Bio³ Seminar Series

Hua Liang, Ph.D.

Professor of Statistics Department of Statistics
George Washington University, Washington D.C.

Title: Why Are Semiparametric Models Useful?

Abstract:
Semi-parametric models, including partial linear additive models and generalized partial linear additive models, can relax structure assumption for linear or generalized linear models. Dr. Hua Liang and his team have developed associated methods to demonstrate how semi-parametric models are useful in health science and biomedical research using several real datasets. Examples of such datasets include a nutritional epidemiology study for exploring the relationship between plasma beta-carotene level dietary and lifestyle factors, a HIV/AIDS study of the relationship between condom use, marital status and other indexes such as CD4 cell count, a study of whether diabetes disease is related to BMI and age, and lastly, a study of the relationship between cancer and genes when the number of gene expressions is larger than the number of subjects.

FRIDAY, SEPTEMBER 11, 2015
10:00am – 11:00am

Warwick Evans Conference Room, Building D
Refreshments will be provided at 9:45am

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This seminar series meets the 2nd and 4th Friday of every month.

Lombardi Comprehensive Cancer Center, Georgetown University Medical Center

Bio³ Seminar Series

Guofen Yan , Ph.D.

Associate Professor of Biostatistics
Department of Public Health
University of Virginia, Charlottesville

Title: CMS claims and disease registry data to assess disparities in chronic disease: opportunities and challenges

Abstract:
While randomization is generally considered the gold standard approach to address most clinical questions, the relationship of race to outcomes, may only be addressed using observational cohort studies. Dr. Yan is currently conducting two ongoing studies that use U.S. Renal Data Systems and CMS data on chronic kidney disease in order to assess: 1) racial differences in accessing nephrologist care and 2) survival gaps among racial subgroups undergoing chronic dialysis. Large sample sizes representing nationally racial/ethnic distribution and extended follow-up periods in these databases provide unique opportunities to examine the geographic determinants and time-varying factors that are important to understanding chronic disease disparities. Statistical design, analysis strategies, and issues of his work will be presented.

FRIDAY, SEPTEMBER 25, 2015
10:00am – 11:00am

Warwick Evans Conference Room, Building D
Refreshments will be provided at 9:45am

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Bio³ Seminar Series

Bhramar Mukherjee, Ph.D.

Professor of Biostatistics and Epidemiology
University of Michigan

Title: Shrinkage Methods Utilizing Auxiliary Information from External Data Sources to Improve Prediction Models with Many Covariates

Abstract: Predicting an outcome Y uses a large number of covariates **X**. However, most data that fits the model contains only Y and **W**, which is a noisy surrogate for **X**, and only in a small number of observations are Y, **X**, and **W** observed. Dr. Mukherjee's team developed Ridge-type shrinkage methods that trade between bias and variance in a data-adaptive way to yield a smaller prediction error using information from both datasets. Her team approached this in full Bayesian context with different forms of adaptive shrinkage and introduced the notion of a hyper-penalty for guiding choices of the tuning parameter to perform adaptive shrinkage. Applying their methods to genomic assay technologies, mRNA expression of a selected number of genes is measured by both quantitative real-time polymerase chain reaction (qRT-PCR, **X**) and microarray technology (**W**) on a small number of lung cancer patients. In addition, only microarray measurements (**W**) are available on a larger number of patients. The goal is to predict survival time (Y) using qRT-PCR (**X**). Does the large dataset containing only **W** aid with prediction of Y using **X**? High-dimensionality, missing covariate information, and predicting a model for Y|**X** (rather than Y|**W**) makes this a non-standard statistical problem. Does integrating/leveraging information from existing diverse data sources to boost prediction have broader application in contemporary scientific studies?

FRIDAY, OCTOBER 9, 2015
10:00am – 11:00am

Warwick Evans Conference Room, Building D
Refreshments will be provided at 9:45am

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Bio³ Seminar Series

Mithat Gonen, Ph.D.

Chief, Biostatistics Service
Department of Epidemiology and Biostatistics
Memorial Sloan-Kettering Cancer Center

Title: Designing Basket Trials

Abstract: The increased sophistication and availability of genomic technologies has sparked an increase in targeted cancer treatments. These treatments work by reversing the consequences of a given genomic alteration. Some targeted cancer treatments are already approved by the FDA (such as the drug Imatinib) and numerous other such drugs are in the process of being development. Basket trials are commonly used for targeted agents in place of traditional Phase II trials. In a basket trial for a given target and agent, all patients expressing the target are enrolled in the study and placed in baskets based on the organ site (histology). In this talk, Dr. Gonen will give examples of basket trials and discuss statistical strategies for their design.

FRIDAY, OCTOBER 23, 2015
10:00am – 11:00am

Warwick Evans Conference Room, Building D
Refreshments will be provided at 9:45am

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Bio³ Seminar Series

Peter Austin, Ph.D.

Senior Core Scientist

ICES Central Cardiovascular Research Program

Title: An introduction to propensity score methods for observational studies

Abstract: Methods based on the propensity score allow one to reduce the effects of measured confounding when using observational data to estimate the effects of treatments, exposures and interventions. During this introductory talk, I will define the propensity score, describe different methods in which it can be used, and discuss good practice when using propensity score methods.

FRIDAY, November 13, 2015
10:00am – 11:00am

Warwick Evans Conference Room, Building D

Refreshments will be provided at 9:45am

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Bio³ Seminar Series

Paul Albert, Ph.D.

Senior Investigator, Biostatistics & Bioinformatics Branch Chief,
Division of Epidemiology, Statistics, and Prevention,
National Institute of Child Health and Human Development (NICHD)

Title: Modeling longitudinal data with a random change point and no time-zero: applications to inference and prediction in single and consecutive labor curves

Abstract: In some longitudinal studies the initiation time of the process is not clearly defined, yet it is important to make inference or do predictions about the longitudinal process. The application of interest in this article is to provide a framework for modeling individualized labor curves (longitudinal cervical dilation measurements) where the start of labor is not clearly defined. This is a well-known problem in obstetrics where the benchmark reference time is often chosen as the end of the process (individuals are fully dilated at 10 cm) and time is run backwards. This approach results in valid and efficient inference unless subjects are censored before the end of the process (due to a c-section, for example), or if we are focused on prediction. Providing dynamic individualized predictions of the longitudinal labor curve prospectively (where backwards time is unknown) is of interest to aid obstetricians to determine if a labor is on a suitable trajectory. We propose a model for longitudinal labor dilation that uses a random-effects with unknown time-zero and a random change point. We present a maximum likelihood approach for parameter estimation that uses adaptive Gaussian quadrature for the numerical integration. A Monte Carlo approach for dynamic prediction of the future longitudinal dilation trajectory from past dilation measurements is proposed. Further, we discuss an extension of this work to the setting for which we have consecutive pregnancy available in the hopes of using prior pregnancy information to predict the labor curves in subsequent pregnancies. We illustrate this methodology with labor dilation data from the Consortium of Safe Labor (CSL) and the Consecutive Pregnancy Study (CPS), both NICHD intramural projects. This work is collaborative research with Drs. Alex McLain of the University of South Carolina and Olive Buhule of NICHD.

FRIDAY, January 8th, 2016
10:00am – 11:00am

Warwick Evans Conference Room, Building D
Refreshments will be provided at 9:45am

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Bio³ Seminar Series

Jan Hannig, Ph.D.

Professor of Statistics and Operations Research
University of North Carolina at Chapel Hill

Title: Generalized Fiducial Inference: A Review

Abstract: R. A. Fisher, the father of modern statistics, proposed the idea of fiducial inference in the 1930's. While his proposal led to some interesting methods for quantifying uncertainty, other prominent statisticians of the time did not accept Fisher's approach because it went against the ideas of statistical inference of the time. Beginning around the year 2000, the authors and collaborators started to re-investigate the idea of fiducial inference and discovered that Fisher's approach, when properly generalized, would open doors to solve many important and difficult inference problems. They termed their generalization of Fisher's idea as generalized fiducial inference (GFI).

After more than a decade of investigations, the authors and collaborators have developed a unifying theory for GFI, and provided GFI solutions to many challenging practical problems in different fields of science and industry. Overall, they have demonstrated that GFI is a valid, useful, and promising approach for conducting statistical inference. The goal of this talk is to deliver a timely and concise introduction to GFI, to present some of the latest results, as well as to list some related open research problems. It is the authors' hope that their contributions to GFI will stimulate the growth and usage of this exciting approach for statistical inference.

FRIDAY, February 12th, 2016
10:00am – 11:00am

Warwick Evans Conference Room, Building D
Refreshments will be provided at 9:45am

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Bio³ Seminar Series

Title: Multiple testing problems in clinical trials. Multistage gatekeeping procedures

George Kordzakhia, Ph. D.

Mathematical Statistician at the Food and Drug Administration
George Washington University

Abstract: The presentation gives a brief introduction to common multiplicity problems arising in clinical trials that involve multiple endpoints, multiple doses, multiple time-points etc. In many cases, multiple objectives in clinical trials have complex hierarchical structure, and power of a multiple test may be optimized by taking into account logical relationships among the null hypotheses.

Analysis of trial with multiple objectives has attracted a lot of attention in the clinical trial literature. Recent developments in the area include a class of methods, known as gatekeeping methods, for hypothesis testing problems with multiple families of null hypotheses. The presentation focuses on multistage gatekeeping methods with a stepwise testing algorithm which facilitates the implementation of gatekeeping procedures and general decision making.

FRIDAY, February 26, 2016
10:00am – 11:00am

Warwick Evans Conference Room, Building D
Refreshments will be provided at 9:45am

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Bio³ Seminar Series

Anindya Roy, Ph.D.

Professor of Statistics,
Department of Mathematics and Statistics,
University of Maryland Baltimore County

Title: Nonparametric Tests for Interaction in Cytotoxicity Response Models

Abstract: We look at cytotoxicity models for exposures to multiple chemicals. To understand the effect of a mixture of agents on cell survival, it is important to understand the interaction between the agents. However, in the absence of well -established parametric response models, the test for interaction maybe sensitive to model misspecification. To build robust tests for interaction we propose new methods for testing interaction in completely nonparametric settings. The tests are developed based on common nonparametric forms of interaction such as Bliss independence and Loewe additivity. We present limited simulation results to illustrate the finite sample properties of the proposed tests. The methodology is illustrated on a real cytotoxicity data.

FRIDAY, April 8th, 2016
10:00am – 11:00am

Warwick Evans Conference Room, Building D
Refreshments will be provided at 9:45am

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