A Bayesian Dynamic Model for Multi-Competitor Sports
Mark Glickman, Boston University School of Public Health

Abstract:
Many games and sports, particularly races, involve outcomes in which competitors are rank ordered rather than simply a single winner being declared. An abundance of approaches exists to estimate competitor ability from rank orderings, often with the purpose of making accurate forecasts for future competitions. We propose a Bayesian state-space framework for rank ordered logit models to rate competitor ability over time. Our approach assumes competitors' performances follow independent Gumbel distributions, with each competitor's mean performance evolving over time as a Gaussian random walk. The model accounts for the possibility of ties, an occurrence that is not atypical in races in which some competitors may not finish and therefore tie for last place. We demonstrate our approach to measuring abilities of 268 women from the results of women's Alpine skiing (downhill) competitions recorded over the period 2002-2013. We discuss the use of our approach in the development of a rating system for multi-competitor games.

Accounting for Unmeasured Confounding of Treatment and Censoring of Survival-Time Outcomes in Comparative Effectiveness Research
James O’Malley, Dartmouth

Abstract:
Ongoing research will be presented on the development and evaluation of methods of accounting for unmeasured confounding of treatment and survival-times measured with incomplete ascertainment due to censoring. The confounding-censoring problem is first characterized using Directed Acyclic Graphs (DAGs). We then consider adapting traditional instrumental variable methods to censored survival-time data and discuss general conditions under which causal effects are identifiable. We apply the methods to evaluate the comparative effectiveness of endovascular surgery and open surgical repair for abdominal aortic aneurysm (AAA) in Medicare patients. Because various physician and patient factors affect treatment selection in observational data, unmeasured factors related to both treatment selection and survival are likely, warranting the use of IV methods. Due to limited follow-up near the end of the study period, censoring is extensive. Therefore, on these data, methods that account for both confounding and censoring have the potential to perform substantially better than naïve methods.

Aporetic Conclusions When Testing the Validity of an Instrumental Variable
Dylan Small, University of Pennsylvania

Abstract:
An instrument or instrumental variable is often used in an effort to avoid selection bias in inference about the effects of treatments when treatment choice is based on thoughtful deliberation. An instrument is a haphazard nudge to accept one treatment or another, where the nudge can affect outcomes only to the extent that it alters the treatment received. There are two key assumptions here: (i) the nudge is haphazard or essentially random once adjustments have been made for observed covariates, (ii) the nudge affects outcomes only by altering the treatment, the so-called exclusion restriction. These assumptions are often said to be untestable; however, that is untrue if testable means checking the compatibility of assumptions with other things we think we know. A test of this sort may result in an aporia, that is, a collection of claims that are individually plausible but mutually inconsistent, without clear indication as to which claim is culpable for the inconsistency. We discuss this subject in the context of our on-going study of the effects of delivery by cesarean section on the survival of extremely
premature infants of 23-24 weeks gestational age. This is joint work with Fan Yang, Jose Zubizarreta, Scott Lorch and Paul Rosenbaum.

Assessing Model Uncertainty via Simulation Optimization
Henry Lam, Boston University

Abstract:
We present a stochastic gradient descent method that is designed to compute worst-case values of performance measures for stochastic models, such as those arising in queueing and service operations, subject to uncertainty of input models that are typically represented by moments or statistical distance constraints. The gradient is obtained via Gateaux differentiation, and can be translated in the form of so-called likelihood ratio method in derivative estimation. Some theoretical convergence and numerical results will be presented.

Asymptotic Behavior of the Prediction Error Variance for Stationary Models
Mamikon Ginovyan, Boston University

Abstract:
One of the main problems in prediction theory of stationary processes, called direct prediction problem, is to describe the asymptotic behavior of the best linear mean squared prediction error variance \( \sigma_n^2(F) \) in predicting the value \( X(1) \) of the process \( \{X(t), t \in \mathbb{Z}\} \) by the observed past of length \( n : X(-n + 1), ..., X(0) \) as \( n \rightarrow \infty \), depending on the regularity nature (deterministic or non-deterministic) and on the memory structure (short-, intermediate-, and long-memory) of the observed process \( X(t) \) parameterized by the spectral function \( F(\lambda), \lambda \in [-\pi, \pi] \).

The second problem of interest, called inverse prediction problem is: for a given rate of decrease of the relative prediction error \( \delta_n^2(F) := \sigma_n^2(F) - \sigma_n^2(F) \) to zero as \( n \rightarrow \infty \), describe the model process \( X(t) \) compatible with that rate. Specify then the dependence structure of the model and the properties of its spectral function \( F(\lambda) \).

In this talk we will discuss these problems both for deterministic and nondeterministic processes. It turns out that for nondeterministic processes the asymptotic behavior of the prediction error variance \( \sigma_n^2(F) \) is determined by the differential properties of the spectral function \( F(\lambda) \) of the model, while for deterministic processes it is determined by the geometric properties of \( F(\lambda) \).

A Bayesian Degree-Corrected Stochastic Block Model for Community Detection in Large Networks
Luis Carvalho. Boston University

Abstract:
We discuss a degree-corrected version of a stochastic block model that aims to achieve a better resolution limit for community identification and is able to handle very large networks. We cast community detection as Bayesian generalized linear models and show that suitable priors are essential to adequately characterize community behavior. To estimate community assignments, we describe a new centroid estimator based on canonical projections and show that while this estimator is similar to Binder's estimator it can be obtained more efficiently. We further propose a latent specification based on "popularity" classes to handle large networks, and show that it identifies communities reliably and efficiently. We demonstrate the proposed model and inference on a number of classical network datasets and real-world large networks from the Stanford network analysis project. Finally, we offer a few concluding remarks on the model implementation and directions for future work. This is joint work with Lijun Peng and Matthew Morse.
**Biomarker Driven Population Enrichment for Adaptive Oncology**

Cyrus Mehta, Cytel Inc & Harvard School of Public Health

**Abstract:**

The development of molecularly targeted therapies for certain types of cancers has led to the consideration of population enrichment designs that explicitly factor in the possibility that the experimental compound might differentially benefit different biomarker subgroups. In such designs, enrollment would initially be open to a broad patient population with the option to restrict future enrollment, following an interim analysis, to only those biomarker subgroups that appeared to be benefiting from the experimental therapy. While this strategy could greatly improve the chances of success for the trial, it poses several statistical and logistical design challenges. Since late-stage oncology trials are typically event driven, one faces a complex trade-off between power, sample size, number of events and study duration. We have developed new statistical methodology for phase 2 population enrichment designs based on generalizations of the conditional error rate approaches of Muller and Schafer. The special difficulties encountered with time-to-event endpoints are addressed by our methods. The crucial role of simulation for guiding the choice of design parameters is emphasized.

**Career Development Session**

This will be a panel discussion of career development issues facing statisticians in a variety of professional roles. The target audience is students, postdocs, recent graduates, and others at the early stages of their career. Discussants will include representatives from different types of academic institutions as well as industry. Discussion topics include the responsibilities involved in different career paths, balancing research priorities, seeking leadership roles, and other career goals.

**Causal Inference in a Partially Randomized Preference Trial with Small Samples**

Cassandra Pattanayak, Wellesley College

**Abstract:**

A randomized medical trial is generalizable to the population of patients who consent to randomization. However, consenting patients often differ importantly from the target population on key baseline covariates. Allowing patients who refuse randomization to choose their own treatment and remain in the study creates an observational study that parallels the randomized trial. This design has been called a "partially randomized preference trial" and allows inference about the causal effect of treatment not only for randomized patients, but also for a larger set of patients that is more similar to the target population. This study design may lead to small sample sizes in at least one of the non-randomized treatment groups. For very small samples, random matching or subclassification algorithms intended to optimize covariate balance are sometimes more effective than a more traditional matching approach. The discussion is motivated by a study on the effect of family-based treatment versus individual supportive psychotherapy for subsyndromal anorexia nervosa in adolescents. This project is joint work with collaborators Katharine L. Loeb (Fairleigh Dickinson University), Sue M. Marcus (Columbia University), and Diana Schron (Wellesley College).

**Detecting Changes in Behavioral Trends of Users on Twitter**

Vasanthan Raghavan, Qualcomm Flarion Technologies, New Jersey

**Abstract:**

We consider the problem of reliable and quick detection of anomalous/suspicious activities in social networks. We propose a coupled HMM that captures the interconnected dynamics between the temporal activity of a user and her social network. We then develop a non-parametric anomaly detection algorithm to detect sudden spurts in activity and demonstrate it to be better suited for practical use than traditional parametric methods.
Detecting Treatment-Covariate Interactions Using Permutation Methods
Rui Wang, Brigham and Women’s Hospital & Harvard School of Public Health

Abstract:
Various interaction tests have been proposed to detect treatment effect heterogeneity; however, they typically examine covariates one at a time and can greatly increase the chance of a false positive finding when the number of covariates is large. We propose a new permutation test for the null hypothesis of no interaction effects for any covariate. The proposed test allows us to consider many covariates simultaneously, applies generally to randomized clinical trials of multiple treatments, and provides an attractive alternative to the standard likelihood ratio test. We illustrate the proposed methods using data from the Treatment of Adolescents with Depression Study.

Efficient Performance Evaluation of the Generalized Shiryaev—Roberts Detection Procedure
Aleksey S. Polunchenko, Binghamton University

Abstract:
We propose a numerical method to evaluate the performance of the emerging Generalized Shiryaev—Roberts change-point detection procedure in a minimax-ish context. We show the method’s rate of convergence to be quadratic and supply a tight bound on the method’s error. To conclude, we demonstrate the proposed method at work in a case study.

“Fat chance” … Looking back at an improbable career in analytics
Doug Newell, Calexus Solutions LLC

Abstract:
Doug Newell is a serial entrepreneur specializing in business and health analytics. He has been the founder or a co-founder of five analytics companies. Over more than 30 years he has lead analytic teams in providing analytics solutions to hundreds of firms in dozens of industries. Doug will talk about his experience building an analytics career and give his insights into successful analytic career paths.

Infusing Statistics Classes with Web-Based Formative Assessments Using ASSISTments and RStudio
Eric Simoneau, Boston Latin School

Abstract:
ASSISTments is a free web-based formative assessment and tutoring tool developed at WPI and funded by the NSF. It allows students to answer questions and get instant feedback. If students find themselves struggling with a question, they can request hints to help them work through the problem. A dashboard of student learning data helps instructors optimize student learning. To date, over 900 high school teachers both in the US and abroad have registered to participate. In this talk, Eric will discuss using ASSISTments along with RStudio's web-based RStudio Server to help students learn basic computation in the introductory statistics course.

Is There an Overuse of Computed Tomography Scanning of Medicare Patients in Hospitals?
Fotios Kokkotos, Partner – Head of Advanced Analytics, Trinity Partners

Abstract:
Radiologists claim that performing two or more CT (Computed Tomography) scans in succession is rarely necessary, yet the practice of multiple CT scanning of patients during the same visit has continued in recent years. This talk discusses how to use the Medicare claims database to review the evidence and identify factors that contribute to this practice. The results corroborate with previous policy studies in concluding that hospitals can and should do more to modify physician behavior by implementing new protocols and to monitor the administration of multiple CT scans. The results also warrant a potential investigation of similar European databases.
Meta-STEPP: Subpopulation Treatment Effect Pattern Plot for Meta-Analysis
Xin Victoria Wang, Dana-Farber Cancer Institute

Abstract:
STEPP (Subpopulation Treatment Effect Pattern Plot) is a method to explore possible treatment-by-covariate interaction in clinical trials where the covariate of interest is continuous. We extend STEPP to the meta-analysis setting where patterns of possible treatment effect heterogeneity can be examined in data from multiple trials. Simulation studies show that Meta-STEPP has adequate type-I error rate recovery as well as power when reasonable window sizes are chosen. When applied to eight breast cancer trials, Meta-STEPP suggests that chemotherapy is less effective for tumors with high estrogen receptor expression compared to those with low expression.

Minimizing Signal Detection Time in Postmarket Sequential Analysis: Balancing Positive Predictive Value and Sensitivity
Judy Maro, Harvard Pilgrim Health Care Institute and Harvard Medical School

Abstract:
Purpose: Outcome misclassification in retrospective epidemiologic analyses has been well-studied, but little is known about such misclassification with respect to sequential statistical analysis during surveillance of medical product-associated risks, a planned capability of the U.S. Food and Drug Administration’s Sentinel System.

Methods: Using a vaccine example, we model and simulate sequential database surveillance in an observational data network using a variety of outcome detection algorithms. We consider how these algorithms, as characterized by sensitivity and positive predictive value, impact the length of surveillance and timeliness of safety signal detection. We show investigators/users of these networks how they can perform preparatory study design calculations that consider outcome misclassification in sequential database surveillance.

Results: Non-differential outcome misclassification generates longer surveillance times and less timely safety signal detection as compared to the case of no misclassification. Inclusive algorithms characterized by high sensitivity but low positive predictive value outperform more narrow algorithms when detecting rare outcomes. This decision calculus may change considerably if medical chart validation procedures were required.

Conclusions: These findings raise important questions regarding the design of observational data networks used for pharmacovigilance. Specifically, there are tradeoffs involved when choosing to populate such networks with component databases that are large as compared to smaller integrated delivery system databases that can more easily access laboratory or clinical data and perform medical chart validation.

A Model for the Joint Estimation of Time to Progression and Survival in the Interval Censored Case.
David A. Schoenfeld, Massachusetts General Hospital.

Abstract:
Clinical Trials often measure disease progression and survival. Disease progression is known to have occurred in the interval between examinations while survival time is known exactly or is right censored. Survival time should provide information on when progression actually occurred. We suggest a joint model for progression and death where the effect of covariates on the hazard of progression and death after progression obey a proportional hazards model and the underlying hazards for progression and death are piecewise constant with the underlying hazard for death after progression depending on the time of progression. The model can be used to test whether treatment improves the disease free interval; whether it improves survival; whether it improves time to progression in surviving patients and survival time in non-surviving patients; and whether it improves time to progression and does not worsen survival. Since the effect of covariates is parametric, all of these inferences can take into account prior knowledge using a Bayesian approach. The method is implemented in a publically available computer program.
Nonparametric Partial Identification of Causal Net and Mechanism Average Treatment Effects (joint with Carlos A. Flores, Cal Poly-San Luis Obispo)
Alfonso Flores-Lagunes, Binghamton University, Institute for the Study of Labor (IZA), Bonn, German

Abstract:
When analyzing the causal effect of a treatment on an outcome it is important to understand the mechanisms or channels through which the treatment works. In this paper we derive informative nonparametric bounds for net and mechanism (mediation) average treatment effects, which provide an intuitive decomposition of the total average treatment effect (ATE) that enables learning about how the treatment affects the outcome. Our bounds allow for heterogeneous effects while not requiring the use of an instrumental variable or having an outcome with bounded support. We employ assumptions requiring weak monotonicity of mean potential outcomes within or across principal strata (subpopulations defined by the potential values of the mechanism variable under each treatment arm). We illustrate the identifying power of our bounds by analyzing what part of the ATE of a training program on weekly earnings and employment is due to the obtainment of a GED, high school, or vocational degree.

On Draw Bias in Horse Racing
John W. Emerson (Jay), Yale University

Abstract:
Some horse races are straight. Others have turns following the contours of specific tracks or courses. Intuition suggests that "running on the inside" ought to offer an advantage, so the draw (or starting position) could offer an advantage. There might even be a draw advantage on some straight tracks due to differences in the running surface or a tilt in the track. What can the data tell us?

openWAR: An Open Source System for Evaluating Overall Player Performance in Major League
Ben Baumer, Smith College

Abstract:
Within baseball analytics, there is substantial interest in comprehensive statistics intended to capture overall player performance. One such measure is Wins Above Replacement (WAR), which aggregates the contributions of a player in each facet of the game: hitting, pitching, base running, and fielding. However, current versions of WAR depend upon proprietary data, ad hoc methodology, and opaque calculations. We propose a competitive aggregate measure, openWAR, that is based upon public data and methodology with greater rigor and transparency. We discuss a principled standard for the nebulous concept of a “replacement” player. Finally, we use simulation-based techniques to provide interval estimates for our openWAR measure.

Optimizing Diagnostic Accuracy of HIV Treatment Failure in Resource-Limited Settings with Selective Use of Viral Load Testing
Tao Liu, Brown University

Abstract:
The WHO guidelines for monitoring HIV treatment in resource-limited settings are mostly based on low-cost markers, and have been shown by recent research to have high misdiagnosis rates. Viral load (VL) is considered “gold standard,” yet its widespread use is limited by cost and infrastructure. We propose a diagnostic algorithm that uses information from routinely-collected markers to guide a selective use of VL testing for diagnosing HIV treatment failure. Our algorithm identifies a patient subpopulation, on whom the limited VL testing minimizes a predefined risk. Diagnostic properties of the algorithm are demonstrated by simulations and application to a real dataset.
Personalized Treatment Selection Based Risk-Benefit Profiles from Clinical Trial Data with Multiple Endpoints
Brian Claggett, Harvard Medical School, Brigham & Women’s Hospital

Abstract:
In a typical randomized clinical study to compare a new treatment with a control, oftentimes each study subject may experience any of several distinct outcomes during the study period, which collectively define the “risk-benefit” profile. To assess the treatment difference, it is desirable to utilize the entirety of such outcome information. The times to these events, however, may not be observed completely due to competing risks. The standard analyses based on the time to the first event, or individual component analyses with respect to each event time, are not ideal. In this paper, we classify each patient’s risk-benefit profile, by considering all event times during follow-up, into several clinically meaningful ordinal categories. We first show how to make inferences for the treatment difference in a two-sample setting with incomplete categorical data. We then present a systematic procedure to identify patients who would benefit from a specific treatment using baseline covariate information. To obtain a valid and efficient system for personalized medicine, we utilize a cross validation method for model building and evaluation and then make inferences using the final selected prediction procedure with an independent data set. The proposal is illustrated with the data from a clinical trial to evaluate a beta-blocker for treating chronic heart failure patients.

A Predictive Enrichment Procedure to Identify Potential Responders to the New Therapy for Randomized, Comparative Controlled Clinical Studies
Junlong Li, Harvard School of Public Health

Abstract:
To evaluate a new therapy vs. a control via a (or a series of) randomized, comparative clinical study, due to heterogeneity of the patient population, a pre-specified, built-in predictive enrichment procedure may be implemented to identify a subpopulation for which the therapy is expected to have a desired risk-benefit profile. Ideally such a companion diagnostic strategy can be conducted using a three-step procedure with three independent data sets generated under the same setting. At the first stage, we create various candidate scoring systems based on the patient's baseline variables parametrically. For the second step, a potentially promising subgroup is identified using these systems. At the final stage, we validate such a selection via two-sample inference procedures for assessing the treatment effectiveness with the data from the so-called holdout sample. When the study size is not large, one may combine the first two steps using a conventional “cross-training-evaluation” algorithm. The entire procedure is illustrated with the data from a cardiovascular trial to evaluate a beta-blocker vs. the standard care for treating chronic heart failure patients.

Prospective Routine Medical Product Safety Surveillance: the FDA Mini-Sentinel System - Overview of Mini-Sentinel
Jeff Brown, Harvard Pilgrim Health Care Institute and Harvard Medical School

Abstract:
The Mini-Sentinel program is part of the FDA’s Sentinel Initiative, a national system under development for monitoring the safety of approved medical products. The system was developed in response to the Food and Drug Administration Amendment Act (FDAAA) of 2007, which requires creation of a post-market active surveillance system that uses electronic health data of 100 million people. Mini-Sentinel, which encompasses more than 30 collaborating organizations, including 18 data partners, provides FDA with rapid querying capability for a large network of electronic health data and enables FDA to develop and test methods to assess medical product safety within a distributed system of electronic healthcare databases. The distributed networking approach allows data to be stored locally, with data partners maintaining direct control over their data and its uses. All data partners have transformed their electronic health data into a common format that is comprised of a set of standardized data files with the same structure, variable names and definitions. Mini-Sentinel has the ability to query
quality-checked administrative and claims data covering over 150 million lives and 380 million person-years of longitudinal observation time between 2000 and 2013. The data partners can access full-text electronic and paper ambulatory and hospital records for over 90% of their members if necessary, and clinical data from electronic health records are available for over 12 million individuals across several data partners. FDA has issued hundreds of rapid-response queries, some of which have contributed to changes in labeling, is conducting several epidemiologic studies, and is beginning to implement prospective surveillance of newly approved medical products.

**R Markdown: Bringing Reproducible Analysis into the Classroom**
Andrew Bray, Smith College

Abstract:
R Markdown is a new technology that makes creating fully-reproducible statistical analysis simple by smoothly integrating computation and written analysis. It provides a solution suitable not only for cutting edge research, but also for use in an introductory statistics course. We present experiential and statistical evidence that R Markdown can be used effectively in introductory statistics courses, and discuss its role in the rapidly-changing world of statistical computation.

**Randomized Clinical Trials to Identify Optimal Antibiotic Treatment Duration**
Michael LaValley, Boston University

Abstract:
Resistance is a major barrier to the continued success of antibiotic treatment and resistance is often generated by overly long durations of antibiotic treatment. A barrier to identifying the shortest effective treatment duration is the cost of the sequence of clinical trials needed to determine shortest optimal treatment duration. We propose a new method to identify the optimal treatment duration of an antibiotic treatment regimen where subjects are randomized to varying treatment durations and the cure proportions of these durations are linked using a logistic regression model, making effective use of information across all treatment duration groups.

**Regression-Based Player Performance Metrics in Hockey**
Brian Macdonald, US Military Academy

Abstract:
We give an introduction to player performance metrics for NHL players. Each metric provides a way to estimate a player’s value to his team while accounting for the strength of his teammates and opponents. We start with the most basic regression model used to compute Adjusted Plus-Minus for skaters and discuss its limitations. We also present improvements that have been made by modifying various aspects of the model. We then shift our attention to goalies. We present a Bayesian hierarchical logistic regression model which can be used to estimate a goalie’s impact on the number of goals his team allows, while accounting for the difficulty of the shots that he faces.

**Robust Dimension Reduction Procedure with Applications**
Yifan Xu, Case Western Reserve University

Abstract:
We propose a new robust non-negative matrix factorization (rNMF) procedure to extract low dimensional structure from high dimensional data; the robustness is with respect to data corruption. We demonstrate the procedure at work in the context of biological data decomposition and simulated corrupted tumor image compression.
Scan Statistics for Vaccine Safety Data Mining
Martin Kulldorff, Harvard Pilgrim Health Care Institute and Harvard Medical School

Abstract:
Post-market drug and vaccine safety surveillance is important to detect adverse events too rare to find in clinical trials. Data mining methods are useful to screen many diagnostic codes for unexpected safety issues in the absence of specific safety concerns. The tree-based scan statistic is a data mining method that simultaneously evaluates a hierarchical system of both specific and broad diagnosis definitions. Self-control methods are widely used in vaccine safety studies, as they adjust for between person confounders. To minimize the number of false signals while evaluating thousands of overlapping disease outcome definitions, we present a self-control tree-based scan statistic. Using electronic claims data from six health insurance plans that are members of the FDA Mini-Sentinel project, we evaluated adverse events after measles-mumps-rubella-varicella and pneumococcal vaccines.

Sequential Estimation of Rare Events in Large Networks
Konstantin M. Zuev, Northeastern University

Abstract:
We consider the problem of reliability assessment in large networks. We propose a new MCMC method for efficient sequential estimation of the probabilities of extreme events (rare occurrence, but high impact) in large networks. The efficiency of the method is demonstrated through an example.

Sequential Tests Controlling False Discovery and Non-discovery Proportions
Shyamal K. De, Binghamton University

Abstract:
We develop test procedures for simultaneous testing of multiple hypotheses for sequentially sampled data and show that the proposed methods keep both tail probabilities of False Discovery and False Non-discovery Proportions (FDP and FNP) at some prescribed levels. The popular False Discovery and False Non-discovery Rates (FDR and FNR) can also be controlled simultaneously by the proposed procedures.

Sequential Online Detection and Classification in 3D Computer Vision
Olympia Hadjiliadis, City University of New York

Abstract:
We consider the problem of online anomaly detection in automatic 3D image reconstruction through laser scan sequential data. After illustrating how modified CUSUM procedures can be applied to distinguish different surface orientations, we introduce a HMM to capture vegetation in urban scenes. We combine this with CUSUM to detect changes in the model thereby illustrating its usefulness.

Subgroup Identification in Personalized Treatment of Alcohol Dependence
Lei Liu, Northwestern University

Abstract:
Identification of patient subgroups of enhanced treatment effects is an important topic in personalized (or tailored) medicine for alcohol research. Recently, several recursive partitioning methods to identify subgroups benefitting from treatment have been proposed. These novel data mining methods improve on the limitation of the traditional regression-based methods via interactions. We propose an exploratory approach, using recursive partitioning methods, e.g., interaction tree and virtual twins, to more flexibly determine subgroups where the treatment effect is likely to be large by prognostic factors. We apply these tree-based methods to a pharmacogenetic trial of ondansetron. Our methods identify several subgroups based on patients genetic and other prognostic covariates. Among the 251 subjects with complete covariate information, the interaction tree method identifies 115 subjects with specific genetic and other prognostic factors, resulting in a 17.9% decrease in the percentage of heavy drinking days.
The virtual twins method identifies 80 subjects with a 19.8% decrease in PHDD. Both methods yield better identifying results than traditional regression methods testing the interaction terms. In summary, the data mining approach is a valid exploratory method for identifying subgroups likely to receive benefit from treatment in a pharmacotherapy trial in alcoholism. Our results can provide new insights into the heterogeneous nature of alcohol use disorder (AUD), helping clinicians to tailor treatment to the biological profile of individual patients, and thereby achieving better treatment outcomes.

State-of-the-Art in Sequential Change-Point Detection
Wenyu Du, Binghampton University

Abstract:
We provide a brief overview of the state-of-the-art in the area of sequential change-point detection. The overview is focused on the discrete-time case and encompasses all major formulations of the underlying optimization problem: Bayesian, generalized Bayesian, minimax and multi-cyclic. Particular attention is paid to the latest advances made in each formulation.

statsTeachR: Open Resources for Teaching Statistics
Nicholas Reich, University of Massachusetts/Amherst

Abstract:
statsTeachR.org is an open-access, online repository of modular lesson plans for teaching statistics and biostatistics using R at the undergraduate and graduate level. Each module focuses on teaching a specific statistical concept. With a focus on hands-on exercises in statistical computing with R, statsTeachR modules provide instruction in fundamental and advanced concepts of statistics and statistical computing. This new collaborative framework enables teachers to use modules in their classroom or to contribute existing materials and lesson plans. Additionally, visitors to the site can curate their own “courses” by creating a collection of existing modules. An overarching goal of the statsTeachR project is to facilitate the development and dissemination of materials for teaching statistics, biostatistics, R, and statistical computing that can be easily incorporated into new or existing classes.

Stratified Bayesian Adaptive Clinical Trials
Lorenzo Trippa, Dana-Farber Cancer Institute

Abstract:
When several experimental treatments are available for testing, multi-arm trials provide gains in efficiency over separate trials. Including interim analyses allows the investigator to effectively use the data gathered during the trial. Bayesian adaptive randomization (AR) and multi-arm multi-stage (MAMS) designs are two distinct methods that use patient outcomes to improve the efficiency and ethics of the trial. AR allocates a greater proportion of future patients to treatments that have performed well; MAMS designs use pre-specified stopping boundaries to determine whether experimental treatments should be dropped. There is little consensus on which method is more suitable for clinical trials, and so in this paper, we compare the two under several simulation scenarios and in the context of a real multi-arm phase II breast cancer trial. We compare the methods in terms of their efficiency and ethical properties. We also consider the practical problem of a delay between recruitment of patients and assessment of their treatment response. Both methods are more efficient and ethical than a multi-arm trial without interim analyses. Delay between recruitment and response assessment attenuates this efficiency gain. We also consider futility stopping rules for response adaptive trials that add efficiency when all treatments are ineffective. Our comparisons show that AR is more efficient than MAMS designs when there is an effective experimental treatment, whereas if none of the experimental treatments is effective, then MAMS designs slightly outperform AR.
The Effect of Medicaid Expansions in the Late 1980s and Early 1990s on the Labor Supply of Pregnant Women
Dhaval Dave, Bentley University & National Bureau of Economic Research

Abstract:
A substantial body of research has found that expansions in Medicaid eligibility increased enrollment in Medicaid, reduced the rate of uninsured, and reduced the rate of private health insurance coverage (i.e., crowd out). Notably, there has been little research that has examined the mechanism by which crowd-out occurs. We provide the first study to examine the effects of expansions in Medicaid eligibility for pregnant women in the late 1980s and the early 1990s on their labor supply, which is one of the possible mechanisms underlying crowd out. Labor market outcomes for women who have given birth in the past year in the Current Population Survey Annual Demographic File are matched with Medicaid eligibility measures by state and year, spanning 1985-1996, the period that witnessed the largest expansions in Medicaid eligibility for pregnant women. Controlling for confounding trends, results based on fixed-effects models indicate that pregnant women’s labor supply is quite sensitive to the offer of Medicaid insurance not tied to employment status. Specifically, estimates suggest that the 20 percentage point increase in Medicaid eligibility during the sample period was associated with a 6% to 7% decrease in the probability that a woman who gave birth in the past year was employed. Among unmarried women with less than a high school education, the change in Medicaid eligibility reduced employment by approximately 13% to 16%. The consistency of these labor-supply estimates in generating observed declines in private coverage plausibly points to shifts in employment as a key driving mechanism behind the crowd-out of private coverage among pregnant women due to the expansions in Medicaid eligibility. Reduced maternal labor supply would have welfare implications for children, who on the one hand may have their mothers home during early life but on the other hand live at least for a while in families with lower income.

The Use of Wearable Technology for Comparative Effectiveness Research
Ani Eloyan, Johns Hopkins University

Abstract:
In many cases the amount of time a person is active as well as the ability of a person to perform certain tasks (e.g., walk, stand, etc.) are used as outcomes when comparing the effectiveness of an intervention or a treatment. For example, the amount of daily activity can be used to identify differences in aging patterns for various interventions, or the functional capacity of patients can be used to assess the recovery patterns after different types of surgery. Often, researchers rely on subjective measurements of these outcomes, such as surveys to measure weekly activity or the 6-minute walk test distance to assess functional capacity. In this talk, the use of wearable technology for obtaining more accurate measurements of the outcomes of interest is discussed. Statistical methods for analyzing activity data are presented in the context of identifying patterns of recovery after two types of heart surgery. This project is joint work with my collaborators V. Zipunnikov, C. Crainiceanu, P. Green, M. Maurer, S. Kodali, M.-Y. Hung, A. Koster and T. Harris.

Unstructured Decentralized Change Detection in Sensor Networks
Grigory Sokolov, University of Southern California

Abstract:
We consider the problem of quickest change-point detection in a decentralized setup with observations made by a distributed sensor network and then transmitted to a fusion center for processing and decision-making. The challenge is that the amount of information the fusion center can receive is limited due to communication channels’ bandwidth constraints. We propose a decentralized sequential change-point detection procedure that (a) requires transmission of least amount of data and (b) is asymptotically optimal for any scenario regarding the unknown subset of affected sensors.
Using Marginal Structural Models to Estimate the Effect of Food Insecurity on Depression in HIV Positive and Negative Injection Drug Users
Norma Terrin, Sally Skinner, & Alice M Tang, Tufts Medical Center

Abstract:
Injection drug users (IDUs) with HIV face a multitude of barriers to HIV treatment, among which are food insecurity and depression. In our previous cross-sectional study of IDUs with and without HIV in Chennai, India, depression was found to be correlated with food insecurity. We hypothesize that symptoms of malnutrition were manifesting as symptoms of depression in this population. In a longitudinal study, we use marginal structural models (MSMs) to test whether food insecurity causes symptoms of depression. The MSMs address confounding (from baseline and time-varying covariates) as well as the bidirectional relationship between food insecurity and depression.

Violation of Detailed Balance and Variance Reduction: a Large Deviations Approach
Kostas Spiliopoulos, Boston University

Abstract:
Monte Carlo methods are very popular methods to sample from high-dimensional target distributions and to approximate integrals of observables integrated against a given measure (distribution), which very often is of Gibbs type. Markov processes that have the target distribution as their invariant measure are used to approximate the equilibrium dynamics and sample the space. In this talk, we explore performance criteria based on the related large deviations theory for random measures and we focus on the diffusion setting. We find that large deviations theory can not only adequately characterize the efficiency of the approximations, but it can also be used as a vehicle to design Markov processes, whose time average optimally (in the sense of variance reduction) approximates the quantities of interest. We quantify the effect that added irreversibility has in the speed of convergence to a target Gibbs measure and to the asymptotic variance of the resulting estimator. One of our main finding is that adding irreversibility reduces the asymptotic variance of generic observables and we give an explicit characterization of when observables do not see their variances reduced in terms of a nonlinear Poisson equation. Theoretical results are supplemented by simulations.

Viral Genetic Linkage Analysis in Cluster Randomized Trials for HIV prevention
Victor DeGruttola (Harvard School of Public Health), Rui Wang, Ravi Goyal

Abstract:
We discuss the design and analytical challenges of the Botswana Combination Prevention Project intended to control HIV infection in Botswana. This study randomizes 30 villages to a combination HIV prevention intervention vs. standard of care. Important in the design is accounting for correlation structure for the HIV infection endpoint, which is driven in part by the sexual network. We investigate analytically and through simulations how different sampling strategies and mechanisms for generating correlation affect study power. To do so, we develop a new method to generate a robust collection of sexual networks utilizing both the estimated features of the mixing matrix and its sampling variability.