences, referred to as structure key genes, were identified and analyzed. Using soybean as an example, we found that the RRD-resistant and susceptible genotypes share only one common key gene, indicating distinct genetic mechanisms underlying disease resistance. These results reveal significant differences in disease-related functional mechanisms and provide new insights for further biological investigation.

Approximation Properties of Locally Optimal Shallow Neural Networks

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Universality, super-convergence, Barron type dimension independence and many other results, show that arbitrary functions can be highly effectively approximated by neural networks. These networks, however, are typically hand-picked or sampled from unknown information. How well such results can be matched by practical training algorithms remains an open problem.

In the simplest case, shallow and one dimensional, neural networks are equivalent to free knot splines. Their knots, are chosen by equi-distribution principles, which ensure that local errors, or local smoothness indicators, are of comparable size. We show that neural network optimization yields similar equi-distribution of Barron smoothness, first for the simple case above and then for shallow networks in high dimensions. The results indicate that practically optimized shallow networks achieve similar approximation properties than known in theory.

From Slow to Fast Dispersal: Impacts on Species Persistence and Infectious Disease Invasion

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In heterogeneous environments, populations of species and infectious diseases are often distributed across patches with different environmental conditions that are connected through dispersal. As dispersal can play a crucial role in determining whether populations and pathogens persist or go extinct in such spatially structured systems, understanding how movement among patches interacts with environmental heterogeneity is a central problem in ecology and epidemiology.

In this talk, we use analytical tools from perturbation theory and group inverse to investigate how slow and fast dispersal influence population dynamics. Our analysis highlights the combined effect of environmental heterogeneity, network connectivity, and dispersal rates.'

Optimal Control of Free Boundary Models for Tumor Growth

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In this talk, we will investigate the optimal control of treatment in free boundary PDE models for tumor growth. The optimal control strategy is designed to inhibit tumor growth while minimizing side effects. In order to characterize it, the optimality system is derived, and a necessary condition is obtained. Numerical simulations will be presented to illustrate the theoretical findings and assess the impact of the optimal control strategy on tumor growth dynamics.
