

Fall 2017

Friday, December 1, 2017

**3:00-4:00PM, Haag Hall 312
Hongjuan Zhou
Department of Mathematics
University of Kansas**

Parameter Estimation for Fractional Ornstein-Uhlenbeck Processes

ABSTRACT

The fractional Ornstein-Uhlenbeck process is defined as the unique pathwise solution to the stochastic differential equation

$$X_t = X_0 - \theta \int_0^t X_s ds + \sigma dB_t^H$$

with initial condition $X_0 \in \mathbb{R}$, where B^H is a fractional Brownian motion of Hurst parameter H . This process has been widely used in many fields such as physics, economics, and finance. In this talk, we will discuss about the estimation of the drift parameter θ . We will use the least squares estimator (LSE). The strong consistency of LSE will be proved, and a central limit theorem is obtained when $H \in (0, \frac{3}{4}]$, and also a noncentral limit theorem is obtained for $H \in (\frac{3}{4}, 1)$. The LSE is also used to study the asymptotics for other alternative estimators, such as the ergodic type estimator. Finally, a Monte Carlo simulation is carried out to validate our results.

Friday, November 3, 2017

Applied Mathematics Public Lecture Series

**3:00-4:00PM, Haag Hall 312
Dr. Noah Rhee
Department of Mathematics and Statistics
University of Missouri - Kansas City**

Jacobi's Method for Symmetric Eigenvalue Problem

ABSTRACT

A typical method for finding all eigenvalues of a square matrix is the QR-method. But in 1992 Demmel and Veselic published a paper titled "Jacob's Method is More Accurate than QR" (SIAM Journal on Matrix Analysis and Applications, Vol 13, pages 1204-1245). In this talk, we review the essential basics of Jacob's method for symmetric eigenvalue problem. Anyone who has undergraduate linear algebra background can understand this talk.

Friday, October 27, 2017

Applied Mathematics Public Lecture Series

3:00-4:00PM, Haag Hall 312

Dr. Xianping Li

Department of Mathematics and Statistics

University of Missouri - Kansas City

Mesh Adaptation for Anisotropic Porous Medium Equations

ABSTRACT

Anisotropic Porous Medium Equation (APME) is developed as an extension of the Porous Medium Equation (PME) for anisotropic porous media. A special analytical solution is derived for APME for time-independent diffusion. Anisotropic mesh adaptation for linear finite element solution of APME is discussed and numerical results for two dimensional examples are presented. The solution errors using anisotropic adaptive meshes show second order convergence.

Friday, October 20, 2017

3:00-4:00PM, Haag Hall 312

Dr. Agnieszka Miedlar

Department of Mathematics

University of Kansas

Flexible Eigenvalue Solvers for Electronic Structure Calculations

ABSTRACT

Determining excited states in quantum physics or calculating the number of valence electrons in the Density Functional Theory (DFT) involve solving eigenvalue problems of very large dimensions. Moreover, very often the interesting features of these complex systems go beyond information contained in the extreme eigenpairs. For this reason, it is important to consider iterative solvers developed to compute a large amount of eigenpairs in the middle of the spectrum of large Hermitian and non-Hermitian matrices. In this talk, we present newly developed Krylov-type methods and compare them with the well-established techniques in electronic structure calculations. We demonstrate their efficiency and robustness through various numerical

examples. This is a joint work with Yousef Saad (University of Minnesota).

Friday, October 6, 2017

3:00-4:00PM, Haag Hall 309

Gerry Baygents

Department of Mathematics and Statistics

University of Missouri - Kansas City

Multi-patch modeling and analysis of hemorrhagic diseases in Missouri's white-tailed deer

ABSTRACT

Hemorrhagic disease (HD) is a vector-borne disease that affects deer and other ruminants in the United States. A delay differential equation for endemic HD involving variable deer and midge (vector) populations is analyzed within a single geographic area (a patch). A threshold parameter R_0 exists and the disease persists if and only if $R_0 > 1$. We examine the value as a function of influx rates, interaction rates, and probability of death while migrating and provide numerical simulation of the changes in R_0 . The model is also analyzed for stability, and a multi-patch extension is proposed.

Friday, September 22, 2017

3:00-4:00PM, Haag Hall 312

Dr. Fengpeng Sun

Department of Geosciences

University of Missouri - Kansas City

A High-Resolution Hybrid Dynamical-Statistical Downscaling Technique and Its Applications to Climate Change Projections for California

ABSTRACT

In this presentation, Dr. Sun will present his recent research activities in development of high-resolution regional climate modeling framework and its applications to projecting future climate change in California's Great Los Angeles Area and Sierra Nevada. Using a combination of dynamical and statistical downscaling techniques, both regions' projected climate and the impacts are examined at the scales of a few kilometers under mitigation and business-as-usual greenhouse gas emissions scenarios. All available global climate models (GCMs) associated with the Coupled Model Intercomparison Project Phase 5 (CMIP5) archive are downscaled. A number of general questions related to the science of climate change at the regional scale will be addressed as well. These include: What information about regional scale change really is latent in the GCM projections? How can one downscale multiple GCMs and multiple time slices efficiently so as to have estimates of ensemble-mean outcomes and associated uncertainties? Given the generally high levels of natural variability at the regional/local scales, how significant is climate change at the scales where climate

change adaptation actually occurs? Dr. Sun will conclude with preliminary results from his Missouri EPSCoR research project and his near future research plans.

Spring 2017

Friday, April 21, 2017

3:00-4:00PM, Haag Hall 309

Dr. Xianping Li

**Department of Mathematics and Statistics
University of Missouri - Kansas City**

Anisotropic Mesh Adaptation in Numerical Computations

ABSTRACT

Mesh adaptation is a powerful and useful tool in mathematical computations that can improve computational efficiency and accuracy. In this talk, we briefly introduce computational methods such as Finite Difference Method and Finite Element Method. Then we introduce anisotropic mesh adaptation techniques in the computations. Applications in image processing and engineering are presented that demonstrate the advantages of anisotropic mesh adaptation.

Wednesday, April 5, 2017

1:00-1:50PM, Haag Hall 313

Dr. Jingjing Yang

**Biostatistics Department,
University of Michigan**

A scalable Bayesian Method for Integrating Functional Information in Genome-wide Association Studies

ABSTRACT

Although genome-wide association studies (GWASs) have identified many complex loci, most of which reside in noncoding regions and have unknown biological functions. Integrative analysis that incorporates known functional information into GWAS can help elucidate the underlying biological mechanisms and prioritize causal-variants. We develop a novel, flexible Bayesian variable selection model with efficient computational techniques for such integrative analysis. Different from previous approaches, our method

models the effect-size distribution and probability of causality for variants with different annotations and jointly models genome-wide variants to account for linkage disequilibrium (LD), thus prioritizing associations based on the quantification of the annotations and allowing for multiple causal-variants per locus. Our method dramatically improves both computational speed and posterior sampling convergence by taking advantage of the block-wise LD structures in human genomes. In simulations, our method accurately quantifies the functional enrichment and performs more powerful for identifying true causal-variants than alternative methods, where the power gain is especially apparent when multiple causal-variants in LD reside in the same locus. We applied our method to an in-depth GWAS of age-related macular degeneration with 33,976 individuals and 9,857,286 variants. We find the strongest enrichment for causality among non-synonymous variants (54x more likely to be causal, 1.4x larger effect-sizes) and variants in active promoter (7.8x more likely, 1.4x larger effect-sizes), as well as identify 5 potentially novel loci in addition to the 32 known AMD risk loci. In conclusion, our method is shown to efficiently integrate functional information in GWASs, helping identify causal-variants and underlying biology.

Friday, March 17, 2017

3:00-4:00PM, Haag Hall 309

**Dr. Ellis Scharfenaker
Department of Economics,
UMKC**

A Tutorial on the Principle of Maximum Entropy Inference

ABSTRACT

This lecture introduces the principle of maximum entropy (PME) from information theory and statistical mechanics as an inductive framework for inferring “statistical equilibrium” distributions in social and economic variables. Particular emphasis will be placed on understanding the PME from an information theoretic perspective and its relationship to Bayesian methods of inference. All those attending are encouraged to read “Foundations of probability theory and statistical mechanics” (available at <http://bayes.wustl.edu/etj/articles/foundations.of.prob.st.pdf>) and “Where do we stand on maximum entropy?” (available at <http://bayes.wustl.edu/etj/articles/stand.on.entropy.pdf>) both by E.T. Jaynes.

Friday, March 10, 2017

3:00-4:00PM, Haag Hall 312

**Dr. Santca Ciupe
Department of Mathematics,
Virginia Tech University**

Mathematical models of HIV-HPV co-infection

ABSTRACT

HIV-infected patients are at increased risk of co-infection with human papilloma virus (HPV), and subsequent malignancies such as oral cancer. To determine the role of HIV-associated immune suppression on HPV persistence and pathogenesis, we developed models of HIV-HPV co-infection and used them to investigate the mechanisms underlying the modulation of HPV infection by HIV. In this talk, I will show how the models can be used to make predictions regarding the HPV persistence in the oral mucosa. We predict that the permissive immune environment created by HIV, as well as molecular interactions between the two viruses, are the reasons for HPV persistence. We address the role of antiretroviral therapy and show that restoration of CD4 T cell count correlates with eventual HPV removal as seen in a recent clinical trial. Lastly, we investigate the effect of HPV on the size of the HIV latent reservoir.

Monday, February 20, 2017

1:00-2:00PM, Haag Hall 312

Mr. Yuwen Gu

Statistics,

University of Minnesota

High-dimensional Generalizations of Asymmetric Least Squares and Their Applications

ABSTRACT

Asymmetric least squares (ALS) regression is a convenient and effective method for summarizing the conditional distribution of a response variable given the covariates. Recent years have seen a growing interest in ALS amongst statisticians, econometricians and financial analysts. However, existing work on ALS only considers the traditional low-dimension-and-large-sample setting. In this talk, we systematically explore the Sparse Asymmetric Least Squares (SALES) regression under high dimensionality. We show the complete theory using penalties such as lasso, MCP and SCAD. A unified efficient algorithm for fitting SALES is proposed and is shown to have a guaranteed linear convergence.

An important application of SALES is to detect heteroscedasticity in high-dimensional data and from that perspective it provides a computationally friendlier alternative to sparse quantile regression (SQR). However, when the goal is to separate the set of significant variables for the mean and that for the standard deviation of the conditional distribution, both SALES and SQR can fail when overlapping variables exist. To that end, we further propose a Coupled Sparse Asymmetric Least Squares (COSALES) regression. We show that COSALES can consistently identify the two important sets of significant variables for the mean and standard deviation simultaneously, even when the two sets have overlaps.

Monday, February 13, 2017

1:00-2:00PM, Haag Hall 312

Ms. Caroline Groth

Biostatistics,

University of Minnesota

Bayesian Models for Analysis of Airborne Chemical Exposures During the Deepwater Horizon Oil Spill Response and Clean-up Efforts

ABSTRACT

In April 2010, the Deepwater Horizon oil rig caught fire and sank, sending approximately 5 million barrels of oil into the Gulf of Mexico over the ensuing 3 months. Thousands of workers were involved in the response and clean-up efforts. Many harmful chemicals were released into the air from crude oil, including total hydrocarbons (THC), benzene, toluene, ethylbenzene, xylene, hexane (BTEXH), and volatile organic compounds (VOCs). NIEHS's GuLF STUDY investigators are estimating the exposures the workers experienced related to the event and evaluating associations between the exposures and detrimental health outcomes.

My research focuses on developing statistical methods to quantify airborne chemical exposure in response to this event and other settings in environmental health. Factors complicating the exposure estimation include analytical method and data collection limitations. All analytical methods used to measure chemical concentrations have a limit of detection (LOD), or a threshold below which exposure cannot be detected with the analytical method (measurements below LOD are called censored measurements). However, even these small exposures must be assessed to provide the most accurate estimates of exposure. Similarly, due to the scope of this event, it was not possible to take measurements in all scenarios where workers were involved in the response.

In this talk, I describe a bivariate left-censored Bayesian model used to quantify exposures under possible LOD censoring in both the response and predictor. I also describe how this method can be expanded to a multivariate framework with multiple chemical predictors with possible censored observations. Then, I briefly describe how we used a database of over 26 million direct-reading VOC area measurements to supplement our exposure information for THC. Finally, I conclude with possible avenues for future research in environmental health and exposure assessment.

Monday, February 6, 2017

1:00-2:00PM, Haag Hall 312

Dr. Abhishek Kaul

**Biostatistics and Computational Biology branch,
National Institute of Environmental Health Sciences**

Estimation and Inference in High Dimensional Error-in-Variables Models and an Application to Microbiome Data

ABSTRACT

We discuss three closely related problems in high dimensional error in variables regression, 1. Additive measurement error in covariates, 2. Missing at random covariates and 3. Precision matrix recovery. We propose a two stage methodology that performs estimation post variable selection in such high dimensional measurement error models. We show that our method provides optimal rates of convergence with only a sub-block of the bias correction matrix, while also providing a higher computational efficiency in comparison to available methods. We then apply the proposed method to human microbiome data, where we classify observations to geographical locations based on corresponding microbial compositions. Lastly, we provide methods for constructing confidence intervals on target parameters in these high dimensional models, our approach is based on the construction of moment conditions that have an additional orthogonality property with respect to nuisance parameters. All

theoretical results are also supported by simulations.

Friday, January 20, 2017

3:00-4:00PM, Haag Hall 312

Dr. David Spade

**Assistant Professor, Dept. of Mathematics & Statistics ,
University of Missouri-Kansas City**

**Modeling Unphased Single-Nucleotide Polymorphism Substitution with a Discussion of Benefits to
Quantitative Trait Locus Detection**

ABSTRACT

Inference of the evolutionary structure of a gene based on genotype data is woefully under-addressed in the statistical and biological literature. This work takes a step toward remedying this issue by construction and evaluation of a time-reversible Markov model for unphased single-nucleotide polymorphism (SNP) substitution. Substitution probabilities, model distances, and reliability of distance estimates are investigated. A simulation study is provided to assess the performance of the model in two common phylogenetic tree estimation procedures. Reliability of distance estimates is also evaluated in the simulation study. This presentation concludes with a discussion of how this model finds a use in the analysis of genome-wide association studies.