Bio^3 Seminar Series

Friday, September 12th, 2014 10:00-11:00 am

New Research Building Auditorium
Refreshments will be provided at 9:45am

Gang Han, Ph.D.

Associate Research Scientist in Public Health (Biostatistics)
School of Public Health, Yale Center for Analytical Sciences

Hybrid Bayesian M-Estimation and Its Application in Calibration and Tuning for Complex Computer Models

Abstract:

Complex computer simulation is critical in biomedical research fields, e.g., the design of prosthetic devices. Tuning and calibration are processes for improving the representativeness of a computer simulation code to a physical phenomenon, which is the key to the success of a computer simulator. In this talk I will introduce a statistical methodology for simultaneously determining tuning and calibration parameters in settings where data are available from a computer code and the associated physical experiment but the number of runs is limited. Tuning parameters are set by minimizing a discrepancy measure while the distribution of each calibration parameter is determined based on a hierarchical Bayesian model. The proposed Bayesian model views the output as a realization of a Gaussian stochastic process with hyperpriors. Draws from the resulting joint posterior distribution are obtained by the Markov chain Monte Carlo simulation. The first and second order properties of the estimates have been derived in the framework of Bayesian frequentist hybrid inference and M-estimation. I will compare the hybrid Bayesian M-estimation and an alternative hierarchical Bayesian approach in an application regarding knee replacement.

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

Lombardi Comprehensive Cancer Center, Georgetown University Medical Center

Bio^3 Seminar Series

Friday, September 26th, 2014 10:00-11:00 am

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

Yi Huang, Ph.D.

Assistant Professor, University of Maryland-Baltimore County
Department of Math and Statistics

Latent Propensity Score Approach for Average Causal Effect Estimation Allowing Covariate Measurement Error

Abstract:

The covariates are often measured with unobserved error in biomedical and policy studies, which is a violation of the strong ignorability assumption. The naive approach is to ignore the error and use the observed covariates in current propensity score framework for average causal effect (ACE) estimation. In the past, we showed that the naive approach typically produces biased ACE inference based on the extended causal assumptions allowing covariate errors. I proposed a flexible finite mixture model framework and estimate average causal treatment effect using EM under continuous outcomes. To extend the model to more flexible type of outcomes and measurement error models, I am working on semiparametric methods for ACE estimations under more flexible framework. Simulations studies are presented to show the performance of new approaches vs. the existing approaches. This is a joint work with Dr. Liang Li, and my students, Elande Baro and Wenxin Lu.

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Bio^3 Seminar Series

Friday, October 24th, 2014 10:00-11:00 am

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

Ulrike Genschel, Ph.D.

Assistant Professor, Department of Statistics
Iowa State University

Point Estimation of the Central Orientation of Random Rotations

Abstract:

Data as three-dimensional rotations have application in computer science, kinematics, and materials sciences, among other areas. Estimating the central orientation from a sample of such data is an important problem, which is complicated by the fact that several different approaches exist for this, motivated by various geometrical and decision-theoretical considerations. However, little is known about how such estimators compare, especially on common distributions for location models with random rotations. We examine four location estimators, three of which are commonly found in different literatures and the fourth estimator (a projected median) is newly introduced. Our study unifies existing literature and provides a detailed numerical investigation of location estimators for three commonly used rotation distributions in statistics and materials science. While the data-generating model influences the best choice of an estimator, the proposed projected median emerges as an overall good performer, which can be suggested without particular distributional assumptions. We illustrate the estimators and our findings with data from a materials science study by approximating the central orientation of cubic crystals on the microsurface of a metal. Accompanying supplementary materials are available online.

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Lombardi Comprehensive Cancer Center, Georgetown University Medical Center

Bio^3 Seminar Series

Friday, November 14th, 2014 11:00 am-12:00 pm

Pre-Clinical Science Building, Room LA2

Refreshments will be provided at 10:45am

Yichuan Zhao, Ph.D.

Professor, Department of Mathematics and Statistics
Georgia State University

Smoothed jackknife Empirical Likelihood Inference for the Difference of ROC Curves

Abstract:

For the comparison of two diagnostic markers at a flexible specificity, people apply the difference of two correlated receiver operating characteristic (ROC) curves to identify the diagnostic test with stronger discriminant ability. In this paper, we employ jackknife empirical likelihood (JEL) method to construct confidence intervals for the difference of two correlated continuous-scale ROC curves. Using the jackknife pseudo-sample, we can avoid estimating several nuisance variables which have to be estimated in existing methods. We prove that the smoothed jackknife empirical log likelihood ratio is asymptotically chi-squared distribution. Furthermore, the simulation studies in terms of coverage probability and average length of confidence intervals show the good performance in small samples with a moderate computational cost. A real data set is used to illustrate our method. This is a joint work with Dr. Hanfang Yang.

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Bio^3 Seminar Series

Friday, January 23rd, 2015 10:00-11:00 am

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

Guoqing Diao, Ph.D.

Associate Professor, Department of Statistics
George Mason University

New Semiparametric Regression Method with Applications to Selection-biased Sampling and Missing Data Problems

Abstract:

We propose a new method to estimate a regression function based on the semiparametric density ratio model, which can be viewed as a generalized linear model with a canonical link function and an unspecified baseline distribution function. Under this model, the distribution of the observed data retains the same structure in the presence of selection-biased sampling or when the predictors are missing at random. Particularly, in the latter case, the new method utilizes all the available information and does not need to specify the distribution of the predictors or the probability of observing the predictors. We establish large sample properties of the proposed regression estimators. Simulation studies demonstrate that the proposed estimators perform well in practical situations. Empirical data from the National Health and Nutrition Examination Survey are presented.

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Bio^3 Seminar Series

Friday, February 27th, 2015 10:00-11:00 am

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

Dr. Zhengjia (Nelson) Chen, Ph.D.

Biostatistics Shared Core of Winship Cancer Institute, Department of Biostatistics and Bioinformatics, Emory University

Bayesian optimal designs for cancer Phase I clinical trials

Abstract:

In cancer Phase I clinical trials, 3+3 design is still used for its simplicity, but it has limitations such as inaccuracy of maximum tolerated dose (MTD) and inflexibility. Escalation With Overdose Control (EWOC) is a Bayesian adaptive design which can overcome these limitations and control the probability of overdosing. However, like other Phase I designs, EWOC treats toxicity response coarsely as a binary indicator (Yes vs No) of dose limiting toxicity (DLT) although patient usually has multiple toxicities and a lot of useful toxicity information is discarded. We establish a novel scoring system to treat toxicity response as a quasi-continuous variable and utilize all toxicities of patients. Our system consists of generally accepted and objective components (a logistic function, grade and type of toxicity, and whether the toxicity is DLT) so that it is relatively objective. We couple our system with EWOC to develop a new design called Escalation With Overdose Control using Normalized Equivalent Toxicity Score (EWOC-NETS) by replacing the binary indicator of DLT and the target probability of DLT with a Normalized Equivalent Toxicity Score (NETS) and a Target NETS (TNETS), respectively. Simulation studies and its application to real trial data demonstrate that EWOC-NETS can treat toxicity response as a quasi-continuous variable, fully utilize all toxicity information, and improve the accuracy of MTD and efficiency of Phase I trial. A user-friendly software of EWOC-NETS is under development and will be available in the future.

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Lombardi Comprehensive Cancer Center, Georgetown University Medical Center

Bio^3 Seminar Series

Friday, March 27th, 2015 10:00-11:00 am

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

Marie Davidian, Ph.D.

William Neal Reynolds Professor of Statistics
North Carolina State University

The Right Treatment for the Right Patient (at the Right Time): Personalized Medicine and Statistics

Abstract:

With the advent of the 'omics era, achieving the goal "personalizing" treatment to the patient based on his/her genetic/genomic as well as physiological, demographic, and other characteristics and past history has become more promising than ever. One perspective on personalized medicine involves identifying subgroups of patients sharing certain characteristics who are likely to benefit from a specific treatment or to whom a new treatment may be targeted ("the right patient"). Another is based on formalizing how clinicians make treatment decisions in practice, where the goal is to identify the most beneficial treatment to administer to a patient from among the available options given his/her characteristics ("the right treatment"). In chronic diseases and disorders like cancer or substance abuse, a series of treatment decisions must be made, and the objective is to determine the "best" treatment option at each decision given all information accrued on the patient to that point, including responses to previous treatments, so as to lead to the most beneficial long term outcome. This sequential decision-making introduces many complications; for example, treatments chosen early on may affect how well treatments given later will work ("at the right time").

Why is a statistician talking about personalized medicine? The development of optimal, evidence-based personalized treatment strategies can be formulated as a fascinating statistical problem. I will provide an overview of challenges involved and of the essential role of statistical methods and study designs in the quest for personalized medicine.

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Bio^3 Seminar Series

Friday, April 10th, 2015 10:00-11:00 am

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

David Mackinnon, Ph.D.

Foundation Professor in the Department of Psychology
Arizona State University

Modern Mediation Analysis: Introduction to Controversies and Solutions

Abstract:

Mediating variables are important for theoretical and applied research in many research areas because they are used to investigate how two variables are related. Examples are the process by which an intervention changes behavior and how a risk factor affects disease. Over the last decade there has been considerable development of new methods and wider substantive application of mediation analysis. Some of the most important recent developments focus on the causal conclusions from statistical mediation analysis. The goal of this presentation is to provide an introduction to statistical and conceptual aspects of mediation analysis with attention to several controversies and methods developed to address those controversies.

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Bio^3 Seminar Series

Friday, April 24th, 2015 10:00-11:00 am

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

Dean Follman, Ph.D.

Assistant Director for Biostatistics, NIAID
Chief Biostatistics Research Branch, National Institute of Allergy and Infectious Diseases

Vaccine Efficacy from the Virion's Perspective

Abstract:

Vaccine clinical trials with typically use the time to consequential infection as the primary endpoint. A common method of analysis for such trials is to compare the times to infection between the vaccine and placebo groups using a Cox regression model. With new technology, we can sometimes additionally record the precise number of virions that cause infection rather than just the indicator that infection occurred. In this paper we develop a unified approach for vaccine trials that couples the time to infection with the number of infecting or founder viruses. We assume that the instantaneous risk of a potentially infectious exposure for individuals in the placebo and vaccine groups follows the same proportional intensity model. Following exposure, the number of founder viruses X* is assumed to be generated from some distribution on 0,1,2,..., which is allowed to be different for the two groups. Exposures that result in X*=0 are unobservable. We denote the placebo and vaccine means of X* by m and m D so that 1- D measures the proportion reduction in the mean number of infecting virions due to vaccination per exposure. We develop different semi-parametric methods of estimating D. We allow the distribution of X* to be Poisson or unspecified, and discuss how to incorporate covariates that impact the time to exposure and/or X*. Interestingly D, which is a ratio of untruncated means, can be reliably estimated using truncated data (X*>0), even if the placebo and vaccine distributions of X* are completely unspecified. We apply our methods to an HIV vaccine trial conducted in injecting drug users.

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