

Fall 2016

Friday, December 2, 2016

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

Dr. Ellis Scharfenaker

Assistant Professor in Dept. of Economics

University of Missouri-Kansas City

Maximum Entropy Inference and Statistical Equilibrium in Economics

ABSTRACT

This talk discusses various concepts of equilibrium in economic theory and emphasizes the role of statistical equilibrium in applied and theoretical economics. Discussion will focus on the problems inherent in the neoclassical concept of Walrasian equilibrium as an analog to force balance in classical thermodynamics and the benefits of adopting the statistical point of view from statistics mechanics and information theory in economic theory.

Friday, November 11, 2016

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

Dr. Jiu Ding

Professor

University of Southern Mississippi

Ergodic Theorems Useful in Computational Ergodic Theory

ABSTRACT

Let P be a linear operator on some Banach space with norm 1. We study the averages of the powers of P to study the fixed point problem of P . Convergence of the averages is usually answered by various ergodic theorems with respect to P . We present some ergodic theorems and their applications in computational ergodic theory.

Friday, November 4, 2016

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

Dr. Phil Lee

Associate Professor

University of Kansas Medical Center

Non-Fourier based spectral localization for magnetic resonance spectroscopy of the human brain

ABSTRACT

Magnetic Resonance (MR) technology offers highly versatile imaging modalities that enable non-invasive assessment of structure, function and metabolic activity in humans and other living organisms. For example, measurements of brain chemical concentrations and turnover rates, cerebral blood flow and brain functional activity are readily possible with the development of a variety of MR techniques. In particular, Magnetic Resonance Spectroscopy (MRS) allows the measurement of a number of brain chemicals simultaneously. However, the spatial resolution of MRS is rather poor due to the intrinsically low concentrations of brain chemicals. Thus, it is challenging to extract brain chemical concentration information from specific structures such as gray matter, white matter as well as lesions and focal or diffuse injury sites. As a viable solution, incorporating MRI information in the spectroscopic reconstruction has been proposed. However, only a few of these approaches for the human brain have been demonstrated, with limited success due to the impact of inhomogeneous magnetic fields. We present our newly developed spectral localization framework, B0-Adjusted and Sensitivity Encoded Spectral Localization by Imaging (BASE-SLIM), which resolves the previous limitations and allows quantitative assessment of brain chemicals from arbitrarily shaped tissue compartments in the human brain.

[Location of MNLC 451](#) (not the interactive learning center), it is in the new part of the library, accessible from E 51st St and Holmes St.

Friday, October 28, 2016

1:00-2:00PM, MNLC 451

Professor Michael Mackey

Center for Applied Mathematics in Bioscience and Medicine

McGill University (Canada)

Using mathematics to understand, treat, and avoid hematological disease: Better medicine through mathematics?

ABSTRACT

This topic is one in which I trace many years of work in my Montréal group in modeling periodic hematological diseases. The ‘understand’ part talks about our use of modeling to figure out what causes cyclical neutropenia, and the ‘treat’ part refers to our work on treating cyclical neutropenia using recombinant cytokines, while the ‘avoid’ part deals with our current ongoing work in trying to obviate the deleterious effects of chemotherapy on blood cell production—one of the major negative side effects of chemo.

[Location of MNLC 451](#) (not the interactive learning center), it is in the new part of the library, accessible from E 51st St and Holmes St.

Friday, October 14, 2016

1:00-2:00PM, MNLC 451

Dr. Anne Gelb
Professor of Mathematics,
Dartmouth College

High order l_1 regularization techniques for reconstructing images from Fourier data
ABSTRACT

In this talk we investigate accurate and efficient l_1 regularization methods for generating images from Fourier data. As a prototype, we will consider synthetic aperture radar (SAR).

Although regularization algorithms are already employed in many imaging applications, in particular magnetic resonance imaging (MRI), tomographic imaging, and SAR, practical and efficient implementation in terms of real time imaging often remain a challenge.

Here we demonstrate that fast numerical operators can be used to robustly implement high order l_1 regularization methods that are as or more efficient than traditional approaches such as back projection, while providing superior image quality. We also develop a sequential joint sparsity model which naturally combines the joint sparsity methodology with composite imaging methods. Our technique is able to reduce the effects of speckle and other noisy artifacts with little additional computational cost. Finally, we show that generalizing total variation regularization to non-integer and higher orders provides improved flexibility and robustness.

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Friday, October 7, 2016

1:00-2:00PM, MNLC 451

Dr. H. T. Banks
Professor of Mathematics,
North Carolina State University

Structured Multi-Scale Models for *Daphnia magna* Population Dynamics
ABSTRACT

In this lecture we discuss statistical validation techniques to verify density-dependent mechanisms hypothesized for populations of *Daphnia magna*. We develop structured population models that exemplify specific mechanisms, and use multi-scale experimental data in order to test their importance. We show that fecundity and survival rates are affected by both time-varying density-independent factors, such as age, and density-dependent factors, such as competition. We perform uncertainty analysis and show that our parameters are estimated with a high degree of confidence. Further, we perform a sensitivity analysis to understand how changes in fecundity and survival rates affect population size and age-structure.

Friday, September 23, 2016

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

Dr. Noah Rhee

Professor of Mathematics

University of Missouri-Kansas City

Constructing Invariant Measures - Part 2

ABSTRACT

The Birkhoff Ergodic Theorem is perhaps the most important theorem in the ergodic theory. The Birkhoff Theorem requires that the given measure must be invariant in a certain sense. So it is very important to construct invariant measures. In this talk, we discuss how Ulam's method can be used to construct invariant measures. **This is a continuation of the talk given last Friday.**

Friday, September 16, 2016

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

Dr. Noah Rhee

Professor of Mathematics

University of Missouri-Kansas City

Constructing Invariant Measures

ABSTRACT

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Spring 2016

[Location of MNLC 451](#) (not the interactive learning center), it is in the new part of the library, accessible from E 51st St and Holmes St.

Friday, May 6, 2016

1:00-2:00PM, MNLC 451

Dr. Pawel Gora

Professor of Mathematics,

Concordia University, Canada

Ergodic, mixing, and exact maps

ABSTRACT

We will define the different types of mixing properties for maps: from ergodicity to exactness. We will also give different equivalent characterizations of these properties using Koopman and Frobenius-Perron operators. Some examples will be given.

Tuesday, April 26, 2016

10:00-11:00AM, Flarsheim Hall 310

Jiwoong Kim

Department of Statistics

Michigan State University

Minimum Distance Estimation in Regression Model with Dependent Errors

ABSTRACT

In this talk, we investigate minimum distance estimation in the linear regression model with dependent errors; regression model with autoregressive errors and panel data model will be discussed. We introduce "strong mixing" and "uniformly locally asymptotically quadratic" conditions. Under these conditions, we discuss asymptotic distributional properties of the minimum distance estimators of both parameters in regression model and ones in autoregressive errors. The minimum distance estimators are robust to dependent errors. Through a simulation study, we compare the minimum distance estimators with existing other estimators, including the generalized least squares and the ordinary least squares estimators. In the case of the regression model with autoregressive errors, we observe some superiority of the minimum distance estimators over the other estimators; the panel data model, however, shows that the minimum distance estimators outperform all other existing estimators. "KoulMde" (R-package for the simulation) is available at "cran.r-project.org."

Friday, April 22, 2016

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

Dr. Leonard Dobens

Associate Professor of Biology

University of Missouri-Kansas City

FijiWings: An Open Source Toolkit for Morphometric Analysis of Insect Wings

ABSTRACT

Automated analysis of photomicrographs assists biologists in quantitatively biological objects from thousands of images. User-friendly programs allow interactive exploration of resulting data to extract complicated and subtle

phenotypes from high-throughput scoring of millions of cells. Measuring the effects of genetic and chemical manipulations on cell structures reveals the influence of genes and gene networks on normal and aberrant cell growth. The wing of the model genetic organism *Drosophila* has landmark features useful to measure the genetic contributions to both tissue and cell size. Image processing and pattern-recognition software can quantify wing features in micrographs, and we have developed a set of macros designed to perform semiautomated morphometric analysis of a wing photomicrograph using a set of plug-ins installed in ImageJ, an open architecture Java-based image processing program developed at the National Institutes of Health. This tool has proven of interest to a broad community of fly geneticists studying both the effect of gene function on wing patterning and the evolution of wing morphology and we have used it to perform a screen for genes that regulate cell and tissue size. Ongoing work to detect cell polarity, reliant on the detection of polarized wing “hairs,” will be presented.

Friday, April 8, 2016

**1:00-2:00PM, MNLC 451
Dr. Carlos Castilo-Chavez
Professor of Mathematics,
Arizona State University**

**Beyond Ebola, Dengue, Influenza and Zika: Lessons learned for mitigating future pandemics
ABSTRACT**

As noted recently, the end of the Ebola outbreak for all three countries predominantly affected, means that it now “the time to consider strategies to prevent future outbreaks of this, and other, zoonotic pathogens. The Ebola outbreak, like many other emerging diseases, illustrates the crucial role of the ecological, social, political, and economic context within which diseases emerge.”

Dispersal, mobility and residence times in risky environments play a significant role on the transmission dynamics of communicable diseases, especially emergent or re-emergent diseases like Influenza or Ebola as well as vector born diseases like Dengue, Chikungunya and Zika. In this talk, the challenges associated with the dynamics of communicable and vector born disease are briefly discussed including the application of phenomenological and mechanistic models that highlight the role of dispersal, mobility, and residence times play on their transmission dynamics.

Friday, March 18, 2016

**3:00-4:00PM, Haag Hall 312
Dr. Brooke L. Fridley
Associate Professor of Biostatistics,
University of Kansas Medical Center**

Ovarian Cancer Research: A synergetic relationship between Investigators and Statisticians

ABSTRACT

“Team science” is at the forefront of cancer research. The American Association for Cancer Research (AACR) gives an annual Team Science Award and the NIH is fostering collaborative research through a variety of initiatives. Much of my statistical research has been directly tied to collaborations with researchers, particular in the area of ovarian cancer and pharmacogenomics. In this seminar, I will present some of the various methodological projects I have worked on over the years motivated by my ovarian cancer research collaborations.

Friday, March 11, 2016

1:00-2:00PM, MNLC 451

Dr. Charles L. Epstein

**Thomas A. Scott Professor of Mathematics,
University of Pennsylvania**

Selective Excitation in MR Imaging

ABSTRACT

The use of Nuclear Magnetic Resonance as an imaging modality requires the ability to selectively excite some spins, while leaving others in their equilibrium state. After a rapid introduction to NMR and MRI, I will explain how the problem of selective excitation is mathematically equivalent to a classical problem in the inverse scattering theory of the AKNS 2×2 system, as well as a practical approach to implementing it called DIST. While related to the well-known SLR approach, this method is superior in that it allows for precise control of the phase of the excitation, as well as the flip-angle profile. I will then show how it is used to design a variety of different types of pulse sequences.

Friday, March 4, 2016

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

Dr. Zhu Li

**Associate Professor, Dept. of Computer Science & Electrical Engineering
(CSEE) ,
University of Missouri-Kansas City**

Visual Recognition over Large Repositories with Subspace Indexing on Grassmann Manifolds

ABSTRACT

In large scale visual pattern recognition applications, when the subject set is large the traditional linear models like PCA/LDA/LPP, become inadequate in capturing the non-linearity and local variations of visual appearance manifold. Kernelized non-linear solutions can alleviate the problem to certain degree, but faces a computational complexity challenge of solving an Eigen problems of size $n \times n$ for number of training samples n . In this work, we developed a novel solution by applying a data partition on the BIGDATA training set first and obtain a rich set of local data patch

models, then the hierarchical structure of this rich set of models are computed with subspace clustering on Grassmanian manifold, via a VQ like algorithm with data partition locality constraint. At query time, a probe image is projected to the data space partition first to obtain the probe model, and the optimal local model is computed by traversing the model hierarchical tree. Simulation results demonstrated the effectiveness of this solution in capturing larger degree of freedom (DoF) of the problem, with good computational efficiency and recognition accuracy, for applications in large subject set face recognition and image tagging.

Friday, February 19, 2016

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

Dr. Daniel Osborne

**Assistant Professor, Department of Mathematics,
Florida A&M University**

Nonparametric Statistical Methods in Medical Imaging

ABSTRACT

Nonparametric statistical analysis on manifolds in the past twenty plus years have been rapidly developed and applied to medical imaging problems. During this time period, statisticians began working more and more with nonlinear object data, regarding their observations as points on manifolds. In this work, we will introduce two different medical imaging problems including a CAT scan application and a DTI application. Next, we provide some nonparametric statistical methods that we developed for addressing some problems in those areas. In particular, regarding the CAT scan application, this work is part of larger project on planning reconstructive surgery in severe skull injuries, includes pre-processing and post-processing steps of CT images. For the DTI application, we developed a two-sample procedure for testing the equality of the generalized Frobenius means of two independent populations on the space of symmetric positive matrices.

Tuesday, February 16, 2016

2:30-3:30PM, Royall Hall 403

Dr. Abhijit Mandal

**Visiting Assistant Professor, Department of Statistics,
University of Pittsburgh**

A Goodness-of-fit Test for the Additive Model

ABSTRACT

In multivariate nonparametric regression the additive models are very useful when a suitable parametric model is difficult to find. The backfitting algorithm is a powerful tool to estimate the additive components. However, due to complexity of the estimators, the asymptotic p -value of the associated test is difficult to calculate without a Monte Carlo simulation. Moreover, the conventional tests assume that the predictor variables are strictly continuous. We introduce a test for the additive components with discrete or categorical predictors, when the model may contain continuous covariates. This method is further extended to the semiparametric regression to test

the goodness-of-fit of the model. These tests are asymptotically optimal in terms of the rate of convergence, as they can detect a specific class of contiguous alternatives at a rate of $n^{-1/2}$. The method is applied to a real data from the Atherosclerosis Risk in Communities (ARIC) to detect genetic association in a genome-wide association study (GWAS).

Wednesday, February 10, 2016

1:00-2:00PM, Haag 201

Dr. Yen-Yi Ho

**Assistant Professor, Department of Biostatistics,
University of Minnesota - Twin Cities**

Statistical Methods for Integrating Large-Scale Genomic Data and Identifying Higher-Order Interactions

ABSTRACT

Genetic molecules and gene products participate in complex inter-connected pathways in biological systems. With a wealth of new data generated through high-throughput technologies, researchers are able to study genetic interactions and cellular pathways at the system level. In this talk, I will discuss two important topics in analyzing large-scale genomic data: (1) combining genomic data from various sources, (2) understanding intricate genetic interactions between biological molecules.

In the first part of the talk, I will present novel approaches to combine SNP and gene expression information. These procedures utilize weights constructed by gene expression measurements to adjust p values from a genome-wide association (GWA) analysis. We apply the weight adjustment procedure to a GWA study on serum interferon regulated chemokine levels in systemic lupus erythematosus patients. In the second part of the talk, I will introduce a measurable three-way interaction—"liquid association"—observed among genes. It could be applied to study mechanisms that prompt cellular pathways to turn on or off. I will present statistical inference procedures to examine the magnitude of liquid association in a given data set and demonstrate the implementation of these methods through simulation and experimental data analysis.

Friday February 5, 2016

1:00-2:00PM, MNLC 451

Dr. Louis J. Gross

**James R. Cox and Alvin and Sally Beaman Distinguished Professor of
Ecology and Evolutionary Biology and Mathematics
Director Emeritus, National Institute for Mathematical and Biological
Synthesis (NIMBioS.org),
University of Tennessee - Knoxville**

"Best" in a Biological Context: Optimization across the Biological Hierarchy

ABSTRACT

Many central concepts in biology involve notions of what is "better" or "best" in the context of evolution, physiology, and behavior. Similarly, in many applied areas of the life sciences, we are concerned with developing a "best" method to carry out drug therapies, resource harvesting, pest management, and epidemic control. I will discuss, with audience participation, what it might mean to be "best" for several problems at different levels of the biological hierarchy. This includes being clear about differences between maximization and optimization, and taking account of constraints, historical and others, on biological systems. Examples will incorporate notions of optimal control, emphasizing spatial problems.