Location: Haag Hall, room 307 (Unless otherwise noted)
Day & Time: Fridays, 3:00-4:00 pm (Unless otherwise noted)
[Campus Map for Talks](#) (PDF Format)

Organizer: [Dr. Majid Bani-Yaghoub](#), 235-2845
Email: baniyaghoubm@umkc.edu

- **[Previous Semester](#)** [Schedule of the Graduate Seminar Series](#)

Dates, Titles, Speakers (with Abstracts as available)

Spring 2013

- **Monday, Feb. 12th , 3:00-3:50 pm**
  David A. Spade, Ph.D.
  [**Department of Statistics, Ohio State University**](#)

  Assessing the Convergence of Markov Chain Monte Carlo Methods for Bayesian Inference of Phylogenetic Trees
  In biology, it is commonly of interest to investigate the ancestral pattern that gave rise to a currently existing group of individuals, such as genes or species. This ancestral pattern is frequently represented pictorially by a phylogenetic tree. Due to the growing popularity of Bayesian statistical methodology, Markov Chain Monte Carlo (MCMC) methods for Bayesian inference of phylogenetic trees have come to the forefront of phylogenetic inference. A common question is that of how long the chain must run before it can provide an approximate sample from the stationary distribution. We answer this question for a Markov chain on phylogenetic tree shapes, and provide insight into how to answer this question for a MCMC algorithm which is designed to obtain samples from the posterior distribution of the branch lengths given the tree shape and a set of DNA sequence data.

- **Wednesday, March 20th , 1:00-1:50 pm**
  Xianping Li, Ph.D.
  Department of Mathematics,
  University of Central Arkansas

  Mesh Adaptation for Anisotropic Diffusion Problems
  Anisotropic diffusion problems arise from many fields of science and engineering including image processing, petroleum engineering and plasma physics. The key feature for those problems is that the diffusion in one direction is much faster than in other directions. One of the challenge is that the numerical solution may contain unphysical solutions (spurious oscillations) when standard numerical methods and regular meshes are used in computation.

Mesh adaptation is widely used in numerical computations to achieve better accuracy and efficiency. In this presentation, I will introduce mesh adaptation strategies that solve the challenge for anisotropic diffusion problems. The mesh is adapted in a special way such that the numerical solutions for time-independent problems are guaranteed to be free of unphysical solutions. For time-dependent problems, conditions for both time step size and mesh are developed such that the numerical solutions are guaranteed to be free of unphysical solutions.

- **Friday, April 5th , 3:00-3:50 pm**
  Dr. José Enrique Figueroa-López
  Associate Professor of Statistics and Mathematics (courtesy)
  Associate Director of the Computational Finance Program,
  Purdue University

  Optimally Thresholded Realized Power Variations for Levy Jump Diffusion Models

  Thresholded Realized Power Variations (TPV) are one of the most popular nonparametric estimators for continuous-time processes with a wide range of applications. In spite of their popularity, a common drawback lies in the necessity of choosing a suitable threshold for the estimator, an issue which so far has mostly been addressed by heuristic selection methods. In this talk, we propose an objective selection method based on desirable optimality properties of the estimators. Concretely, we develop a well-posed optimization problem which, for a fixed sample size and time horizon, selects a threshold that minimizes the expected total number of jump misclassifications committed by the thresholding mechanism associated with these estimators. We solve the optimization problem under mild regularity conditions on the density of the underlying jump distribution, allowing us to provide an explicit infill asymptotic characterization of the resulting optimal thresholding sequence at a fixed time horizon. Furthermore, we develop an estimation algorithm, which allows for a feasible implementation of the newfound optimal sequence. Simulations demonstrate the improved finite sample performance offered by optimal TPV estimators in comparison to other popular alternatives. This is joint work with Jeff Nisen.

- **Friday, April 19th , 3:00-3:50 pm**
  Professor Jiu Ding,
  Department of Mathematics,
  University of Southern Mississippi

  The Mean Ergodic Theorem of Matrices and Its Application to Solving the Yang-Baxter Matrix Equation

  The equation AXA=XAX is called the Yang-Baxter matrix equation, where the given matrix A and the unknown matrix X are square matrices of the same order. Some solutions of the Yang-Baxter matrix equation are constructed with the help of the mean ergodic theorem for matrices.

- **Friday, April 26th , 3:00-3:50 pm**
  [Professor Lingling An](#),
  Department of Agriculture and Biosystems Engineering,

  Statistical methods on functional analysis of metagenomes

  The advent of next-generation sequencing technologies has greatly promoted the field of metagenomics which studies genetic material recovered directly from an environment. However, due to the massive short DNA sequences produced by the new sequencing technologies, there is an urgent need to develop efficient statistical methods to rapidly analyze the massive sequencing data generated from microbial communities and to accurately detect the features/functions present in a metagenomic sample/community. In particular, there lack of statistical methods focusing on functional analysis of metagenoimics at the low level, i.e., more specific level. This study focuses on detecting all possible functional roles that are present in a metagenomic sample/community and at the low level. In this research we propose a statistical mixture model to describe the probability of short reads assigned to the candidate functional roles, with sequencing error taken into account. The proposed method is evaluated in comprehensive simulation studies. It is shown that the method is more accurate in assigning reads to relative functional roles, compared with other existing method in functional metagenomic analysis. The method is also employed to analyze some real data sets.

- **Wednesday, May 8th , 1:00-1:30 pm**
  Ashley Walker (graduate student),
  Department of Mathematics and Statistics,
  University of Missouri-Kansas City

  Modeling hepatitis C virus dynamics: Liver regeneration and critical drug efficacy

  By modeling the hepatitis C virus with differential equations, researchers have been given a means of evaluating the antiviral effectiveness of current therapy, estimating parameters such as the rate infected hepatocytes are lost, and providing a tool for action against the hepatitis C virus for both interferon and ribarvirin. However, the original model produced by Neumann in 1998, has many limitations when it comes to modeling all of the observed responses to current treatment. In particular, the original model cannot explain a triphasic viral decay that has been seen in many patients. The original model also cannot fit patients who experience a flat second phase of viral decay, and it cannot predict viral load reappearance to pretreatment level upon completion of therapy. By extending the model Dahari, Lo, Ribeiro, and Perelson show that by including hepatocyte growth and reproduction, the model provides a more realistic representation of typical responses to therapy. Additionally they define a bifurcation point for drug efficacy. For efficacies above the bifurcation point the virus is eventually cleared, while for efficacies below it, a chronically infected viral steady state is ultimately reached.

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Organizer: [Dr. Naveen Vaidya](#) , (816) 235-2847
Email: [vaidyan@umkc.edu](#)

Dates, Titles, Speakers (with Abstracts as available)

Fall 2013

- **Friday, Sep. 6**

Using the Joint Modeling Approach to Handling Incomplete Data in Longitudinal and Coarse Data in Cross-Sectional Studies

[Dr. Hung-Wen (Henry) Yeh](#) [The University of Kansas Medical Center]

Incomplete and coarse data are common in medical and public health research. In longitudinal studies, observations that investigators intend to collect may be missing because subjects may omit scheduled visits (intermittent missing) or lost to follow-up/drop-out (monotone missing). Coarse data is a general type of incomplete data where data may be grouped/rounded (aka heaped), censored, or missing. When data are incomplete or coarse, missing/coarse data always cause reduction in precision of estimates due to the information loss, and, of greater concern, may introduce a potential bias in estimation. The validity of analysis methods depends on the assumption of missing/coarse mechanism, or whether the reasons of missing/coarsening are related to the outcome of interest. In this talk, I will use two examples from smoking research to demonstrate the utilization of the joint modeling approach that takes into account non-ignorable missing/coarsening mechanisms in analyzing repeated binary measures in a longitudinal study and coarse count data in a cross-sectional study.

- **Friday, Sep. 13**

Mathematical & Computational Models for Spreading of Infectious Diseases

[Dr. Caterina M. Scoglio](#) [Kansas State University]

In this talk, I will fist give an overview of my group's research work in the field of mathematical models for infectious disease spreading. In the second part of the talk, I will provide details on some recent results concerning the impact of human behavior changes in the evolution of the spreading process, and prove how the dissemination of preventive information can reduce the size of an epidemic. To this end, we have developed the Susceptible-Alert-Infected-Susceptible (SAIS) model as an extension of the SIS (Susceptible-Infected-Susceptible) model. In the SAIS model, "alert" individuals observe the health status of neighbors in their contact network, and as a result, they may adopt a set of cautious behaviors to reduce their infection rate. This alertness, when incorporated in the mathematical model, results in an increase of the range of effective/relative infection rates for which initial infections die out. Built upon the SAIS model, our work also has investigated how information dissemination increases this range hence boosting the population against epidemic spreading. The information dissemination is realized through an additional network among individuals, such as an online social network, sharing the same nodes (individuals) with the contact network but with different links. These "information links" provide

the health status of one individual to all the individuals she/he is connected to in the information dissemination network. Using an information dissemination index of a quadratic form in terms of the adjacency matrix of the information dissemination network and the dominant eigenvector of the contact network adjacency matrix, we propose an optimal information dissemination strategy. We show that monitoring the health status of a small, but "central", subgroup of individuals and circulating their incidence information enhances the resilience of the society against infectious diseases most efficiently. Extensive numerical simulations on a survey–based contact network for a rural community in Kansas support these findings.

- **Friday, Sep. 20**

Sign-preserving of principal eigenfunctions in P1 finite element approximation of eigenvalue problems of second-order elliptic operators

Dr. **Weizhang Huang** [University of Kansas]

This talk is concerned with the P1 finite element approximation of the eigenvalue problem of second-order elliptic operators subject to the Dirichlet boundary condition. The focus is on the preservation of basic properties of the principal eigenvalue and eigenfunctions of continuous problems. We shall show that when the stiffness matrix is an irreducible M-matrix, the algebraic eigenvalue problem maintains those properties such as the smallest eigenvalue being real and simple and the corresponding eigenfunctions being either positive or negative inside the physical domain. Mesh conditions leading to such a stiffness matrix are also discussed. A sufficient condition is that the mesh is simplicial, acute when measured in the metric specified by the inverse of the diffusion matrix, and interiorly connected. The acute requirement can be replaced by the Delaunay condition in two dimensions. Numerical results are presented to verify the theoretical findings.

- **Friday, Sep. 2**7

Mean Reversion Trading: Optimal Double Stopping Approach

Dr. Tim S. T. Leung [Columbia University]

We study the problem of trading under mean-reverting price dynamics subject to transaction cost. We formulate an optimal double stopping problem to analyze the optimal timing to enter and subsequently exit the market, when prices are driven by an Ornstein-Uhlenbeck (OU), exponential OU, or Cox-Ingersoll-Ross (CIR) process. In the OU and CIR cases, the investor's optimal strategy is characterized by a lower level for entry and an upper level for exit. However, in the exponential OU case, we find that it is optimal to delay entry not only when the current price is high, but surprisingly also when the price is sufficiently close to zero. Both analytical and numerical results are provided to illustrate the dependence of timing strategies on model parameters such as mean-reversion level and transaction cost. As extensions, we further impose a stop-loss constraint or a minimum holding period, and examine their effects on the timing of trades.

- **Friday, Oct. 11**

Occupation Time, Investment, and Approximation

Dr. Allanus Tsoi [University of Missouri, Columbia]

An investment strategy based on the occupation time of a certain financial state of a corporation is discussed. One example is that if a certain business corporation keeps distributing dividends of considerably attractive amount every year up to a certain number of years, then certain financial group will take action to invest in a certain financial market. We will employ filtering techniques to estimate the chance that the above sequence of events will occur, which will favor the financial group to take the corresponding action of investing.

- **Friday, Oct. 18**

Dr. Alan S. Perelson [Los Alamos National Laboratory] **talk cancelled**

- **Friday, Oct. 25**

Sequential Designs with Application in Software Engineering

Wei Wu, PhD. Candidate [UMKC]

Presented here is a Bayesian approach to test case allocation in the software reliability estimation. Bayesian analysis allows us to update our beliefs about the reliability of a particular partition as we test, and thus, dynamically refine our allocation of test cases during the reliability testing process. We started with a fully sequential sampling scheme to estimate the reliability of a software system using partition testing. We have shown both theoretically and through simulation that the proposed scheme always performs at least as well as fixed sampling approaches where test case allocation is predetermined, and in all but the most unlikely circumstances, outperforms them. Based on the sequential allocation, a multistage sampling scheme is established, which is less time consuming and more affordable. Meanwhile, an efficient sampling scheme is also developed to accommodate more situations. At last, we extend our study from parallel systems to series systems. We again use a Bayesian approach to allocate test cases to estimate the reliability of a series system with two components. A second-order lower bound for the incurred Bayes risk is established theoretically and Monte Carlo simulations with several proposed sequential designs are implemented to achieve this second-order lower bound.

- **Friday, Nov. 1**

A Reduced Rank Model for Analyzing Multivariate Spatial Datasets

Dr. Jonathan R. Bradley [University of Missouri- Columbia]

We introduce the multivariate spatial mixed effects (MSME) model to analyze multivariate spatial data. The MSME model can be specified to have a "low rank" structure, which lends itself to efficient computation of parameter estimates, the optimal kriging predictor, and associated measures of prediction error. This approach to fitting generic mixed effects models for multivariate spatial data is novel; however, our approach to statistical analysis also includes interpreting and evaluating the fitted MSME model. Thus, the well-known deviance information criterion (DIC) is used to evaluate the optimal kriging predictor. Also, a diagnostic criterion called the residual nonstationarity is introduced to interpret the covariance between observations in a spatial context. This approach to statistical analysis (i.e., fitting, interpreting and evaluating the MSME model) is demonstrated using a simulation example, and a real data application. In the real data application, we jointly analyze several demographic variables, obtained from the American Community Survey, using the MSME model.

- **Friday, Nov. 8**

Anisotropic finite element meshes and stability of explicit Runge-Kutta methods for linear parabolic equations

Dr. Lennard Kamenski [Weierstrass Institute for Applied Analysis and Stochastics Berlin, Germany]

We study the stability of explicit Runge-Kutta time integration schemes for the linear finite element approximation of linear parabolic equations. The derived bound on the largest permissible time step is tight for any mesh and any diffusion matrix within a factor of at most 2(d+1), where d is the spacial dimension. Both full mass matrix and mass lumping are considered. The bound reveals that the stability condition is affected by two factors: the first factor depends on number of mesh elements and corresponds to the classic bound for the Laplace operator on a uniform mesh, the other factor reflects the effects of the interplay of the mesh geometry and the diffusion matrix. It is shown that it is not the mesh geometry itself but the mesh geometry in relation to the diffusion matrix that is crucial to the stability of explicit methods. Numerical results are presented to verify the theoretical findings.

- **Friday, Nov. 15**

Sequential Monte Carlo Methods and Their Applications: An Overview and Recent Developments

Dr. Rong Chen [Department of Statistics, Rutgers University, New Jersey]

The sequential Monte Carlo (SMC) methodology emerged in the fields of statistics and engineering has shown a great promise in solving a large class of highly complex inference and optimization problems, opening up new frontiers for crossfertilization between statistical science and many application areas.

SMC can be loosely defined as a family of techniques that use Monte Carlo simulations to solve on-line estimation and prediction problems in stochastic dynamic systems. By recursively generating random samples of the state variables, SMC adapts flexibly to the dynamics of the underlying stochastic systems. In this talk, we present an overview of the current status of SMC, its applications and some recent developments. Specifically, we will introduce a general framework of SMC, and discuss various strategies on fine-tuning the different components in the SMC algorithm, in order to achieve maximum efficiency. SMC applications, especially those in science, engineering, bioinformatics, and financial data analysis will be discussed

- **Friday, Nov. 22**

Modeling Bubonic Plague Persistence: Dynamical System Approach

Robert Schmitt [UMKC Department of Mathematics and Statistics]

The bubonic plague - the reason of the Black Death of medieval Europe – is caused by the bacterium Yersinia pestis. Despite being considered a historical disease, cases of plague still continue to occur worldwide, and particularly the evolution of antibiotic resistance in Y. pestis possesses a threat of future large-scale epidemics. Y. pestis is known to be maintained in rodent populations, and typically, the disease is introduced to the human population by fleas leaving an infected rodent that has died nearby. In this talk, I will give an overview of the history of Y.pestis and the problems that arise in the epidemiology of the disease. I will further discuss how existing models, including the ones with the

presence of resistant rats and meta-population structure, help explain the maintenance of the plague in wild rodent populations. I will then propose a novel model, which takes a more realistic approach to the heritability of resistance to plague and the possible means of transmission. Applying the Next Generation Matrix Method to our model, we calculate the basic reproduction number of Y. pestis infection. I will further present simulation results of our model, and discuss how our results compare with those from the previous models and the observed data.

- **Wednesday, Dec. 4**

Relationship between Mothers' health behaviors and Preterm births

Jing Yi (Jennie) Yan [UMKC Department of Mathematics and Statistics]

All we know that smoking, alcohol, and illicit drug will affect our health, but we don't know how harmful effect to pregnancy and case preterm birth. In this presentation, I will use Chi-Squared test and logistic regression model to analyze a large data set which includes 83,685 live births to black and white mothers from 1990-2002 in Kansas City, MO. And we tried to determine whether there were combined effects of smoking, alcohol, and illicit drug during pregnancy on the frequency of preterm births. We defined health compromising behaviors as the use of cigarettes, alcohol, and illicit drugs. The effect of these behaviors on preterm births was considered for each substance individually, and in combination. The rates of preterm births for these groups were calculated. Using logistic regression, adjusted odds ratios were used to estimate the relative risk of preterm births among these groups. Also, I will use the other new data set to prove the objectives and find the important factors which case preterm births. The main idea for this presentation is to use all the statistically results to prove our objectives.