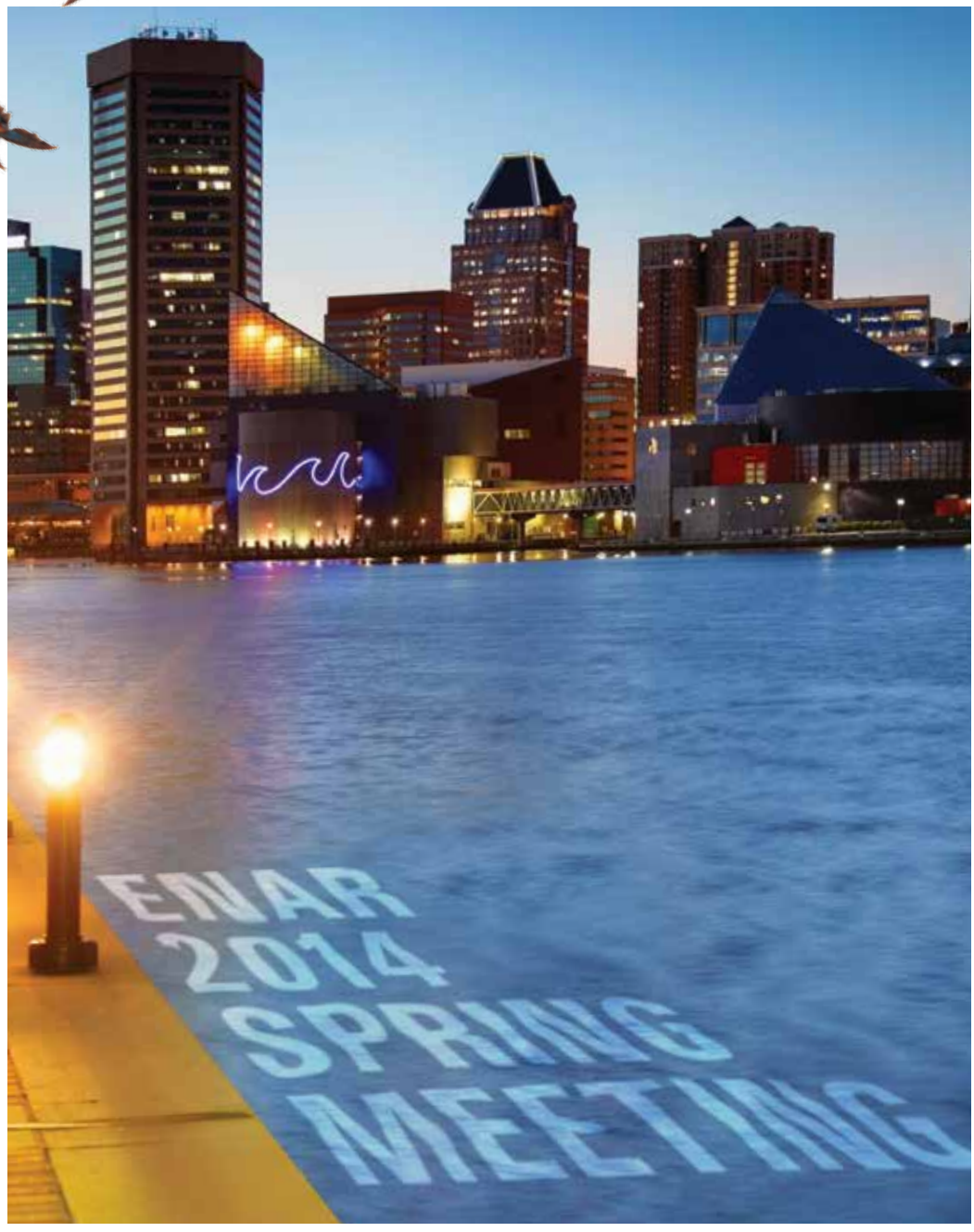
ENAR
MARCH 16–19, 2014
Baltimore Marriott Waterfront Hotel
Baltimore, Maryland
ENAR
2014
SPRING
MEETING
with IMS and Sections of ASA
Program

ENAR



ENAR 2014
SPRING MEETING
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Welcome and Overview 4–5

Acknowledgements 6–9

Special Thanks 10

Baltimore, Maryland Highlights 12–13

Presidential Invited Speaker 15

IMS Medallion Lecture 16

Short Courses 17–19

Turorials 20–22

Roundtables 23–25

Program Summary 27–39

Scientific Program 40–98

Index 100–115

Grand Ballroom Floor Plan 116

Harborside Ballroom Floor Plan 117

Waterview Ballroom Floor Plan 118

ENAR 2014 SPRING MEETING
MARCH 16–19, 2014

Welcome

I am delighted to welcome you to the 2014 ENAR Spring Meeting!

I am indebted to a dedicated team of individuals for diligently planning what promises to be an exciting and enriching program.

For first time attendees of the ENAR Spring Meeting, I extend a heartfelt welcome and hope that you will continue to enjoy the annual meeting for many years to come. For returning attendees, I trust that this year's meeting will be most fulfilling and will energize you to continue to carry out the vital work of statistical practice, research and development. The ENAR Spring Meeting is a wonderful opportunity to attend stimulating scientific sessions targeting the most pressing issues in our field, to deepen our understanding of cutting-edge statistical methods and software through our education program, to connect with old friends and meet new ones, to identify prospective employees/employers, to explore the latest books and software from our exhibitors, and so much more.

Scientific Program Led by Program Chair, Dr. Hernando Ombao of the University of California at Irvine, and Associate Chair, Dr. Qi Long of Emory University, the Program Committee has assembled an outstanding invited scientific program. This would not be possible without the contributions from many of you who volunteered to participate in the invited sessions as organizers, chairs, and speakers. The invited program features recent advances in a broad set of topics such as statistical methods for longitudinal data, emerging methodology for big data (including, genomics, bioinformatics, imaging, etc.), clinical trials, functional data analysis, survival analysis, and epidemiologic and public health data. The scientific program will feature an expanded number of poster presentations, including invited posters, and contributed poster presentations. The ENAR Regional Advisory Board (RAB) will conduct a poster competition, which has been a resounding success in recent years. Finally, there will be numerous contributed oral presentations, which are an integral part of the Spring Meeting.

Education Program Come and learn from the best! There is no better opportunity to bolster your understanding of methodology and software that may be beneficial in the workplace, to learn about a topic outside of your primary area of specialization, or to deepen your background in an area of interest. The Education Advisory Committee has compiled a set of fabulous short courses and tutorials featuring internationally renowned instructors.

The short course topics cover a range of areas such as advanced high performance computing techniques and strategies for massive data, longitudinal data (including missing data, surrogate endpoints, and joint modeling with survival outcomes), next generation sequencing, adaptive clinical trials, evaluation of prognostic biomarkers, causal analysis, and functional data analysis, among others.

The program will also offer a series of roundtable luncheons with distinguished discussion leaders addressing topics of interest to statisticians in academia, government, and industry.

Keynote Lectures Highlights of the ENAR 2014 Program include speakers for the Presidential Invited Address and the IMS Medallion lecture. I am thrilled that these lectures will be given by preeminent scholars who have made vast contributions within statistics and biostatistics. Dr. Robert Tibshirani, from Stanford University, will deliver the Presidential Invited Address entitled "A Significance Test for the Lasso." Professor Tibshirani has made seminal contributions in penalized regression, most notably the lasso, as well as the analysis of high throughput microarray array data. He has received numerous awards including some of the most distinguished honors in statistics and in science more broadly. He is a member of the National Academy of Sciences, was a recipient of the Committee of Presidents of Statistical Societies (COPSS) Presidents' Award and the Statistical Society of Canada's Gold Medal, and is a fellow of the Institute of Mathematical Statistics (IMS), the American Statistical Association (ASA), and the Royal Society of Canada.

Dr. Xihong Lin, from Harvard School of Public Health, will give the IMS Medallion Lecture. Professor Lin has made a tremendous impact to the theory and practice of biostatistics, including contributions to methodology for mixed models, nonparametric and semiparametric regression, and statistical genetics and genomics. Among Professor Lin's numerous honors, she is the recipient of the COPSS Presidents' Award, the Spiegelman Award, and the National Cancer Institute MERIT Award. She is a Fellow of the ASA and IMS.

Additional Meeting Activities There are a host of other activities at the ENAR Spring Meeting for participants to find opportunities to engage. The Spring Meeting will feature the popular Career Placement Center. For participants seeking employment, be sure to register to gain access to many of the leading organizations in the field including government, academic, and private institutions. The Fostering Diversity in Biostatistics Workshop will be held on Sunday, March 16th. This workshop targets undergraduate students, undergraduate faculty, graduate students, graduate faculty, and professionals from industry and government, with a focus on recruitment, retention, and promotion of biostatisticians from traditionally under-represented groups. I thank Dr. Knashawn Morales of the University of Pennsylvania and Dr. Simone Gray of the Centers for Disease Control and Prevention for their leadership in organizing this year's workshop. The Council for Emerging and New Statisticians (CENS) will hold an inaugural social event to increase networking opportunities for graduate students and recent graduates. Indicate your interest during the ENAR Spring Meeting registration process. There is a new member reception, and you will find a host of activities for student members at the meeting.

A favorite for many is the Tuesday night social event, which I am excited to announce will be held at the National Aquarium in Baltimore. Those who participate in this year's event will enjoy a wonderful evening of networking, a dinner including authentic Maryland crab cakes, and the National Aquarium which features over 16,000 animals including sharks, birds, frogs, turtles, dolphins, and jellies. This is an event that you do not want to miss!

Meeting Venue The conference hotel, the Marriott Waterfront, is located along Harbor East, which is conveniently situated near the Inner Harbor, Little Italy, and Fell's Point, which offer an array of dining options, bars, and entertainment.

Acknowledgements I would like to thank the Local Arrangements Committee, led by Professor Ciprian Crainiceanu, for their planning efforts to ensure that meeting participants will experience the best that Baltimore has to offer. Finally, I wish to express my sincere gratitude to Kathy Hoskins, our ENAR Executive Director, Katie Earley, Challee Blackwelder, and their other colleagues at Drohan Management for their incredible support in planning the ENAR Spring Meeting. Kathy and her team have been vital in the growing success of ENAR and its annual Spring Meeting. It has indeed been a pleasure working with you!

DuBois Bowman
ENAR 2014 President

ACKNOWLEDGEMENTS

ENAR would like to acknowledge the generous support of the 2014 Local Arrangements Committee Chaired by

Ciprian M. Crainiceanu
Department of Biostatistics
Johns Hopkins University

and our student volunteers!

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LOCAL INFORMATION

BALTIMORE, CHARM CITY

Baltimore, or *Charm City*, is a thriving all-American city with world leading research universities such as Johns Hopkins University and the University of Maryland. Baltimore has a thriving economy powered by tourism and a thriving industry including Under Armor, Black and Decker, Domino Sugar, the Port of Baltimore, T. Rowe Price, and Northrop Grumman. Charm City is also the home of the Ravens football team, the 2000 and 2012 Super Bowl champions, and the Orioles baseball team, the 1966, 1970, and 1983 World Series champions.

Baltimore National Aquarium

The Aquarium is just short walk away from the Baltimore Marriott Waterfront Hotel and is the home of a new Australian wing and of the newly remodeled Blacktip Reef. Atlantic bottlenose dolphins, jellyfish, poison frogs, sharks, corals, and octopuses are just some of attractions that will make every visit unforgettable.

Inner Harbor

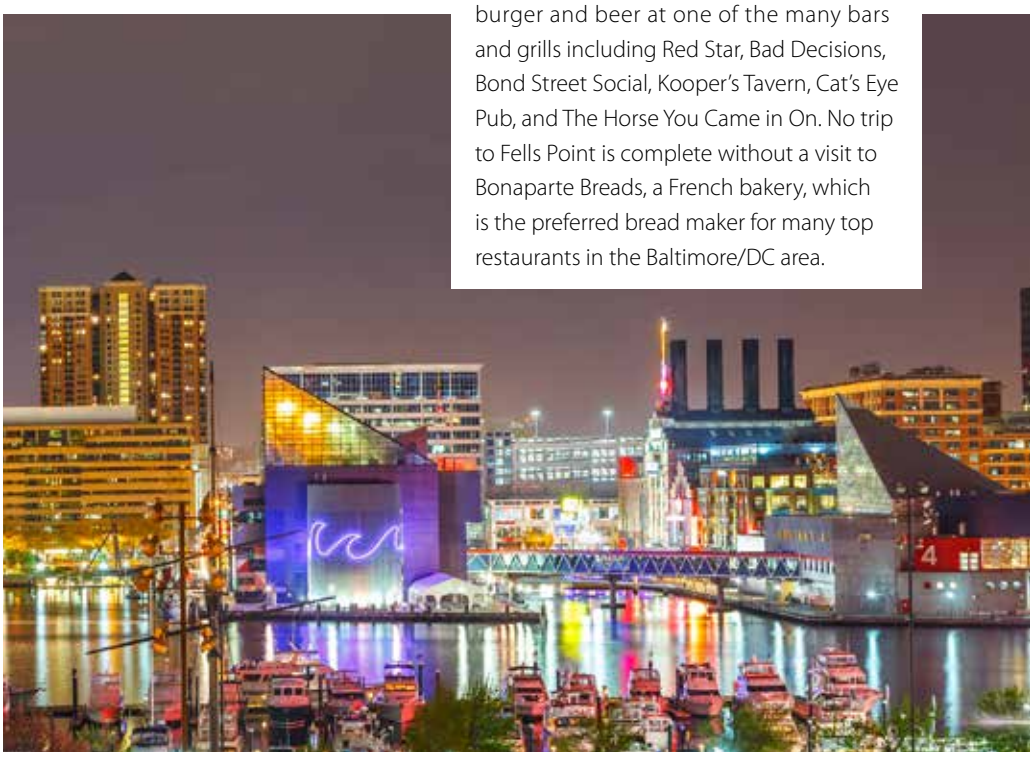
The Baltimore inner harbor is spectacular, a symbol of the dynamic remaking of the city, and the major touristic attraction of Baltimore. The waterfront provides beautiful views of the marina and easy access to many attractions including the National Aquarium, Maryland Science Center, and the American Visionary Art Museum. Not to be missed are the Fudgery, the water taxy ride to Fort McHenry, or one of the many hour-long water cruises that can be booked on the spot.

Walter's Museum

The Walter's is an internationally renowned art museum with exhibitions spanning more than 5000 years from pre-dynastic Egypt to 20th-century Europe. General admission is free, but watch for the paid special exhibitions; they are a must see.

Fells Point

Fells Point is a historic waterfront neighborhood and an absolute favorite with the locals. Walking around Fells Point marina provides excellent opportunities to dine in some of the best city restaurants including Mezze, The Black Olive, Kali's Court, the Nanami Café or enjoy an all American burger and beer at one of the many bars and grills including Red Star, Bad Decisions, Bond Street Social, Kooper's Tavern, Cat's Eye Pub, and The Horse You Came in On. No trip to Fells Point is complete without a visit to Bonaparte Breads, a French bakery, which is the preferred bread maker for many top restaurants in the Baltimore/DC area.



BALTIMORE
SO MANY THINGS TO DO!

Little Italy

This charming neighborhood is located in the heart of downtown Baltimore and within walking distance of the meeting hotel. Located between the Inner Harbor and historic Fells Point Little Italy has almost 30 restaurants, outdoor movies, bocce tournaments, and friendly narrow streets to explore.

Crabs and Crab Cakes

Picking steamed crabs spiced with Old Bay and eating crab cakes are quintessential Baltimore experiences. There are many places to enjoy an authentic Baltimore culinary experience including Captain James, Nick's Fish House, LP Steamers, Canton Dockside, Riptide by the Bay, Jimmy's Famous Seafood, and Costas Inn. Some may require planning, transportation and calling ahead to check for crab size and availability.

Restaurants

Baltimore offers an amazing assortment of restaurants with a great selection of cuisine including Afghani (The Helmand), American (Charleston, Salt Tavern, The Fleet Street Kitchen, Woodberry Kitchen, Wit & Wisdom, Blue Hill Tavern, Brewer's Art), Ethiopian (Dukem), Greek (Mezze, The Black Olive, Ouzo Bay), Italian (La Scala, Cinghiale, La Tavola), Japanese (Nanami cafe), Jewish (Goldberg's Bagels, Umami), Lebanese (The Lebanese Taverna), French (Petit Louis), Russian (Ze Mean Bean Café, Vernisage), Spanish (Tio Pepe), Turkish (Cazbar). This is just a small selection and there are many, many more restaurants to choose from.

Water Taxi

The water taxi is a wonderful way to visit the inner harbor's best attractions, restaurants, bars, and shopping. It has 17 stops including the Aquarium, Science Center, Harbor East, Fell's Point, and Fort McHenry. On a warm day this is probably the best way to enjoy crabs at Captain James Landing and learn about the history of the American national anthem by visiting Fort McHenry.

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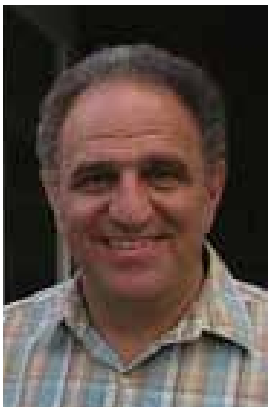
Presidential Invited Speaker



A Significance Test for the Lasso

Robert J. Tibshirani, Ph.D.
Departments of Statistics
and Health Research and Policy
Stanford University

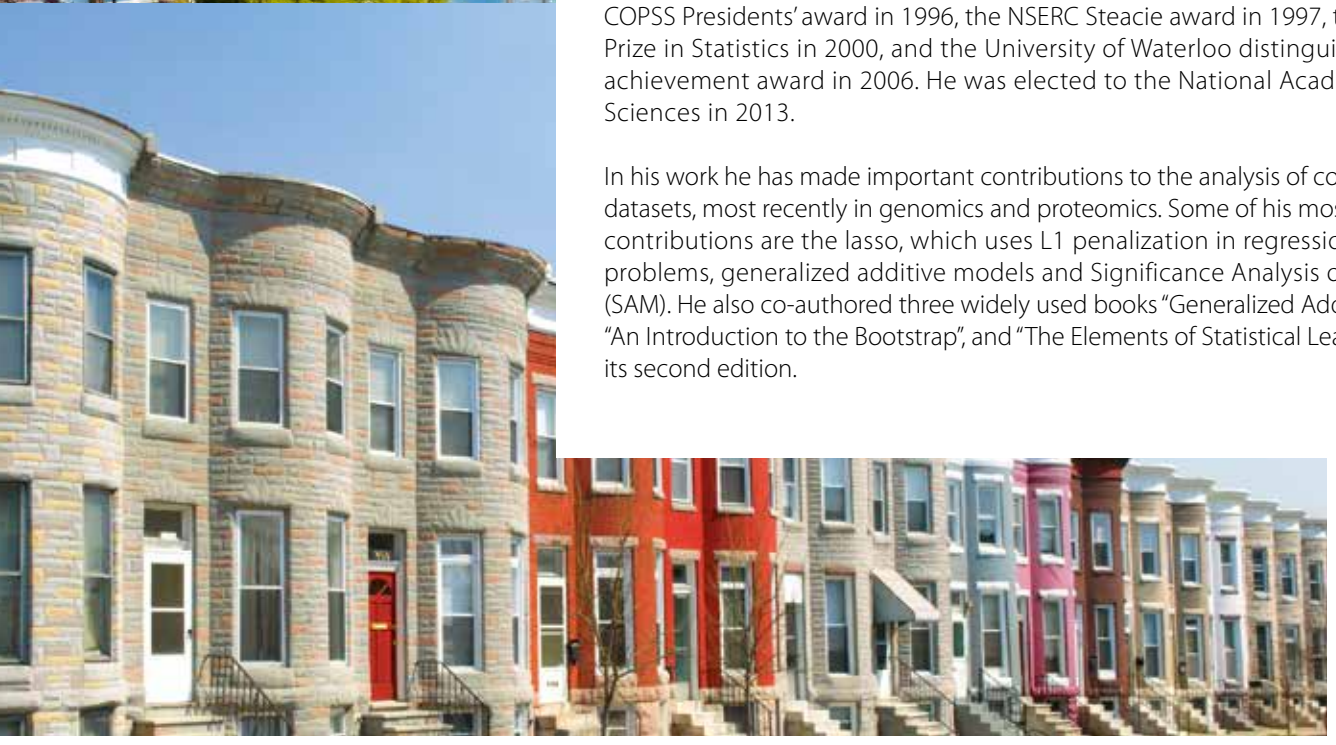
In this talk, I consider testing the significance of the terms in a fitted regression, fit via the lasso. I propose a novel test statistic for this problem, and show that it has a simple asymptotic null distribution. This work builds on the least angle regression approach for fitting the lasso, and the notion of degrees of freedom for adaptive models (Efron 1986) and for the lasso (Efron et. al 2004, Zou et al 2007). I give examples of this procedure, discuss extensions to generalized linear models and the Cox model, and describe an R language package for its computation. In addition, generalizations to a broad range of adaptive fitting such as graphical models and clustering will be outlined. This work is joint with Richard Lockhart (Simon Fraser University), Jonathan Taylor (Stanford University) and Ryan Tibshirani (Carnegie Mellon University).

Biography

Robert Tibshirani is a Professor in the Departments of Statistics and Health Research and Policy at Stanford University. He received a bachelor's degree from the University of Waterloo, a master's degree from the University of Toronto and a Ph.D. from Stanford University. He was a Professor at the University of Toronto from 1985 to 1998.

Professor Tibshirani is a Fellow of the American Statistical Association, the Institute of Mathematical Statistics and the Royal Society of Canada. He won the prestigious COPSS Presidents' award in 1996, the NSERC Steacie award in 1997, the CRM-SSC Prize in Statistics in 2000, and the University of Waterloo distinguished alumni achievement award in 2006. He was elected to the National Academy of Sciences in 2013.

In his work he has made important contributions to the analysis of complex datasets, most recently in genomics and proteomics. Some of his most well-known contributions are the lasso, which uses L1 penalization in regression and related problems, generalized additive models and Significance Analysis of Microarrays (SAM). He also co-authored three widely used books "Generalized Additive Models", "An Introduction to the Bootstrap", and "The Elements of Statistical Learning", now in its second edition.



IMS Medallion Lecture

Statistical Genetics and Genomics in the Big Data Era: Opportunities and Challenges in Research and Training

Xihong Lin, Ph.D.
Department of Biostatistics
Harvard School of Public Health

The human genome project in conjunction with the rapid advance of high throughput technology has transformed the landscape of health science research. The genetic and genomic era provides an unprecedented promise of understanding genetic underpinnings of complex diseases or traits, studying gene-environment interactions, predicting disease risk, and improving prevention and intervention, and advancing personalized medicine. A large number of genome-wide association studies conducted in the last ten years have identified over 1,000 common genetic variants that are associated with many complex diseases and traits. Massive next generation sequencing data as well as different types of 'omics data have become rapidly available in the last few years. These big genetic and genomic data present statisticians with many exciting opportunities as well as challenges in data analysis and in interpretation of results. They also call for more interdisciplinary knowledge and research, e.g., in statistics, machine learning, data curation, molecular biology, genetic epidemiology and clinical science. In this talk, I will discuss some of these challenges, such as low-level pre-processing, analysis of rare variants in next generation sequencing association studies; integrative genomics, which integrates different types of 'oimcs data; and study of gene-environment and gene-treatment interactions. I will also discuss strategies of training next generation quantitative genomic scientists at the interface of statistical genetics and genomics, computational biology and genetic epidemiology, to meet these challenges.

Biography

Xihong Lin is Professor of Biostatistics and Coordinating Director of the Program of Quantitative Genomics at the Harvard School of Public Health (HSPH). She received PhD degree from the Department of Biostatistics of the University of Washington in 1994 under the direction of Professor Norman Breslow. She was on the faculty of the Department of Biostatistics at the University of Michigan between 1994 and 2005 before she joined the HSPH in 2005. Lin received the 2002 Mortimer Spiegelman Award from the American Public Health Association, and the 2006 Presidents' Award from the Committee of the Presidents of Statistical Societies (COPSS). She is an elected fellow of the American Statistical Association, Institute of Mathematical Statistics, and International Statistical Institute. Lin was the former Chair of the COPSS (2010-2012). She is currently a member of the Committee of Applied and Theoretical Statistics of the US National Academy of Science. Lin is a recipient of the MERIT (Method to Extend Research in Time) award from the National Cancer Institute, which provides a long term support for her methodological research. She is the PI of the T32 training grant on interdisciplinary training in statistical genetics and computational biology. She has served on numerous editorial boards of statistical and genetic journals. She was the former Coordinating Editor of Biometrics, and currently the co-editor of Statistics in Biosciences, and the Associate Editor of Journal of the American Statistical Association and American Journal of Human Genetics. She was a permanent member of the NIH study section of Biostatistical Methods and Study Designs (BMRD), and has served on a large number of other study sections of NIH and NSF.

SHORT COURSES | SUNDAY, MARCH 16

SC1: Longitudinal and Incomplete Data

FULL DAY 8:00 am – 5:00 pm

Geert Molenberghs
Universiteit Hasselt and
the Katholieke Universiteit Leuven in Belgium

Geert Verbeke
KU Leuven

Overview

We first briefly present linear mixed models for continuous hierarchical data. The focus lies on the modeler's perspective and on applications. Emphasis will be on model formulation, parameter estimation, and hypothesis testing, as well as on the distinction between the random-effects (hierarchical) model and the implied marginal model.

Second, models for non-Gaussian data will be discussed, with a strong emphasis on generalized estimating equations (GEE) and the generalized linear mixed model (GLMM). To usefully introduce this theme, a brief review of the classical generalized linear modeling framework will be presented. Similarities and differences with the continuous case will be discussed. The differences between marginal models, such as GEE, and random-effects models, such as the GLMM, will be explained in detail.

Third, when analyzing hierarchical and longitudinal data, one is often confronted with missing observations, i.e., scheduled measurements have not been made, due to a variety of (known or unknown) reasons. It will be shown that, if no appropriate measures are taken, missing data can cause seriously jeopardizing results, and interpretation difficulties are bound to occur. Methods to properly analyze incomplete data, under flexible assumptions, are presented. All developments will be illustrated with worked examples using the SAS System.

The Course

- **Session 1:** Linear mixed models, model formulation, parameter interpretation, hierarchical versus marginal model interpretation, estimation and inference, empirical Bayes
- **Session 2:** Model families for discrete outcomes, marginal models, generalized estimating equations (GEE)
- **Session 3:** Generalized mixed models, estimation methods (Laplace, MQL, PQL, Quadrature), comparison with GEE
- **Session 4:** Missing data mechanisms, problems with nonrandom dropout (i.e., bias, loss of efficiency, etc.), modeling frameworks to handle dropout (selection, pattern mixture and shared parameter models), sensitivity analyses

SC2: Bayesian Methods for Data Analysis, Meta-Analysis, and Adaptive Clinical Trials

FULL DAY 8:00 am – 5:00 pm

Brad Carlin
University of Minnesota

Overview

This course will provide a review of Bayesian inference, meta-analysis, and Bayesian adaptive methods for clinical trials. To begin, the review of Bayesian methods will include prior determination, point and interval estimation, hypothesis testing, prediction, and model choice. There will also be a review of Bayesian computation, including Markov chain Monte Carlo (MCMC) methods, Gibbs sampling, and other extensions. To facilitate practical implementation of topics covered, there will be a computer demonstration of the WinBUGS software in a few standard models. After the lunch break, the course turns to the basics of Bayesian clinical trial design, including the notions of range of equivalence, community of priors, and a discussion of available software. Bayesian adaptive methods will include rule- (3+3) and model-based (CRM, EWOC) designs for finding the maximum tolerated dose (MTD), sequential stopping for futility, efficacy, and/or toxicity, and adaptive randomization and dose allocation. There will also be a discussion of network meta-analysis, as well as the closely related topic of incorporation of historical data in clinical trial design and analysis.

SC3: Statistical Computing for Big Data

FULL DAY 8:00 am – 5:00 pm

Deepak Agarwal
LinkedIn

Overview

Massive data get generated, stored and analyzed every day in various fields like bioinformatics, climatology, internet, telecommunications, and many more. Hadoop has become the most popular distributed file storage (and computing) system in the world. A challenging and growing research area concerns the development of appropriate statistical methods for analyzing such large-scale data. The objective of this short course is to provide a high level introduction to the open-source Hadoop system that uses Map-Reduce framework, and more importantly, to illustrate the use of Map-Reduce and Hadoop for real statistical applications, starting from basics like computing means and variances.

The course will then cover more advanced topics of fitting statistical models to large data via Hadoop. We will mainly focus on applications like computational advertising and content recommendation where the goal is to recommend items to users when visiting a website to maximize some positive response like clicks. This is a high dimensional bandit problem since there is positive utility in showing items that have low mean and high variance. A practical approach is to reduce the dimension through multi-level bilinear random effects model and couple it with classical bandit solutions. Numerous examples of real systems the author has deployed at big web companies like Yahoo! and LinkedIn will be used to illustrate the methods. Special focus will be on scalable model fitting of mixed effects generalized linear models fitted to datasets consisting of hundreds of millions of observations and hundreds of thousands of predictors.

SC4: Statistical Methods for Genome Wide Regional Analysis with Next Generation Sequencing Data

HALF DAY 8:00 am – 12:00 noon

Rafael Irizarry
Harvard University

Hao Wu
Emory University

Overview

Genome wide regional analysis is the task of detecting genomic regions of certain interest from whole-genome data. Examples of these regions include protein-binding sites where different proteins interact with DNA, histone modification regions, and regions exhibiting differential DNA methylation between different biological contexts. High-throughput experiments such as next-generation sequencing (NGS) enable the detection of these regions at the whole-genome scale. The data collected from these experiments are tightly spaced on the linear genome. At the regions of interest, the data show different distribution from the majority of the genome, and sometimes look like short and pointy "peaks" or broad "blocks" when plotting against the genomic coordinates. So the methods of detecting these regions have the general theme of "peak/block detection".

In this half-day short course, we will cover the statistical methods and software for peak/block detection from NGS data. We will first provide a general introduction to NGS technology and its applications. Then we will focus on two specific applications of NGS: ChIP-seq for protein binding site and histone modification region detection, and bisulfite sequencing (BS-seq) for detection of DNA methylation regions. The data from each application suffer from systematic biases

that need to be carefully accounted for in order to design sound statistical methods for analyses. We will introduce the biological motivation, technical procedures, raw data formats, characteristics of the data, and then provide an in-depth review of the statistical methods. In the computer lab, we will provide hands-on exercise of sequence mapping and statistical analysis using open source software such as R/Bioconductor.

The Course

— Introduction to NGS technologies

— Statistical methods for ChIP-seq and BS-seq data analyses

— Computer lab includes following exercises

— Sequence alignment using bowtie

— Use GenomicRanges and GenomicFeatures Bioconductor package to analyze and annotate ChIP-seq analysis results

— Use bsseq Bioconductor package to analyze BS-seq data

SC5: Statistical Evaluation of Prognostic Biomarkers

HALF DAY 8:00 am – 12:00 noon

Patrick Heagerty
University of Washington

Overview

This course will introduce predictive accuracy concepts that allow evaluation of time-dependent sensitivity and specificity for prognosis of a subsequent event time. We will overview options that are appropriate for both baseline markers and for longitudinal markers. Methods will be illustrated using examples from HIV and cancer research and we will highlight R packages that are currently available.

SC6: Joint Modeling of Longitudinal and Survival Data

HALF DAY 1:00 pm – 5:00 pm

Joseph G. Ibrahim
University of North Carolina at Chapel Hill

Overview

In this short course, we will examine in depth statistical methods for joint modeling of longitudinal and survival data. Both frequentist and Bayesian approaches will be examined. The types of joint models that will be discussed are selection models, pattern mixture models, and shared parameter models. Both linear mixed models as well as generalized linear mixed models will be discussed for the longitudinal models and Cox-type, piecewise constant hazard, as well as cure rate models will be discussed for the survival component. Both univariate and multivariate survival models will be discussed as well as multivariate longitudinal models. Several types of applications will also be discussed including ones in cancer, vaccine studies, quality of life studies, and AIDS research. Missing data issues will also be examined, and SAS and R software for fitting joint models will be illustrated in detail.

The Course

— Introduction to joint models: selection, pattern mixture and shared parameter models

— A review of the existing frequentist and Bayesian methodologies for joint modeling with applications to cancer, vaccine studies, quality of life studies, and AIDS research

— SAS and R software for fitting joint models with applications to cancer, vaccine studies, quality of life studies, and AIDS research

— Multivariate joint models of longitudinal and survival data

— Joint cure rate models

— Model assessment and diagnostics

— Clinical trials design using joint models

SC7: Bayesian Disease Mapping with INLA: An Introduction

HALF DAY 1:00 pm – 5:00 pm

Andrew Lawson
Medical University of South Carolina

Overview

This course will cover methodology and computational strategies for Bayesian disease mapping, beginning with an introduction to the Bayesian modeling paradigm and basic disease mapping concepts. The course will proceed to discuss disease mapping models with hierarchical structure and posterior sampling versus posterior approximation. For approximation methods, particular attention will be devoted to the integrated nested Laplace approximation (INLA) and its implementation with the R package INLA. Examples of fitting disease mapping models using INLA will be presented, and sample R programs will be provided to course attendees.

TUTORIALS

MONDAY, MARCH 17

T1: An Introduction to Comparative Effectiveness Research

8:30 am – 10:15 am

Sharon-Lise Normand
Harvard School of Public Health

Description

Comparative Effectiveness Research (CER) refers to a body of research that generates and synthesizes evidence on the comparative benefits and harms of alternative interventions to prevent, diagnose, treat, and monitor clinical conditions, or to improve the delivery of health care. The evidence from CER is intended to support clinical and policy decision making at both the individual and the population level. While the growth of massive health care data sources has given rise to new opportunities for CER, several statistical challenges have also emerged. This tutorial will provide an overview of the types of research questions addressed by CER, review the main statistical methodology currently utilized, and highlight areas where new methodology is required. Examples from cardiology and mental illness will illustrate substantive and methodological issues.

T2: Functional Data Analysis: Techniques and Applications

10:30 am – 12:15 pm

R. Todd Ogden and Jeff Goldsmith
Columbia University

Description

As modern technological advances allow the collection of increasingly large and complex datasets, there is urgent need for practitioners to be able to analyze and model such data. We will focus on one special type of data: functional data, which consists of all data measured over some continuum and thus can be regarded as being a function of some continuous variable. Examples include growth curves (any data collected over time), spectral data, imaging data, and so on.

This tutorial will provide an introduction to the general topic of functional data analysis targeted to the practitioner. We will describe various techniques in common use in the area (see outline below) and illustrate these with real data examples. In addition, we will provide code used to carry out the various analyses, allowing participants to quickly get up to speed in performing their own analyses of functional data.

The Tutorial

— Functional data examples and terminology

— Descriptive analysis techniques

— Smoothing techniques and basis functions

— Functional principal component analysis

— Linear regression models with functional data

— Scalar-on-function regression

— Function-on-scalar regression

— Function-on-function regression

— Brief overview of other modern advances

— Nonparametric functional data analysis

— Multilevel and longitudinal functional data

T3: Nonparametric Bayesian Data Analysis

1:45 pm – 3:30 pm

Peter Müller
University of Texas, Austin

Description

All models are wrong, but some are useful. Many statisticians know and appreciate G.E.P. Box's comment on statistical modeling. Often the choice of the final model is a compromise between an accurate representation of the experimental conditions, a preference for parsimony and the need for a practicable implementation. The competing goals are not always honestly spelled out, and the resulting uncertainties are not fully described. Over the last 20 years, a powerful inference approach that allows mitigating some of these limitations has become increasingly popular. Bayesian nonparametric (BNP) inference allows acknowledging uncertainty about an assumed sampling model while maintaining a practically feasible inference approach. We could take this feature as a pragmatic characterization of BNP as flexible prior probability models that generalize traditional models by allowing for positive prior probability for a very wide range of alternative models, while centering the prior around a parsimonious traditional model. A formal definition of BNP is as probability models on infinite dimensional parameter spaces. A typical application of BNP is to density estimation.

In this tutorial we review some of the popular models, including Dirichlet process (DP) models, Polya tree models, DP mixtures and dependent DP (DDP) models. We will review some of the general modeling principles, including species sampling models, stick breaking priors, product partition models for random partition and normalized random measures with independent increments. We will briefly discuss some of the main computational algorithms and available software. The discussion will be illustrated by applications to problems in biostatistics and bioinformatics.

T4: Quantile Regression for Survival Analysis

3:45 pm – 5:30 pm

Limin Peng
Emory University

Description

Quantile regression, as a significant extension of the traditional accelerated failure time model, has many natural appeals for survival analysis. It offers flexibility to dynamically assess the relationships between survival outcomes and covariates while retaining easy physical interpretation. Many methods developed for quantile regression with survival data also have nice computational features, which are expected to foster their biomedical applications. In this tutorial, the main questions to be addressed include: (1) what can quantile regression offer beyond standard survival analysis? (2) what are the well-developed approaches that can readily be used for analyzing survival data? (3) how to implement these methods in practice? We will conclude with some remarks on limitations and challenges in this field.

TUTORIALS

TUESDAY, MARCH 18

T5: An Introduction to High-Performance Computing with R

8:30 am – 10:15 am

John Emerson
Yale University

Description

This tutorial will introduce you to topics in high-performance computing with R. We will quickly explore the new parallel package (containing snow and multicore). We will then concentrate on the elegant framework for parallel programming offered by packages foreach and the associated parallel backends. We will touch upon a range of related topics including memory management and algorithmic efficiency. Time permitting, we will conclude with basic examples of handling larger-than-RAM numeric matrices and use of shared memory.

T6: Causal Mediation Analysis

1:45 pm – 3:30 pm

Tyler VanderWeele
Harvard School of Public Health

Description

This tutorial will cover some of the recent developments in causal mediation analysis and provide practical tools to implement these techniques. Mediation analysis concerns assessing the mechanisms and pathways by which causal effects operate. The lecture will cover the relationship between traditional methods for mediation in epidemiology and the social sciences and those that have been developing within the causal inference literature using natural direct and indirect effects. Methods for dichotomous, continuous, and time-to-event outcomes will be described. Special attention will be given to the strong assumptions about confounding that must be made to identify direct and indirect effects. The tutorial will discuss the use and implementation of sensitivity analysis techniques to assess how sensitive conclusions are to violations of confounding assumptions. Discussion will be given to how such mediation analysis approaches can be extended to settings in which data come from a case-control study design. The methods will be illustrated by various applications to perinatal, genetic and social epidemiology.

T7: Cure Models and Their Applications

3:45 pm – 5:30 pm

Jeremy M. G. Taylor
University of Michigan

Paul Y. Peng
Queen's University

Description

Cure models refer to a class of extended survival models for survival data with a cure fraction. The standard survival models often assume that subjects in a study will experience the event of interest with sufficient follow-up without censoring. However, this assumption may not be appropriate in situations such as cancer studies where patients may be cured and will not experience relapse, however long the follow-up, and cure models must be considered to analyze survival data in such studies. Cure models also find applications in other disciplines, such as epidemiology, psychology, public health and economics. The last 15 years witnessed a rapid growth in extending survival models to accommodate potentially cured subjects. New statistical methodologies were developed to extend the existing survival models, and the newly proposed cure models greatly expand the applicability of cure models to various types of survival data with a cured fraction and provide appealing ways to interpret the results of analysis, compared to standard survival analysis models. The tutorial will cover the mixture model and bounded cumulative hazard formulation of cure models, estimation methods, identifiability issues, software and extensions to clustered data. The instructors will introduce some real life data sets from clinical studies, present necessary details of the cure models and recent advances, and demonstrate the use of the cure models on the data with software.

ROUNDTABLES

MONDAY, MARCH 17 | 12:15 PM – 1:30 PM

R1: Writing a Successful Grant in a Challenging Funding Climate: Strategies for Statistical and Other Scientific Review Panels

Amita Manatunga
Emory University

Description
I will focus on strategies for writing a successful NIH grant application to support statistical methodological research. I will begin with an outline of the grant submission and review processes and descriptions of popular NIH grant mechanisms, namely R01, R03 and R21 grants. I will describe characteristics of high-quality grant applications including the formulation of specific aims and preliminary data with the emphasis on significance and innovation. Other discussions will include strategies for submitting methodological grants to other Study Sections besides to the Biostatistical Methods and Research Design (BMRD) study section.

R2: Key Elements of a Successful Career as a Tenure Track Faculty Member

Francesca Dominici
Harvard School of Public Health

Description
We will have an informal discussion regarding challenges and opportunities for junior tenure track faculty in quantitative departments. We will discuss topics related to: balancing papers and grant submissions, management of interdisciplinary collaborations, teaching, negotiation skills, work family balance etc.

R3: Statistics and the Law: Statisticians as Expert Witnesses

Bruce Levin
Columbia University

Description
How is statistical evidence presented and used in legal proceedings, especially from the perspective of an expert witness? Statistical evidence plays an important role in legal proceedings such as toxic tort cases, class actions in the areas of equal employment opportunity and equal opportunity in housing, voting rights cases, patent disputes, challenged elections, adverse events in drug trials, calculation of damages resulting from theft, collusion, health insurance fraud, and other audits involving sampling, and many more, in settings ranging from jury trials, bench trials, administrative hearings, arbitration hearings, depositions, and the lawyer's office. In addition, studies of the legal system itself are proliferating and are increasingly statistical in nature, with entire journals devoted to the subject. We will discuss the following topics (as time permits): communicating statistical concepts and findings clearly and effectively, in both verbal testimony and written reports; do's and don't's of being an expert witness; how lawyers make effective use of experts; what experts should expect in and out of the courtroom; the adversarial paradigm versus the academic research paradigm; and relevant ethical issues. The discussion leader has over 35 years of experience working with lawyers in litigation support, publishing scholarly legal articles with attorneys, and testifying as an expert statistical witness in legal proceedings. He is co-author with lawyer Michael O. Finkelstein of the textbook Statistics for Lawyers (2nd edition, Springer, 2001), the third edition of which is forthcoming.

R4: Research Opportunities at the US Census Bureau

Thomas A. Louis
Johns Hopkins and U.S. Census Bureau

Description
In order to meet the challenges of efficiently obtaining valid demographic, economic, and activity-based information, making it available to the public while protecting confidentiality, research at the U.S. Census Bureau and other federal statistical agencies, indeed survey research more generally, burgeons. At the roundtable I'll briefly describe the Research & Methodology directorate, list major research goals with related statistical and computational issues and methods. Many are similar to those addressed by and used in Biostatistics and Informatics, and we can consider a subset. We'll close with a discussion of career opportunities. Visit (http://www.census.gov/research/) for some background.

R5: The Leadership Role of a Statistician on Interdisciplinary Research Teams

Scarlett Bellamy
University of Pennsylvania

Description
Informal discussion will primarily focus on identifying leadership opportunities and roles in the context of interdisciplinary research teams. These may be research based (e.g., statistical leadership for an analytical core for a large Center) or training-focused (e.g., serving as PI for an institutional training grant). We will also discuss key elements for successful leadership as well as identify strategies for being invited to take on such roles.

R6: The Role of Statisticians at the FDA

Dionne L. Price
Food and Drug Administration

Description
The Food and Drug Administration (FDA) is composed of seven centers which collectively employ over 250 statisticians. Statisticians at the FDA are an integral part of multidisciplinary teams dedicated to assuring the safety and efficacy of human and veterinary drugs, biological products, medical devices, our nation's food supply, cosmetics, and products that emit radiation. Statisticians analyze and evaluate data, provide leadership, promote innovation in study designs and statistical techniques, and conduct methodological research aimed at addressing the many complex issues that arise in a regulatory environment. FDA statisticians utilize their statistical training and knowledge to directly impact the public health. Roundtable participants will learn the role of statisticians at the FDA and potential paths to successful careers with the Agency.

R7: Publishing Without Perishing: Strategies for Success in Publishing in (Bio)statistical Journals

Marie Davidian
North Carolina State University

Description
Contributing to the advance of our discipline through publication of articles in peer-reviewed journals is a fundamental expectation for both junior and not-so-junior biostatistical researchers alike. Success in publishing one's work ensures that it will be widely disseminated to researchers and practitioners who stand to benefit. In addition, funding agencies and academic institutions place considerable importance on a successful record of publication. Accordingly, understanding the peer review and editorial processes of top journals and mastering the art of writing an effective journal article are keys to success in publishing. How does one determine the best outlet for one's work? What are the essential elements of a successful journal article? How does one maximize the chance of acceptance? What strategies can ensure that a published paper is read and cited? How does one make optimal use of limited space and additional supplementary material in conveying the message? What are the roles of the editor, associate editor, and referees? What considerations do editors use when evaluating a paper? This roundtable will provide a forum for candid discussion of these and other questions.

R8: Preparing for Leadership Opportunities in the Pharmaceutical Industry

Aarti Shah
Eli Lilly and Company

Description

Tom Davenport in his book Competing on Analytics writes "The companies that are winning are those which are deriving business benefits through deep and sophisticated analytics." Who will lead companies to translate the sophisticated analytics to business benefits? Is it the statistician? If yes, what leadership skills does a statistician need in addition to his or her deep technical knowledge? In this session, we will discuss leadership skills that are absolutely necessary for today's statistician to be successful and how one goes about developing these skills. We will explore the topic of "Statistical Leadership".

R9: Preparing for Leadership in Statistics

Michael Kosorok
University of North Carolina at Chapel Hill

Description

We will discuss how statisticians can prepare for leadership roles during the course of their career. This will include a review of fundamental leadership skills applicable to both small and large groups, as well as specialized leadership skills needed to lead academic departments and other similar organizations. We will explore the benefits of delegation, empowering others, and maintaining flexibility and balance. We will also discuss ways to help students prepare for future leadership roles and the pros and cons of accepting leadership positions.

ENAR 2014
SPRING MEETING

PROGRAM SUMMARY

Saturday, March 15

3:30 pm – 5:30 pm	Conference Registration	Grand Ballroom Registration (3rd Floor)

Sunday, March 16

7:30 am – 6:30 pm	Conference Registration	Grand Ballroom Registration (3rd Floor)
8:00 am – 12:00 pm	**SHORT COURSES**	
	SC4: Statistical Methods for Genome Wide Regional Analysis with Next Generation Sequencing Data	Grand Ballroom VIII (3rd Floor)
	SC5: Statistical Evaluation of Prognostic Biomarkers	Grand Ballroom X (3rd Floor)
8:00 am – 5:00 pm	**SHORT COURSES**	
	SC1: Longitudinal and Incomplete Data	Grand Ballroom III (3rd Floor)
	SC2: Bayesian Methods for Data Analysis, Meta-Analysis and Adaptive Clinical Trials	Grand Ballroom IV (3rd Floor)
	SC3: Statistical Computing for Big Data	Grand Ballroom I (3rd Floor)
12:30 pm – 5:30 pm	**DIVERSITY WORKSHOP**	Essex Room (4th Floor)
1:00 pm – 5:00 pm	**SHORT COURSES**	
	SC6: Joint Modeling of Longitudinal and Survival Data	Grand Ballroom X (3rd Floor)
	SC7: Bayesian Disease Mapping with INLA: An Introduction	Grand Ballroom VIII (3rd Floor)

Sunday, March 16 *(continued)*

3:00 pm – 6:00 pm	Exhibits Open	Grand Ballroom Foyer (3rd Floor)
4:00 pm – 6:30 pm	**PLACEMENT SERVICE**	Waterview Rooms ABC (Lobby Level)
4:30 pm – 7:00 pm	**ENAR EXECUTIVE COMMITTEE** (by Invitation Only)	Waterview D (Lobby Level)
7:30 pm – 8:00 pm	**NEW MEMBER RECEPTION**	Grand Ballroom (3rd Floor)
8:00 pm – 11:00 pm	**SOCIAL MIXER AND POSTER SESSION**	Grand Ballroom (3rd Floor)

1.
Posters: Invited Poster Session

2.
Posters: Clinical Trials and Study Design

3.
Posters: Bayesian Methods

4.
Posters: Statistical Genetics and Genomics

5.
Posters: Prediction, Prognostics, Diagnostic Testing

6.
Posters: Survival Analysis

7.
Posters: Imaging, High Dimensional Data, Biomarkers, and Microarray

8.
Posters: Environmental and Longitudinal Data Analysis

9.
Posters: Epidemiology and Causal Inference

10.
Posters: Non Parametric and Non Linear Methods

11.
Posters: Variable Selection, Machine Learning and Other

Monday, March 17

7:30 am – 5:00 pm	Conference Registration	Grand Ballroom (3rd Floor)
7:30 am – 5:00 pm	Speaker Ready Room	Boardroom (3rd Floor)
8:30 am – 5:30 pm	Exhibits Open	Grand Ballroom Foyer (3rd Floor)
8:30 am – 10:15 am	**TUTORIAL**	
	T1: An Introduction to Comparative Effectiveness Research	Harborside A (4th Floor)
	SCIENTIFIC PROGRAM	
	12. Massive Online Open Statistics (MOOS): Should we be Teaching Statistics to 100,000s of Thousands at a Time?	Grand Ballroom I (3rd Floor)
	13. Council for Emerging and New Statisticians (CENS) Invited Session: Should I do a PostDoc?	Grand Ballroom V (3rd Floor)
	14. Adaptive Randomized Trial Designs and Improved Analysis Methods to Learn which Subpopulations Benefit from which Treatments	Grand Ballroom II (3rd Floor)
	15. Statistical Methods for Complex Structured Biomedical Object Data	Grand Ballroom VI (3rd Floor)
	16. Multivariate Analysis in High Dimensions	Grand Ballroom III (3rd Floor)
	17. Recent Advances in Lifetime Data Analysis	Grand Ballroom IV (3rd Floor)
	18. Contributed Papers: Epidemiologic Methods	Atlantic Room (3rd Floor)
	19. Contributed Papers: Computational Methods and Implementation	Bristol Room (3rd Floor)
	20. Contributed Papers: Non-parametric and Semiparametric Methods in Functional Data Analysis	Grand Ballroom X (3rd Floor)
	21. Contributed Papers: Statistical Methods for Microarray and Biomarker Data	Grand Ballroom VII (3rd Floor)

Monday, March 17 *(continued)*

	22. **Contributed Papers: Machine Learning**	Grand Ballroom IX (3rd Floor)
	23. **Contributed Papers: Multiple Testing**	Chasseur Room (3rd Floor)
	24. **Contributed Papers: Methods for Statistical Genetics**	Grand Ballroom VIII (3rd Floor)
9:30 am – 4:30 pm	**PLACEMENT SERVICE**	Waterview Rooms (Lobby Level)
10:15 am – 10:30 am	Refreshment Break with Our Exhibitors	Grand Ballroom Foyer (3rd Floor)
10:30 am – 12:15 pm	**TUTORIAL**	
	T2: Functional Data Analysis: Techniques and Applications	Harborside A (4th Floor)
	SCIENTIFIC PROGRAM	
	25. **Statistical Innovations for Studying the Human Brain Function**	Grand Ballroom II (3rd Floor)
	26. **Meta-analysis of Gene-environment Interaction in the Post-GWAS Era**	Grand Ballroom VI (3rd Floor)
	27. **Statistics Methods for High-Throughput Genomics**	Grand Ballroom V (3rd Floor)
	28. **Personalized Medicine: Better Treatment for the Patient or the Right Patient for the Treatment?**	Grand Ballroom VIII (3rd Floor)
	29. **Recent Advances in Statistical Methods for Meta-Analysis**	Grand Ballroom III (3rd Floor)
	30. **Subgroup Analysis and Personalized Prediction**	Grand Ballroom IX (3rd Floor)
	31. **Latent Variable Modeling for Multiple Outcomes and Growth Models in Psychiatric Studies**	Grand Ballroom VII (3rd Floor)
	32. **Contributed Papers: Bayesian Analysis of High Dimensional Data**	Grand Ballroom I (3rd Floor)
	33. **Contributed Papers: Genetics and Epidemiologic Study Design**	Grand Ballroom IV (3rd Floor)
	34. **Contributed Papers: Non-linear Models**	Grand Ballroom X (3rd Floor)

Monday, March 17 *(continued)*

	35. **Contributed Papers: Survival Analysis for Clinical Trial Data**	Atlantic Room (3rd Floor)
	36. **Contributed Papers: Clustered Data Methods**	Bristol Room (3rd Floor)
	37. **Contributed Papers: Statistical Methods for Longitudinal Data**	Chasseur Room (3rd Floor)
12:15 pm – 1:30 pm	**ROUNDTABLE LUNCHEONS**	Dover Rooms (3rd Floor)
12:30 pm – 4:30 pm	**REGIONAL ADVISORY BOARD (RAB) LUNCHEON MEETING** (by Invitation Only)	Falkland Room (4th Floor)
1:45 pm – 3:30 pm	**TUTORIAL**	
	T3: **Nonparametric Bayesian Data Analysis**	Harborside A (4th Floor)
	SCIENTIFIC PROGRAM	
	38. **Recent Developments in Estimating the Health Effects of Air Pollution and Regulation**	Grand Ballroom VIII (3rd Floor)
	39. **Recent Advances in Casual Reference**	Grand Ballroom III (3rd Floor)
	40. **Social Network Data: Challenges and Opportunities**	Grand Ballroom II (3rd Floor)
	41. **Statistics and Computing for High-throughput Sequencing Data**	Grand Ballroom V (3rd Floor)
	42. **Variable Selection and Analysis of High Dimensional Data**	Grand Ballroom I (3rd Floor)
	43. **Functional Data Analysis and its Applications in Genetics**	Grand Ballroom VI (3rd Floor)
	44. **Emerging Statistical Challenges with Complex Longitudinal or Functional Data**	Grand Ballroom IX (3rd Floor)
	45. **Contributed Papers: Genome Wide Association Studies**	Grand Ballroom IV (3rd Floor)

Monday, March 17 *(continued)*

	46. **Contributed Papers: Applications of Bayesian Methods**	Atlantic Room (3rd Floor)
	47. **Contributed Papers: High Dimensional Data**	Grand Ballroom VII (3rd Floor)
	48. **Contributed Papers: Clinical Trials**	Bristol Room (3rd Floor)
	49. **Contributed Papers: Personalized Medicine and Variable Subset Selection**	Grand Ballroom X (3rd Floor)
	50. **Contributed Papers: Analysis of Clustered Data**	Chasseur Room (3rd Floor)
3:30 pm – 3:45 pm	Refreshment Break with Our Exhibitors	Grand Ballroom Foyer (3rd Floor)
3:45 pm – 5:30 pm	**TUTORIAL**	
	T4: **Quantile Regression for Survival Analysis**	Harborside A (4th Floor)
	SCIENTIFIC PROGRAM	
	51. **The Role of Statistics in Shaping Public Policy**	Grand Ballroom II (3rd Floor)
	52. **Having it all: Weighting to Achieve Balance**	Grand Ballroom V (3rd Floor)
	53. **Biostatistical Methods for Integrative Genomics**	Grand Ballroom VI (3rd Floor)
	54. **Safety Surveillance Monitoring through Signal Detection**	Grand Ballroom I (3rd Floor)
	55. **Multiple Testing and Simultaneous Inferences in Complex Settings**	Grand Ballroom III (3rd Floor)

Monday, March 17 *(continued)*

	56. **New Developments in Bayesian Nonparametrics**	Grand Ballroom IX (3rd Floor)
	57. **Contributed Papers: Statistical Genetics and Genomics**	Grand Ballroom VIII (3rd Floor)
	58. **Contributed Papers: Imaging**	Grand Ballroom IV (3rd Floor)
	59. **Contributed Papers: Semi-Parametric and Non-Parametric Models in Survival Analysis**	Grand Ballroom VII (3rd Floor)
	60. **Contributed Papers: Hierarchical Models**	Atlantic Room (3rd Floor)
	61. **Contributed Papers: Methods for Removing Selection Bias and Confounding**	Grand Ballroom X (3rd Floor)
	62. **Contributed Papers: Functional Data Analysis**	Bristol Room (3rd Floor)
	63. **Contributed Papers: Recent Advances in Bayesian Methods**	Chasseur Room (3rd Floor)
5:30 pm – 6:30 pm	**CENS STUDENT MIXER**	Dover Room (3rd Floor)
6:00 pm – 7:30 pm	**PRESIDENT'S RECEPTION** (by Invitation Only)	Laurel Room A (4th Floor)

Tuesday, March 18

7:30 am – 5:00 pm	Conference Registration	Grand Ballroom (3rd Floor)
7:30 am – 5:00 pm	Speaker Ready Room	Boardroom (3rd Floor)
9:30 am – 3:30 pm	**PLACEMENT SERVICE**	Waterview Rooms (Lobby Level)
8:30 am – 5:30 pm	Exhibits Open	Grand Ballroom Foyer (3rd Floor)
8:30 am – 10:15 am	**TUTORIAL**	
	T5: **An Introduction to High-Performance Computing with R**	Dover Room (3rd Floor)
	SCIENTIFIC PROGRAM	
	64. **Statistical Learning for Complex Multivariate Biomedical Data**	Grand Ballroom VIII (3rd Floor)
	65. **Statistical Challenges in Studies of Environmental, Reproductive and Perinatal Health**	Harborside Room A (4th Floor)
	66. **New Developments in Statistical Methodologies for the Analysis of Disease Data**	Grand Ballroom II (3rd Floor)
	67. **Recent Development and Application of Bayesian Methods for the Probability of Success and Decision Making in Clinical Trials**	Harborside Room B (4th Floor)
	68. **Functional Data Analysis: Show Me the Data**	Grand Ballroom III (3rd Floor)
	69. **Latent Class Models for Diagnostic Testing with Applications in Psychiatry**	Grand Ballroom IV (3rd Floor)
	70. **Statistical Methods for Biomarker Evaluation**	Grand Ballroom I (3rd Floor)
	71. **Contributed Papers: Semi-Parametric and Non-Parametric Models**	Grand Ballroom X (3rd Floor)
	72. **Contributed Papers: Joint Models for Longitudinal and Survival Data**	Bristol Room (3rd Floor)
	73. **Contributed Papers: Statistical Methods in Epidemiology**	Grand Ballroom VII (3rd Floor)

Tuesday, March 18 *(continued)*

	74. **Contributed Papers: Adaptive Designs and Randomization**	Atlantic Room (3rd Floor)
	75. **Contributed Papers: Next Generation Sequencing**	Grand Ballroom IX (3rd Floor)
	76. **Contributed Papers: Statistical Methods for Survival Analysis**	Chasseur Room (3rd Floor)
10:15 am – 10:30 am	Refreshment Break with Our Exhibitors	Grand Ballroom Foyer (3rd Floor)
10:30 am – 12:15 pm	**77. PRESIDENTIAL INVITED ADDRESS**	Grand Ballrooms V and VI (3rd Floor)
12:30 pm – 4:30 pm	**REGIONAL COMMITTEE MEETING** (by Invitation Only)	James Room (4th Floor)
1:45 pm – 3:30 pm	**TUTORIAL**	
	T6: **Causal Mediation Analysis**	Dover Room (3rd Floor)
	SCIENTIFIC PROGRAM	
	78. **JABES Invited Session**	Grand Ballroom VIII (3rd Floor)
	79. **Recent Advances in Statistical Methods for Missing Data**	Grand Ballroom III (3rd Floor)
	80. **Big Data Methods in Biostatistics**	Grand Ballroom II (3rd Floor)
	81. **Statistical Prediction Models for Medical Decision Making**	Grand Ballroom IV (3rd Floor)
	82. **Recent Developments in Statistical Genetics, Genomics, and their Applications**	Grand Ballroom V (3rd Floor)
	83. **Improved Statistical Modeling and Understanding of Gene Expression and Transcription Regulation using Next Generation Sequencing and Other High Throughput Technologies**	Grand Ballroom VI (3rd Floor)
	84. **Statistical Challenges in Public Health Research at the CDC**	Grand Ballroom VII (3rd Floor)

Tuesday, March 18 *(continued)*

	85. **Innovative Bayesian Nonparametrics in Biostatistics**	Grand Ballroom I (3rd Floor)
	86. **Contributed Papers: New Developments in Survival Analysis**	Grand Ballroom X (3rd Floor)
	87. **Contributed Papers: Causal Inference**	Atlantic Room (3rd Floor)
	88. **Contributed Papers: Non-Parametric Analysis of Biomedical Data**	Bristol Room (3rd Floor)
	89. **Contributed Papers: High Dimensional Imaging Data**	Grand Ballroom IX (3rd Floor)
	90. **Contributed Papers: New Methods in Genomics**	Chasseur Room (3rd Floor)
3:30 pm – 3:45 pm	Refreshment Break with Our Exhibitors	Grand Ballroom Foyer (3rd Floor)
3:45 pm – 5:30 pm	**TUTORIAL**	
	T7: **Cure Models and Their Applications**	Dover Room (3rd Floor)
	SCIENTIFIC PROGRAM	
	91. **IMS Medallion Lecture**	Grand Ballroom VI (3rd Floor)
	92. **Parametric Or Nonparametric, Which Is The Answer?**	Grand Ballroom VII (3rd Floor)
	93. **Causal Inference in High Dimensional Settings**	Grand Ballroom II (3rd Floor)
	94. **Advances in Time Series Analysis of Biomedical Signals**	Grand Ballroom III (3rd Floor)
	95. **Frontiers in Statistical Genetics for Complex Trait Association**	Grand Ballroom V (3rd Floor)
	96. **Functional Data Approaches to Neurological and Mental Disease**	Harborside Room A (4th Floor)

Tuesday, March 18 *(continued)*

	97. **Modeling Neurological Diseases With Imaging Data**	Harborside Room B (4th Floor)
	98. **Making Sense of Sensors: Statistical Methods for Wearable Computing**	Grand Ballroom I (3rd Floor)
	99. **Contributed Papers: Survival Analysis**	Grand Ballroom IV (3rd Floor)
	100. **Contributed Papers: Personalized Medicine**	Grand Ballroom VIII (3rd Floor)
	101. **Contributed Papers: Spatial Temporal Models**	Grand Ballroom IX (3rd Floor)
	102. **Contributed Papers: Statistical Methods in Cancer Applications**	Grand Ballroom X (3rd Floor)
	103. **Contributed Papers: Diagnostic and Screening Tests**	Atlantic Room (3rd Floor)
	104. **Contributed Papers: Statistical Methods for Biomarker Discovery**	Bristol Room (3rd Floor)
5:30 pm – 6:30 pm	**ENAR BUSINESS MEETING** (Open to All ENAR Members)	Bristol Room (3rd Floor)
6:30 pm – 10:00 pm	**Tuesday Night Event at the Baltimore Aquarium** (We will walk as a group to the aquarium)	**Please meet PROMPTLY at 6:15 pm in the hotel lobby**

Wednesday, March 19

7:30 am – 12:00 pm	Speaker Ready Room	Boardroom (3rd Floor)
7:30 am – 9:00 am	**PLANNING COMMITTEE MEETING** (by Invitation Only)	James Room (4th Floor)
8:00 am – 12:30 pm	Conference Registration	Grand Ballroom Registration (3rd Floor)
8:00 am – 12:00 pm	Exhibits Open	Grand Ballroom Foyer (3rd Floor)
8:30 am – 10:15 am	**SCIENTIFIC PROGRAM**	
	105. Modern Survival Analysis in Observational Studies	Grand Ballroom IX (3rd Floor)
	106. Recent Development on Personalized Medicine	Grand Ballroom II (3rd Floor)
	107. Causal Inference in the Assessment of Surrogate Markers	Grand Ballroom III (3rd Floor)
	108. New Developments in Multiple Comparisons Procedures and Variable Selection	Grand Ballroom VIII (3rd Floor)
	109. Spatial Models and Dynamics Applied to Environmental Sciences and Public Health	Grand Ballroom V (3rd Floor)
	110. Advances in Longitudinal studies for Predicting Clinical Outcomes	Grand Ballroom VI (3rd Floor)
	111. Contributed Papers: New Developments in Education, Consulting, and Health Policy	Atlantic Room (3rd Floor)
	112. Contributed Papers: Latest Advances in Functional and Imaging Data Analysis	Grand Ballroom I (3rd Floor)
	113. Contributed Papers: Bayesian Methods	Grand Ballroom IV (3rd Floor)
	114. Contributed Papers: Multivariate Survival Analysis	Grand Ballroom VII (3rd Floor)
	115. Contributed Papers: Statistical Analysis in the Presence of Missing Data	Grand Ballroom X (3rd Floor)
	116. Contributed Papers: Tools for Longitudinal Data Analysis	Bristol Room (3rd Floor)
	117. Contributed Papers: Analysis of Data from Clinical Trials	Chasseur Room (3rd Floor)

Wednesday, March 19 *(continued)*

10:15 am – 10:30 am	Refreshment Break with Our Exhibitors	Grand Ballroom Foyer (3rd Floor)
10:30 am – 12:15 pm	**SCIENTIFIC PROGRAM**	
	118. **Human Health and Environmental Statistics at the U.S. EPA's Office of Research and Development**	Grand Ballroom V (3rd Floor)
	119. **Power Analysis for Mixed Models: Where We Stand**	Grand Ballroom III (3rd Floor)
	120. **New Developments in Estimating Causal Effects of Time-varying Treatments**	Grand Ballroom II (3rd Floor)
	121. **Inside the Biostatistical Collaborative Process**	Grand Ballroom VI (3rd Floor)
	122. **Contributed Papers: Non-Parametric Methods**	Atlantic Room (3rd Floor)
	123. **Contributed Papers: Variable Subset Selection**	Chasseur Room (3rd Floor)
	124. **Contributed Papers: High Dimensional Data in Genetics and Genomics**	Grand Ballroom VIII (3rd Floor)
	125. **Contributed Papers: Tools for Survival Analysis**	Grand Ballroom IV (3rd Floor)
	126. **Contributed Papers: Meta-Analysis**	Grand Ballroom I (3rd Floor)
	127. **Contributed Papers: Statistical Methods for Handling Missing Data**	Grand Ballroom X (3rd Floor)
	128. **Contributed Papers: Longitudinal Data Analysis**	Bristol Room (3rd Floor)
	129. **Contributed Papers: Prediction and Prognostic Modeling**	Grand Ballroom VII (3rd Floor)
	130. **Contributed Papers: New Methods for GWAS**	Grand Ballroom IX (3rd Floor)

✱ = Presenter | ■ = Student Award Winner

SCIENTIFIC PROGRAM

Sunday, March 16

8:00 – 11:00 pm

POSTER PRESENTATIONS

Grand Ballroom (3rd Floor)

1. INVITED POSTER SESSION

Sponsor: ENAR

1A. SuBLIME and OASIS for Multiple Sclerosis Lesion Segmentation in Structural MRI
Elizabeth M. Sweeney*, Johns Hopkins Bloomberg School of Public Health
Russell T. Shinohara, University of Pennsylvania
Ciprian M. Crainiceanu, Johns Hopkins Bloomberg School of Public Health

1B. Elastic Statistical Shape Analysis of 3D Objects using Square Root Normal Fields
Sebastian Kurtek*, The Ohio State University

1C. Epidemiological Models for Browser-Based Malware
Natallia Katenka*, University of Rhode Island
Eric Kolaczyk and **Mark Crovella**, Boston University
Tom Britton, Stockholm University

1D. Meta-analysis of Rare Variants Based on Single-variant Statistics
Yijuan Hu*, Emory University
Sonja I. Berndt, National Cancer Institute, National Institutes of Health
Stefan Gustafsson and **Andrea Ganna**, Uppsala University Hospital
Joel Hirschhorn, Boston Children's Hospital
Kari E. North, University of North Carolina, Chapel Hill
Erik Ingelsson, Uppsala University Hospital
Danyu Lin, University of North Carolina, Chapel Hill

1E. Spatial Quantile Regression for Neuroimaging Data
Linglong Kong*, University of Alberta
Hongtu Zhu, University of North Carolina, Chapel Hill

1F. Enhancements for Model-b[illegible]lustering of Array-based DNA Meth[illegible]ta
CANCELLED
Devin C. Koestler*, [illegible] Kansas Medical Center
Andres Housen[illegible] [illegible] State University
Carmen J. [illegible]rock C. Christensen, Dartmouth College

1G. Disease Surveillance using Dynamic Screening System
Peihua Qiu*, University of Florida

1H. Heat Kernel Wavelets on Manifolds and its Application to Brain Imaging
Moo K. Chung*, University of Wisconsin, Madison

1I. Data Visualizations Should be More Interactive
Karl W. Broman*, University of Wisconsin, Madison

1J. Introducing the Evolving Evolutionary Spectrum, with Applications to a Learning Association Study
Mark Fiecas*, University of Warwick

1K. Improving Rare Variant Association Test with Prior Information
Xin He* and **Li Liu**, Carnegie Mellon University
Bernie Devlin, University of Pittsburgh School of Medicine
Kathryn Roeder, Carnegie Mellon University

✱ = Presenter | ■ = Student Award Winner

2. POSTERS: CLINICAL TRIALS AND STUDY DESIGN

Sponsor: ENAR

2A. A New Statistical Test of Heterogeneity in Treatment Response
Hongbo Lin* and **Changyu Shen**, Indiana University, Indianapolis

2B. Comparing Methods of Tuning Adaptively Randomized Trials
John Cook, Yining Du* and **Jack Lee,** University of Texas MD Anderson Cancer Center

2C. Multi-regional Issues in Equivalence Assessment of Test and References
Yi Tsong*, U.S. Food and Drug Administration

2D. Statistical Methods for Analyzing Count Data — A Case Study on Adverse Event Data from Vaccine Trials
Qin Jiang*, Pfizer Inc.

2E. An Alternate Study Design Approach for Multilevel Counts Subject to Overdispersion, with Illustrations Reflective of a Motivating Cluster-randomized Community Trial
Kenneth J. Wilkins*, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health and Uniformed Services University of the Health Sciences
Shweta Padmanaban, Georgetown University
Stephanie M. Rodriguez, Uniformed Services University of the Health Sciences

2 F. Leveraging Baseline Variables to Improve Estimators of the Average Treatment Effect in Randomized Trials
Elizabeth A. Colantuoni* and **Michael Rosenblum**, Johns Hopkins Bloomberg School of Public Health

2G. Identifying Comparable Populations using Entropy Matching: The Comparison of Drug Effectiveness between Clinical Trials and EMRs
Haoda Fu, Eli Lilly and Company
Jin Zhou*, University of Arizona

2H. Re-estimating Sample Size in a Randomized Clinical Trial using Participant Compliance Data
Peter D. Merrill* and **Leslie A. McClure**, University of Alabama, Birmingham

2I. Variable Group Sizes in Cluster Randomized Trials Reduces Power
Stephen A. Lauer* and **Nicholas G. Reich**, University of Massachusetts, Amherst
Ken P. Kleinman, Harvard Medical School and Harvard Pilgrim Health Care Institute

2J. CoGaussian Statistical Model for Right Skewed Data
Govind Mudholkar and **Ziji Yu***, University of Rochester
Saria Awadalla, University of Illinois, Chicago

2K. Use of Historical Data in Clinical Trials
Kert Viele*, Berry Consultants

3. POSTERS: BAYESIAN METHODS

Sponsor: ENAR

3A. A Bayesian Approach to ROC Curve Estimation using Conditional Means Priors
Jack S. Knorr* and **John W. Seaman**, Baylor University

3B. Benchmark Dose Model Averaging in Toxicology
Otis R. Evans*, University of North Carolina, Wilmington

3C. Dirichlet Process Mixture Extension Model to Accommodate Complex Sample Designs for Linear and Quantile Regression
Xi Xia* and **Michael Elliott**, University of Michigan

3D. On Bayesian Model Selection for Robust Likelihood-free Methods based on Moment Conditions
Cheng Li* and **Wenxin Jiang**, Northwestern University

3E. Robustness of Multilevel Item Response Theory Model to Outliers using Normal/Independent Distribution on both Random Effects and Outcomes
Geng Chen* and **Sheng Luo**, University of Texas School of Public Health

3 F. Bayesian Sample Size Determination for Informative Hypotheses
Kristen M. Tecson* and **John W. Seaman**, Baylor University

3G. Block Total Response Designs: A Bayesian Approach
Michelle S. Marcovitz*, Baylor University
Damaraju Raghavarao, Temple University
John W. Seaman, Baylor University

3H. Priors and Sample Size Determination for Hurdle Models
Joyce Cheng*, **John W. Seaman** and **David Kahle**, Baylor University

3I. Bayesian Models for Facility-level Adverse Medical Device Event Rates among Hospitalized Children
Laura A. Hatfield* and **Vanessa Azzone**, Harvard Medical School
Sharon-Lise T. Normand, Harvard Medical School and Harvard School of Public Health

* = Presenter | ■ = Student Award Winner

3J. Group Comparison of Pulsatile Hormone Times Series

TingTing Lu* and **Timothy D. Johnson**, University of Michigan

3K. A Bayesian Approach to Detecting Changes in the Visual System

Raymond G. Hoffmann* and **Edgar A. Deyoe**, Medical College of Wisconsin

3L. A Comparison of MCMC and Variational Bayes Algorithms for 3D Log-Gaussian Cox Processes

Ming Teng*, University of Michigan
Farouk S. Nathoo, University of Victoria
Timothy D. Johnson, University of Michigan

3M. A Bayesian Hierarchical Model for Estimating HIV Testing Hazard

Qian An* and **Jian Kang**, Emory University

3N. Bayesian Inference of the Asymmetric Laplace Distribution with Partial Information

Shiyi Tu*, Min Wang and **Xiaoqian Sun**, Clemson University

3O. An Efficient Bayesian Sampling Approach for Continuous Bayesian Network Structure Learning

Shengtong Han* and **Hongmei Zhang**, University of Memphis

3P. Two-sample Empirical Likelihood based Tests for Mean: From Frequentists to Bayesian Type Techniques with Applications to Case-control Studies

Ge Tao* and **Albert Vexler**, State University of New York at Buffalo

3Q. Bayes Regularized Graphical Model Estimation in High Dimensions

Suprateek Kundu* and **Bani Mallick**, Texas A&M University
Amin Momin and **Veera Baladandayuthapani**, University of Texas MD Anderson Cancer Research Center

4. POSTERS: STATISTICAL GENETICS AND GENOMICS

Sponsor: ENAR

4A. LDA Topic Model of an Unknown Number of Topics via MCMC

Zhe Chen* and **Hani Doss**, University of Florida

4B. Controlling the Local False Discovery Rate in the Adaptive Lasso

Joshua N. Sampson* and **Nilanjan Chatterjee**, National Cancer Institute, National Institutes of Health
Raymond Carroll, Texas A&M University
Samuel Muller, University of Sydney

4C. Integrated Analysis of MicroRNA and Messenger RNA Expression Profiles of Essential Thrombocytosis

Erya Huang*, **Wei Zhu**, **Dmitri V. Gnatenko** and **Wadie F. Bahou**, Stony Brook University

4D. The Power Comparison of the Haplotype-based Collapsing Tests and the Variant-based Collapsing Tests for Detecting Rare Variants in Pedigrees

Wei Guo* and **Yin Yao Shugart**, National Institute of Mental Health, National Institutes of Health

4E. Functional Normalization (FunNorm): A Better Alternative to Quantile Normalization for Methylation Data

Jean-Philippe Fortin*, Johns Hopkins University
Aurélie Labbe, McGill University
Mathieu Lemire, University of Toronto
Brent W. Zanke, Ottawa Hospital Research Institute
Thomas J. Hudson, University of Toronto
Elana J. Fertig, Sidney Kimmel Cancer Center at Johns Hopkins University
Celia M.T. Greenwood, McGill University
Kasper D. Hansen, Johns Hopkins University

4F. MetaOC: Meta-analysis with One-sided Correction to Detect Differentially Expressed Genes with Concordant Direction

Xingbin Wang*, **M. Ilyas Kamboh** and **George C. Tseng**, University of Pittsburgh

4G. Normalization of DNA Methylation Microarrays using Technical Covariates

Paul T. Manser* and **Mark Reimers**, Virginia Commonwealth University

4H. Sequence Kernel Association Test for Quantitative Traits in Twin Samples

Kai Xia*, Wonil Chung, Zhaoyu Yin, Rebecca C. Santelli and **Fei Zou**, University of North Carolina, Chapel Hill

4I. An Alternative Approach to Model RNA-seq Data with GLMM

Han Sun*, Cleveland Clinic
Jiayang Sun, Case Western Reserve University

* = Presenter | ■ = Student Award Winner

4J. Classifying Family Relationships using Dense SNP Data and Putative Pedigree Information

Zhen Zeng* and **Eleanor Feingold**, University of Pittsburgh

4K. Identifying Multiple-Role Genes Dynamic in Distinct Environments

Yaqun Wang*, Ningtao Wang, Han Hao and **Rongling Wu,** The Pennsylvania State University

4L. ChIP-seq Meta-Caller: An Assembly Method to Combine Multiple ChIP-seq Peak Callers to Identify and Reprioritize the Peaks

Rui Chen*, University of Pittsburgh
Qunhua Li, The Pennsylvania State University
George C. Tseng, University of Pittsburgh

4M. Fast Annotation-Agnostic Differential Expression Analysis

Leonardo Collado-Torres*, Johns Hopkins University Bloomberg School of Public Health and Maltz Research Laboratories
Andrew E. Jaffe, Maltz Research Laboratories
Jeffrey T. Leek, Johns Hopkins University Bloomberg School of Public Health

4N. Sample Size and Power Determination for Association Tests in Case-parent Trio Studies

Holger Schwender*, Heinrich Heine University Duesseldorf
Christoph Neumann, TU Dortmund University
Margaret A. Taub, Samuel G. Younkin, Terri H. Beaty and **Ingo Ruczinski**, Johns Hopkins University

4O. A Hierarchical Bayesian Approach to Detect Differential Methylation in Both Mean and Variance for Next Generation Sequencing

Shuang Li*, Varghese George, Duchwan Ryu, Xiaoling Wang, Shaoyong Su and **Huidong Shi**, Georgia Regents University
Robert H. Podolsky, Wayne State University
Hongyan Xu, Georgia Regents University

4P. Bayesian Mixture Models for Complex Copy Number Polymorphisms Inferred from Genotyping Arrays

Stephen Cristiano*, **Robert B. Scharpf** and **Lynn Mireless**, Johns Hopkins University

4Q. Multiple Phenotype Analysis for Genome-Wide Association Studies

Shelley Liu*, Harvard School of Public Health
Sheng Feng, Biogen-Idec

4R. EBSeq-HMM: An Empirical Bayes Hidden Markov Model for Ordered RNA-seq Experiments

Ning Leng*, University of Wisconsin, Madison
Brian E. Mcintosh, Morgridge Institute for Research
Yuan Li, University of Wisconsin, Madison
Bao K. Nguyen, Bret Duffin, Shulan Tian, James A. Thomson and **Ron Stewart**, Morgridge Institute for Research
Christina Kendziorski, University of Wisconsin, Madison

5. POSTERS: PREDICTION, PROGNOSTICS, DIAGNOSTIC TESTING

Sponsor: ENAR

5A. Joint Confidence Region Estimation for Area Under ROC Curve and Youden Index

Jingjing Yin* and **Lili Tian**, University at Buffalo

5B. Building Risk Models with Calibrated Margins

Paige Maas*, National Cancer Institute, National Institutes of Health
Raymond Carroll, Texas A&M University
Nilanjan Chatterjee, National Cancer Institute, National Institutes of Health

5C. Meta-TSP: A Meta-analysis Framework of Top Scoring Pair Algorithm to Combine Multiple Transcriptomic Studies in Inter-study Prediction Analysis

SungHwan Kim* and **George C. Tseng**, University of Pittsburgh

5D. A Modified Tree-Based Method for Personalized Medicine Decisions

Wan-Min Tsai*, Heping Zhang, Stephanie O'Malley and **Ralitza Gueorguieva**, Yale University

5E. A Simple Method for Evaluating Within-Sample Prognostic Balance Achieved by Published Comorbidity Summary Measures

Brian L. Egleston*, Robert G. Uzzo, J. Robert Beck and **Yu-Ning Wong**, Fox Chase Cancer Center, Temple University Health System

5F. Effect Size Measures for Functional Modifiers of Treatment Response

Adam Ciarleglio*, New York University School of Medicine

5G. Power Calculations for Prognostic Biomarker Validation Studies with Time to Event Data

Marshall D. Brown* and **Yingye Zheng**, Fred Hutchinson Cancer Research Center
Tianxi Cai, Harvard School of Public Health

5H. Generalized Incremental Forward Stagewise Ordinal Models: Application Predicting Stage of Alzheimer's Disease

Kellie J. Archer* and **Jiayi Hou**, Virginia Commonwealth University

* = Presenter | ■ = Student Award Winner

6. POSTERS: SURVIVAL ANALYSIS

Sponsor: ENAR

6A. Non-parametric Confidence Bands for Survival Function using Martingale Method
Eun-Joo Lee*, Millikin University

6B. On the Estimators and Tests for the Semiparametric Hazards Regression Model
Seung-Hwan Lee*, Illinois Wesleyan University

6C. Regression Analysis of Bivariate Current Status Data with the Proportional Hazards Model and Bernstein Polynomials
Tao Hu, Capital Normal University
Qingning Zhou* and **Jianguo Sun**, University of Missouri, Columbia

6D. Joint Structure Selection and Estimation in the Time-varying Coefficient Cox Model
Wei Xiao* and **Wenbin Lu**, North Carolina State University
Hao Helen Zhang, University of Arizona

6E. Weighted Log-rank Tests for 'Flipped-Data' Survival Analysis of Data with Non-Detects
Eric R. Siegel*, **Songthip T. Ounpraseuth** and **Ralph L. Kodell**, University of Arkansas for Medical Sciences

6F. A Frailty Approach for Survival Analysis with Error-prone Covariate
Sehee Kim* and **Yi Li**, University of Michigan
Donna Spiegelman, Harvard School of Public Health

6G. LC-Morph: A Morphological Image Signature for Predicting Lung Cancer Survival
Yuchen Yang*, **Fuyong Xing**, **Hai Su**, **Chi Wang**, **Li Chen**, **Lin Yang** and **Arnolod Stromberg**, University of Kentucky

7. POSTERS: IMAGING, HIGH DIMENSIONAL DATA, BIOMARKERS, AND MICROARRAY

Sponsor: ENAR

7A. On the Distribution of Photon Counts with Censoring in Two-Photon Microscopy
Burcin Simsek* and **Satish Iyengar**, University of Pittsburgh
David Kleinfeld, University of California, San Diego

7B. Bayesian Gaussian Process Regression for High-dimensional Data
Qing He*, Jian Kang and **Qi Long**, Emory University

7C. Effects of Alcohol use on Brain Networks: A Dynamic Causal Model Study with EEG Data
Benjamin T. Brown*, Lynn Eberly, Steve Malone and **Kathleen Thomas**, University of Minnesota

7D. C.Logic: A Classification Algorithm for Discovering Interactions that Lead to Disease Susceptibility
Sybil L. Nelson*, Bethany Wolf and **Viswanathan Ramakrishnan**, Medical University of South Carolina

7E. A Direct Approach to False Discovery Rate Regression
Simina M. Boca*, National Cancer Institute, National Institutes of Health
Jeffrey T. Leek, Johns Hopkins Bloomberg School of Public Health

7F. A Study of the Correlation Structure of Microarray Gene Expression Data Based on Mechanistic Modelling of Cell Population Kinetics
Linlin Chen*, Rochester Institute of Technology
Lev Klebnov, Charles University
Anthony Almudevar and **Christoph Proschel**, University of Rochester

7G. Making Computerized Adaptive Testing a Diagnostic Tool
Hua-Hua Chang*, University of Illinois, Urbana-Champaign
Ya-Hui Su, National Chung Cheng University

7H. Missing Value Imputation in High-dimensional Phenomic Data: Imputable or Not? And How?
Serena Liao* and **George C. Tseng**, University of Pittsburgh

7I. Age Prediction using Supervised PCA
Valerie J. Watkins* and **Yishi Wang**, University of North Carolina, Wilmington

7J. Tensor Regression with Applications in Neuroimaging Data Analysis
Xiaoshan Li*, Hua Zhou and **Lexin Li**, North Carolina State University

7K. Investigating Spatiotemporal Covariance Structures for Modeling Longitudinal Imaging Data
Brandon J. George* and **Inmaculada Aban**, University of Alabama, Birmingham

7L. Nonparametric Regression with Tree-structured Response
Yuan Wang*, University of Texas MD Anderson Cancer Center
J. S. Marron, University of North Carolina, Chapel Hill
Haonan Wang, Colorado State University
Burcu Aydin, Alim Ladha and **Elizabeth Bullitt**, University of North Carolina, Chapel Hill

7M. Improving Scan-Rescan Reliability of Resting State fMRI Parcellation
Amanda Mejia*, Johns Hopkins School of Public Health
Mary Beth Nebel and **Stewart Mostofsky**, Kennedy Krieger Institute
Brian Caffo and **Martin Lindquist**, Johns Hopkins School of Public Health

* = Presenter | ■ = Student Award Winner

7N. SGPP: Spatial Gaussian Predictive Process Models for Neuroimaging Data

Jung Won Hyun* and **Yimei Li**, St. Jude Children's Research Hospital
John H. Gilmore, Zhaohua Lu, Martin Styner and **Hongtu Zhu**, University of North Carolina, Chapel Hill

7O. Dimension Reduction using Inverse Spline Regression

Kijoeng Nam, U.S. Food and Drug Administration
Paul J. Smith, University of Maryland, College Park

7P. Interpreting Large Dense (Scary) Linear Models along Predictor Groups

Yuval Benjamini*, Stanford University
Julien Mairal, INRIA, Grenoble
Bin Yu, University of California, Berkeley

8. POSTERS: ENVIRONMENTAL AND LONGITUDINAL DATA ANALYSIS

Sponsor: ENAR

8A. Accounting for Complex Survey Design in Modeling Temporal Trends of Phthalate Metabolites in the U.S. Population

Min Chen*, Kevin Kransler, Rosemary Zaleski and **Hua Qian**, ExxonMobil Biomedical Sciences, Inc.

8B. Non-stationary Covariance Functions via Domain Segmentation

Douglas C. Hom*, Timothy D. Johnson and **Veronica J. Berrocal**, University of Michigan

8C. The Effect of Exposure to Air Toxics on Age of Diagnosis and Subtype of Childhood Leukemia — A Joint Modeling Approach

Ting-Yu Chen*, Elaine Symanski and **Wenyaw Chan**, University of Texas School of Public Health

8D. Investigating the Health Risks Associated with Long Term Exposure to Coarse PM

Helen L. Powell* and **Roger D. Peng**, Johns Hopkins Bloomberg School of Public Health

8E. Functional Data Analysis to Guide a Conditional Likelihood Regression in a Case-Crossover Study Investigating whether Social Characteristics Modify the Health Effects of Air Pollution

Juana M. Herrera*, Joan Staniswalis and **Sara E. Grineski**, University of Texas, El Paso

8F. Dependence Modeling of Spatio-Temporal Weather Extreme Events

Whitney Huang* and **Hao Zhang**, Purdue University

8G. Identifying the Constellation of Emergency Health Conditions most Sensitive to Extreme Heat

Jennifer Bobb*, Harvard School of Public Health

8H. Statistical Strategies for Constructing Health Risk Models with Multiple Pollutants and their Interactions

Zhichao Sun*, Yebin Tao, Shi Li, Kelly K. Ferguson, John D. Meeker, Sung Kyun Park, Stuart A. Batterman and **Bhramar Mukherjee**, University of Michigan

8I. Mixed Effects Models for Investigating Dietary Regimens Intended to Extend Lifespan in Caenorhabditis Elegans

Jeffrey Burton*, Robbie Beyl, Jolene Zheng and **William D. Johnson**, Pennington Biomedical Research Center

8J. Simulation from a known Cox MSM using Standard Parametric Models for the g-formula

Jessica G. Young* and **Eric J. Tchetgen Tchetgen**, Harvard School of Public Health

8K. Reflecting the Orientation of Teeth in Random Effects Models for Periodontal Outcomes

Rong Xia* and **Thomas M. Braun**, University of Michigan

8L. A Longitudinal Beta-binomial Model for Over-dispersed Binomial Data

Hongqian Wu* and **Ying Zhang**, University of Iowa

9. POSTERS: EPIDEMIOLOGY AND CAUSAL INFERENCE

Sponsor: ENAR

9A. Methods of Missing-Data Exploration that Reveal Potential Extrapolation

Victoria Liublinska*, Harvard University

9B. Exploring Mobile Technology to Enhance Birth Outcomes in Rural Mozambique: Pilot Study Results

Manoj T. Rema*, Ike Okosun and **Sheryl Strasser**, Georgia State University

9C. Transformations to the Zero-inflated Negative Binominal Model for Overall Exposure Effects: An Analysis of Blood Lead and Dental Caries in a Complex Survey

D. Leann Long* and **R. Constance Wiener**, West Virginia University

9D. Applying Multiple Imputation using External Calibration to Propensity Score Methods

Yenny G. Webb-Vargas* and **Elizabeth A. Stuart**, Johns Hopkins Bloomberg School of Public Health

* = Presenter | ■ = Student Award Winner

9E. Efficient Estimation of Partial Rank-based Correlation with Missing Data
Wei Ding* and **Peter X.K Song**, University of Michigan

9F. Data Analysis of Contributing Factors for Obesity in Low-Income Neighborhoods
Sujin Kim* and **Rukmana Deden**, Savannah State University

10. POSTERS: NON PARAMETRIC AND NON LINEAR METHODS

Sponsor: ENAR

10A. Comparison of Area Under the Curve and Mixed Effects Models Methodologies for Profile Analysis
Robbie A. Beyl*, Jeffrey Burton and **William Johnson**, Pennington Biomedical Research Center

10B. Inferential Approaches to Relative Risk Regression
Yi Lu* and **Daniel O. Scharfstein**, Johns Hopkins Bloomberg School of Public Health

10C. Fractional Polynomial Regression with Multilevel Data
Paul Kolm*, Daniel Elliot and **Joann Brice**, Christiana Care Health System
Robert Young, Northwestern University

10D. BLUP Estimation in Unbalanced Mixed-Effects Models
Samaradasa Weerahandi, Pfizer Inc.
Peijin Xie, Hershey's Company
Ching-Ray Yu and **Kelly H. Zou***, Pfizer Inc.

10E. Flexible Test for Interactions in Smoothing Spline ANOVA Models through the Use of Distance Correlation
Sebastian J. Teran Hidalgo*, Michael Wu and **Michael Kosorok**, University of North Carolina, Chapel Hill

10F. Optimal Global Test for Functional Linear Regression Models and its Applications
Xiao Wang and **Simeng Qu***, Purdue University

10G. Model Tumor Pattern and Compare Treatment Effects using Semiparametric Linear Mixed-Effects Models
Changming Xia*, University of Rochester
Jianrong Wu, St. Jude Children's Research Hospital
Hua Liang, The George Washington University

10H. Robust Variance Component Analysis with Applications in Biological Assay Validation
Binbing Yu*, MedImmune, LLC.

10I. Oracle Inference for GMM Models
Mihai C. Giurcanu* and **Brett D. Presnell**, University of Florida

10J. Covariate-dependent Functional Inference for the Life-time Circadian Rhythm of Physical Activity
Luo Xiao*, Lei Huang and **Ciprian Crainiceanu**, Johns Hopkins Bloomberg School of Public Health

11. POSTERS: VARIABLE SELECTION, MACHINE LEARNING AND OTHER

Sponsor: ENAR

11A. An Extended Beta Regression Model
Min Yi* and **Nancy Flournoy**, University of Missouri, Columbia

11B. Model-Adjusted Standardization to Account for Unmeasured Cluster-Level Covariates with Complex Survey Data
Zhuangyu Cai* and **Babette Brumback**, University of Florida

11C. A New Multiple Comparisons with the Best Procedure
Tianshuang Wu* and **Susan Murphy**, University of Michigan

11D. Mixture of D-vine Copulas for Modeling Dependence
Daeyoung Kim, Sungkyunkwan University, Korea
Jong-Min Kim, University of Minnesota, Morris
Shu-Min Liao, Amherst College
Yoonsung Jung*, Prairie View A&M University

11E. Ensemble Variable Selection and Estimation (EVE)
Sunyoung Shin*, Yufeng Liu and **Jason Fine**, University of North Carolina, Chapel Hill

11F. Support Vector Classifiers and Missing Data: An Investigation of the Complete-Case Solution and a Proposal of an EM-like Solution
Thomas G. Stewart*, Donglin Zeng and **Michael C. Wu**, University of North Carolina, Chapel Hill

11G. Evaluating Novel Intradialytic Sampling Designs for Individual Pharmacokinetic Analysis using Monte Carlo Simulation
Minchun Zhou*, William Henry Fissell and **Matthew Stephen Shotwell**, Vanderbilt University

11H. A Study on the Statistical Properties of the European Pharmacopoeia Test for Uniformity of Dosage Units using Large Sample Sizes
Meiyu Shen*, Yi Tsong and **Xiaoyu Dong**, U.S. Food and Drug Administration

11I. Variable Selection When Some Predictors are Measured with Error
Guangning Xu* and **Leonard A. Stefanski**, North Carolina State University

* = Presenter | ■ = Student Award Winner

11J. Variable Selection for Optimal Treatment Regimes

Na Zhang*, Eric Laber and **Howard Bondell**, North Carolina State University

11K. Promoting Similarity of Model Sparsity Structures in Integrative Analysis

Yuan Huang* and **Runze Li**, The Pennsylvania State University
Jian Huang, University of Iowa
Shuangge Ma, Yale University

Monday, March 17

8:30 am – 10:15 a.m.

12. MASSIVE ONLINE OPEN STATISTICS (MOOS): SHOULD WE BE TEACHING STATISTICS TO 100,000 AT A TIME?

Grand Ballroom I (3rd Floor)

Sponsors: ENAR, ASA Section on Statistical Education, ASA Statistical Learning and Data Mining Section

Organizer: Jeffrey Leek, Johns Hopkins Bloomberg School of Public Health

Chair: Brian Caffo, Johns Hopkins Bloomberg School of Public Health

8:30
MOOCs for Statistics and the Statistics of MOOCs
Joseph Blitzstein*, Harvard University

8:55
Can We Teach 100,000 People Data Analysis at a Time?
Jeffrey T. Leek*, Johns Hopkins Bloomberg School of Public Health

9:20
Statistical Reasoning for the Masses
John McGready*, Johns Hopkins Bloomberg School of Public Health

9:45
Massive Online Open Statistics (MOOS): Should We be Teaching Statistics to 100,000 at a Time?
Rebecca Nugent*, Carnegie Mellon University

10:10
Floor Discussion

13. COUNCIL FOR EMERGING AND NEW STATISTICIANS (CENS) INVITED SESSION: SHOULD I DO A POSTDOC?

Grand Ballroom V (3rd Floor)

Sponsors: ENAR, ASA Mental Health Statistics Section

Organizer: Tapan Mehta, University of Alabama, Birmingham

Chair: Naomi Brownstein, Florida State University

8:30
My Experiences as a Postdoc in Biostatistics
Joshua Warren*, University of North Carolina, Chapel Hill

9:00
Is Post-Doctoral Fellowship Key to Academic Success?
Hemant K. Tiwari*, University of Alabama, Birmingham

9:30
Should I do a Post-Doctoral Fellowship? The NICHD Experience
Paul S. Albert*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

10:10
Floor Discussion

14. ADAPTIVE RANDOMIZED TRIAL DESIGNS AND IMPROVED ANALYSIS METHODS TO LEARN WHICH SUBPOPULATIONS BENEFIT FROM WHICH TREATMENTS

Grand Ballroom II (3rd Floor)

Sponsors: IMS, ASA Biometrics Section, ASA Biopharmaceutical Section

Organizer: Michael Rosenblum, Johns Hopkins Bloomberg School of Public Health

Chair: Yi (Yvonne) Huang, Johns Hopkins Bloomberg School of Public Health

8:30
Impacts of Predictive Genomic Classifier Performance on Subpopulation-Specific Treatment Effects Assessment
Sue-Jane Wang*, U.S. Food and Drug Administration
Ming-Chung Li, National Cancer Institute, National Institutes of Health

8:55
SHINE Shadow: A Bayesian Adaptive Trial vs. a Group Sequential Trial in Stroke
Jason T. Connor* and **Kristine R. Broglio**, Berry Consultants
Valerie L. Durkalski, Medical University of South Carolina

* = Presenter | ■ = Student Award Winner

9:20

Adaptive Enrichment Designs for Clinical Trials
Noah Simon*, University of Washington
Richard Simon, National Cancer Institute, National Institutes of Health

9:45

Constructing Confidence Sets for the Optimal Regime
Sherri Rose*, Harvard University
Tuo Zhao, Johns Hopkins University
Han Liu, Princeton University
Michael Rosenblum, Johns Hopkins University

10:10

Floor Discussion

15. STATISTICAL METHODS FOR COMPLEX STRUCTURED BIOMEDICAL OBJECT DATA

Grand Ballroom VI (3rd Floor)

Sponsors: ENAR, ASA Statistical Learning and Data Mining Section

Organizer: Veera Baladandayuthapani, University of Texas MD Anderson Cancer Center

Chair: Veera Baladandayuthapani, University of Texas MD Anderson Cancer Center

8:30

Object Oriented Data Analysis: Backwards PCA
J. S. Marron*, University of North Carolina, Chapel Hill

8:55

Additive and Interaction Models for Nonparametric Functional and Object Regression, with Application to Ophthalmological Multi-level Functional Data on Spherical Domains
Jeffrey S. Morris* and **Veera Baladandayuthapani**, University of Texas MD Anderson Cancer Center
Massimo Fazio, University of Alabama, Birmingham

9:20

On Synergy Between Statistical Shape Analysis (SSA) and Functional Data Analysis (FDA)
Anuj Srivastava*, Florida State University
Sebastian Kurtek, The Ohio State University
Eric Klassen, Florida State University
Jingyong Su, Texas Tech University

9:45

Bayesian Spatial Functional Models for High-dimensional Genomics Data
Veerabhadran Baladandayuthapani*, Lin Zhang, Jeffrey Morris and **Keith Baggerly**, University of Texas MD Anderson Cancer Center

10:10

Floor Discussion

16. MULTIVARIATE ANALYSIS IN HIGH DIMENSIONS

Grand Ballroom III (3rd Floor)

Sponsor: IMS

Organizer: Adam Rothman, University of Minnesota

Chair: Mark Fiecas, University of Warwick, UK

8:30

Laplacian Shrinkage for Estimation of Inverse Covariance Matrices from Heterogenous Samples
Takumi Saegusa and **Ali Shojaie***, University of Washington

8:55

Joint Mean-Covariance Models for Incomplete Multivariate Longitudinal Data
Mohsen Pourahmadi*, Texas A&M University

9:20

Prediction in Abundant High-dimensional Linear Regression
Dennis Cook*, University of Minnesota
Liliana Forzani, Instituto de Matem´atica Aplicada del Litoral and Facultad de Ingenier´ıa Qu´ımica CONICET and UNL
Adam J. Rothman, University of Minnesota

9:45

Properties of Optimizations used in Penalized Gaussian Likelihood Inverse Covariance Matrix Estimation
Adam J. Rothman*, University of Minnesota
Liliana Forzani, Instituto de Matem´atica Aplicada del Litoral and Facultad de Ingenier´ıa Qu´mica CONICET and UNL

10:10

Floor Discussion

17. RECENT ADVANCES IN LIFETIME DATA ANALYSIS

Grand Ballroom IV (3rd Floor)

Sponsor: ENAR

Organizer: Mei-Ling Ting Lee, University of Maryland, College Park

Chair: Xin He, University of Maryland, College Park

8:30

Bayesian Threshold Regression for Informatively Censored Current Status Data
Tao Xiao, University of Maryland, College Park and The Ohio State University
Michael L. Pennell*, The Ohio State University

* = Presenter | ■ = Student Award Winner

8:55

Semiparametric Estimation for the Additive Hazards Model with Left-truncated and Right-censored Data
Chiung-Yu Huang*, Johns Hopkins University
Jing Qin, National Institute of Allergy and Infectious Diseases, National Institutes of Health

9:20

Semiparametric Inference on the Absolute Risk Reduction and the Restricted Mean Survival Difference
Song Yang*, National Heart, Lung, and Blood Institute, National Institutes of Health

9:45

Evaluating Calibration of Risk Prediction Models
Ruth Pfeiffer*, National Cancer Institute, National Institutes of Health

10:10

Floor Discussion

18. CONTRIBUTED PAPERS: EPIDEMIOLOGIC METHODS

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Emily Mitchell, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

8:30

Modeling Epidemiological Features of Disease Outbreaks
Manasi Sheth-Chandra*, Booz Allen Hamilton
N. Rao Chaganty, Old Dominion University

8:45

A Stochastic Model for Explicit Estimation of Effect Modification in Finite Sample
Xiaoshan Wang* and **Jacqueline Starr**, Forsyth Institute

9:00

Modeling the Effects of Climate Change and Air Quality on Asthma, Accounting for Uncertainty
Stacey E. Alexeeff*, Stephan R. Sain and **Doug Nychka**, National Center for Atmospheric Research

9:15

One Novel Approach to Handle Random Measurement Error using Hidden Markov Models
Lola Luo*, Dylan Small and **Jason A. Roy**, University of Pennsylvania

9:30

Quantifying Circadian Trajectory of Fatigability using the Proportional Intensity Model
Jiawei Bai*, Jennifer Schrack and **Mei-Cheng Wang**, Johns Hopkins University
Luigi Ferrucci, National Institute of Aging, National Institutes of Health
Ciprian M. Crainiceanu, Johns Hopkins University

9:45

A Comparison of Methods for Biomarker Associations with Endogenous Treatment
Andrew J. Spieker*, Joseph AC Delaney and **Robyn L. McClelland**, University of Washington

10:00

Modeling Temporal Patterns in Exposure/Response Relationships with Change Points, with an Application to Incident Obstructive Airway Disease in Firefighters Exposed to the World Trade Center Rescue/Recovery Effort
Charles B. Hall*, Albert Einstein College of Medicine of Yeshiva University
Michelle Glaser, Mayris Webber, Xiaoxue Liu and **Rachel Zeig-Owens**, Montefiore Medical Center
David Prezant, Fire Department of the City of New York

19. CONTRIBUTED PAPERS: COMPUTATIONAL METHODS AND IMPLEMENTATION

Bristol Room (3rd Floor)

Sponsor: ENAR

Chair: Ruiwen Zhang, SAS Inc.

8:30

Performance of Shannon's Maximum Entropy Distribution under Some Restrictions
Sinan Saracli* and **Hatice Cicek**, Afyon Kocatepe University

8:45

Propensity Score Matching with Survival Outcomes: Critical Considerations in the Choice of the Caliper Size
Adin-Cristian Andrei*, Zhi Li, S. Chris Malaisrie, Edwin McGee, Jane Kruse and **Patrick M. McCarthy**, Bluhm Cardiovascular Institute, Northwestern University

9:00

Model Free Variable Rank using Randomized Decision Tree, an Ensemble of Trees
Bong-Jin Choi* and **Chris P. Tsokos**, University of South Florida

* = Presenter | ■ = Student Award Winner

9:15

Optimal Computational and Statistical Rates of Convergence for Sparse Nonconvex Learning Problems

Zhaoran Wang* and **Han Liu**, Princeton University
Tong Zhang, Rutgers University

9:30

A Modified EM Algorithm for Regression Analysis of Data with Non-ignorable Non-response

Yang Zhang* and **Gong Tang**, University of Pittsburgh

9:45

A Computationally Fast and Asymptotically Efficient Approach for the Broken-stick Model

Ritabrata Das*, Moulinath Banerjee and **Bin Nan**, University of Michigan

20. CONTRIBUTED PAPERS: NON-PARAMETRIC AND SEMIPARAMETRIC METHODS IN FUNCTIONAL DATA ANALYSIS

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Adam Ciarleglio, NYU School of Medicine

8:30

Restricted Likelihood Ratio Tests for Linearity in Scalar-on-Function Regression

Mathew W. McLean*, Texas A&M University
Giles Hooker and **David Ruppert**, Cornell University

8:45

Incorporating Covariates in Skewed Functional Data Models

Meng Li*, Ana-Maria Staicu and **Howard D. Bondell**, North Carolina State University

9:00

Simultaneous Inference for Repeated Functional Data

Guanqun Cao*, Auburn University
Lily Wang, University of Georgia

9:15

Generalized Functional Concurrent Model

Janet S. Kim*, **Arnab Maity** and **Ana-Maria Staicu**, North Carolina State University

9:30

Variable-Domain Functional Regression

Jonathan E. Gellar ■ and **Elizabeth Colantuoni**, Johns Hopkins Bloomberg School of Public Health
Dale M. Needham, Johns Hopkins School of Medicine
Ciprian M. Crainiceanu, Johns Hopkins Bloomberg School of Public Health

9:45

Interaction Models for Functional Data

Joseph Usset*, Ana-Maria Staicu and **Arnab Maity**, North Carolina State University

10:00

A Novel Statistical Method based on Dynamic Models for Classification

Lerong Li* and **Momiao Xiong**, University of Texas School of Public Health, Houston

21. CONTRIBUTED PAPERS: STATISTICAL METHODS FOR MICROARRAY AND BIOMARKER DATA

Grand Ballroom VII (3rd Floor)

Sponsor: ENAR

Chair: Danping Liu, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

8:30

Modeling qRT-PCR Dynamics with Application to Cancer Biomarkers Quantification

Inna Chervoneva*, Thomas Jefferson University

8:45

Evaluation Drug Efficacy in the Presence of the Imperfect Companion Diagnostic Device

Meijuan Li*, U.S. Food and Drug Administration

9:00

Joint Graphical Models for Relational Structures in Multi-Dimensional Phenotypic Data

Vivian H. Shih*, Novartis Pharmaceuticals
Catherine A. Sugar, University of California, Los Angeles

9:15

Sample Size Methods for Training Classifiers Developed from Regularized Logistic Regression

Sandra Safo*, Xiao Song and **Kevin K. Dobbin**, University of Georgia

9:30

Bilaterally Contaminated Normal Model with Nuisance Parameter and Its Applications

Qian Fan*, University of Kentucky
Hongying Dai, Children's Mercy Hospital
Richard J. Charnigo, University of Kentucky

9:45

Correlation Coefficient Inference for Left-Censored Biomarker Data with Known Detection Limits

Courtney E. McCracken, Emory University
Stephen W. Looney*, Georgia Regents University

10:00

A Semi-parametric Model for Time-dependent Predictive Accuracy Curves of Biomarkers

Weining Shen*, Jing Ning and **Ying Yuan**, University of Texas MD Anderson Cancer Center

* = Presenter | ■ = Student Award Winner

22. CONTRIBUTED PAPERS: MACHINE LEARNING

Grand Ballroom IX (3rd Floor)

Sponsor: ENAR

Chair: Qing He, Emory University

8:30

Joint Estimation of Multiple Graphical Models from High Dimensional Dependent Data

Huitong Qiu ■ and **Fang Han**, Johns Hopkins University
Han Liu, Princeton University
Brian S. Caffo, Johns Hopkins University

8:45

MBACT - Multiclass Bayesian Additive Classification Trees

Bereket P. Kindo*, Hao Wang and **Edsel A. Pena**, University of South Carolina

9:00

Random Forest Importance Scores: Significance Testing and Conditional Importance

Eric Bair* and **Lira Pi**, University of North Carolina, Chapel Hill

9:15

Large-Margin Classifier Selection via Decision Boundary Instability

Wei Sun* and **Guang Cheng**, Purdue University
Yufeng Liu, University of North Carolina, Chapel Hill

9:30

Bias Correction for Selecting the Minimal-error Classifier from Many Machine Learning Models

Ying Ding*, Shaowu Tang, Ge Liao, Jia Jia, Yan Lin and **George C. Tseng**, University of Pittsburgh

9:45

Ensemble Learning of Inverse Probability Weights for Marginal Structural Modeling in Large Observational Datasets

Susan Gruber* and **Roger W. Logan**, Harvard School of Public Health
Inmaculada Jarrin and **Susana Monge**, Instituto de Salud Carlos III, Madrid, Spain
Miguel Hernan, Harvard School of Public Health

10:00

Ordinal Logic Forest: Discovering Interactions Among Binary Predictors for Classifying Ordinal Responses

Bethany J. Wolf* and **Elizabeth G. Hill**, Medical University of South Carolina
Elizabeth H. Slate, Florida State University

23. CONTRIBUTED PAPERS: MULTIPLE TESTING

Chasseur Ballroom (3rd Floor)

Sponsor: ENAR

Chair: Simina M. Boca, National Cancer Institute, National Institutes of Health

8:30

Sizing Clinical Trials that Compare Two Interventions using Two Time-to-Event Outcomes

Yuki Ando, Pharmaceuticals and Medical Devices Agency
Toshimitsu Hamasaki*, Osaka University Graduate School of Medicine and National Cerebral and Cardiovascular Center
Tomoyuki Sugimoto, Hirosaki University Graduate School of Science & Technology
Scott R. Evans, Harvard School of Public Health
Yuko Ohno, Osaka University Graduate School of Medicine

8:45

Multiple Simultaneous Tests for Noninferiority and Superiority: A Graphical Approach

Heng Li and **Vandana Mukhi***, U.S. Food and Drug Administration

9:00

Multiple Testing that Considers Assumptions and Network

Demba Fofana*, E. O. George and **Dale Bowman**, University of Memphis

9:15

Testing the Disjunction Hypothesis using Voronoi Diagrams, with Applications to Genetics

Daisy Phillips* and **Debashis Ghosh**, The Pennsylvania State University

9:30

A Class of Improved Hybrid Hochberg-Hommel Type Step-Up Multiple Test Procedures

Jiangtao Gou* and **Ajit C. Tamhane**, Northwestern University
Dong Xi, Novartis Pharmaceuticals Corporation
Dror Rom, Prosoft Software, Inc.

9:45

Identifying Multiple Regulation Across a Diverse Set of Outcomes

Denis M. Agniel* and **Tianxi Cai**, Harvard University

10:00

Dorfman Testing with Correlated Responses

Elena K. Bordonali*, Michael G. Hudgens and **Bahjat F. Qaqish**, University of North Carolina, Chapel Hill

✱ = Presenter | ■ = Student Award Winner

24. CONTRIBUTED PAPERS: METHODS FOR STATISTICAL GENETICS

Grand Ballroom VIII (3rd Floor)

Sponsor: ENAR

Chair: Peng Wei, University of Texas School of Public Health

8:30

Fitting Generalized Linear Mixed Models to Family Data in Genetic Association Studies

Tao Wang*, Peng He and **Kwang Woo Ahn**, Medical College of Wisconsin
Xujing Wang, University of Alabama, Birmingham
Soumitra Ghosh, GlaxoSmithKline
Purushottam Laud, Medical College of Wisconsin

8:45

Kernel Methods for Regression Analysis of Microbiome Compositional Data

Jun Chen*, Harvard School of Public Health
Hongzhe Li, University of Pennsylvania

9:00

Latent Class Quantitative Trait Loci (QTL) Mapping

Shuyun Ye*, Xiaomao Li, Mark Keller, Alan Attie and **Christina Kendziorski**, University of Wisconsin, Madison

9:15

Using Gene Expression to Improve the Power of Genome-Wide Association Analysis

Yen-Yi Ho* and **Emily C. Baechler**, University of Minnesota
Ward Ortmann, Timothy W. Behrens, Robert R. Graham and **Tushar R. Bhangale**, Genentech, Inc.
Wei Pan, University of Minnesota

9:30

Extending Linear Predictors to Impute Genotypes in Pedigrees

Wenan Chen* and **Daniel J. Schaid**, Mayo Clinic

9:45

Inferring Rare Disease Risk Variants based on Exact Probabilities of Sharing by Multiple Affected Relatives

Alexandre Bureau*, Institut universitaire en santé mentale de Québec
Samuel Younkin, University of Wisconsin, Madison
Margaret M. Parker, Johns Hopkins Bloomberg School of Public Health
Joan E. Bailey-Wilson, National Human Genome Research Institute, National Institutes of Health
Mary L. Marazita, University of Pittsburgh
Jeffrey C. Murray, University of Iowa
Elisabeth Mangold, University of Bonn
Hasan Albacha-Hejazi, Dr. Hejazi Clinic
Terri H. Beaty and **Ingo Ruczinski**, Johns Hopkins Bloomberg School of Public Health

10:00

People Can't See Statistical Significance: A Massive Randomized Trial on the Visual Perception of Relationships

Aaron Fisher*, Georgiana B. Anderson and **Jeff Leek**, Johns Hopkins Bloomberg School of Public Health

Monday, March 17

10:15 am – 10:30 pm

Refreshment Break with our Exhibitors

Grand Ballroom Foyer (3rd Floor)

Monday, March 17

10:30 am – 12:15 pm

25. STATISTICAL INNOVATIONS FOR STUDYING THE HUMAN BRAIN FUNCTION

Grand Ballroom II (3rd Floor)

Sponsors: ENAR, ASA Section on ASA Section on Statistics in Imaging

Organizer: Mark Fiecas, University of Warwick

Chair: Mark Fiecas, University of Warwick

10:30

A New Method for Estimating Changes in Granger Causality in EEG Data

Ivor Cribben*, University of Alberta

10:55

Genome-wide Scan of Brain Phenotypes Discovers Common Genetic Variants Influencing Cortical Surface Area

Chi-Hua Chen*, Andrew Schork and **Wes Thompson**, University of California, San Diego
Ole Andreasssen, University of Oslo
Anders Dale, University of California, San Diego

11:20

Comparison of Parametric and Semiparametric Statistical Methods and Signal Processing Methodology for fMRI Signal Analysis Illustrated using a Gustatory Experiment

Jaroslaw Harezlak*, Indiana University Fairbanks School of Public Health
Mario Dzemidzic, Indiana University School of Medicine
Maria A. Kudela and **Jacek Urbanek**, Indiana University Fairbanks School of Public Health
Brandon G. Oberlin and **David A. Kareken**, Indiana University School of Medicine

* = Presenter | ■ = Student Award Winner

11:45
A Semi-parametric Quadratic Inference Approach for Longitudinal fMRI Data
Yu Chen*, Timothy D. Johnson and **Min Zhang**, University of Michigan

12:10
Floor Discussion

26. META-ANALYSIS OF GENE-ENVIRONMENT INTERACTION IN THE POST-GWAS ERA

Grand Ballroom VI (3rd Floor)

Sponsors: ENAR, ASA Section on Statistics and the Environment

Organizer: Bhramar Mukherjee, University of Michigan

Chair: Jaeil Ahn, University of Texas MD Anderson Cancer Center

10:30
Testing GxE in Genome-wide Association Studies
Li Hsu*, Fred Hutchinson Cancer Research Center

10:55
Bayesian Meta-analysis Methods for Detecting G-E Interactions in Genomic Data
Xiaoquan Wen*, University of Michigan

11:20
The Role of Covariate Heterogeneity in Meta-analysis of Gene-environment Interactions with Quantitative Traits
Bhramar Mukherjee*, University of Michigan
Shi Li, Eli Lilly and Company

11:45
Meta and Mega Analysis of G x E Interactions with Complex Disease Outcomes: Experience and Insights from the CHARGE Consortium
Kenneth Rice* and **Colleen Sitlani**, University of Washington

12:10
Floor Discussion

27. STATISTICS METHODS FOR HIGH-THROUGHPUT GENOMICS

Grand Ballroom V (3rd Floor)

Sponsors: ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section

Organizer: Hui Jiang, University of Michigan

Chair: Hui Jiang, University of Michigan

10:30
Statistical Issues with RNAseq Data
Rafael Irizarry*, Dana-Farber Cancer Institute and Harvard School of Public Health

10:55
Model-based Estimation of Abundances of Species, Microbial Genes and Pathways in Metagenomic Data
Hongzhe Li* and **Eric Chen**, University of Pennsylvania

11:20
Statistical Analysis of Time Course ChIP-seq Data
Xuekui Zhang and **Hongkai Ji***, Johns Hopkins Bloomberg School of Public Health

11:45
Sequencing Thousands of Human Genomes
Goncalo R. Abecasis, University of Michigan School of Public Health

12:10
Floor Discussion

28. PANEL DISCUSSION: PERSONALIZED MEDICINE: BETTER TREATMENT FOR THE PATIENT OR THE RIGHT PATIENT FOR THE TREATMENT?

Grand Ballroom VIII (3rd Floor)

Sponsors: ENAR, ASA Biopharmaceutical Section

Organizer: Olga Marchenko, Innovation, Quintiles

Chair: Olga Marchenko, Innovation, Quintiles

10:30
Personanalized Medicine: Better Treatment for the Patient or the Right Patient for the Treatments?
Anastasios A. Tsiatis, North Carolina State University

10:55
Keaven M. Anderson, Merck & Company, Inc.

11:20
Discussion
Stephen J. Ruberg, Eli Lilly and Company — Distinguished Research Fellow
Sandeep M. Menon, Pfizer Inc. and Boston University
Lisa M. LaVange, U.S. Food and Drug Administration
Ilya Lipkovich, Quintiles

12:00
Floor Discussion

* = Presenter | ■ = Student Award Winner

29. RECENT ADVANCES IN STATISTICAL METHODS FOR META-ANALYSIS

Grand Ballroom III (3rd Floor)

Sponsors: ENAR, ASA Section on Bayesian Statistical Science, ASA Biopharmaceutical Section

Organizer: Yong Chen, University of Texas Health Science Center at Houston

Chair: Haitao Chu, University of Minnesota

10:30
Bayesian Network Meta-Analysis for Categorical Outcomes
Christopher H. Schmid* and **Thomas A. Trikalinos**, Brown University

11:00
Incorporation of Mixed Bivariate Outcomes and Individual Patient Data in Network Meta Analysis
Bradley P. Carlin* and **Hwanhee Hong**, University of Minnesota
Haoda Fu and **Karen L. Price**, Eli Lilly and Company

11:30
Meta-analysis of Diagnostic Test Accuracy Comparisons: Network Methods
Wei Cheng, Constantine Gatsonis*, Christopher Schmid and **Thomas Trikalinos**, Brown University

12:00
Floor Discussion

30. SUBGROUP ANALYSIS AND PERSONALIZED PREDICTION

Grand Ballroom IX (3rd Floor)

Sponsors: ENAR, ASA Biopharmaceutical Section

Organizer: Annie Qu, University of Illinois, Urbana-Champaign

Chair: Annie Qu, University of Illinois, Urbana-Champaign

10:30
Personalized Prediction
Yunzhang Zhu, Xiaotong Shen*, and **Changqing Ye**, University of Minnesota

10:55
Personalized Treatment for Longitudinal Data
Hyunkeun Cho*, Western Michigan University
Peng Wang, Bowling Green State University
Annie Qu, University of Illinois, Urbana-Champaign

11:20
Multiway Clustering with Hidden Structure
Bruce G. Lindsay*, The Pennsylvania State University
Francesco Bartolucci, University of Perugia
Francesca Chiaromonte, The Pennsylvania State University

11:45
Model-based Inference in Subgroup Analysis
Xuming He* and **Juan Shen**, University of Michigan

12:10
Floor Discussion

31. LATENT VARIABLE MODELING FOR MULTIPLE OUTCOMES AND GROWTH MODELS IN PSYCHIATRIC STUDIES

Grand Ballroom VII (3rd Floor)

Sponsors: ENAR, ASA Mental Health Statistics Section

Organizer: Samprit Banerjee, Cornell University

Chair: Yuanjia Wang, Columbia University

10:30
Shared Versus Specific Effects of Treatment on Multiple Outcomes in Clinical Trials using Latent Variable Modeling
Melanie Wall*, Columbia University

10:55
Using Multiple Imputation to Harmonize Data Across Multiple Trials that use Different Outcome Measures
Juned Siddique*, Northwestern University
Ahnalee Brinks, University of Miami
Charles H. Brown, Northwestern University
Jerome P. Reiter, Duke University

11:20
Simultaneous Estimation of Mixture Model for Multilevel Data
Haiqun Lin*, Shu-xia Li, Xiao Xu and **Harlan M. Krumholz**, Yale University

11:45
Three Novel Applications of Latent Variable Modeling: A Discussion
Samprit Banerjee*, Cornell University

12:10
Floor Discussion

32. CONTRIBUTED PAPERS: BAYESIAN ANALYSIS OF HIGH DIMENSIONAL DATA

Grand Ballroom I (3rd Floor)

Sponsor: ENAR

Chair: Mark Reimers, Virginia Commonwealth University

10:30
Constrained Priors and X-inactivation
Alan B. Lenarcic*, John Calaway, Fernando Pardo and **William Valdar**, University of North Carolina, Chapel Hill

* = Presenter | ■ = Student Award Winner

10:45

Bayesian Approach for Predicting Protein Secondary Structure

David B. Dahl, Brigham Young University
Qiwei Li* and **Marina Vannucci**, Rice University
Hyun Joo and **Jerry W. Tsai**, University of the Pacific

11:00

A Hierarchical Bayesian Model for Inference of Copy Number Variants and Their Association to Gene Expression

Alberto Cassese*, Rice University
Michele Guindani, University of Texas MD Anderson Cancer Center
Mahlet G. Tadesse, Georgetown University
Francesco Falciani, University of Liverpool
Marina Vannucci, Rice University

11:15

Sampling Designs for Multi-Species Assemblage with Unknown Heterogeneity

Hongmei Zhang, University of South Carolina
Kaushik Ghosh*, University of Nevada, Las Vegas
Pulak Ghosh, Indian Institute of Management, Bangalore

11:30

Bayes Multiple Classification Function in Logic Regression Models

Wensong Wu* and **Tan Li**, Florida International University

11:45

Using Informative Priors Obtained from Historical Data Significantly Improves Detection of Differentially Expressed Genes using Microarray Data

Ben Li* and **Qing He**, Emory University
Zhaonan Sun and **Yu Zhu**, Purdue University
Zhaohui Qin, Emory University

12:00

Smoothing Functional Data with a Hierarchical Bayesian Model

Jingjing Yang*, Rice University
Hongxiao Zhu, Virginia Tech
Dennis D. Cox, Rice University

33. CONTRIBUTED PAPERS: GENETICS AND EPIDEMIOLOGIC STUDY DESIGN

Grand Ballroom IV (3rd Floor)

Sponsor: ENAR

Chair: Osorio Meirelles, National Institute on Aging, National Institutes of Health

10:30

Control Function Assisted IPW Estimation with a Secondary Outcome in Case-control Studies

Tamar Sofer* and **Eric J. Tchetgen Tchetgen**, Harvard School of Public Health

10:45

Prediction of Cancer Drugs' Sensitivities using High-Dimensional Genomic Features

Ting-Huei Chen* and **Wei Sun**, University of North Carolina, Chapel Hill

11:00

Enhancing Genetic Case-control Studies using Sample Surveys

Parichoy Pal Choudhury* and **Daniel Scharfstein**, Johns Hopkins University
Joshua Galanter and **Chris Gignoux**, University of California, San Francisco
Lindsey Roth, Kaiser Permanente
Sam Oh, Esteban Burchard and **Saunak Sen**, University of California, San Francisco

11:15

The Effect of FTO Gene Variants and Physical Activity Interaction on Trunk Fat Percentage Among the Population of Newfoundland

Anthony Payne, Taraneh Abarin*, Farrell Cahill, Guang Sun and **J Concepción Loredo-Osti**, Memorial University

11:30

On the Underlying Assumptions of Threshold Boolean Networks as a Model for Genetic Regulatory Network Behavior

Van Tran*, Mathew N. McCall, Helene McMurray and **Anthony Almudevar**, University of Rochester Medical Center

11:45

Evaluation of Illumina Infimium 450K Methylation Chip using Technical Replicates

Maitreyee Bose*, Weihua Guan, Chong Wu, James Pankow, Ellen Demerath and **Jan Bressler**, University of Minnesota

12:00

Leveraging Family History in Genetic Association Studies

Arpita Ghosh*, Public Health Foundation of India
Patricia Hartge, National Cancer Institute, National Institutes of Health
Peter Kraft and **Amit D. Joshi**, Harvard School of Public Health
Regina G. Ziegler, National Cancer Institute, National Institutes of Health
Myrto Barrdahl, German Cancer Research Center
Stephen J. Chanock, Sholom Wacholder and **Nilanjan Chatterjee**, National Cancer Institute, National Institutes of Health

* = Presenter | ■ = Student Award Winner

34. CONTRIBUTED PAPERS: NON-LINEAR MODELS

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Phebe Brenne Kemmer, Emory University

10:30

Single Index Change Point Model with an Application of Environmental Health Study on Mortality and Temperature

Hamdy Mahmoud* and **Inyoung Kim**, Virginia Tech
Ho Kim, Seoul National University

10:45

A Model for Extreme Stacking of Data Censored at Endpoints of a Distribution with a Continuous Interior: Illustration with W-shaped Data

Robert Gallop*, Randall H. Rieger and **Scott McClintock**, West Chester University
David C. Atkins, University of Washington

11:00

Estimating a Dengue Ordinary Differential Equation Model with the Mesh Adaptive Direct Search Method

Yu-Ting Weng*, University of Pittsburgh
Shawn T. Brown and **Nathan Stone**, Pittsburgh Supercomputing Center
Abdus S. Wahed, University of Pittsburgh

11:15

Parametric and Nonparametric Spherical Regression

Michael M. Rosenthal ■, Wei Wu, Eric Klassen and **Anuj Srivastava**, Florida State University

11:30

Non-parametric Tests for One-Sided Interaction in Shape Restricted Models

Mingyu Xi*, University of Maryland, Baltimore County

11:45

Sparse Kernel Machine Regression for Ordinal Outcomes

Yuanyuan Shen*, Harvard School of Public Health
Katherine Liao, Brigham and Women's Hospital
Tianxi Cai, Harvard School of Public Health

12:00

Regression Models on Riemannian Symmetric Spaces

Emil A. Cornea*, Hongtu Zhu and **Joseph G. Ibrahim**, University of North Carolina, Chapel Hill

35. CONTRIBUTED PAPERS: SURVIVAL ANALYSIS FOR CLINICAL TRIAL DATA

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Chi Hyun Lee, University of Minnesota

10:30

Sample Size Calculation Based on Efficient Unconditional Tests for Clinical Trials with Historical Controls

Guogen Shan* and **Sheniz Moonie**, University of Nevada, Las Vegas

10:45

Sieve Estimation in a Markov Illness-Death Process Under Dual Censoring

Audrey Boruvka* and **Richard J. Cook**, University of Waterloo

11:00

A Simple Locally Efficient Estimator for Relative Risk in Case-cohort Studies

Emmanuel Sampene* and **Abdus S. Wahed**, University of Pittsburgh

11:15

Generation of Virtual Control Groups for Single Arm Prostate Cancer Adjuvant Trials

Zhenyu Jia*, University of Akron and Northeast Ohio Medical University
Michael B. Lilly, Medical University of South Carolina
Dan A. Mercola, University of California, Irvine

11:30

Imbalanced Randomization in Non-inferiority Trials can be Highly Efficient

Rick Chappell*, University of Wisconsin Madison

11:45

Estimating Survival Benefit in Randomized Clinical Trials with Treatment Arm Switching After Disease Progression

Shan Kang* and **Thomas M. Braun**, University of Michigan

12:00

Semiparametric Proportional Rates Regression for the Composite Endpoint of Recurrent and Terminal Events

Lu Mao* and **Danyu Lin**, University of North Carolina, Chapel Hill

* = Presenter | ■ = Student Award Winner

36. CONTRIBUTED PAPERS: CLUSTERED DATA METHODS

Bristol Room (3rd Floor)

Sponsor: ENAR

Chair: Michael D. Larsen, The George Washington University

10:30

A New Semiparametric Approach to Finite Mixture of Regressions using Penalized Regression via Fusion
Erin Austin*, Wei Pan and **Xiaotong Shen**, University of Minnesota

10:45

Semi-Parametric Models for Clustered Survival Data with Random Cluster Size
Shuling Liu*, Amita K. Manatunga and **Limin Peng**, Emory University

11:00

Identification of Biologically Relevant Subtypes via Preweighted Sparse Clustering
Sheila Gaynor*, Harvard University
Eric Bair, University of North Carolina, Chapel Hill

11:15

Estimation Methods for Copula Models for Discrete Clustered and Longitudinal Data
N. Rao Chaganty*, Old Dominion University

11:30

Biclustering via Sparse Clustering
Qian Liu ■, Guanhua Chen, Michael R. Kosorok and **Eric Bair**, University of North Carolina, Chapel Hill

11:45

Composite Likelihood Inference for Multivariate Finite Mixture Models with Application to Flow Cytometry Data
Fei Ma* and **Ollivier Hyrien**, University of Rochester

12:00

Weighted Quartile Sum Regression for Assessing the Association of Environmental Chemical Mixtures and Oral Health
Bhanu M. Evani* and **Chris Gennings**, Virginia Commonwealth University

37. CONTRIBUTED PAPERS: STATISTICAL METHODS FOR LONGITUDINAL DATA

Chasseur Room (3rd Floor)

Sponsor: ENAR

Chair: Chulmin Kim, University of West Georgia

10:30

Sample Size Determination for Longitudinal Binary Response Data based on Testing the Difference in Rate of Change in Log Odds Ratio between Groups
Kush Kapur*, Boston Children's Hospital and Harvard Medical School
Dulal K. Bhaumik, University of Illinois, Chicago

10:45

Model Selection of Generalized Estimating Equations with Multiple Imputation and High-dimensional Covariates for Missing Longitudinal Data
Ming Wang*, The Pennsylvania State College of Medicine

11:00

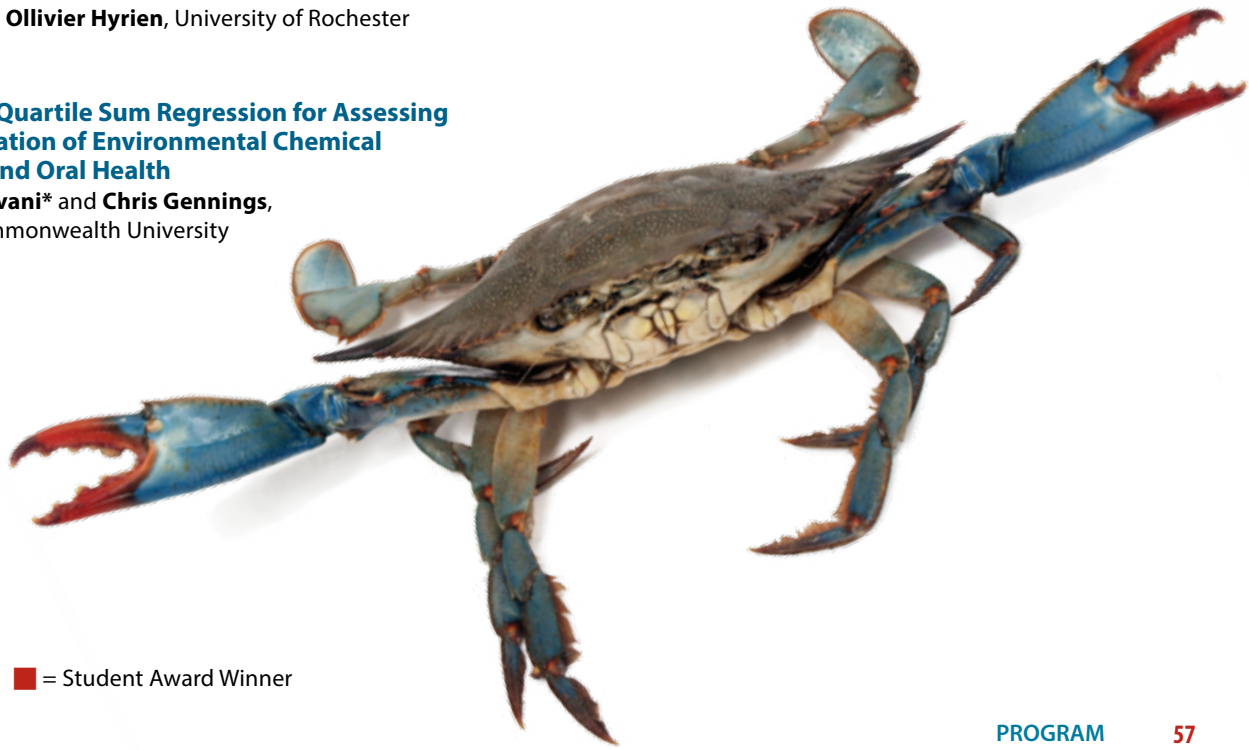
An EM Algorithm for Multilevel Multivariate Mixed Effect Model with Unstructured Error Covariance
Yun Ling* and **Stewart J. Anderson**, University of Pittsburgh

11:15

Regression Methodology for Comparing Longitudinal Rates of Change
Matthew W. Bryan*, University of Pennsylvania
Patrick Heagerty, University of Washington

11:30

Three-step Estimation via Local Polynomial Smoothing for Unevenly Sampled Longitudinal Data
Lei Ye*, Ada O. Youk, Susan M. Sereika and **Lora E. Burke**, University of Pittsburgh



✱ = Presenter | ■ = Student Award Winner

11:45

The Use of Tight Clustering Techniques for Group-based Trajectory Modeling of Longitudinal Data Accounting for Random Intercepts
Ching-Wen Lee* and **Lisa A. Weissfeld**, University of Pittsburgh

12:00

Monotone Spline-based Nonparametric Estimation of Longitudinal Data with Mixture Distribution
Wenjing Lu* and **Ying Zhang**, University of Iowa

Monday, March 17

12:15 pm – 1:30 pm

ROUNDTABLE LUNCHEONS

Dover Rooms (3rd Floor)

Monday, March 17

1:45 pm – 3:30 pm

38. RECENT DEVELOPMENTS IN ESTIMATING THE HEALTH EFFECTS OF AIR POLLUTION AND REGULATION

Grand Ballroom VIII (3rd Floor)

Sponsors: ENAR, ASA Section on Bayesian Statistical Science, Statistics and the Environment

Organizer: Brian Reich, North Carolina State University

Chair: Brian Reich, North Carolina State University

1:45

A Distributed Exposure Time-to-Event Model for Estimating Associations Between Air Pollution and Preterm Birth
Howard H. Chang*, Emory University
Joshua L. Warren, University of North Carolina, Chapel Hill
Lyndsey A. Darrow, Emory University
Brian J. Reich, North Carolina State University
Lance A. Waller, Emory University

2:10

Bayesian Kernel Machine Regression for Estimating the Health Effects of Pollution Mixtures
Brent A. Coull* and **Jennifer F. Bobb**, Harvard School of Public Health
Gregory A. Wellenius, Brown University
Murray Mittleman, Beth Israel Deaconess Medical Center

2:35

Estimating the Health Benefit of Reducing Indoor Air Pollution in a Randomized Environmental Intervention
Roger D. Peng*, Arlene Butz, Amber J. Hackstadt, D'Ann L. Williams, Gregory B. Diette, Patrick N. Breysse and **Elizabeth C. Matsui**, Johns Hopkins University

3:00

Influence of Time-varying Air Pollution Exposure on Rate of Change Estimates for Progression of Cardiovascular Disease
Lianne Sheppard* and **Adel Lee**, University of Washington

3:25

Floor Discussion

39. RECENT ADVANCES IN CAUSAL INFERENCE

Grand Ballroom III (3rd Floor)

Sponsors: IMS, ASA Mental Health Statistics Section, ASA Biometrics Section

Organizer: Dylan Small, University of Pennsylvania

Chair: Dylan Small, University of Pennsylvania

1:45

Causal Inference with Social Network Data: Inflated Effective Sample Sizes, Deflated Standard Errors, and Other Perils
Elizabeth Ogburn *, Johns Hopkins University

2:10

Causal Inference with Continuous Treatments
Yeying Zhu*, University of Waterloo
Donna L. Coffman and **Debashis Ghosh**, The Pennsylvania State University

2:35

Balancing Covariates via Propensity Score Weighting: A New Perspective
Fan Li*, Duke University
Alan Zaslavsky, Harvard Medical School
Kari Lock Morgan, Duke University

3:00

Robust Estimation of Causal Effects of Erythropoiesis-stimulating Agents (ESAs) on Mortality
Roee Gutman* and **David D. Dore**, Brown University

3:25

Floor Discussion

* = Presenter | ■ = Student Award Winner

40. SOCIAL NETWORK DATA: CHALLENGES AND OPPORTUNITIES

Grand Ballroom II (3rd Floor)

Sponsors: IMS, ASA Statistical Learning and Data Mining Section

Organizer: Elizabeth Ogburn, Harvard University

Chair: Iván Díaz, Johns Hopkins University

1:45
What, if Anything, Do We Learn by Fitting an Exponential-family Random Graph Model?
Cosma Shalizi* and **Alessandro Rinaldo**, Carnegie Mellon University

2:10
Bayesian Inference for Non-Ignorable Sampling in Social Networks
Simon Lunagomez* and **Edoardo M. Airoldi**, Harvard University

2:35
Targeted Learning of Causal Effects for Networks
Mark J. van der Laan*, University of California, Berkeley

3:00
Diffusion Matters, But How?
Kevin A. Bryan*, Northwestern University

3:25
Floor Discussion

41. STATISTICS AND COMPUTING FOR HIGH-THROUGHPUT SEQUENCING DATA

Grand Ballroom V (3rd Floor)

Sponsors: ENAR, ASA Statistical Learning and Data Mining Section

Organizer: Hongkai Ji, Johns Hopkins School of Public Health

Chair: Hongkai Ji, Johns Hopkins School of Public Health

1:45
Computational Challenges in Exome and RNA-Seq Analysis
Steven L. Salzberg*, Johns Hopkins University

2:10
Statistical Modeling of Alternative Splicing with RNA-Seq Data
Hui Jiang*, University of Michigan
Julia Salzman, Stanford University
Yang Shi, University of Michigan

2:35
Statistical Analysis of Deep Sequencing Data from Tumor Samples
Lin Hou, Yale School of Public Health
Mengjie Chen, Yale University
Hongyu Zhao*, Yale School of Public Health

3:00
Models and Statistics for Detection of Genome Structural Variation
Nancy R. Zhang*, University of Pennsylvania
David Siegmund, Stanford University
Benjamin Yakir, The Hebrew University

3:25
Floor Discussion

42. VARIABLE SELECTION AND ANALYSIS OF HIGH DIMENSIONAL DATA

Grand Ballroom I (3rd Floor)

Sponsors: ENAR, ASA Statistical Learning and Data Mining Section

Organizer: Lily Wang, University of Georgia

Chair: Lily Wang, University of Georgia

1:45
Regularized Semiparametric Functional Linear Regression
Helen Zhang*, University of Arizona

2:10
Dimension Reduction for Tensor Regression
Peng Zeng*, Auburn University
Wenxuan Zhong, University of Georgia

2:35
Sparse Group LASSO for Pathway Based GWAS
Tatiyana V. Apanasovich*, The George Washington University

3:00
Floor Discussion

* = Presenter | ■ = Student Award Winner

43. FUNCTIONAL DATA ANALYSIS AND ITS APPLICATIONS IN GENETICS

Grand Ballroom VI (3rd Floor)

Sponsor: ENAR

Organizer: Ruzong Fan, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

Chair: Yifan Wang, National Institutes of Health

1:45

Most Predictive Interval Selection for Functional Predictors, with Application to Classifying Tumor Stages from Mass Spectra

Andreas Kryger Jensen, University of Southern Denmark, Odense
Hans-Georg Müller*, University of California, Davis

2:10

Restricted Likelihood Ratio Tests for Functional Effects in the Functional Linear Model

Bruce J. Swihart*, Johns Hopkins Bloomberg School of Public Health
Jeff Goldsmith, Columbia University
Ciprian M. Crainiceanu, Johns Hopkins Bloomberg School of Public Health

2:35

Gene-gene Interaction Analysis for Next-generation Sequencing

Momiao Xiong*, University of Texas School of Public Health
Yun Zhu and **Jinying Zhao**, Tulane University

3:00

Functional Regression Models for Association Analysis of Complex Traits

Ruzong Fan*, Yifan Wang and **James L. Mills**, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health
Alexander F. Wilson and **Joan E. Bailey-Wilson**, National Human Genome Research Institute, National Institutes of Health
Momiao Xiong, University of Texas, Houston

3:25

Floor Discussion

44. EMERGING STATISTICAL CHALLENGES WITH COMPLEX LONGITUDINAL OR FUNCTIONAL DATA

Grand Ballroom IX (3rd Floor)

Sponsor: ENAR, ASA Biometrics Section

Organizer: Lu Wang, University of Michigan

Chair: Lu Wang, University of Michigan

1:45

Consistent Estimation of Covariate Effects for Some Between-/Within-Cluster Covariate Decomposition Methods When Data are Missing at Random

John Neuhaus* and **Charles McCulloch**, University of California, San Francisco

2:10

Handling Missing Data for Multiple Waves of Longitudinal Data

Xuan Bi and **Annie Qu***, University of Illinois, Urbana-Champaign

2:35

A Broad Framework for Joint Modeling and Some Tales from the Unexpected

Geert Molenberghs*, I-BioStat, Hasselt Universiteit and Katholieke Universiteit Leuven, Belgium
Michael G. Kenward, London School of Hygiene and Tropical Medicine, UK
Marc Aerts, Hasselt Universiteit, Belgium
Geert Verbeke, Katholieke Universiteit Leuven and Hasselt Universiteit, Belgium
Anastasios Tsiatis and **Marie Davidian**, North Carolina State University
Dimitris Rizopoulos, Erasmus University, The Netherlands

3:00

Modeling and Estimation Methods for Physical Activity Data

Haocheng Li and **Raymond J. Carroll***, Texas A&M University
John Staudenmayer, University of Massachusetts, Amherst

3:25

Floor Discussion

✱ = Presenter | ■ = Student Award Winner

45. CONTRIBUTED PAPERS: GENOME WIDE ASSOCIATION STUDIES

Grand Ballroom IV (3rd Floor)

Sponsor: ENAR

Chair: Alexandre Bureau, Université Laval

1:45

Testing Calibration of Risk Models at Extremes of Disease-risk

Minsun Song*, National Cancer Institute, National Institutes of Health
Peter Kraft and **Amit D. Joshi**, Harvard School of Public Health
Myrto Barrdahl, German Cancer Research Center
Nilanjan Chatterjee, National Cancer Institute, National Institutes of Health

2:00

An Adaptive Genetic Association Test using Double Kernel Machines

Xiang Zhan* and **Debashis Ghosh**, The Pennsylvania State University

2:15

Multi-Marker Tests for Joint Association in Longitudinal Studies using the Genetic Random Field Model

Zihuai He*, Min Zhang, Jennifer Smith, Sharon Kardia, Ana Diez Roux and **Seunggeun Lee**, University of Michigan
Xiuqing Guo and **Walter Palmas**, Columbia University
Bhramar Mukherjee, University of Michigan

2:30

More Powerful Genetic Association Testing via a New Statistical Framework for Integrative Genomics

Sihai D. Zhao*, Tony Cai and **Hongzhe Li**, University of Pennsylvania

2:45

Principal Component Regression and Linear Mixed Model in Association Analysis of Structured Samples: Competitors or Complements?

Yiwei Zhang ■, Novartis Pharmaceuticals
Wei Pan, University of Minnesota

3:00

A Versatile Omnibus Test for Detecting Mean and Variance Heterogeneity for Quantitative Traits

Peng Wei*, Ying Cao and **Taylor Maxwell**, University of Texas School of Public Health

3:15

Flexible and Robust Methods for Rare-variant Testing of Quantitative Traits in Pedigrees

Yunxuan Jiang*, Karen N. Conneely and **Michael P. Epstein**, Emory University

46. CONTRIBUTED PAPERS: APPLICATIONS OF BAYESIAN METHODS

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Jing Zhang, University of Minnesota

1:45

Semi-parametric Bayesian Clustering of Ophthalmology Data

Xin Tong*, University of South Carolina
Hongmei Zhang, University of Memphis

2:00

A Nonparametric Bayesian Latent Factor Model for Body Image Evaluation

Kassie Fronczyk*, Rice University
Michele Guindani, University of Texas MD Anderson Cancer Center
Marina Vannucci, Rice University

2:15

Bayes Sensitivity Analysis with Fisher-Rao Metric

Sebastian Kurtek and **Karthik Bharath***, The Ohio State University

2:30

Bayesian Inference on Multiple Proportions for Misclassified Binomial Data

Dewi Rahardja and **Haiwen Shi***, U.S. Food and Drug Administration

2:45

Longitudinal Mediation Analysis

Chanmin Kim* and **Michael J. Daniels**, University of Texas, Austin
Jason A. Roy, University of Pennsylvania
Beth H. Marcus, University of California, San Diego

3:00

Estimation of Contact Network Properties using Multiple HIV Epidemic Data Sources

Ravi Goyal* and **Nicole B. Carnegie**, Harvard University

3:15

Bayesian Variable Selection for a Regression Model with a Misclassified Binary Covariate

Daniel P. Beavers*, Wake Forest School of Medicine
James D. Stamey, Baylor University

* = Presenter | ■ = Student Award Winner

47. CONTRIBUTED PAPERS: HIGH DIMENSIONAL DATA

Grand Ballroom VII (3rd Floor)

Sponsor: ENAR

Chair: Yuval Benjamini, Stanford University

1:45

Inference for Survival Prediction in the High Dimensional Setting

Jennifer A. Sinnott* and **Tianxi Cai**, Harvard University

2:00

Testing High-dimensional Nonparametric Function with Application to Gene Set Analysis

Tao He*, Ping-Shou Zhong, Yuehua Cui and **Vidyadhar Mandrekar**, Michigan State University

2:15

Variable Selection and Inference for Ultra-High Dimensional Survival Data With Missing Covariates Under Proportional Hazards Models

Yang Ning* and **Grace Yi**, University of Waterloo
Baojiang Chen, University of Nebraska
Nancy Reid, University of Toronto

2:30

An EM Test for the Contaminated Chi-Square Model

Feng Zhou*, University of Kentucky
Hongying Dai, Children's Mercy Hospital
Richard Charnigo, University of Kentucky

2:45

Biostatistical Matrix Time Series Models

Seyed Yaser Samadi* and **Lynne Billard**, University of Georgia

3:00

Supervised Singular Value Decomposition and Its Asymptotic Properties

Gen Li ■ and **Haipeng Shen**, University of North Carolina, Chapel Hill
Dan Yang, Rutgers, The State University of New Jersey
Andrew Nobel, University of North Carolina, Chapel Hill

3:15

brainR: Interactive 3 and 4d Images of High Resolution Neuroimage Data

John Muschelli*, Elizabeth M. Sweeney and **Ciprian M. Crainiceanu**, Johns Hopkins Bloomberg School of Public Health

48. CONTRIBUTED PAPERS: CLINICAL TRIALS

Bristol Room (3rd Floor)

Sponsor: ENAR

Chair: Ashutosh Ranjan, University of Alabama, Birmingham

1:45

Outcome-adaptive Allocation with Natural Lead-in for Three-group Trials with Binary Outcomes

Ghalib A. Bello* and **Roy T. Sabo**, Virginia Commonwealth University

2:00

Trial Design and Analysis Challenges When Studying Therapies Designed to Control Growth of Brain Metastases in Cancer Patients

Sujata M. Patil*, Memorial Sloan-Kettering Cancer Center

2:15

Understanding Inconsistencies Between Replicate Trials: Insomnia Case Study

Richard Entsuah, Kenneth Liu*, Junshui Ma, Duane Snavely and **Ellen Snyder**, Merck

2:30

Sample Size Determination for a Three-arm Equivalence Trial of Normally Distributed Responses

Yu-Wei Chang*, Temple University
Yi Tsong and **Xiaoyu Dong**, U.S. Food and Drug Administration
Zhigen Zhao, Temple University

2:45

The Utility of Bayesian Predictive Probabilities for Interim Monitoring of Clinical Trials

Benjamin R. Saville*, Vanderbilt University School of Medicine
Jason Connor, Berry Consultants
Gregory Ayers and **JoAnn Alvarez**, Vanderbilt University School of Medicine

3:00

Evaluation of Bias for Outcome Response Adaptive Randomization Designs

Yaping Wang*, University of Texas MD Anderson Cancer Center and University of Texas School of Public Health
Hongjian Zhu, University of Texas School of Public Health
J. Jack Lee, University of Texas MD Anderson Cancer Center

3:15

Analysis of the Anticipated Power of a Test: Browne (1995) Revisited

Paul W. Stewart*, University of North Carolina, Chapel Hill

✱ = Presenter | ■ = Student Award Winner

49. CONTRIBUTED PAPERS: PERSONALIZED MEDICINE AND VARIABLE SUBSET SELECTION

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Na Zhang, North Carolina State University

1:45

Multivariate Markov Models for the Conditional Probability of Toxicity in Phase II Trials
Laura L. Fernandes*, Susan Murray and **Jeremy MG Taylor**, University of Michigan

2:00

Latent Supervised Learning for Estimating Treatment Effect Heterogeneity
Susan Wei* and **Michael R. Kosorok**, University of North Carolina, Chapel Hill

2:15

Personalized Selection of Radiation Therapy Dose using Statistical Models for Toxicity and Efficacy with Dose and Biomarkers as Covariates
Matthew Schipper* and **Jeremy MG Taylor**, University of Michigan
Feng-Ming Kong, Georgia Regents University
Randy TenHaken and **Martha Matuzak**, University of Michigan

2:30

Simultaneous Inference for Assessing the Effects of a SNP on Treatment Efficacy in Personalized Medicine
Ying Ding*, University of Pittsburgh
Grace Li and **Stephen J. Ruberg**, Eli Lilly and Company
Jason C. Hsu, Eli Lilly and Company and The Ohio State University

2:45

Consistent Variable Selection for Quantile Regression with Varying Covariate Effects
Qi Zheng* and **Limin Peng**, Emory University

3:00

Consistent Bi-level Variable Selection via Composite Group Bridge Regression
Indu Seetharaman, Kansas State University
Kun Chen*, University of Connecticut

3:15

Penalized Regression for Interval-Censored Times of Disease Progression: Selection of HLA Markers in Psoriatic Arthritis
Ying Wu* and **Richard Cook**, University of Waterloo

50. CONTRIBUTED PAPERS: ANALYSIS OF CLUSTERED DATA

Chasseur Room (3rd Floor)

Sponsor: ENAR

Chair: Jacek Urbanek, Indiana University Fairbanks School of Public Health

1:45

Statistical Methods for Assessing Perception in Children with Cochlear Implants
Michael D. Larsen* and **Cynthia Core**, The George Washington University
Janean Wilson, Children's National Medical Center
James Mahshie, The George Washington University

2:00

Identify Common Clusters in Independent Populations with Application to Psychiatry
Yun Zhang*, Kehui Chen, Allan Sampson and **David Volk**, University of Pittsburgh

* = Presenter | ■ = Student Award Winner

2:15

Generalized Estimating Equation in Analyzing Group-Randomized Trials with Limited Number of Groups
Peng Li* and **David T. Redden**, University of Alabama, Birmingham

2:30

Accounting for Covariates in Differential Methylation Analysis with Next-generation Sequencing
Hongyan Xu*, Georgia Regents University
Robert Podolsky, Wayne State University
Duchwan Ryu and **Varghese George**, Georgia Regents University

2:45

Evaluating Predictors of Individual Dietary Intake Latent Values under Different Mixed Models
Shuli Yu* and **Edward J. Stanek III**, University of Massachusetts, Amherst

3:00

A Markov Mixture Model for Longitudinal Course of Youth Bipolar Disorder
Jieyu Fan*, Satish Iyengar and **Boris Birmaher**, University of Pittsburgh
Adriana Lopez, Carnegie Mellon University, Qatar
Rasim S. Diler, University of Pittsburgh
David Axelson, The Ohio State University
Benjamin Goldstein, University of Toronto
Tina Goldstein, University of Pittsburgh
Fangzi Liao and **Mary K. Gill**, Western Psychiatric Institute and Clinic

3:15

Longitudinal Multivariate Outcome Data from Couples: Application to HPV Transmission Couple Studies
Xiangrong Kong*, Johns Hopkins University Bloomberg School of Public Health

Monday, March 17

3:30 pm – 3:45 pm

Refreshment Break with Our Exhibitors

Grand Ballroom Foyer (3rd Floor)

Monday, March 17

3:45 pm – 5:30 pm

51. THE ROLE OF STATISTICS IN SHAPING PUBLIC POLICY

Grand Ballroom II (3rd Floor)

Sponsors: ENAR, ASA Government Statistics Section

Organizer: Hernando Ombao, University of California at Irvine

Chair: Hernando Ombao, University of California at Irvine

3:45

Statisticians: Guardians of Democracy!
Roderick J. Little*, University of Michigan

4:30

Big Statistics, Major Policies, and... a Little Politics
Sally C. Morton*, University of Pittsburgh

5:15

Floor Discussion

52. PANEL DISCUSSION: HAVING IT ALL: WEIGHTING TO ACHIEVE BALANCE

Grand Ballroom V (3rd Floor)

Sponsor: ENAR

Organizers: Shari Messinger, University of Miami and **Leslie McClure**, University of Alabama, Birmingham

Chairs: Shari Messinger, University of Miami and **Leslie McClure**, University of Alabama at Birmingham

3:45

Thomas M. Braun, University of Michigan
Mary D. Sammel, University of Pennsylvania
Telba Z. Irony, U.S. Food and Drug Administration
Aarti Shah, Eli Lilly & Company
Francesca Dominici, Harvard School of Public Health

5:15

Floor Discussion

* = Presenter | ■ = Student Award Winner

53. BIOSTATISTICAL METHODS FOR INTEGRATIVE GENOMICS

Grand Ballroom VI (3rd Floor)

Sponsor: ENAR

Organizer: Wei Sun, University North Carolina, Chapel Hill

Chair: Wei Sun, University North Carolina, Chapel Hill

3:45
A Brief Overview of Modelling Approaches in Integrative Genomics, with Special Reference to eQTL Analyses
Sylvia T. Richardson*, Cambridge Institute of Public Health

4:25
Information Integrative Framework for Sparse K-means to Combine multi-Cohort and Multi-omics Data
Zhiguang Huo, Sunghwan Kim and **George C. Tseng***, University of Pittsburgh

4:45
EgoNet: Identification of Disease Ego-network Modules
Rendong Yang, Zhaohui S. Qin and **Tianwei Yu***, Emory University

5:05
Extensions to Hidden Markov Models and Their Application to Integrated Analysis of Multiple Chromatin Immunoprecipitation Data
Hyung Won Choi, National University of Singapore
Damian Famian and **Alexey Nesvizhskii**, University of Michigan
Debashis Ghosh, The Pennsylvania State University
Zhaohui S. Qin*, Emory University

5:25
Floor Discussion

54. SAFETY SURVEILLANCE MONITORING THROUGH SIGNAL DETECTION

Grand Ballroom I (3rd Floor)

Sponsors: ENAR, ASA Biopharmaceutical Section

Organizer: Theodore Lystig, Medtronic, Inc.

Chair: Laura Hatfield, Harvard Medical School

3:45
Methodological Challenges for Sequential Medical Product Safety Surveillance using Observational Healthcare Data
Andrea J. Cook* and **Jennifer C. Nelson**, Group Health Research Institute

4:10
Graphical Approaches for Disproportionality Analysis of Spontaneously-Reported Adverse Events in Pharmacovigilance
Richard C. Zink*, JMP Life Sciences at SAS Insitute, Inc.

4:35
Likelihood Ratio Tests for Active Surveillance
Ram C. Tiwari*, U.S. Food and Drug Administration

5:00
Discussion of Safety Surveillance Monitoring Through Signal Detection
Theodore Lystig*, Medtronic, Inc.

5:25
Floor Discussion

55. MULTIPLE TESTING AND SIMULTANEOUS INFERENCES IN COMPLEX SETTINGS

Grand Ballroom III (3rd Floor)

Sponsors: ENAR, ASA Statistical Learning and Data Mining Section, ASA Biopharmaceutical Section

Organizer: Yi-Hui Zhou, North Carolina State University

Chair: Yi-Hui Zhou, North Carolina State University

3:45
False Discovery Rate Control and Group Testing for Complex Omics Data
Andrew B. Nobel* and **Gen Li**, University of North Carolina, Chapel Hill
Andrey Shabalin, Virginia Commonwealth University
Ivan Rusyn, University of North Carolina, Chapel Hill
Fred A. Wright, North Carolina State University

4:10
Another Look at Robust PC-based Stratification Control for Multiple Testing
Yi-Hui Zhou*, North Carolina State University

4:35
Simultaneous Inference of Multiple Rare Variants: Design, Power and Interpretation of Findings
Andriy Derkach, University of Toronto
Jerry F. Lawless, University of Waterloo
Lei Sun*, University of Toronto

5:00
Extending the Projack to Complex Settings
Fred A. Wright* and **Yi-Hui Zhou**, North Carolina State University

5:25
Floor Discussion

* = Presenter | ■ = Student Award Winner

56. NEW DEVELOPMENTS IN BAYESIAN NONPARAMETRICS

Grand Ballroom IX (3rd Floor)

Sponsors: IMS, ASA Section on Bayesian Statistical Science

Organizer: Jian Kang, Emory University School of Public Health

Chair: Jian Kang, Emory University School of Public Health

3:45
Scalable Bayesian ASA Section on Nonparametric Statistics
David B. Dunson*, Duke University

4:10
Bayesian Models of Structured Sparsity for Discovery of Regulatory Genetic Variants
Ryan P. Adams*, Harvard University
Barbara Engelhardt, Duke University

4:35
Bayesian Nonparametric Inference of Population Admixtures
Maria De Iorio* University College London
Stefano Favaro, Universita' degli Studi di Torino
Yee Whye Teh, University of Oxford
Lloyd Elliott, University College London

5:00
Pre-surgical Assessment of Peritumoral Brain Activation Via a Bayesian Non-parametric Potts Model
Timothy D. Johnson*, University of Michigan

5:25
Floor Discussion

57. CONTRIBUTED PAPERS: STATISTICAL GENETICS AND GENOMICS

Grand Ballroom VIII (3rd Floor)

Sponsor: ENAR

Chair: Sihai Dave Zhao, University of Pennsylvania

3:45
Sparse Multivariate Factor Analysis Regression Models and Its Applications to Integrative Genomics Analysis
Yan Zhou* and **Peter Song**, University of Michigan
Pei Wang, Fred Hutchinson Cancer Research Center
Ji Zhu, University of Michigan

4:00
A General Statistical Framework for Transcript Assemblies
Alyssa Frazee*, Geo Pertea, Steven Salzberg and **Jeff Leek**, Johns Hopkins University

4:15
Nonparametric Test for Differential Binding Analysis with ChIP-Seq Data
Qian Wu*, Kyoung-Jae Won and **Hongzhe Li**, University of Pennsylvania

4:30
A Statistical Framework for Expression QTL Mapping via Two-way Mixture Model
Ningtao Wang*, Yaqun Wang, Bruce Lindsay and **Rongling Wu**, The Pennsylvania State University

4:45
SVM with Bootstrap for Soft Clustering of Populations
Matey Neykov*, Harvard University

5:00
Functional Principal Component Analysis for Next Generation Sequencing
Lieven Clement*, Ghent University

5:15
The Generalized Higher Criticism for Testing SNP-sets in Genetic Association Testing
Ian J. Barnett ■ and **Xihong Lin**, Harvard University

58. CONTRIBUTED PAPERS: IMAGING

Grand Ballroom IV (3rd Floor)

Sponsor: ENAR

Chair: Sheng Luo, University of Texas Health Science Center at Houston

3:45
Modeling Covariate Effects in Group Independent Component Analysis with Applications to Functional Magnetic Resonance Imaging
Ran Shi* and **Ying Guo**, Emory University

4:00
Quantile Mapping for Multi-modal Imaging Data
Huaihou Chen*, Philip T. Reiss, Clare Kelly and **Xavier F. Castellanos**, New York University School of Medicine

4:15
Latent Variable Models for Longitudinal MR Imaging Data with Multiple Outcomes
Xiao Wu*, University of Florida
Michael J. Daniels, University of Texas, Austin

4:30 A Novel Brain Connectivity Network Model: Build Bridges Between Network Communities
Shuo Chen*, University of Maryland, College Park

✱ = Presenter | ■ = Student Award Winner

4:45

A Bayesian Model for Brain Activation and Connectivity

Zhe Yu* and **Hernando Ombao**, University of California, Irvine
Raquel Prado, University of California, Santa Cruz
Erin Burke and **Steve Cramer**, University of California, Irvine

5:00

Pre-Surgical fMRI Data Analysis using a Spatially Adaptive Conditional Autoregressive Model

Zhuqing Liu*, Veronica J. Berrocal and **Timothy D. Johnson**, University of Michigan

5:15

Spatial and Temporal Pattern in the Brain Accounting Cognitive Changes After Mild Traumatic Brain Injury

Namhee Kim*, Craig A. Branch and **Michael L. Lipton**, Albert Einstein College of Medicine

59. CONTRIBUTED PAPERS: SEMI-PARAMETRIC AND NON-PARAMETRIC MODELS IN SURVIVAL ANALYSIS

Grand Ballroom VII (3rd Floor)

Sponsor: ENAR

Chair: Tian Dai, Emory University

3:45

Semiparametric Bayes Estimation of Gap-Time Distribution with Correlated Recurrent Event Data

AKM F. Rahman* and **Edsel A. Pena**, University of South Carolina, Columbia

4:00

Quantile Regression Models for Current Status Data

Fang-Shu Ou ■, Donglin Zeng and **Jianwen Cai**, University of North Carolina, Chapel Hill

4:15

Competing Risks Regression Under Random Signs Censoring

Jonathan Yabes* and **Joyce Chang**, University of Pittsburgh

4:30

Regression Analysis of Informatively Interval-censored Failure Time Data with Cox Model

Ling Ma*, University of Missouri, Columbia
Tao Hu, Capital Normal University, China
Jianguo Sun, University of Missouri, Columbia

4:45

Floor Discussions

5:00

Weighted Estimation of the Accelerated Failure Time Model in the Presence of Dependent Censoring

Youngjoo Cho* and **Debashis Ghosh**, The Pennsylvania State University

5:15

Model Assisted Cox Regression

Shoubhik Mondal* and **Sundarraman Subramanian**, New Jersey Institute of Technology

60. CONTRIBUTED PAPERS: HIERARCHICAL MODELS

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Michelle Ross, University of Pennsylvania

3:45

Examining the Spatio-temporal Trend Between Alcohol Outlets and Violence using Integrated Nested Laplace Approximations

Loni P. Tabb*, Drexel University
Tony H. Grubesic, Oregon State University

4:00

The Role of Prior Effective Sample Size in the Design of Bayesian Medical Device Studies

Gene A. Pennello and **Laura Thompson***, U.S. Food and Drug Administration

4:15

A Hybrid Bayesian Hierarchical Model Combining Cohort and Case-control Studies for Meta-analysis of Diagnostic Tests: Accounting for Disease Prevalence and Partial Verification Bias

Xiaoye Ma*, University of Minnesota
Yong Chen, University of Texas
Stephen Cole, University of North Carolina, Chapel Hill
Haitao Chu, University of Minnesota

4:30

Group Comparison of Pulsatile Hormone Times Series

TingTing Lu* and **Timothy D. Johnson**, University of Michigan

4:45

Population Size Estimation with Inactive Lists: Hierarchical Mixture Models and Missing Data with Application to Armed Conflict Data

Shira Mitchell* and **Al Ozonoff**, Harvard University
Kristian Lum, Virginia Polytechnic Institute and State University
Alan M. Zaslavsky and **Brent A. Coull**, Harvard University

* = Presenter | ■ = Student Award Winner

5:00

Bayesian Hierarchical Joint Modeling of Repeatedly Measured Continuous and Ordinal Markers of Disease Severity

Olive D. Buhule*, Abdus S. Wahed and **Ada O. Youk**, University of Pittsburgh

5:15

Hierarchical Nearest-Neighbor Gaussian Process Models for Massive Geostatistical Datasets

Abhirup Datta* and **Sudipto Banerjee**, University of Minnesota
Andrew O. Finley, Michigan State University

61. CONTRIBUTED PAPERS: METHODS FOR REMOVING SELECTION BIAS AND CONFOUNDING

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Yenny Webb-Vargas, Johns Hopkins Bloomberg School of Public Health

3:45

Stable Weights that Balance Covariates for Causal Inference and Estimation with Incomplete Data

Jose Zubizarreta ■, Columbia University

4:00

Matching using Propensity Score Methods for Time-varying Treatments

Pallavi S. Mishra-Kalyani*, Brent A. Johnson and **Qi Long**, Emory University

4:15

Estimating Causal Effects in an Observational Study with a Survival Time Endpoint

Jaeun Choi* and **Mary Beth Landrum**, Harvard Medical School
A. James O'Malley, Dartmouth College
Bruce Landon, Harvard Medical School

4:30

Weighting to Strengthen an Instrumental Variable

Doug Lehmann*, Yun Li and **Yi Li**, University of Michigan

4:45

Propensity Score Bin Bootstrapping Method in Estimation of Cost-Effectiveness

Zugui Zhang*, Paul Kolm and **William S. Weintraub**, Christiana Care Health System

5:00

Maximum Likelihood Adjustment for Mis-measured Exposure using External Validation Data and Propensity Scores

Danielle Braun*, Harvard School of Public Health and Dana-Farber Cancer Institute
Malka Gorfine, Israel Institute of Technology
Corwin Zigler and **Francesca Dominici**, Harvard School of Public Health
Giovanni Parmigiani, Harvard School of Public Health and Dana-Farber Cancer Institute

5:15

Examination of Statistical Power in a Propensity Score Analysis Approach

Falynn C. Turley* and **David Redden**, University of Alabama, Birmingham

62. CONTRIBUTED PAPERS: FUNCTIONAL DATA ANALYSIS

Bristol Room (3rd Floor)

Sponsor: ENAR

Chair: Guanqun Cao, Auburn University

3:45

Structured Functional Principal Component Analysis

Haochang Shou*, Vadim Zipunnikov and **Ciprian M. Crainiceanu**, Johns Hopkins Bloomberg School of Public Health
Sonja Greven, Ludwig-Maximilians-Universitat, Germany

4:00

A Robust Approach for Functional Linear Regression Model

Yihong Zhao*, New York University Medical Center
R. Todd Ogden, Columbia University Medical Center
Huaihou Chen, New York University Medical Center

4:15

Nonlinear Functional Regression Models with Application to Copy Number Data

Adrian Coles* and **Arnab Maity**, North Carolina State University
Ganiraju Manyam and **Veerabhadran Baladandayuthapani**, University of Texas MD Anderson Cancer Center

4:30

Generalized Functional Linear Models for Case-Control Association Studies

Ruzong Fan, Yifan Wang* and **James L. Mills**, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health
Iryna Lobach, University of California, San Francisco
Momiao Xiong, University of Texas, Houston

* = Presenter | ■ = Student Award Winner

4:45

Wavelet-based Function-on-Function Mixed Models

Mark J. Meyer* and **Brent A. Coull**, Harvard University
Francesco Versace and **Jeffrey S. Morris**, University of Texas MD Anderson Cancer Center

5:00

A Computational Framework for Genetic Mapping of Heterochrony

Han Hao*, **Ningtao Wang** and **Yaqun Wang**, The Pennsylvania State University
Jianxin Wang and **Zhong Wang**, Beijing Forestry University
Rongling Wu, The Pennsylvania State University

63. CONTRIBUTED PAPERS: RECENT ADVANCES IN BAYESIAN METHODS

Chasseur Room (3rd Floor)

Sponsor: ENAR

Chair: Karthik Bharath, The Ohio State University

3:45

Incorporating Spatial Dependence into Bayesian Multiple Testing of Statistical Parametric Maps in Functional Neuroimaging

Andrew Brown*, Clemson University
Nicole A. Lazar and **Gauri S. Datta**, University of Georgia
Woncheol Jang, Seoul National University
Jennifer E. McDowell, University of Georgia

4:00

Multivariate Bayesian Censored Models for Predicting Exposure to Multiple Chemical Agents

Caroline Groth*, Sudipto Banerjee, Tran Huynh and **Gurumurthy Ramachandran**, University of Minnesota
Richard Kwok, National Institute of Environmental Health Sciences, National Institutes of Health
Mark Stenzel, Exposure Assessment Applications, LLC
Patricia Stewart, Stewart Exposure Assessments, LLC

4:15

Methods in Functional Data Analysis for Curve Comparison in Spectroscopic Protein Unfolding Data: Applications using Bayesian Inferential Methods

Miranda L. Lynch*,
University of Connecticut Health Center

4:30

Bayesian Variable Selection for High Dimensional Datasets in the Presence of Error-prone Time-to-event Outcomes

Xiangdong Gu* and **Raji Balasubramanian**,
University of Massachusetts, Amherst

4:45

Cortical Thickness Thinning and Cognitive Impairment in Parkinson's Disease Without Dememtia

Lijun Zhang*, Ming Wang, Nicholas Sterling, EunYoung Lee, Guangwei Du, Mechelle Lewis and **Xuemei Huang**,
The Pennsylvania State University,
Milton S. Hershey Medical Center

5:00

Bayesian Modeling of Mixed Outcome Types using Random Effect

Hua Wei*, Eli Lilly and Company

5:15

An Objective Stepwise Bayes Approach to Small Area Estimation

Yanping Qu*, U.S. Food and Drug Administration
Glen D. Meeden, University of Minnesota

Tuesday, March 18

8:30 am – 10:15 am

64. STATISTICAL LEARNING FOR COMPLEX MULTIVARIATE BIOMEDICAL DATA

Grand Ballroom VIII (3rd Floor)

Sponsors: ENAR, ASA Mental Health Statistics Section, ASA Statistical Learning and Data Mining Section

Organizer: Huaihou Chen, New York University

Chair: Huaihou Chen, New York University

8:30

Linear Conditioning for Clustering Functional Data

Thaddeus Tarpey*, Wright State University

8:55

Multiple Kernel Statistical Learning to Combine Heterogeneous Data Sources for Prediction

Tianle Chen, Columbia University
Donglin Zeng, University of North Carolina, Chapel Hill
Yuanjia Wang*, Columbia University

9:20

Margin-based Learning of Minimum Clinically Important Difference

Tu Xu and **Samad Hedayat**, University of Illinois, Chicago
Junhui Wang*, City University of Hong Kong

* = Presenter | ■ = Student Award Winner

9:45

Dynamic Directional Model for Effective Brain Connectivity using Electrocorticographic (ECoG) Time Series

Tingting Zhang* and **Jingwei Wu**, University of Virginia
Fan Li, Duke University
Dana Boatman-Reich and **Brian Caffo**, Johns Hopkins University

10:10

Floor Discussion

65. STATISTICAL CHALLENGES IN STUDIES OF ENVIRONMENTAL, REPRODUCTIVE AND PERINATAL HEALTH

Harborside Room A (4th Floor)

Sponsors: ENAR, ASA Section on Statistics and the Environment

Organizer: Kirsten Lum, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

Chair: Kirsten Lum, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

8:30

The Current Duration Approach to Estimating Time to Pregnancy

Niels Keiding*, University of Copenhagen, Denmark

8:55

Prediction of Fecundity Based on Joint Modeling of Multiple Time Scale Longitudinal Intercourse and Menstrual Cycle Characteristics

Rajeshwari Sundaram*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

9:20

Air Pollution Metric Analysis while Determining Susceptible Periods of Pregnancy for Low Birth Weight and Birth Defects

Montse Fuentes*, North Carolina State University
Joshua L. Warren and **Amy H. Herring**, University of North Carolina, Chapel Hill
Peter H. Langlois, Texas Department of State Health Services, Austin

9:45

Identifying "Bad Actors" in Mixtures of Prenatal Exposures Associated with Reproductive Health using Weighted Quantile Sum Regression

Chris Gennings*, Virginia Commonwealth University
Caroline K. Carrico, Health Diagnostics Laboratory

10:10

Floor Discussion

66. NEW DEVELOPMENTS IN STATISTICAL METHODOLOGIES FOR THE ANALYSIS OF DISEASE DATA

Grand Ballroom II (3rd Floor)

Sponsor: ENAR

Organizer: Sujay Datta, University of Akron

Chair: Sujay Datta, University of Akron

8:30

Making the Cut: Improved Ranking and Selection in Large-scale Inference

Nicholas Henderson and **Michael A. Newton***, University of Wisconsin, Madison

8:55

Generation of Virtual Control Groups for Single Arm Prostate Cancer Adjuvant Trials

Zhenyu Jia*, University of Akron and Northeast Ohio Medical University
Michael B. Lilly, Medical University of South Carolina
Dan A. Mercola, University of California, Irvine

9:20

Differential Network Analysis using Microarray Gene Expression Data

Susmita Datta*, University of Louisville

9:45

Fused Lasso with the Adaptation of Parameter Ordering (FLAPO) in Meta Analysis of Repeated Measurements

Fei Wang, Ford Motor Credit
Lu Wang and **Peter XK Song***, University of Michigan

10:10

Floor Discussion

67. RECENT DEVELOPMENT AND APPLICATION OF BAYESIAN METHODS FOR THE PROBABILITY OF SUCCESS AND DECISION MAKING IN CLINICAL TRIALS

Harborside Room B (4th Floor)

Sponsors: ENAR, ASA Section on Bayesian Statistical Science, ASA Biopharmaceutical Section

Organizer: Ming-Hui Chen, University of Connecticut

Chair: Mani Y. Lakshminarayanan, Pfizer Inc.

8:30

Using Prior Information to Help Determine Appropriate Metrics for Sound Decision Making in Drug Development

Christy Chuang-Stein*, Pfizer Inc.

* = Presenter | ■ = Student Award Winner

8:55
Average Power and Average Conditional Power in Clinical Trial Design and Interim Analysis
Kuang-Kuo G. Lan*, Janssen R&D, Johnson & Johnson

9:20
Bayesian Probability of Success for Superiority Trials in the Presence of Historical Data
Joseph G. Ibrahim*, University of North Carolina, Chapel Hill
Ming-Hui Chen, University of Connecticut
Mani Y. Lakshminarayanan, Guanghan Liu, Joseph F. Heyse, Merck, Inc.

9:45
Evaluating Regression-to-the-Mean of Treatment Effect from Phase 2 to Phase 3
Jianliang Zhang*, MedImmune, LLC

10:10
Floor Discussion

68. FUNCTIONAL DATA ANALYSIS: SHOW ME THE DATA

Grand Ballroom III (3rd Floor)

Sponsors: IMS, ASA Biometrics Section, ASA Section on Nonparametric Statistics

Organizer: Ciprian Crainiceanu, Johns Hopkins University

Chair: Jaroslaw Harezlak, Indiana University School of Medicine

8:30
CSI Statistics: Functional Data Analysis for Dead Bodies
John Aston*, University of Cambridge and University of Warwick
Anjali Mazumder, University of Warwick
Anna Zylbersztejn, University of Warwick and University of Leicester

8:55
Surviving in the ICU: The Case for Uneven Support Functional Data Analysis
Ciprian Crainiceanu* and **Jonathan Gellar**, Johns Hopkins University

9:20
Studying the Relationship Between Cerebral Vessel Morphology and Hemodynamic Forces in Arteries Affected by Aneurysms: A Spatial Functional Data Analysis Approach
Laura M. Sangalli*, Laboratory for Modeling and Scientific Computing MOX, Italy
Bree Ettinger, Emory University
Simona Perotto, Laboratory for Modeling and Scientific Computing MOX, Italy

9:45
Functional Prediction of Traffic Streams
Jeng-Min Chiou*, Academia Sinica

10:10
Floor Discussion

69. LATENT CLASS MODELS FOR DIAGNOSTIC TESTING WITH APPLICATIONS IN PSYCHIATRY

Grand Ballroom IV (3rd Floor)

Sponsor: ENAR

Organizer: Jeffrey Douglas, University of Illinois, Urbana-Champaign

Chair: Jeffrey Douglas, University of Illinois, Urbana-Champaign

8:30
Theory and Applications of the Self-learning Q-matrix
Jingchen Liu*, Columbia University

8:55
Making Computerized Adaptive Testing a Diagnostic Tool
Hua-Hua Chang*, University of Illinois, Urbana-Champaign
Ya-Hui Su, National Chung Cheng University

9:20
Heterogeneous Variance Classification Models for Psychiatric Assessment Survey Data
Jonathan Templin*, University of Kansas
Lesa Hoffman, **Ryan Walters** and **Meghan Sullivan**, University of Nebraska, Lincoln

9:45
Use of Latent Product Lattice Classification Models for Self-reported Measures of Depression
Curtis Tatsuoka*, Case Western Reserve University

10:10
Floor Discussion

70. STATISTICAL METHODS FOR BIOMARKER EVALUATION

Grand Ballroom I (3rd Floor)

Sponsor: ENAR

Organizer: Shanshan Li, Indiana University, Fairbanks School of Public Health

Chair: Mei-Cheng Wang, Johns Hopkins Bloomberg School of Public Health

8:30
Semi-parametric ROC Analysis using Accelerated Regression Models
Eunhee Kim*, Brown University
Donglin Zeng, University of North Carolina, Chapel Hill

* = Presenter | ■ = Student Award Winner

8:55

Nonparametric ROC Based Evaluation for Survival Outcomes
Xiao Song*, University of Georgia
Xiao-Hua Zhou, Puget Sound Health Care System and University of Washington
Shuangge Ma, Yale University

9:20

A Generalized C-index for Survival Data
Patrick J. Heagerty*, University of Washington

9:45

Estimating Time-Dependent ROC Curve using Data Under Outcome-Dependent Sampling
Shanshan Li*, Indiana University Fairbanks School of Public Health
Mei-Cheng Wang, Johns Hopkins Bloomberg School of Public Health

10:10

Floor Discussion

71. CONTRIBUTED PAPERS: SEMI-PARAMETRIC AND NON-PARAMETRIC MODELS

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Mathew McLean, Texas A&M University

8:30

Robust Estimations of Scale, Dependence and Correlation Based on Quick Estimators
Lai Wei*, U.S. Food and Drug Administration
Alan Hutson, State University of New York at Buffalo

8:45

An RKHS Approach to Estimating High-dimensional Graphs
Kuang-Yao Lee*, Yale University
Bing Li, The Pennsylvania State University
Hongyu Zhao, Yale University

9:00

Quantile Association Regression Models
Ruosha Li* and **Yu Cheng**, University of Pittsburgh
Jason Fine, University of North Carolina, Chapel Hill

9:15

Calibrated Smoothed Bootstrap Confidence Intervals
Santu Ghosh*, Wayne State University

9:30

Semiparametric Group Testing Regression Models
Dewei Wang*, Christopher S. McMahan and **Colin M. Gallagher,** Clemson University
Kurunarathna B. Kulasekera, University of Louisville

9:45

A Novel Pairwise Conditional Likelihood Ratio Test in a Semiparametric Model for vQTL Mapping
Chuan Hong* and **Yong Chen**, University of Texas School of Public Health, Houston
Yang Ning, University of Waterloo
Peng Wei, University of Texas School of Public Health, Houston

10:00

Fused Kernel-Spline Smoothing for Repeatedly Measured Outcomes in a Generalized Partially Linear Model with Functional Single Index
Fei Jiang ■, Rice University
Yanyuan Ma, Texas A & M University
Yuanjia Wang, Columbia University

72. CONTRIBUTED PAPERS: JOINT MODELS FOR LONGITUDINAL AND SURVIVAL DATA

Bristol Room (3rd Floor)

Sponsor ENAR

Chair: Kush Kapur, Boston Children's Hospital and Harvard Medical School

8:30

Joint Latent Class Models With Interval-Censored Survival Data
Lan Kong* and **Guodong Liu**, The Pennsylvania State University College of Medicine

8:45

A Fast EM Algorithm for Fitting Joint Models of a Binary Response and Multiple Longitudinal Covariates Subject to Detection Limits
Paul W. Bernhardt*, Villanova University
Daowen Zhang and **Huixia J. Wang**, North Carolina State University

9:00

Regression Modeling of Longitudinal Binary Outcomes with Outcome-Dependent Observation Times
Kay See Tan ■**, Andrea B. Troxel, Stephen E. Kimmel, Kevin G. Volpp** and **Benjamin French**, University of Pennsylvania Perelman School of Medicine

✱ = Presenter | ■ = Student Award Winner

9:15

Joint Model for a Diagnostic Test without a Gold Standard in the Presence of a Dependent Terminal Event

Sheng Luo*, Xiao Su and **Stacia DeSantis**, University of Texas, Houston
Xuelin Huang, Min Yi and **Kelly Hunt**, University of Texas MD Anderson Cancer Center

9:30

Modeling Short- and Long-Term Characteristics of Follicle Stimulating Hormone as Predictors of Severe Hot Flashes in Penn Ovarian Aging Study

Bei Jiang* and **Naisyin Wang**, University of Michigan
Mary D. Sammel, University of Pennsylvania
Michael R. Elliott, University of Michigan

9:45

Regression Analysis of Longitudinal Data with Correlated Censoring and Observation Times

Yang Li*, University of North Carolina, Charlotte
Haiying Wang, University of New Hampshire
Jianguo Sun, University of Missouri, Columbia

10:00

Mixtures of Gaussian Processes Applied to Medical Monitoring of Lung Function Decline and Pulmonary Exacerbations in Cystic Fibrosis

Leo L. Duan*, John P. Clancy and **Rhonda D. Szczesniak**, Cincinnati Children's Hospital Medical Center

73. CONTRIBUTED PAPERS: STATISTICAL METHODS IN EPIDEMIOLOGY

Grand Ballroom VII (3rd Floor)

Sponsor: ENAR

Chair: Ming Wang, The Pennsylvania State University

8:30

Comparing Parametric and Semi-Parametric Regression Models for a Skewed, Pooled Outcome

Emily M. Mitchell*, National Institute of Child Health and Human Development, National Institutes of Health
Robert H. Lyles, Emory University
Michelle Danaher, Neil J. Perkins and **Enrique F. Schisterman**, National Institute of Child Health and Human Development, National Institutes of Health

8:45

Effect Modification and Design Sensitivity in Observational Studies

Jesse Y. Hsu*, Dylan S. Small and **Paul R. Rosenbaum**, University of Pennsylvania

9:00

Structural Nested Mean Model for Clustered Outcomes

Jiwei He* and **Marshall Joffe**, University of Pennsylvania

9:15

Flexible Models for Comparing Cumulative Effects of Time-dependent Exposures

Chenkun Wang*, Hai Liu and **Sujuan Gao**, Indiana University School of Medicine and Richard M. Fairbank School of Public Health

9:30

Instrumental Variables Estimation with Some Invalid Instruments and Its Application to Mendelian Randomization

Hyunseung Kang*, Anru Zhang, T. Tony Cai and **Dylan S. Small**, University of Pennsylvania

9:45

Variable Selection for Case-Cohort Studies with A Diverging Number of Parameters

Ai Ni ■ and **Jianwen Cai**, University of North Carolina, Chapel Hill

10:00

Weighted Model Selection for Fractional Polynomial Models

Michael D. Regier*, Ruoxin Zhang and **John Honaker**, West Virginia University

74. CONTRIBUTED PAPERS: ADAPTIVE DESIGNS AND RANDOMIZATION

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Qin Jiang, Pfizer Inc.

8:30

Two-Stage Adaptive Optimal Design with Fixed First Stage Sample Size

Adam Lane*, Cincinnati Children's Hospital Medical Center
Nancy Flournoy, University of Missouri

8:45 Phase II/III Seamless Adaptive Dose Selection Design for Longitudinal Patient Data

Caitlyn Ellerbe*, Jordan Elm and **Viswanathan Ramakrishnan**, Medical University of South Carolina
Bruce Turnbull, Cornell University
Edward Jauch, Medical University of South Carolina
Stacia DeSantis, University of Texas Health Sciences
Valerie Durkalski, Medical University of South Carolina

9:00

The Use of Decreasingly Informative Priors in Adaptive Clinical Trial Designs

Roy T. Sabo*, Virginia Commonwealth University

✱ = Presenter | ■ = Student Award Winner

9:15

An Adaptive Bayesian Dose Finding Approach for Drug Combinations with Drug-drug Interaction

Yang Yang*, University of Maryland, Baltimore County
Hong-Bin Fang, Georgetown University
Anindya Roy, University of Maryland, Baltimore County
Ming Tan, Georgetown University

9:30

Dose Escalation with Over-dose and Under-dose Controls for Phase I/II Clinical Trial

Zheng Li* and **Michael Kutner**, Emory University
Ying Yuan, University of Texas MD Anderson Cancer Center
Zhengjia Chen, Emory University

9:45

An Adaptive Treatment Strategy for the Management of White-Nose Syndrome

Nick Meyer*, Eric Laber, Krishna Pacifici and **Brian Reich**, North Carolina State University

10:00

Floor Discussion

75. CONTRIBUTED PAPERS: NEXT GENERATION SEQUENCING

Grand Ballroom IX (3rd Floor)

Sponsor: ENAR

Chair: Prasad Patil, Johns Hopkins University

8:30

Genotype Calling and Haplotyping in Extended Families

Lun-Ching Chang, University of Pittsburgh
Bingshan Li, Vanderbilt University
George C. Tseng and **Wei Chen***, University of Pittsburgh

8:45

Meta-Analysis of Sequencing Studies Under Random-Effects Models

Zheng-Zheng Tang* and **Dan-Yu Lin**, University of North Carolina, Chapel Hill

9:00

Likelihood Based Complex Trait Association Testing for Arbitrary Depth Sequencing Data

Song Yan* and **Yun Li**, University of North Carolina, Chapel Hill

9:15

Design Issue and Power Calculation in RNA-seq Applications

Chien-Wei Lin* and **George C. Tseng**, University of Pittsburgh

9:30

A Simulation-based Comparative Study of the Relative Power of Family-based Association Tests

Jia Jia* and **Daniel E. Weeks**, University of Pittsburgh

9:45

A DNA Variant Caller Adapted to Assess Mitochondrial DNA Variation from Whole-Genome Sequencing Data

Jun Ding*, National Institute on Aging, National Institutes of Health
Carlo Sidore, Istituto di Ricerca Genetica e Biomedica, Consiglio Nazionale delle Ricerche, Monserrato, Cagliari, Italy
Osorio Meirelles, National Institute on Aging, National Institutes of Health
Mary Kate Wing, University of Michigan
Fabio Busonero, Istituto di Ricerca Genetica e Biomedica, Consiglio Nazionale delle Ricerche, Monserrato, Cagliari, Italy
Ramaiah Nagaraja, National Institute on Aging, National Institutes of Health
Francesco Cucca, Istituto di Ricerca Genetica e Biomedica, Consiglio Nazionale delle Ricerche, Monserrato, Cagliari, Italy
Goncalo R. Abecasis, University of Michigan
David Schlessinger, National Institute on Aging, National Institutes of Health

10:00

Analysis of Sequence Data Under Multivariate Trait-Dependent Sampling

Ran Tao*, Donglin Zeng, Nora Franceschini and **Kari E. North**, University of North Carolina, Chapel Hill
Eric Boerwinkle, University of Texas Health Science Center, Houston
Dan-Yu Lin, University of North Carolina, Chapel Hill

* = Presenter | ■ = Student Award Winner

76. CONTRIBUTED PAPERS: STATISTICAL METHODS FOR SURVIVAL ANALYSIS

Chasseur Room (3rd Floor)

Sponsor: ENAR

Chair: Jennifer Sinnott, Harvard University

8:30
Distributional Properties and Peculiarities in HPP-Based Recurrent Event Models
Piaomu Liu* and **Edsel A. Peña**, University of South Carolina, Columbia

8:45
Vertical Modeling: Analysis of Multi-state Data with a Cured Fraction
Mioara Alina Nicolaie* and **Catherine Legrand**, Université catholique de Louvain

9:00
Sequential Stratification for Recurrent Event Outcomes
Abigail Smith* and **Douglas Shaubel**, University of Michigan

9:15
Random Survival Forests for Interval-censored Outcomes in the Presence of Imperfect Diagnostic Tests
Hui Xu*, Xiangdong Gu and **Raji Balasubramanian**, University of Massachusetts, Amherst

9:30
Analysis of MD STARnet Data
Ke Liu*, Ying Zhang, Paul Romitti, Soman Puzhankara and **Kristin Caspers**, University of Iowa
Elinora Price, Jennifer Andrews and **Chris Cunniff**, University of Arizona

9:45
Time-Dependent Tree-Structured Survival Analysis with Unbiased Variable Selection
Meredith L. Wallace*, University of Pittsburgh

10:00
Quantile Regression in Semiparametric Varying-Coefficient Partially Linear Models for Right Censored Length-biased Data
Xuerong Chen, Georgetown University
Yeqian Liu* and **Jianguo Sun**, University of Missouri, Columbia
Yong Zhou, Chinese Academy of Sciences, Beijing

Tuesday, March 18

10:15 am – 10:30 am

Refreshment Break with Our Exhibitors
Grand Ballroom Foyer (3rd Floor)

Tuesday, March 18

10:30 am – 12:15 pm

77. PRESIDENTIAL INVITED ADDRESS

Grand Ballroom (3rd Floor)

Sponsor: ENAR

Organizer/Chair: DuBois Bowman, Columbia University

10:30
Introduction

10:35
Distinguished Student Paper Awards

10:45
A Significance Test for the Lasso
Robert J. Tibshirani, PhD, Department of Statistics and Health Research and Policy, Stanford University

Tuesday, March 18

1:45 pm – 3:30 pm

78. JABES INVITED SESSION

Grand Ballroom VIII (3rd Floor)

Sponsors: ENAR, ASA Section on Statistics and the Environment, ASA Government Statistics Section

Organizer: Montserrat Fuentes, North Carolina State University

Chair: Montserrat Fuentes, North Carolina State University

1:45
Estimating Velocity for Processive Motor Proteins with Random Detachment
John Hughes*, University of Minnesota
Shankar Shastry, William O. Hancock and **John Fricks**, The Pennsylvania State University

* = Presenter | ■ = Student Award Winner

2:10

Bayesian 2-stage Space-Time Mixture Modeling with Spatial Misalignment

Andrew B. Lawson*, Medical University of South Carolina
Jungsoon Choi, Hangyang University, Korea
Bo Cai, University of South Carolina, Columbia
Monir Hossain, University of Cincinnati
Russell Kirby, University of South Florida
Jihong Liu, University of South Carolina, Columbia

2:35

Identifying Genes that are Differentially Expressed in Both of Two Independent Experiments

Megan Orr*, North Dakota State University
Peng Liu and **Dan Nettleton**, Iowa State University

3:00

A Bayesian Approach to Fitting Gibbs Processes with Temporal Random Effects Generalisations and Challenges

Ruth King, Janine B. Illian*, Stuart E. King and **Glenna F. Nightingale**, University of St Andrews
Ditte K. Hendrichsen, Norwegian Institute for Nature Research

3:25

Floor Discussion

79. RECENT ADVANCES IN STATISTICAL METHODS FOR MISSING DATA

Grand Ballroom III (3rd Floor)

Sponsors: ENAR, ASA Biometrics Section, ASA Government Statistics Section

Organizer: Qi Long, Emory University

Chair: Pallavi Mishra-Kalyani, Emory University

1:45

Identification and Multiple Imputation of Implausible Gestational Ages for the Study of Preterm Births

Nathaniel Schenker*, National Center for Health Statistics, Centers for Disease Control and Prevention

2:10

Adjusting for Verification Bias in Estimation of Covariate-specific Areas under the ROC Curves

Xiao-Hua A. Zhou*, University of Washington
Danping Liu, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

2:35

Multiple Imputation Via Flexible, Joint Models

Jerome Reiter*, Duke University

3:00

On the Use of Box-Cox Transformation for Missing Data Imputation

Yulei He*, Don Malec and **Nathaniel Schenker**, National Center for Health Statistics, Centers for Disease Control and Prevention

3:25

Floor Discussion

80. BIG DATA METHODS IN BIOSTATISTICS

Grand Ballroom II (3rd Floor)

Sponsors: IMS, ASA Statistical Learning and Data Mining Section, ASA Biopharmaceutical Section

Organizer: Babak Shahbaba, University of California, Irvine

Chair: Babak Shahbaba, University of California, Irvine

1:45

Some Post-GWAS Strategies for Identifying the Remaining Genetic Determinants

Zhaoxia Yu*, University of California, Irvine

2:10

Interactive, Exploratory Visualization and Statistical Analysis of Genome-Scale Data

Hector Corrada Bravo* and **Florin Chelaru**, University of Maryland, College Park

2:35

A Semiparametric Bayesian Model for Detecting Multiway Synchrony Among Neurons

Babak Shahbaba*, Bo Zhou, Shiwei Lan and **Hernando Ombao**, University of California, Irvine
David Moorman, Medical University of South Carolina
Sam Behseta, Cal State Fullerton

3:00

Algebraic Properties and Fast Large Covariance Estimation

Xi Luo*, Brown University

3:25

Floor Discussion

* = Presenter | ■ = Student Award Winner

81. STATISTICAL PREDICTION MODELS FOR MEDICAL DECISION MAKING

Grand Ballroom IV (3rd Floor)

Sponsors: ENAR, ASA Mental Health Statistics Section

Organizer: Jing Ning, University of Texas MD Anderson Cancer Center

Chair: Jing Ning, University of Texas MD Anderson Cancer Center

1:45
Dynamic Prediction of Survival Outcomes and Medical Decision Making
Xuelin Huang*, Sangbum Choi and **Jing Ning**, University of Texas MD Anderson Cancer Center

2:10
Statistical Prediction Models for Medical Decision Making
Michael W. Kattan*, Cleveland Clinic

2:35
ROC Analysis for Multiple Markers with Tree-based Classification
Mei-Cheng Wang*, Johns Hopkins University
Shanshan Li, Indiana University Fairbanks School of Public Health

3:00
Efficient Evaluation of Risk Markers for Censored Failure Time Outcome: Analyses and Designs
Yingye Zheng*, Fred Hutchinson Cancer Research Center
Tianxi Cai, Harvard School of Public Health

3:25
Floor Discussion

82. RECENT DEVELOPMENTS IN STATISTICAL GENETICS, GENOMICS, AND THEIR APPLICATIONS

Grand Ballroom V (3rd Floor)

Sponsors: ENAR, ASA Biometrics Section

Organizer: Mingyao Li, University of Pennsylvania School of Medicine

Chair: Mingyao Li, University of Pennsylvania School of Medicine

1:45
Joint Analysis of SNP and Gene Expression Data in Genetic Association Studies of Complex Diseases Using Causal Mediation Analysis
Yen-Tsung Huang, Brown University
Tyler VanderWeele and **Xihong Lin***, Harvard School of Public Health

2:10
The Magic of Score Statistics
Danyu Lin*, University of North Carolina, Chapel Hill

2:35
Assessing the Sensitivity of Genetic Associations to Unmeasured Confounding Under a Causal Framework
Nandita Mitra*, University of Pennsylvania
Elizabeth Handorf, Fox Chase Cancer Center
Peter Kanetsky and **Steve Kawut**, University of Pennsylvania

3:00
Robust and Powerful Sibpair Test for Rare Variant Association
Keng-Han Lin and **Sebastian Zoellner***, University of Michigan

3:25
Floor Discussion

83. IMPROVED STATISTICAL MODELING AND UNDERSTANDING OF GENE EXPRESSION AND TRANSCRIPTION REGULATION USING NEXT GENERATION SEQUENCING AND OTHER HIGH THROUGHPUT TECHNOLOGIES

Grand Ballroom VI (3rd Floor)

Sponsor: ENAR

Organizer: Michael Y. Zhu, Purdue University

Chair: Zhaohui Qin, Emory University

1:45
Deconvolution of Base Pair Level RNA-Seq Read Counts for Quantification of Transcript Expression Levels
Han Wu* and **Yu Zhu**, Purdue University

2:10
Accounting for Nuisance Covariates when using RNA-Seq Data to Identify Differentially Expressed Genes
Dan Nettleton* and **Yet Nguyen**, Iowa State University

2:35
Bayesian Models for Integrative Genomics
Marina Vannucci* and **Alberto Cassese**, Rice University
Michele Guindani, University of Texas MD Anderson Cancer Center

* = Presenter | ■ = Student Award Winner

3:00

Understanding Spatial Organizations of Chromosomes via Statistical Analysis of Hi-C Data
Ming Hu*, New York University
Ke Deng, Tsinghua University
Zhaohui Qin, Emory University
Jun S. Liu, Harvard University

3:25

Floor Discussion

84. STATISTICAL CHALLENGES IN PUBLIC HEALTH RESEARCH AT THE CDC

Grand Ballroom VII (3rd Floor)

Sponsors: ENAR, ASA Government Statistics Section

Organizer: Simone Gray, Centers for Disease Control and Prevention

Chair: Dr. Craig Borkowf, Centers for Disease Control and Prevention

1:45

Exploring the Optimal Al... Sample Sizes in Dual-Frame RDD T... Surveys
Haci Akcin, Cente... Control and Prevention
Denise Bradf... ...op Grumman

CANCELLED

2:10

Area Level Models for County Level Prevalence Estimates using Publically Available BRFSS Data
Betsy L. Cadwell*, Theodore J. Thompson and **Lawrence E. Barker**, Centers for Disease Control and Prevention

2:35

Multiple Imputation of Linked National Health Interview Survey and Medicare data files
Guangyu Zhang*, Jennifer D. Parker and **Nathaniel Schenker**, National Center for Health Statistics, Centers for Disease Control and Prevention

3:00

Using Longitudinal Data Analysis to Link Policy and Legislation to Public Health Impacts
Simone Gray*, Patricia Sweeney, Joseph Prejean, David W. Purcell, Aruna Surendera Babu, Brett Williams, Jenny Sewell and **Jonathan Mermin**, Centers for Disease Control and Prevention

3:25

Discussant: Craig Borkowf, Centers for Disease Control and Prevention

85. INNOVATIVE BAYESIAN NONPARAMETRICS IN BIOSTATISTICS

Grand Ballroom I (3rd Floor)

Sponsors: ENAR, ASA Section on Bayesian Statistical Science, ASA Biometrics Section

Organizer: Michael Daniels, University of Texas, Austin

Chair: Antonio Linero, University of Florida

1:45

Longitudinal Data Analysis using a Random Partition Model with Regression on Covariates
Gary L. Rosner*, Johns Hopkins University
Peter Mueller, University of Texas, Austin
Fernando Quintana, Pontificia Universidad Catolica de Chile
Michael Maitland, University of Chicago

2:10

A Bayesian Feature Allocation Model for Tumor Heterogeneity
Peter Mueller*, University of Texas, Austin
Juhee Lee, University of California, Santa Cruz
Yuan Ji, NorthShore University Health System

2:35

A Bayesian Nonparametric Approach to Monotone Missing Data in Longitudinal Studies with Informative Missingness
Antonio Linero, University of Florida
Michael Daniels*, University of Texas, Austin

3:00

Bayesian Quantile Regression for Censored Data
Brian J. Reich* and **Luke B. Smith**, North Carolina State University

3:25

Floor Discussion

86. CONTRIBUTED PAPERS: NEW DEVELOPMENTS IN SURVIVAL ANALYSIS

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Adin-Cristian Andrei, Bluhm Cardiovascular Institute

1:45

A Local Agreement Index Based on Hazard Functions for Survival Outcomes
Tian Dai* and **Ying Guo**, Emory University

2:00

A Frailty Model for Bivariate Interval-censored Data Allowing Weak Dependence and Independence
Naichen Wang* and **Lianming Wang**, University of South Carolina

* = Presenter | ■ = Student Award Winner

2:15

Survival Analysis with Correlated Frailties and the Bootstrap

J. C. Loredo-Osti*, Memorial University

2:30

Semiparametric Methods to Contrast Restricted Mean Gap Times

Xu Shu ■ and **Douglas E. Schaubel**, University of Michigan

2:45

Extending the Peters-Belson Approach for Assessing Disparities to Right Censored Time-to-Event Outcomes

Lynn E. Eberly*, James S. Hodges, Kay Savik, Olga Gurvich and **Donna Z. Bliss**, University of Minnesota

3:00

Consistency on Change-point Estimators on Hazard Regression Models with Long-term Survivors and Right Censoring

Wei Zhang* and **Lianfen Qian**, Florida Atlantic University

3:15

Nonparametric Estimation of Quantile Residual Life for Length-Biased Survival Data

Samia H. Lopa* and **Jong-Hyeon Jeong**, University of Pittsburgh

87. CONTRIBUTED PAPERS: CAUSAL INFERENCE

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Jessica G. Young, Harvard School of Public Health

1:45

Estimation of the Optimal Regime in Treatment of Prostate Cancer Recurrence from Observational Data using Flexible Weighting Models

Jincheng Shen*, Lu Wang and **Jeremy M.G. Taylor**, University of Michigan

2:00

A Simulation Study of a Multiply-Robust Approach for Causal Inference with Missing Covariates

Jia Zhan* and **Changyu Shen**, Indiana University School of Medicine
Lingling Li, Harvard Medical School
Xiaochun Li, Indiana University School of Medicine

2:15

Estimating Causal Treatment Effect for Complex Intervention Study Designs

Pan Wu*, Christiana Care Health System

2:30

Regression Analysis of Sequentially Randomized Trials through Artificial Randomization

Semhar B. Ogbagaber* and **Abdus S. Wahed**, University of Pittsburgh

2:45

Why Do Treatments Work Differently for Some People? Understanding Treatment-effect Mechanisms in Stratified Medicine

Sabine Landau*, King's College London
Richard Emsley, **Hanhua Liu** and **Graham Dunn**, University of Manchester, United Kingdom

3:00

Inference for Surrogate Endpoint Validation in the Binary Case

Ionut Bebu*, Uniformed Services University of the Health Sciences
Thomas Mathew, University of Maryland Baltimore County
Brian K. Agan, Uniformed Services University of the Health Sciences

3:15

Longitudinal Analyses of the Causal Path Between Multiple Sclerosis and Depression using Structural Equation Modeling

Douglas Gunzler*, Case Western Reserve University

88. CONTRIBUTED PAPERS: NON-PARAMETRIC ANALYSIS OF BIOMEDICAL DATA

Bristol Room (3rd Floor)

Sponsor: ENAR

Chair: Leo Duan, Cincinnati Children's Hospital Medical Center

1:45

A Spatio-Temporal Nonparametric Bayesian Variable Selection Model of fMRI Data for Clustering Correlated Time Courses

Linlin Zhang*, Rice University
Michele Guindani, University of Texas MD Anderson Cancer Center
Marina Vannucci, Rice University

2:00

Inferences about the Mean Area Under the Curve in Pre-Clinical Destructive Sampling Designs

Yi Shi*, State University of New York at Buffalo
Rameela Chandrasekhar, Vanderbilt University
Alan Hutson and **Gregory Wilding**, State University of New York at Buffalo

2:15

Investigating a Method for Testing a Hypothesis about the Ratio of Two Medians using Conover's Rank Transformation Method

Donald J. Schuirmann*, U.S. Food and Drug Administration

✱ = Presenter | ■ = Student Award Winner

2:30

Restricted Confidence Intervals for Ordered Binary and Survival Data

Yongseok Park*, University of Pittsburgh
Jeremy M G Taylor, University of Michigan

2:45

Novel Algorithm for Stratifying Patients into Survival Risk Groups using Mutation Data at Selected Genes

Irina Ostrovnaya*, Sean Devlin and **Mithat Gönen**, Memorial Sloan-Kettering Cancer Center

3:00

Two-sample Parameter Estimation using Empirical Characteristic Functions

Cornelis J. Potgieter*, Southern Methodist University
Fred Lombard, North-West University, Potchefstroom, South Africa

3:15

Multiple Imputation Methods for Nonparametric Inference on Cumulative Incidence with Missing Cause of Failure

Minjung Lee*, Seoul National University
James J. Dignam, University of Chicago
Junhee Han, University of Arkansas, Fayetteville

89. CONTRIBUTED PAPERS: HIGH DIMENSIONAL IMAGING DATA

Grand Ballroom IX (3rd Floor)

Sponsor: ENAR

Chair: Feng Liu, University of North Carolina, Chapel Hill

1:45

A Parallel Group Independent Component Analysis Algorithm

Shaojie Chen*, Lei Huang, Huitong Qiu, Ani Eloyan and **Brian Caffo**, Johns Hopkins University

2:00

Ultra-high Dimensional Test Via Sparse Projections

Qiang Sun*, Hongtu Zhu and **Joseph G. Ibrahim**, University of North Carolina, Chapel Hill

2:15

Statistical Approaches for Exploring Brain Connectivity with Multi-Modal Neuroimaging Data

Phebe B. Kemmer* and **Ying Guo** Emory University
F. DuBois Bowman, Columbia University

2:30

Spatially Regularizing High Angular Resolution Diffusion Imaging

Shangbang Rao*, Hongtu Zhu, Jian Cheng, Pew-Thian Yap and **Joseph Ibrahim**, University of North Carolina, Chapel Hill

2:45

Parametrization of White Matter Manifold-like Structures using Principal Surfaces

Chen Yue* and **Vadim Zipunnikov**, Johns Hopkins University
Pierre-Louis Bazin, Max Planck Institute
Dzung Pham and **Daniel S. Reich**, National Institute of Neurological Disorders and Stroke, National Institutes of Health
Ciprian Crainiceanu and **Brian Caffo**, Johns Hopkins University

3:00

Predicting Enhancement in Magnetic Resonance Images using Scan Stratified Case Control Sampling

Gina-Maria Pomann*, North Carolina State University
Elizabeth M. Sweeney, Johns Hopkins University
Russel (Taki) Shinohara, University of Pennsylvania
Ana-Maria Staicu, North Carolina State University
Daniel S. Reich, National Institute of Neurological Disorders and Stroke, National Institutes of Health

3:15

Persistence Landscape of Functional Signal and Its Application to Epileptic Electroencaphalogram Data

Yuan Wang ■, University of Wisconsin, Madison
Hernando Ombao, University of California, Irvine
Moo K. Chung, University of Wisconsin, Madison

✱ = Presenter | ■ = Student Award Winner

90. CONTRIBUTED PAPERS: NEW METHODS IN GENOMICS

Chasseur Room (3rd Floor)

Sponsor: ENAR

Chair: Emily Huang, Stony Brook University

1:45

Inference of Epigenetic Modulation of Gene Expression with Meta-pathway Analysis
Elana J. Fertig*, Johns Hopkins University
Ana Markovic, University of California, San Francisco
Ludmila V. Danilova, Daria A. Gaykalova, Leslie Cope, Christine H. Chung and **Joseph A. Califano**, Johns Hopkins University
Michael F. Ochs, The College of New Jersey

2:00

Integrative Modeling of Multiplatform Genomic Data
Yen-Tsung Huang*, Brown University

2:15

The Most Informative Spacing Test as an Outlier and Subgroup Identification Method
Iwona Pawlikowska*, Gang Wu, Michael Edmonson, Tanja Gruber, Jinghui Zhang and **Stan Pounds**, St. Jude Children's Research Hospital

2:30

Cross-Platform Gene Expression Profile Classification using Top-Scoring Pairs
Prasad Patil*, Johns Hopkins School of Public Health
Benjamin Haibe-Kains, Institut de Recherches Clinques de Montreal
Jeffrey T. Leek, Johns Hopkins School of Public Health

2:45

A Survival Copula Mixture Model for Comparing Two Genomic Rank List
Yingying Wei* and **Hongkai Ji**, Johns Hopkins University

3:00

An Integrated Method for Detecting MicroRNA Target Proteins through Reverse-phase Protein Lysate Arrays
Jiawen Zhu*, Song Wu and **Jie Yang**, Stony Brook University

3:15

Testing in Metagenomic Profiling Studies with the Microbiota Regression-based Kernel Association Test (MiRKAT)
Ni Zhao* and **Michael C. Wu**, Fred Hutchinson Cancer Research Center

Tuesday, March 18

3:30 pm – 3:45 pm

Refreshment Break with Our Exhibitors

Grand Ballroom Foyer (3rd Floor)

Tuesday, March 18

3:45 pm – 5:30 pm

91. IMS MEDALLION LECTURE

Grand Ballroom VI (3rd Floor)

Sponsor: IMS

Chair: Daniel Scharfstein, Johns Hopkins University School of Public Health

3:45

Statistical Genetics and Genomics in the Big Data Era: Opportunities and Challenges in Research and Training
Xihong Lin*. Harvard School of Public Health

92. PARAMETRIC OR NONPARAMETRIC; WHICH IS THE ANSWER?

Grand Ballroom VII (3rd Floor)

Sponsors: ENAR, ASA Mental Health Statistics Section, Non-Parametric

Organizer: Zhehui Luo, Michigan State University

Chair: Zhehui Luo, Michigan State University

3:45

Super Learning to Hedge Against Incorrect Inference from Arbitrary Parametric Assumptions in Marginal Structural Modeling
Romain Neugebauer*, Kaiser Permanente

4:10

Fitting ICU Data Complexity: Need for Innovative Prediction Tools Mortality Prediction by SuperLearner
Romain Pirracchio*, Hôpital Saint Louis, Paris, France
Maya Petersen, University of California, Berkeley
Sylvie Chevret, Hôpital Saint Louis, Paris, France
Mark van der Laan, University of California, Berkeley

4:35

Sensitivity Analysis for Causal Inference under Unmeasured Confounding and Measurement Error Problems
Iván Díaz*, Johns Hopkins Bloomberg School of Public Health
Mark van der Laan, University of California, Berkeley

* = Presenter | ■ = Student Award Winner

5:00

From Causal Roadmaps to Hedging Your Bets in the Adventures of Comparative Effectiveness Research: An Illustration using an Effect Modification Analysis of Star*D

Wenjing Zheng, University of California, Berkeley
Zhehui Luo*, Michigan State University
Mark van der Laan, University of California, Berkeley

5:25

Floor Discussion

93. CAUSAL INFERENCE IN HIGH DIMENSIONAL SETTINGS

Grand Ballroom II (3rd Floor)

Sponsors: ENAR, ASA Section on ASA Section on Statistics in Imaging

Organizer: Yenny WebbVargas, Johns Hopkins School of Public Health

Chair: Bruce Swihart, Johns Hopkins School of Public Health

3:45

Calibrated Observational Studies

David Madigan*, Columbia University

4:10

Connectivity and Causality in Brain Imaging

Martin A. Lindquist*, Johns Hopkins Bloomberg School of Public Health

4:35

Causal Inference for fMRI Time Series Data with Systematic Errors of Measurement in a Balanced On/Off Study of Social Evaluative Threat

Michael E. Sobel*, Columbia University
Martin A. Lindquist, Johns Hopkins Bloomberg School of Public Health

5:00

Data Adaptive Target Parameters in Causal Inference

Alan E. Hubbard* and **Mark van der Laan**, University of California, Berkeley

5:25

Floor Discussion

94. ADVANCES IN TIME SERIES ANALYSIS OF BIOMEDICAL SIGNALS

Grand Ballroom III (3rd Floor)

Sponsors: ENAR, ASA Section on ASA Section on Statistics in Imaging

Organizer: Robert Krafty, Temple University

Chair: Sarah Ratcliffe, University of Pennsylvania

3:45

Spatial Identification of Epileptic Brain Regions

Giovanni Motta*, Columbia University
Michael M. Haglund and **Daryl Hochman**, Duke University

4:10

Time Series Analysis of Molecular Motor-Cargo Complexes

John Fricks*, The Pennsylvania State University

4:35

Penalized Multivariate Whittle Likelihood for Power Spectrum Estimation

Robert T. Krafty*, Temple University
William O. Collinge, University of Pittsburgh

5:00

A Bayesian Model of Activation and Functional Connectivity for Event-Related fMRI

Wesley K. Thompson*, University of California, San Diego

5:25

Floor Discussion

95. FRONTIERS IN STATISTICAL GENETICS FOR COMPLEX TRAIT ASSOCIATION

Grand Ballroom V (3rd Floor)

Sponsor: ENAR

Organizer: Yijuan Hu, Emory University

Chair: Yijuan Hu, Emory University

3:45

Genetic Architecture of Complex Traits: Implications for Discovery, Prediction and Prevention

Nilanjan Chatterjee*, National Cancer Institute, National Institutes of Health
JuHyun Park, Dongukk University, South Korea

4:10

Statistical Approaches for Rare-Variant Association Testing in Families

Michael P. Epstein*, Emory University

4:35

A Novel Collapsing Method for Rare Copy Number Variants

Jung-Ying Tzeng*, North Carolina State University
Jin P. Szatkiewicz and **Patrick F. Sullivan**, University of North Carolina, Chapel Hill

* = Presenter | ■ = Student Award Winner

5:00

Testing Association without Calling Genotypes Allows for Systematic Differences in Read Depth and Sequencing Error Rate between Cases and Controls

Glen A. Satten*, Centers for Disease Control and Prevention
Richard Johnston and **Peizhou Liao**, Emory University
Yu Jiang and **Andrew S. Allen**, Duke University
Yijuan Hu, Emory University

5:25

Floor Discussion

96. FUNCTIONAL DATA APPROACHES TO NEUROLOGICAL AND MENTAL DISEASE

Harborside Room A (4th Floor)

Sponsors: ENAR, ASA Mental Health Statistics Section, ASA Section on Statistics in Imaging, ASA Section on Nonparametric Statistics

Organizer: Russell Shinohara, University of Pennsylvania

Chair: Adam Ciarleglio, New York University

3:45

Distance Splines, Nonparametric Functional Regression, and Multimodal Neuroimaging

Philip T. Reiss*, New York University and Nathan Kline Institute
Lei Huang, Johns Hopkins University
Huaihou Chen, New York University
David L. Miller, University of St Andrews

4:10

Assessing Systematic Effects of Stroke on Motor Control using Hierarchical Function-on-Scalar Regression

Jeff Goldsmith* and **Tomoko Kitago**, Columbia University

4:35

Flexible Concurrent Regression Models for Functional Data

Janet Kim, Ana-Maria Staicu* and **Arnab Maity**, North Carolina State University

5:00

Biosignatures Based on Imaging Data

Todd Ogden*, Columbia University
Adam Ciarleglio and **Eva Petkova**, New York University
Thaddeus Tarpey, Wright State University

5:25

Floor Discussion

97. MODELING NEUROLOGICAL DISEASES WITH IMAGING DATA

Harborside Room B (4th Floor)

Sponsors: ENAR, ASA Section on Statistics in Imaging, ASA Biometrics Section

Organizer: Jeff Goldsmith, Columbia University

Chair: Daniel B. Shin, University of Pennsylvania

3:45

Developmental Disorders and Neuroimaging: Tools, Results and Issues

Brian S. Caffo*, Johns Hopkins Bloomberg School of Public Health

4:10

Learning Brain Connectivity Network of Depression via Multi-Attribute Canonical Correlation Graphs

Jian Kang*, Emory University
Han Liu, Princeton University
DuBois F. Bowman, Columbia University
Helen S. Mayberg, Emory University

4:35

Normalization Techniques for Statistical Inference from Magnetic Resonance Imaging

Russell T. Shinohara*, University of Pennsylvania
Elizabeth M. Sweeney, Johns Hopkins University
Jeff Goldsmith, Columbia University
Navid Shiee, Henry M. Jackson Foundation
Farrah J. Mateen, Harvard University
Peter A. Calabresi and **Samson Jarso**, Johns Hopkins University
Dzung L. Pham, Henry M. Jackson Foundation
Daniel S. Reich, National Institute of Neurological Disorders and Stroke, National Institutes of Health
Ciprian M. Crainiceanu, Johns Hopkins University

5:00

Voxel-wise Marginal Longitudinal Modelling of Brain Atrophy Data

Bryan Guillaume, University of Warwick and Université de Liège
Thomas E. Nichols*, University of Warwick
Lourens Waldorp, University of Amsterdam

5:25

Floor Discussion

* = Presenter | ■ = Student Award Winner

98. MAKING SENSE OF SENSORS: STATISTICAL METHODS FOR WEARABLE COMPUTING

Grand Ballroom I (3rd Floor)

Sponsor: ENAR

Organizer: Vadim Zipunnikov, Johns Hopkins Bloomberg **School** of Public Health

Chair: Sherri Rose, Harvard School of Medicine

3:45

ActiVis: An R Package for Visualizing Functional Actigraphy Data
Abbass Sharif*, University of Southern California
Juergen Symanzik, Utah State University

4:10

From Humans to Monkeys and Back: Physical Activity Patterns in Humans and Primates
Vadim Zipunnikov*, Johns Hopkins University
Jeff Goldsmith, Columbia University
Haochang Shou and **Ciprian Crainiceanu**, Johns Hopkins University

4:35

Measurement Error Models for Physical Activity: Accelerometers and Self Report
John W. Staudenmayer*, University of Massachusetts, Amherst

5:00

Statistical Methods for Development and Temporal Organization of Repetitive Behavior
Nikolay Bliznyuk*, Isaac H. Duerr, Amber Muehleman and **Mark Lewis**, University of Florida

5:25

Floor Discussion

99. CONTRIBUTED PAPERS: SURVIVAL ANALYSIS

Grand Ballroom IV (3rd Floor)

Sponsor: ENAR

Chair: J C. Loredo-Osti, Memorial University

3:45

A Semiparametric Bayesian Approach to Modelling Destructive Weighted Poisson Cure Rate Model
Arpita Chatterjee*, Georgia Southern University
Narayanaswamy Balakrishnan, McMaster University

4:00

Support Vector Hazards Regression for Predicting Survival Outcome
Xiaoxi Liu ■, University of North Carolina, Chapel Hill
Yuanjia Wang, Columbia University
Donglin Zeng, University of North Carolina, Chapel Hill

4:15

Semiparametric Extreme-value Regression Model for Analyzing Biomarker-defined Time-to-Event
Noorie Hyun*, Donglin Zeng and **David J. Couper**, University of North Carolina, Chapel Hill

4:30

Spatial Extended Hazard Model with Application to South Carolina Prostate Cancer Data
Li Li*, University of South Carolina

4:45

Local Polynomial Density Estimation with Interval Censored Data
Derick R. Peterson*, University of Rochester
Mark J. van der Laan, University of California, Berkeley

5:00

Stacking Survival Models
Andrew Wey*, John Connett and **Kyle Rudser**, University of Minnesota

5:15

Semiparametric Approach for Regression with Covariate Subject to Limit of Detection
Shengchun Kong* and **Bin Nan**, University of Michigan

100. CONTRIBUTED PAPERS: PERSONALIZED MEDICINE

Grand Ballroom VIII (3rd Floor)

Sponsor: ENAR

Chair: Susan Wei, University of North Carolina, Chapel Hill

3:45

Combining Biomarkers to Optimize Patient Treatment Recommendations
Chaeryon Kang*, Holly Janes and **Ying Huang**, Fred Hutchinson Cancer Research Center

4:00

Simple Approximations to Optimal Treatment Regimes in Randomized Clinical Trial Data
Jared C. Foster*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health
Bin Nan and **Jeremy MG Taylor**, University of Michigan

4:15

Regularized Outcome Weighted Subgroup Identification for Differential Treatment Effects
Yaoyao Xu ■**, Menggang Yu, Yingqi Zhao, Quefeng Li** and **Jun Shao**, University of Wisconsin, Madison

4:30

Finding Optimal Treatment Dose using Outcome Weighted Learning
Guanhua Chen*, Donglin Zeng and **Michael R. Kosorok**, University of North Carolina, Chapel Hill

✱ = Presenter | ■ = Student Award Winner

4:45

Assessing the Heterogeneity of Treatment Effects via Potential Outcomes of Individual Patients
Zhiwei Zhang*, U.S. Food and Drug Administration
Chenguang Wang, Johns Hopkins University School of Medicine
Lei Nie and **Guoxing Soon**, U.S. Food and Drug Administration

5:00

Identifying Subpopulations with Differential Risk Benefit Profiles
Junlong Li* and **Tianxi Cai**, Harvard School of Public Health

5:15

Active Learning Clinical Trials for Personalized Medicine
Yingqi Zhao*, University of Wisconsin, Madison
Stanislav Minsker, Duke University
Guang Cheng, Purdue University

101. CONTRIBUTED PAPERS: SPATIAL TEMPORAL MODELS

Grand Ballroom IX (3rd Floor)

Sponsor: ENAR

Chair: Helen Louise Powell, Johns Hopkins Bloomberg School of Public Health

3:45

A Bayesian Hierarchical Spatial Model for Dental Caries Assessment using Non-gaussian Markov Random Fields
Ick Hoon Jin* and **Ying Yuan**, University of Texas MD Anderson Cancer Center
Dipankar Bandyopadhyay, University of Minnesota

4:00

Spatial Analysis of Hotel Room Rate: Evidence from Star Rated Hotels in Beijing
Chuan Wang*, University of Florida
Yang Yang, Temple University

4:15

A Sparse Reduced Rank Framework for Group Analysis of Functional Neuroimaging Data
Mihye Ahn*, Haipeng Shen, Weili Lin and **Hongtu Zhu**, University of North Carolina, Chapel Hill

4:30

Bayesian Hierarchical Models for Two-Phase Studies
Michelle E. Ross*, University of Pennsylvania
Jon Wakefield, University of Washington

4:45

Spatially Varying Distributed Lag Models
Jongyu Baek*, Brisa Sanchez and **Veronica Berrocal**, University of Michigan

5:00

Efficient Data-Driven Knot Selection for Reduced Rank Spatial Models
Casey M. Jelsema* and **Shyamal D. Peddada**, National Institute of Environmental Health Sciences, National Institutes of Health

5:15

Spatiotemporal Hurdle Models for Zero-inflated Count Data: Exploring Trends in Emergency Department Visits
Brian Neelon*, Duke University
Howard H. Chang and **Qiang Ling**, Emory University
Nicole Hastings, Duke University

102. CONTRIBUTED PAPERS: STATISTICAL METHODS IN CANCER APPLICATIONS

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Minsun Song, National Cancer Institute, National Institutes of Health

3:45

High-dimensional Nonparametric Surface Estimation with Applications to Drug Combination Studies
Xuerong Chen*, Hong-Bin Fang and **Ming Tan**, Georgetown University

4:00

Meta-analysis Sparse K-means Framework for Disease Subtype Discovery
Zhiguang Huo* and **George C. Tseng**, University of Pittsburgh

4:15

Identifying Driver Genes from Somatic Mutations: An Integrative Model-Based Approach
Keegan D. Korthauer* and **Christina Kendziorski**, University of Wisconsin, Madison

4:30

Additive Regression Model with Frailty on Semi-competing Risks Data
Jinheum Kim*, University of Suwon
Youn Nam Kim, Clinical Trials Center Severance Hospital
Chung Mo Nam, Yonsei University College of Medicine

* = Presenter | ■ = Student Award Winner

4:45

Investigating Herpes Simplex Virus Type 1 and KB Oral Cancer using Fractional Factorial Designs for Drug Combination Determination
Hongquan Xu, University of California, Los Angeles
Jessica Jaynes*, University of Nevada, Las Vegas
Xianting Ding, Shanghai Jiao Tong University
Weng Kee Wong and **Chih-Ming Ho**, University of California, Los Angeles

5:00

Recursive Reclassification using Genomic Markers
Sean Devlin*, Irina Ostrovnaya and **Mithat Gönen**, Memorial Sloan-Kettering Cancer Center

5:15

Impact of Copula Directional Specification on Multi-trial Evaluation of Surrogate Endpoints
Lindsay A. Renfro*, Mayo Clinic
Hongwei Shang, University of Connecticut
Daniel J. Sargent, Mayo Clinic

103. CONTRIBUTED PAPERS: DIAGNOSTIC AND SCREENING TESTS

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Le Kang, U.S. Food and Drug Administration

3:45

A New Diagnostic Accuracy Measure and Cut-off Point Selection Criterion
Tuochuan Dong*, State University of New York at Buffalo
Kristopher Attwood, Roswell Park Cancer Institute
Lili Tian, State University of New York at Buffalo

4:00

A Bayesian Missing Data Analysis Model for Estimating and Comparing Diagnostic Test Accuracy
Yi Hua*, University of Illinois, Urbana Champaign
Chenguang Wang, Johns Hopkins University

4:15

Application of Latent Class Analysis for Screening Test of Adolescents Suicidal Behavior in United States (1991-2011 YRBSS Survey)
Hani Samawi*, Georgia Southern University
Ryan Butterfield, Odumosu and Butterfield, LLC.

4:30

Issues in Reviewing Precision Studies of Quantitative Measurement in Medical Device Submissions in FDA
Haiwen Shi and **Qin Li***, U.S. Food and Drug Administration

4:45

On the Relationship between FROC and ROI Analyses for Detection-Localization Data
Andriy I. Bandos*, University of Pittsburgh
Nancy A. Obuchowski, Cleveland Clinic Lerner College of Medicine of Case Western Reserve University

5:00

Comparison of Diagnostic Performance Levels using Partial AUC
Hua Ma*, Andriy I. Bandos and **David Gur**, University of Pittsburgh

5:15

A Simplifying Reformulation of the Binormal Likelihood-Ratio Model
Stephen L. Hillis*, University of Iowa

104. CONTRIBUTED PAPERS: STATISTICAL METHODS FOR BIOMARKER DISCOVERY

Bristol Room (3rd Floor)

Sponsor: ENAR

Chair: Kaushik Ghosh, University of Nevada, Las Vegas

3:45

New Class of Bivariate Weibull Distributions to Accommodate the Concordance Correlation Coefficient for Left-censored Data
Uthumporn Domthong* and **Vernon M. Chinchilli**, The Pennsylvania State Hershey College of Medicine

4:00

A Semi-parametric ROC Method for Assessing Biomarkers Subject to Measurement Errors and Limit of Detection
Le Kang*, Weijie Chen and **Lucas Tcheuko**, U.S. Food and Drug Administration

4:15

Clustering and DMR Identification Using Illumina Methylation Microarray
Jeff Campbell*, Duchwan Ryu, Varghese George, Hongyan Xu and **Jaejik Kim**, Georgia Regents University

4:30

Confidence Metrics for Identification of Proteins, Post-translational Modifications (PTMs) and Proteoforms
Naomi C. Brownstein* and **Nicolas L. Young**, Florida State University

4:45

Feature Selection for Ranked-based Classifiers Applied to Cancer Biomarker Discovery
Bahman Afsari*, Luigi Marchionni and **Elana J. Fertig**, Johns Hopkins University
Ulissess Braga-Neto, Texas A&M University
Donald Geman, Johns Hopkins University

* = Presenter | ■ = Student Award Winner

5:00

Meta-analysis of Regulatory Network on Major Depressive Disorder by Liquid Association
Shuchang Liu*, Ying Ding and **George C. Tseng**, University of Pittsburgh

5:15

Modeling Physical Mixtures of Test Samples to Improve Class Prediction
Niels R. Hansen* and **Martin Vincent**, University of Copenhagen

5:30– 6:00 pm

ENAR BUSINESS MEETING
(OPEN TO ALL ENAR MEMBERS)

Bristol Room (3rd Floor)

Wednesday, March 19

8:30 am – 10:15 am

105. MODERN SURVIVAL ANALYSIS IN OBSERVATIONAL STUDIES

Grand Ballroom IX (3rd Floor)

Sponsor: ENAR

Organizer: **Kevin He**, University of Michigan

Chair: Kevin He, University of Michigan

8:30

More Efficient Estimator for Additive Hazard Model for Case-Cohort Studies
Jianwen Cai*, University of North Carolina, Chapel Hill
Soyoung Kim, Fred Hutchinson Cancer Research Center
David Couper, University of North Carolina, Chapel Hill

8:55

Contrasting Group-specific Cumulative Means Associated with Marked Recurrent Events in the Presence of a Terminating Event
Rick Ma, Regeneron Pharmaceuticals
Douglas E. Schaubel*, University of Michigan

9:20

Gateau Differential Based Boosting for Time-varying Survival Models
Yi Li*, Ji Zhu and **Kevin He**, University of Michigan

9:45

Screening for Osteoporosis in Postmenopausal Women: A Case Study in Interval Censored Competing Risks Data
Jason Fine*, University of North Carolina, Chapel Hill

10:10

Floor Discussion

106. RECENT DEVELOPMENT ON PERSONALIZED MEDICINE

Grand Ballroom II (3rd Floor)

Sponsors: ENAR, ASA Mental Health Statistics Section, ASA Biopharmaceutical Section

Organizer: Rui Song, North Carolina State University

Chair: Rui Song, North Carolina State University

8:30

Q-learning with L1 Regularization
Min Qian*, Columbia University

8:55

Personalized Medicine and Artificial Intelligence
Michael R. Kosorok*, University of North Carolina, Chapel Hill

9:20

Bayesian Methods for Dose-Finding with Targeted Agents in Early Phase Trials
Peter F. Thall*, University of Texas MD Anderson Cancer Center

9:45

Use of DNA Sequencing in Oncology Discovery Clinical Trials
Richard Simon*, National Cancer Institute, National Institutes of Health

10:10

Floor Discussion

107. CAUSAL INFERENCE IN THE ASSESSMENT OF SURROGATE MARKERS

Grand Ballroom III (3rd Floor)

Sponsors: ENAR, ASA Biopharmaceutical Section

Organizer: Michael R. Elliott, University of Michigan

Chair: Marshall Joffe, University of Pennsylvania School of Medicine

8:30

Measures of Surrogacy using Principal Stratification
Jeremy MG Taylor*, Anna Conlon and **Michael R. Elliott**, University of Michigan

8:55

Assessing the Surrogacy Paradox
Michael R. Elliott*, Anna Conlon, Yun Li and **Jeremy MG Taylor**, University of Michigan

* = Presenter | ■ = Student Award Winner

9:20

Direct Estimation of Joint Counterfactual Probabilities for the Assessment of Binary Surrogate Endpoints
Marc Buyse*, IDDI Inc.
Tomasz Burzykowski, Hasselt University, Belgium
Ariel Alonso, Maastricht University, The Netherlands
Geert Molenberghs, Leuven University, Belgium

9:45

Evaluation of Surrogates of Protection in Pre-clinical HIV Vaccine Trials
Dustin M. Long, West Virginia University
Michael G. Hudgens*, University of North Carolina, Chapel Hill

10:10

Floor Discussion

108. NEW DEVELOPMENTS IN MULTIPLE COMPARISONS PROCEDURES AND VARIABLE SELECTION

Grand Ballroom VIII (3rd Floor)

Sponsor: IMS

Organizer: Debashis Ghosh, The Pennsylvania State University

Chair: Debashis Ghosh, The Pennsylvania State University

8:30

False Discovery Control in Large-scale Spatial Multiple Testing
Wenguang Sun*, University of Southern California
Brian Reich, North Carolina State University
Tony Cai, University of Pennsylvania
Michele Guindani, University of Texas MD Anderson Cancer Center
Armin Schwartzman, North Carolina State University

8:55

Estimating the Evidence of Replicability in 'Omics' Research
Ruth Heller*, Tel-Aviv University
Marina Bogomolov, Technion

9:20

Statistics Coauthor and Citation Network
Jiashun Jin*, Carnegie Mellon University
Pengsheng Ji, University of Georgia

9:45

Adaptive Controls of FWER and FDR Under Block Dependence
Wenge Guo, New Jersey Institute of Technology
Sanat K. Sarkar*, Temple University

10:10

Floor Discussion

109. SPATIAL MODELS AND DYNAMICS APPLIED TO ENVIRONMENTAL SCIENCES AND PUBLIC HEALTH

Grand Ballroom V (3rd Floor)

Sponsors: ENAR, ASA Section on Bayesian Statistical Science, ASA Section on Statistics and the Environment

Organizer: Veronica J. Berrocal, University of Michigan

Chair: Howard Chang, Emory University

8:30

A Nonparametric Bayesian Model for Spatial Point Processes with Application to Raccoon Rabies Spread
Gavino Puggioni*, University of Rhode Island
Luca Gerardo-Giorda, Basque Center for Applied Mathematics, Spain
Lance Waller and **Leslie Real**, Emory University

8:55

The Role of Weather in Meningitis Spread in Africa
Yolanda Hagar*, University of Colorado, Boulder
Mary Hayden, National Center of Atmospheric Research
Abudulai Adams Forgor, War Memorial Hospital, Ghana
Tom Hopson, National Center of Atmospheric Research
Patricia Akweongo, University of Ghana
Abraham Hodgson, Ghana Health Service
Andrew Monoghan and **Christine Wiedinmyer**, National Center of Atmospheric Research
Raj Pandya, University Corporation for Atmospheric Research
Vanja Dukic, University of Colorado, Boulder

9:20

A Spatial Point Process Model for Viral Infections
Murali Haran*, Joshua Goldstein, John Fricks and **Francesca Chiaromonte**, The Pennsylvania State University

9:45

Using Genetic Sequences to Infer Population Dynamics: Phylodynamic Analysis of HIV Transmission in SE Michigan
Edward L. Ionides*, University of Michigan

10:10

Floor Discussion

* = Presenter | ■ = Student Award Winner

110. ADVANCES IN LONGITUDINAL STUDIES FOR PREDICTING CLINICAL OUTCOMES

Grand Ballroom VI (3rd Floor)

Sponsor: ENAR

Organizer: Abdus Sattar, Case Western Reserve University School of Medicine

Chair: Abdus Sattar, Case Western Reserve University School of Medicine

8:30

Multi-state Analysis of Serial Biomarkers, Non-Terminal, and Terminal Events

Richard J. Cook*, University of Waterloo

8:55

Generalized Quasi-Likelihood Ratio Tests for Semiparametric Analysis of Covariance Models in Longitudinal Data

Jin Tang, University of Georgia
Yehua Li*, Iowa State University

9:20

A Semi-parametric Longitudinal Model for Predicting Clinical Outcomes

Sanjoy Sinha*, Carleton University
Abdus Sattar, Case Western Reserve University School of Medicine

9:45

Predicting Outcomes using Generalized Linear Mixed Models

Sophia Rabe-Hesketh*, University of California, Berkeley
Anders Skrondal, Norwegian Institute of Public Health

10:10

Floor Discussion

111. CONTRIBUTED PAPERS: NEW DEVELOPMENTS IN EDUCATION, CONSULTING, AND HEALTH POLICY

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Sybil Nelson, Medical University of South Carolina

8:30

The Use of Analogies to Help Clinicians and Investigators Better Understand the Principles and Practice of Biostatistics

Martin L. Lesser*, Meredith Akerman and **Nina Kohn**, Feinstein Institute for Medical Research

8:45

Distributed Data, Confidentiality and Specimen Pooling: Using an Old Tool for New Challenges

Paramita Saha Chaudhuri*, Duke University

9:00

Analysis of Resting Metabolic Rate in a Latin Square Design with Repeated Measures

William D. Johnson*, Robbie Beyl and **Jeffrey Burton**, Pennington Biomedical Research Center

9:15

Small Area Estimation of Vaccination Coverage Rates by Combining Time Series and Cross Sectional Data

Santanu Pramanik* and **Ramanan Laxminarayan**, Public Health Foundation of India

9:30

Challenges using Survey Data to Estimate Problem Gambling Prevalence in the SEIG-MA Project

Edward J. Stanek III* and **Rachel A. Volberg**, University of Massachusetts, Amherst
Robert J. Williams, University of Lethbridge, Alberta, Canada

9:45

Practical and Statistical Challenges in Developing an HIV Drug Resistance Surveillance Protocol

Natalie Exner* and **Marcello Pagano**, Harvard University

10:10

Floor Discussion

112. CONTRIBUTED PAPERS: LATEST ADVANCES IN FUNCTIONAL AND IMAGING DATA ANALYSIS

Grand Ballroom I (3rd Floor)

Sponsor: ENAR

Chair: Jaroslaw Harezlak, Indiana University Fairbanks School of Public Health

8:30

Online Functional Principal Component Analysis

David Degras*, DePaul University

8:45

Modeling Binary Functional Data with Application to Animal Husbandry

Jan Gertheiss*, University of Göttingen
Verena Maier, Ludwig-Maximilians-University Munich
Engel F. Hessel, University of Göttingen
Ana-Maria Staicu, North Carolina State University

* = Presenter | ■ = Student Award Winner

9:00

Using Regression Models to Infer Active Connections in Cortex

Mark A. Reimers*, Virginia Commonwealth University

9:15

Parametric Modulation of Functional MRI Signals: A Mixed Effect Model Approach

Lei Huang* and **Martin Lindquist**, Johns Hopkins University
Philip Reiss, New York University Child Study Center
Ciprian Crainiceanu, Johns Hopkins University

9:30

Pre-processing of the Longitudinal Structural Brain Imaging Data: A Case Study

Jacek Urbanek* and **Jaroslaw Harezlak**, Indiana University Fairbanks School of Public Health
Elizabeth M. Sweeney, Johns Hopkins Bloomberg School of Public Health

9:45

Clustering of Ultra High Dimensional Longitudinal Data

Seonjoo Lee*, Columbia University
Vadim Zipunnikov, Johns Hopkins University
Navid Shiee, Amazon Inc.
Daniel S. Reich, National Institute of Neurological Disorders and Stroke, National Institutes of Health
Dzung L. Pham, The Henry Jackson Foundation
Brian S. Caffo and **Ciprian M. Crainiceanu**, Johns Hopkins University

10:00

Effects of Registration on Statistical Analysis of MRI Data

Ani Eloyan* and **Haochang Shou**, Johns Hopkins University
Russell T. Shinohara, University of Pennsylvania
Elizabeth M. Sweeney and **Mary B. Nebel**, Johns Hopkins University
Daniel S. Reich, National Institute of Neurological Disorders and Stroke, National Institutes of Health
Martin A. Lindquist and **Ciprian M. Crainiceanu**, Johns Hopkins University

✱ = Presenter | ■ = Student Award Winner

113. CONTRIBUTED PAPERS: BAYESIAN METHODS

Grand Ballroom IV (3rd Floor)

Sponsor: ENAR

Chair: Kassie Fronczyk, Rice University

8:30

Joint Models for Multivariate Longitudinal Measurements and a Binary Event: An Application to a Fetal Growth Study with Longitudinal Ultrasound Measurements

Sungduk Kim* and **Paul S. Albert**, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

8:45

Bayesian Peer Calibration Based on Network Position with Application to Alcohol Use

Miles Q. Ott*, Carleton College
Joseph H. Hogan, Brown University
Krista J. Gile, University of Massachusetts, Amherst
Crystal Linkletter, Mathworks
Nancy P. Barnett, Brown University

9:00

Modeling Long-term HIV Dynamics with Left Censoring Measurements

Tao Lu*, State University of New York at Albany

9:15

A Bayesian Missing Data Framework for Generalized Multiple Outcome Mixed Treatment Comparisons

Hwanhee Hong*, Haitao Chu, Jing Zhang and **Bradley P. Carlin**, University of Minnesota

9:30

Clustering Significant Regions of Brain Activation Using fMRI Meta Data

Meredith Ray*, University of South Carolina
Hongmei Zhang, University of Memphis
Jian Kang, Emory University

9:45

Bayesian Factorizations of Big Sparse Tensors

Jing Zhou ■, University of North Carolina, Chapel Hill
Anirban Bhattacharya, Duke University
Amy H. Herring, University of North Carolina, Chapel Hill
David B. Dunson, Duke University

10:00

Floor Discussion

114. CONTRIBUTED PAPERS: MULTIVARIATE SURVIVAL ANALYSIS

Grand Ballroom VII (3rd Floor)

Sponsor: ENAR

Chair: Hui Xu, University of Massachusetts, Amherst

8:30

Inference on Quantile Residual Life for Semi-competing Risks Data

Wen-Chi Wu* and **Jong-Hyeon Jeong**, University of Pittsburgh

8:45

Model Selection and Goodness-of-Fit Test Procedures for Copula Models

Antai Wang*, New Jersey Institute of Technology

9:00

Analysis of Recurrent Events Data based on Accelerated Recurrence Time Model

Xiaoyan Sun*, Limin Peng, Yijian Huang and **Amita K. Manatunga**, Emory University
Hui-Chuan Lai, University of Wisconsin, Madison

9:15

Simple Two-stage Semiparametric Estimation of the Positive Stable Shared Frailty Model

Yu Han*, Changyong Feng and **Xin Tu**, University of Rochester

9:30

Nonparametric Estimation of Joint Distribution of Time from Umbilical Cord Blood Transplantation to First Infection and Gap Times between Recurrent Infections

Chi Hyun Lee ■ and **Xianghua Luo**, University of Minnesota
Chiung-Yu Huang, Johns Hopkins University
Todd DeFor, University of Minnesota

9:45

Safe Trials for Equivalence of Two Survival Functions: Alternative to the Tests under Proportional Hazards

Elvis Martinez*, Florida State University
Wenting Wang, University of Texas MD Anderson Cancer Center
Debajyoti Sinha, Florida State University
Stuart Lipsitz, Harvard Medical School
Richard Chappell, University of Wisconsin, Madison

10:00

Composite Likelihood For Joint Analysis of Multiple Multistate Processes via Copulas

Liqun Diao*, University of Rochester
Richard J. Cook, University of Waterloo

115. CONTRIBUTED PAPERS: STATISTICAL ANALYSIS IN THE PRESENCE OF MISSING DATA

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Jiwei Zhao, University of Waterloo

8:30

Variable Selection and Prediction with Incomplete High-Dimensional Data

Ying Liu*, Yang Feng, Yuanjia Wang and **Melanie Wall**, Columbia University

8:45

Quantile Regression in the Presence of Monotone Missingness with Sensitivity Analysis

Minzhao Liu*, University of Florida
Michael Daniels, University of Texas, Austin

9:00

Improving the Robustness of Doubly Robust Estimators

Peisong Han*, University of Waterloo
Lu Wang, University of Michigan

9:15

Nonparametric MANOVA Approaches for Non-Normal Multivariate Outcomes with Missing Values

Fanyin He*, Sati Mazumdar, Gong Tang and **Stewart J. Anderson**, University of Pittsburgh

9:30

Model Independent Diagnostic for Multiple Imputations

Irina Bondarenko* and **Trivellore Raghunathan**, University of Michigan

9:45

Simple Relaxed Conditional Likelihood

John J. Hanfelt and **Lijia Wang***, Emory University

10:00

Floor Discussion

✱ = Presenter | ■ = Student Award Winner

116. CONTRIBUTED PAPERS: TOOLS FOR LONGITUDINAL DATA ANALYSIS

Bristol Room (3rd Floor)

Sponsor: ENAR

Chair: **Ozgur Asar**, Lancaster Medical School

8:30

Longitudinal Outcome Evaluation of a Pilot Study of Provider Delivered Care Management
Hsiu-Ching Chang*, BlueCross BlueShield of Michigan

8:45

Properties and Applications of Multivariate Antedependence Models
Chulmin Kim*, University of West Georgia

9:00

Antedependence Models for Skew Normal Longitudinal Data
Shu-Ching Chang* and **Dale Zimmerman**, University of Iowa

9:15

Bayesian Shared Parameter Models for Dyadic Longitudinal Data with Intermittent Dropouts
Jaeil Ahn*, Georgetown University
Ying Yuan and **Wenyi Wang**, University of Texas MD Anderson Cancer Center

9:30

An R Package for Sensitivity Analysis on Longitudinal Data with Non-Ignorable Intermittent Missingness
Jing Wang*, The George Washington University
Chenguang Wang, Johns Hopkins University

9:45

A Novel Mixture Model Estimates Time to Onset of Disease or Drug Effects and its Association with Key Covariates
Mengyuan Xu*, National Institute of Environmental Health Sciences, National Institutes of Health
Yin Yao, The National Institute of Mental Health, National Institutes of Health

10:00

A Two-part Mixture Model for Zero-inflated Longitudinal Measurements with Heterogeneous Random Effects
Huirong Zhu*, Sheng Luo and **Stacia M. DeSantis**, University of Texas Health Science Center at Houston

117. CONTRIBUTED PAPERS: ANALYSIS OF DATA FROM CLINICAL TRIALS

Chasseur Room (3rd Floor)

Sponsor: ENAR

Chair: Adam Lane, Cincinnati Children's Hospital Medical Center

8:30

Finding the Optimal Allocation in Sequential Binary Response Experiments with Two Possibly Correlated Endpoints
Lu Wang* and **Hongjian Zhu**, University of Texas Health Science Center at Houston

8:45

A General Class of Correlation Coefficients between Binary and Continuous Variables for the 2 × 2 Crossover Design
Luojun Wang* and **Vernon Chinchilli**, Penn State Hershey College of Medicine

9:00

Weighted and Replicated Estimator for Comparing Dynamic Treatment Regimens with a Binary Outcome using SMART Data: Practical Issues and a Simulations-based Sample Size Calculator
Kelley M. Kidwell* and **Inbal Nahum-Shani**, University of Michigan
Connie Kasari, University of California, Los Angeles
Daniel Almirall, University of Michigan

9:15

Marginal Meta Analysis for Combining Randomized Clinical Trials with Rare Binary Outcomes — Reevaluating the Safety Concern of Avandia
Yi Huang* and **Elande Baro**, University of Maryland, Baltimore County
Guoxing Soon, U.S. Food and Drug Administration

9:30

Design Issues and their Effect on Power and Sampling Frequency Requirements for N-of-1 Clinical Trials
Yanpin Wang*, Andrew Viterbi and **Nicholas Schork**, Scripps Health

9:45

Using Internal Pilots to Design Cluster Randomized Trials with Unequal Cluster Sizes
Ashutosh Ranjan*, University of Alabama, Birmingham
Christopher S. Coffey, University of Iowa
Leslie A. McClure, University of Alabama, Birmingham

10:00

Designing Balanced Patient-specific Treatment Stimuli for Post-stroke Language Interventions
Minming Li*, Edward J. Stanek III and **Jacquie Kurland**, University of Massachusetts, Amherst

* = Presenter | ■ = Student Award Winner

Wednesday, March 19

10:15 am – 10:30 am

Refreshment Break with Our Exhibitors

Grand Ballroom Foyer (3rd Floor)

Wednesday, March 19

10:30 am – 12:15 pm

118. HUMAN HEALTH AND ENVIRONMENTAL STATISTICS AT THE U.S. EPA'S OFFICE OF RESEARCH AND DEVELOPMENT

Grand Ballroom V (3rd Floor)

Sponsors: ENAR, ASA Section on Statistics and the Environment, ASA Government Statistic Section

Organizer: James L. Crooks, U.S. Environmental Protection Agency

Chair: Ana Rappold, U.S. Environmental Protection Agency

10:30

Exploring Chemically Induced Change in Neuronal Networks

Diana Hall*, University of North Carolina, Chapel Hill

10:50

Development and Evaluation of Two Reduced Form Versions of a Deterministic Air Quality Model for Ozone and Particulate Matter

Kristen M. Foley*, Sergey L. Napelenok, Sharon B. Phillips and **Carey Jang**, U.S. Environmental Protection Agency

11:10

Fully Bayesian Analysis of High-Throughput Targeted Metabolomics Assays

James L. Crooks*, Denise K. MacMillan and **Jane E. Gallagher**, U.S. Environmental Protection Agency

11:30

Implications of Nonlinear Concentration Response Curve for Ozone related Mortality on Risk Assessment

Ana G. Rappold* and **James L. Crooks**, U.S. Environmental Protection Agency

11:50

Modeling the Effect of Temperature on Ozone-Related Mortality

Ander Wilson*, North Carolina State University
Ana G. Rappold and **Lucas M. Neas**, U.S. Environmental Protection Agency
Brian J. Reich, North Carolina State University

119. POWER ANALYSIS FOR MIXED MODELS: WHERE WE STAND

Grand Ballroom III (3rd Floor)

Sponsor: ENAR

Organizer: Yueh-Yun Chi, University of Florida

Chair: Keith E. Muller, University of Florida

10:30

Introduction

Keith Muller*, University of Florida

10:35

Quick (but Accurate) Power and Precision Approximation using Generalized Linear Mixed Model Software

Walter W. Stroup*, University of Nebraska, Lincoln

10:55

Sample Size for Fixed Effect Inference in Longitudinal and Multilevel Mixed Models

Yueh-Yun Chi*, University of Florida

11:15

Optimal Combination of Number of Participants and Number of Repeated Measurements in Longitudinal Studies with Time-Varying Exposure

Donna Spiegelman*, Harvard School of Public Health
Jose Barrera-Gomez and **Xavier Basagana**, Centre for Research in Environmental Epidemiology (CREAL), Barcelona, Spain

11:35

Panel Discussion

120. NEW DEVELOPMENTS IN ESTIMATING CAUSAL EFFECTS OF TIME-VARYING TREATMENTS

Grand Ballroom II (3rd Floor)

Sponsor: ENAR

Organizer: Edward Kennedy, University of Pennsylvania School of Medicine

Chair: Edward Kennedy, University of Pennsylvania School of Medicine

10:30

Double Robust Estimation Strategies for Longitudinal Censored Data

Mireille E. Schnitzer*, Université de Montréal
Judith J. Lok, Harvard School of Public Health

10:55

Nonparametric Smoothing for Causal Inference with Continuous Treatments

Edward H. Kennedy* and **Marshall M. Joffe**, University of Pennsylvania

* = Presenter | ■ = Student Award Winner

11:20
Overcoming Challenges Associated with Artificial Censoring in Structural Nested Failure Time Models
David M. Vock*, University of Minnesota

11:45
Inference for Causal Effects of Time-varying Treatment in the Presence of Selective Measurement Error
Marshall M. Joffe*, University of Pennsylvania

12:10
Floor Discussion

121. INSIDE THE BIOSTATISTICAL COLLABORATIVE PROCESS

Grand Ballroom VI (3rd Floor)

Sponsors: ENAR, ASA Mental Health Statistics Section

Organizer: Bhramar Mukherjee and **Brisa Sanchez**, University of Michigan

Chair: Brisa Sánchez, University of Michigan

10:30
Mass Spectrometry-based Metabolomics to Understand Human Health and Disease
Andrew Patterson*, The Pennsylvania State University

11:00
Kernel Machines for Metabolomics Data Analysis
Xiang Zhan, Debashis Ghosh* and **Andrew Patterson**, The Pennsylvania State University

11:45
Discussant: Wei Pan, University of Minnesota

122. CONTRIBUTED PAPERS: NON-PARAMETRIC METHODS

Atlantic Room (3rd Floor)

Sponsor: ENAR

Chair: Kuang-Yao Lee, Yale University

10:30
On Inverse Probability Weighted Estimators in the Presence of Interference
Lan Liu*, Michael G. Hudgens and **Sylvia Becker-Dreps**, University of North Carolina, Chapel Hill

10:45
Association of Time to Recovery and a Subsequent Depressive or Mania Episode
Xiaotian Chen* and **Yu Cheng**, University of Pittsburgh

11:00
Bayesian Doubly Semiparametric Proportional Hazards Model with Commensurate Priors that Facilitate Borrowing from a Nonexchangeable Data Source
Thomas A. Murray*, University of Minnesota
Brian P. Hobbs, University of Texas MD Anderson Cancer Center
Bradley P. Carlin, University of Minnesota

11:15
Bivariate Penalized Splines for Regression
Ming-Jun Lai and **Lily Wang***, University of Georgia

11:30
Signed Rank with Responses Missing at Random
Huybrechts F. Bindele*, University of South Alabama

11:45
Combination of Nonparametric Regression Based Classifiers for Breast Tissue Diagnosis from Raman Spectra
Jing Guo*, Richard Charnigo and **Cidambi Srinivasan**, University of Kentucky
Ramachandra Dasari, Massachusetts Institute of Technology
Maryann Fitzmaurice, Case Western Reserve University
Abigail Haka, Cornell University

12:00
Gene-Trait Similarity U Test
Changshuai Wei* and **Qing Lu**, Michigan State University

✱ = Presenter | ■ = Student Award Winner

123. CONTRIBUTED PAPERS: VARIABLE SUBSET SELECTION

Chasseur Room (3rd Floor)

Sponsor: ENAR

Chair: Sunyoung Shin, University of North Carolina, Chapel Hill

10:30

Time-varying Networks Estimation and Dynamic Model Selection

Xinxin Shu* and **Annie Qu**, University of Illinois, Urbana-Champaign

10:45

Simultaneous Variable Selection for Joint Models of Longitudinal and Survival Outcomes

Zangdong He*, Indiana University School of Medicine and Fairbanks School of Public Health
Wanzhu Tu, Indiana University School of Medicine, Fairbanks School of Public Health and Regenstrief Institute, Inc.
Sijian Wang, University of Wisconsin, Madison
Haoda Fu, Eli Lilly & Company
Zhangsheng Yu, Indiana University School of Medicine and Fairbanks School of Public Health

11:00

Local Feature Selection in Varying-Coefficient Models

Lan Xue, Oregon State University
Xinxin Shu and **Peibei Shi***, University of Illinois, Urbana-Champaign
Colin O. Wu, National Heart, Lung and Blood Institute, National Institutes of Health
Annie Qu, University of Illinois, Urbana-Champaign

11:15

Structured Feature Selection for Longitudinal Biomarker Data

Anthony V. Pileggi* and **Brent A. Johnson**, Emory University
DuBois Bowman, Columbia University

11:30

Parsimonious Covariate and Conditional-Mean Model Selection with Multiple Candidate Predictors

Greg DiRienzo*, State University of New York at Albany

11:45

Floor Discussion

124. CONTRIBUTED PAPERS: HIGH DIMENSIONAL DATA IN GENETICS AND GENOMICS

Grand Ballroom VIII (3rd Floor)

Sponsor: ENAR

Chair: Jun Ding, National Institute on Aging, National Institutes of Health

10:30

Strategies for Developing Prediction Models from Genome-wide Association Studies

Jincao Wu*, Ruth M. Pfeiffer and **Mitchell H. Gail**, National Cancer Institute, National Institutes of Health

10:45

A Penalized Multi-trait Mixed Model for Association Mapping in Pedigree-based GWAS

Jin Liu*, University of Illinois, Chicago
Can Yang, Yale University
Xingjie Shi, Shanghai University of Finance and Economics, China
Cong Li, Yale University
Jian Huang, University of Iowa
Hongyu Zhao and **Shuangge Ma**, Yale University

11:00

A Mixture of Experts Approach for the Analysis of SNP Data

Julia Schiffner* and **Holger Schwender**, Heinrich-Heine-Universitaet Duesseldorf

11:15

Joint Estimation of Multiple Dependent Gaussian Graphical Models

Yuying Xie ■, Yufeng Liu and **William Valdar**, University of North Carolina, Chapel Hill

11:30

Gateau Differential Boosting for Analysis of Gene Effects and Gene-gene Interaction

Kevin He*, Yi Li and **Ji Zhu**, University of Michigan

11:45

Concordant Integrative Analysis of Multiple Gene Expression Data Sets

Fanni Zhang* and **Yinglei Lai**, The George Washington University

12:00

D_CDF Test of Negative Log Transformed P-values with Application to Genetic Pathway Analysis

Hongying Dai*, Children's Mercy Hospital
Richard Charnigo, University of Kentucky

✱ = Presenter | ■ = Student Award Winner

125. CONTRIBUTED PAPERS: TOOLS FOR SURVIVAL ANALYSIS

Grand Ballroom IV (3rd Floor)

Sponsor: ENAR

Chair: Jonathan Yabes, University of Pittsburgh

10:30

Robust Prediction of Cumulative Incidence Function under Non-proportional Subdistribution Hazards
Qing Liu* and **Chung-Chou H Chang**, University of Pittsburgh

10:45

Dynamics Model of Diabetes Disease Progression to End-Stage-Renal Disease and Mortality
Ying Jiang, Nathaniel Osgood, Roland Dyck and **Hyun J. Lim***, University of Saskatchewan, Canada

11:00

On the Consistency of Maximum Likelihood Estimators for the Three Parameter Lognormal Distribution
HaiYing Wang*, University of New Hampshire
Nancy Flournoy, University of Missouri, Columbia

11:15

Regression When the Predictor may be Censored
David Oakes*, University of Rochester

11:30

Nonparametric Discrete Survival Function Estimation with Uncertain Endpoints using an Internal Validation Subsample
Jarcy Zee* and **Sharon X. Xie**, University of Pennsylvania Perelman School of Medicine

11:45

A New Flexible Association Measure for Semi-competing Risks
Jing Yang* and **Limin Peng**, Emory University

12:00

Pseudo-value Approach for Comparing Survival Medians for Dependent Data
Kwang Woo Ahn*, Medical College of Wisconsin
Franco Mendolia, German Aerospace Center, Institute of Aerospace Medicine, Germany

126. CONTRIBUTED PAPERS: META-ANALYSIS

Grand Ballroom I (3rd Floor)

Sponsor: ENAR

Chair: Sujin Kim, Savannah State University

10:30

Estimation of Treatment Effects in Matched-Pair Cluster Randomized Trials by Calibrating Covariate Imbalance Between Clusters
Zhenke Wu* and **Constantine E. Frangakis**, Johns Hopkins Bloomberg School of Public Health
Thomas A. Louis, Johns Hopkins Bloomberg School of Public Health and U.S. Census Bureau
Daniel O. Scharfstein, Johns Hopkins Bloomberg School of Public Health

10:45

A Unification of Models for Meta-analysis of Diagnostic Accuracy Studies Without a Gold Standard
Yulun Liu* and **Yong Chen**, University of Texas Health Science Center at Houston
Haitao Chu, University of Minnesota

11:00

Meta-analysis Methods for Combining Multiple Expression Profiles: Comparisons, Statistical Characterization and an Application Guideline
Lun-Ching Chang*, Hui-Min Lin and **George C. Tseng**, University of Pittsburgh

11:15

Investigation on Adaptively Weighted Evidence Aggregation Meta-analysis Methods
Shaowu Tang* and **George C. Tseng**, University of Pittsburgh

11:30

Bayesian Hierarchical Models for Network Meta-analysis Incorporating Nonignorable Missingness
Jing Zhang ■, Haitao Chu, Hwanhee Hong and **James D. Neaton**, University of Minnesota
Guoxing Greg Soon, U.S. Food and Drug Administration
Beth A. Virnig and **Bradley P. Carlin**, University of Minnesota

11:45

Plug-in Tests for Non-equivalence of Means of Independent Normal Populations
Sungwoo Choi* and **Junyong Park**, University of Maryland Baltimore County

✱ = Presenter | ■ = Student Award Winner

127. CONTRIBUTED PAPERS: STATISTICAL METHODS FOR HANDLING MISSING DATA

Grand Ballroom X (3rd Floor)

Sponsor: ENAR

Chair: Victoria Liublinska, Harvard University

10:30

Censoring Adjustment Methods for Source Apportionment Models

Jenna R. Krall*, Johns Hopkins Bloomberg School of Public Health
Charles H. Simpson, Havoc Engineering
Roger D. Peng, Johns Hopkins Bloomberg School of Public Health

10:45

A Hot Deck Imputation Procedure for Multiply Imputing Nonignorable Missing Data: The Proxy Pattern-Mixture Hot Deck

Danielle M. Sullivan* and **Rebecca R. Andridge**, The Ohio State University

11:00

Analysis of Incomplete Derived Responses: Multiple Imputation for Body Mass Index Data

Jiwei Zhao*, Richard Cook and **Changbao Wu**, University of Waterloo

11:15

Longitudinal Latent Variable Models Given Incompletely Observed Biomarkers and Covariates

Chunfeng Ren* and **Yongyun Shin**, Virginia Commonwealth University

11:30

Clustering Incomplete Data using Normal Mixture Models

Chantal Larose*, Dipak Dey and **Ofer Harel**, University of Connecticut

11:45

Causal Inference in Longitudinal Studies with Dropout and Truncation by Death

Michelle Shardell*, University of Maryland
Gregory Hicks, University of Delaware
Luigi Ferrucci, National Institute on Aging, National Institutes of Health

12:00

The Effect of Imputing a Complex Outcome on the Rejection Rate of Pearson's Chi-Square Test of Independence and a Permutation-Based Correction Factor

Megan J. Olson Hunt* and **Gong Tang**, University of Pittsburgh

128. CONTRIBUTED PAPERS: LONGITUDINAL DATA ANALYSIS

Bristol Room (3rd Floor)

Sponsor: ENAR

Chair: Douglas Gunzler, Case Western Reserve University

10:30

Generalized p-Values for Testing Zero-Variance Components in Linear Mixed-effects Models

Haiyan Su*, Montclair State University
Xinmin Li, ShanDong University of Technology
Hua Liang, The George Washington University
Hulin Wu, University of Rochester

10:45

Sufficient Dimension Reduction for Longitudinal Data

Xuan Bi* and **Annie Qu**, University of Illinois, Urbana-Champaign

11:00

Real Time Monitoring of Progression Towards Renal Failure in Primary Care Patients

Peter J. Diggle, Lancaster University, United Kingdom and University of Liverpool, United Kingdom
Ines Sousa, University of Minho, Portugal
Ozgur Asar*, Lancaster University, United Kingdom

11:15

AR(1) Latent Class Models for Longitudinal Count Data

Nicholas Henderson* and **Paul Rathouz**, University of Wisconsin, Madison

11:30

Time-varying Coefficient Models to Identify and Model Time-clusters in Recurrent Event Data

Xiaoxue Li*, Stewart J. Anderson and **Saul Shiffman**, University of Pittsburgh

11:45

Identifying Multiple Change-points in a Linear Mixed Effects Model

Yinglei Lai*, The George Washington University
Paul S. Albert, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

12:00

Regression Analysis of Mixed Recurrent-event and Panel-count Data

Liang Zhu*, St. Jude Children's Research Hospital
Xingwei Tong, Beijing Normal University
Jianguo Sun, University of Missouri, Columbia
Kumar Srivastava, St. Jude Children's Research Hospital
Wendy Leisenring, Fred Hutchinson Cancer Research Center
Leslie Robinson, St. Jude Children's Research Hospital

129. CONTRIBUTED PAPERS: PREDICTION AND PROGNOSTIC MODELING

Grand Ballroom VII (3rd Floor)

Sponsor: ENAR

Chair: Kellie J. Archer, Virginia Commonwealth University

10:30

Predicting Probabilities of Competing Risk Outcomes under Informative Censoring, with Application to Safety and Efficacy of Initial ART in HIV-Positive Patients

Judith J. Lok* and **Michael D. Hughes**, Harvard School of Public Health

10:45

The Optimality of a Pseudo-Likelihood Approach to Bayesian Classification

Josephine K. Asafu-Adjei* and **Rebecca A. Betensky**, Harvard School of Public Health

11:00

Local Likelihood-Based Estimation for Quantile Classification in Binary Regression Models

John D. Rice* and **Jeremy M. G. Taylor**, University of Michigan

11:15

Combination of Longitudinal Biomarkers in Predicting Binary Events with Application in a Fetal Growth Study

Danping Liu* and **Paul S. Albert**, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

11:30

Predictive Accuracy of Time-dependent Markers for Survival Outcomes

Li Chen*, University of Kentucky
Donglin Zeng and **Danyu Lin**, University of North Carolina, Chapel Hill

11:45

An Investigation of the Assumptions of the Current Status Model

Jian-Lun Xu*, National Cancer Institute

12:00

Floor Discussion

130. CONTRIBUTED PAPERS: NEW METHODS FOR GWAS

Grand Ballroom IX (3rd Floor)

Sponsor: ENAR

Chair: Tamar Sofer, Harvard School of Public Health

10:30

Lassot: A Hybrid of Lasso and t-regularization for Penalized Regression and Applications to Genomic Selection

Long Qu*, Wright State University

10:45

SHAVE: Shrinkage Estimator Measured for Multiple Visits Increases Power in GWAS of Quantitative Traits

Osorio D. Meirelles*, **Jun Ding** and **Toshiko Tanaka**, National Institute on Aging, National Institutes of Health
Serena Sanna, Istituto di Ricerca Genetica e Biomedica, Consiglio Nazionale delle Ricerche, Monserrato, Cagliari, Italy
Hsih-Te Yang, Taiwan Food and Drug Administration
Dawood B. Dudekula, National Institute on Aging, National Institutes of Health
Francesco Cucca, Istituto di Ricerca Genetica e Biomedica, Consiglio Nazionale delle Ricerche, Monserrato, Cagliari, Italy
Luigi Ferrucci, National Institute on Aging, National Institutes of Health
Goncalo Abecasis, University of Michigan
David Schlessinger, National Institute on Aging, National Institutes of Health

11:00

Secondary Trait Analysis for Case-Control Association Studies in the Presence of Covariates

Godwin Yung* and **Xihong Lin**, Harvard University

11:15

Penalized Multi-Marker versus Single-Marker Regression Methods for Genome-Wide Association Studies of Quantitative Traits

Hui Yi*, Netsanet Imam and **Ina Hoeschele**, Virginia Tech

11:30

Association Studies with Imputed SNPs Using Expectation-Maximization-Likelihood-Ratio Test

Kuan-Chieh Huang* and **Yun Li**, University of North Carolina, Chapel Hill

11:45

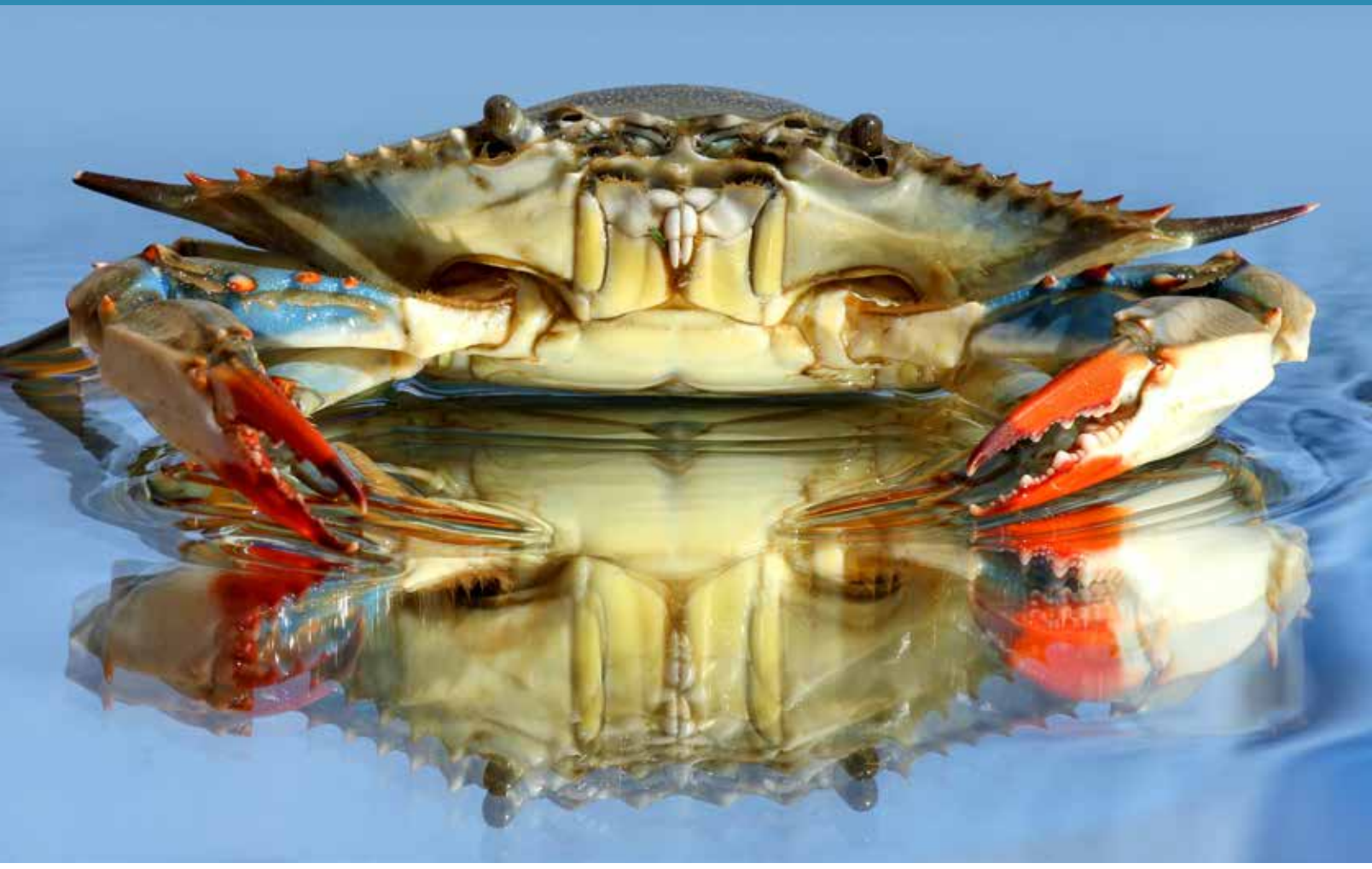
Statistical Calibration of qRT-PCR, Microarray and RNA-Seq Gene Expression Data with Measurement Error Models

Zhaonan Sun*, Thomas Kuczek and **Yu Zhu**, Purdue University

12:00

IUTA: A Statistical Method to Detect Differential Isoform Usage from mRNA-Seq Data

Liang Niu*, Weichun Huang, David M. Umbach and **Leping Li**, National Institute of Environmental Health Sciences, National Institutes of Health



ENAR 2014
SPRING MEETING

INDEX

Aban, Inmaculada 7k
Abarin, Taraneh 33
Abecasis, Goncalo R. 27, 75, 130
Adams, Ryan P. 56
Aerts, Marc 44
Afsari, Bahman 104
Agan, Brian K. 87
Agarwal, Deepak SC3
Agniel, Denis M. 23
Ahn, Jaeil 116
Ahn, Kwang Woo 24, 125
Ahn, Mihye 101
Airoldi, Edoardo M. 40
Akcin, Haci 84
Akerman, Meredith 111
Akweongo, Patricia 109
Albacha-Hejazi, Hasan 24
Albert, Paul S. 13, 113, 128, 129
Alexeeff, Stacey E. 18
Allen, Andrew S. 95
Almirall, Daniel 117
Almudevar, Anthony 7f, 33
Alonso, Ariel 107
Alvarez, JoAnn 48
An, Qian 3m
Anderson, Georgiana B. 24
Anderson, Keaven M. 28
Anderson, Stewart J. 37, 115, 128
Ando, Yuki 23
Andreasssen, Ole 25
Andrei, Adin-Cristian 19
Andrews, Jennifer 76
Andridge, Rebecca R. 127
Apanasovich, Tatiyana V. 42
Archer, Kellie J. 5h
Asafu-Adjei, Josephine K. 129
Asar, Ozgur 128
Aston, John 68
Atkins, David C. 34
Attie, Alan 24
Attwood, Kristopher 103
Austin, Erin 36
Awadalla, Saria 2j
Axelson, David 50
Aydin, Burcu 7l
Ayers, Gregory 48
Azzone, Vanessa 3i
Baechler, Emily C. 24
Baek, Jongyu 101
Baggerly, Keith 15
Bahou, Wadie F. 4c
Bai, Jiawei 18
Bailey-Wilson, Joan E. 24, 43
Bair, Eric 22, 36
Baladandayuthapani, Veerabhadran 3q, 15 62
Balakrishnan, Narayanaswamy 99
Balasubramanian, Raji 63, 76
Bandos, Andriy I. 103
Bandyopadhyay, Dipankar 101
Banerjee, Moulinath 19
Banerjee, Samprit 31
Banerjee, Sudipto 60, 63
Barker, Lawrence E. 84
Barnett, Ian J. 57
Barnett, Nancy P. 113
Baro, Elande 117
Barrdahl, Myrto 33, 45
Barrera-Gomez, Jose 119
Bartolucci, Francesco 30

Basagana, Xavier 119
Batterman, Stuart A. 8h
Bazin, Pierre-Louis 89
Beaty, Terri H. 4n, 24
Beavers, Daniel P. 46
Bebu, Ionut 87
Beck, J. Robert 5e
Becker-Dreps, Sylvia 122
Behrens, Timothy W. 24
Behseta, Sam 80
Bellamy, Scarlett R5
Bello, Ghalib A. 48
Benjamini, Yuval 7p
Berndt, Sonja I. 1d
Bernhardt, Paul W. 72
Berrocal, Veronica J. 8b, 58, 101
Betensky, Rebecca A. 129
Beyl, Robbie A. 8i, 10a, 111
Bhangale, Tushar R. 24
Bharath, Karthik 46
Bhattacharya, Anirban 113
Bhaumik, Dulal K. 37
Bi, Xuan 44, 128
Billard, Lynne 47
Bindele, Huybrechts F. 122
Birmaher, Boris 50
Bliss, Donna Z. 86
Bliznyuk, Nikolay 98
Blitzstein, Joseph 12
Boatman-Reich, Dana 64
Bobb, Jennifer F. 8g, 38
Boca, Simina M. 7e
Boerwinkle, Eric 75
Bogomolov, Marina 108
Bondarenko, Irina 115
Bondell, Howard D. 11j, 20
Bordonali, Elena K. 23
Boruvka, Audrey 35
Bose, Maitreyee 33
Bowman, Dale 23
Bowman, DuBois 89, 97, 123
Bradford, Denise 84
Braga-Neto, Ulissess 104
Branch, Craig A. 58
Braun, Danielle 61
Braun, Thomas M. 8k, 35, 52
Bressler, Jan 33
Breysse, Patrick N. 38
Brice, Joann 10c
Brinks, Ahnalee 31
Britton, Tom 1c
Broglio, Kristine R. 14
Broman, Karl W. 1i
Brown, Andrew 63
Brown, Benjamin T. 7c
Brown, Charles H. 31
Brown, Marshall D. 5g
Brown, Shawn T. 34
Brownstein, Naomi C. 104
Brumback, Babette 11b
Bryan, Kevin A. 40
Bryan, Matthew W. 37
Buhule, Olive D. 60
Bullitt, Elizabeth 7l
Burchard, Esteban 33
Bureau, Alexandre 24
Burke, Erin 58
Burke, Lora E. 37
Burton, Jeffrey 8i, 10a, 111
Burzykowski, Tomasz 107
Busonero, Fabio 75
Butterfield, Ryan 103
Butz, Arlene 38
Buyse, Marc 107
Cadwell, Betsy L. 84
Caffo, Brian S. 7m, 22, 64, 89, 97, 112
Cahill, Farrell 33
Cai, Bo 78
Cai, Jianwen 59, 73, 105
Cai, Tianxi 5g, 23, 34, 47, 81, 100
Cai, Tony 45, 73, 108
Cai, Zhuangyu 11b
Calabresi, Peter A. 97
Calaway, John 32
Califano, Joseph A. 90
Campbell, Jeff 104
Cao, Guanqun 20
Cao, Ying 45
Carlin, Bradley P. 29, 113, 122, 126, SC2
Carnegie, Nicole B. 46
Carrico, Caroline K. 65
Carroll, Raymond J. 4b, 5b, 44
Caspers, Kristin 76
Cassese, Alberto 32, 83
Castellanos, Xavier F. 58
Chaganty. N. Rao 18, 36
Chan, Wenyaw 8c
Chandrasekhar, Rameela 88
Chang, Chung-Chou H 125
Chang, Hsiu-Ching 116
Chang, Howard H. 38, 101
Chang, Hua-Hua 7g, 69
Chang, Joyce 59

Chang, Lun-Ching 75, 126
Chang, Shu-Ching 116
Chang, Yu-Wei 48
Chanock, Stephen J. 33
Chappell, Richard 35, 114
Charnigo, Richard J. 21, 47, 122, 124
Chatterjee, Arpita 99
Chatterjee, Nilanjan 4b, 5b, 33, 45, 95
Chelaru, Florin 80
Chen, Baojiang 47
Chen, Chi-Hua 25
Chen, Eric 27
Chen, Geng 3e
Chen, Guanhua 36, 100
Chen, Huaihou 58, 62, 96
Chen, Jun 24
Chen, Kehui 50
Chen, Kun 49
Chen, Li 6g, 129
Chen, Linlin 7f
Chen, Mengjie 41
Chen, Min 8a
Chen, Ming-Hui 67
Chen, Rui 4l
Chen, Shaojie 89
Chen, Shuo 58
Chen, Tianle 64
Chen, Ting-Huei 33
Chen, Ting-Yu 8c
Chen, Wei 75
Chen, Weijie 104
Chen, Wenan 24
Chen, Xiaotian 122
Chen, Xuerong 76, 102
Chen, Yong 60, 71, 126
Chen, Yu 25
Chen, Zhe 4a
Chen, Zhengjia 74
Cheng, Guang 22, 100
Cheng, Jian 89
Cheng, Joyce 3h
Cheng, Wei 29
Cheng, Yu 71, 122
Chervoneva, Inna 21
Chevret, Sylvie 92
Chi, Yueh-Yun 119
Chiaromonte, Francesca 30, 109
Chinchilli, Vernon M. 104, 117
Chiou, Jeng-Min 68
Cho, Hyunkeun 30
Cho, Youngjoo 59
Choi, Bong-Jin 19
Choi, Hyung Won 53
Choi, Jaeun 61
Choi, Jungsoon 78
Choi, Sangbum 81
Choi, Sungwoo 126
Christensen, Brock C. 1f
Chu, Haitao 60, 113, 126
Chuang-Stein, Christy 67
Chung, Christine H. 90
Chung, Moo K. 1h, 89
Chung, Wonil 4h
Ciarleglio, Adam 5f, 96
Cicek, Hatice 19
Clancy, John P. 72
Clement, Lieven 57
Coffey, Christopher S. 117
Coffman, Donna L. 39
Colantuoni, Elizabeth A. 2f, 20
Cole, Stephen 60
Coles, Adrian 62
Collado-Torres, Leonardo 4m
Collinge, William O. 94
Conlon, Anna SC 107
Conneely, Karen N. 45
Connett, John 99
Connor, Jason T. 14, 48
Cook, Andrea J. 54
Cook, Dennis 16
Cook, John 2b
Cook, Richard J. 35, 49, 110, 114, 127
Cope, Leslie 90
Core, Cynthia 50
Cornea, Emil A. 34
Corrada Bravo, Hector 80
Coull, Brent A. 38, 60, 62
Couper, David J. 99, 105
Cox, Dennis D. 32
Crainiceanu, Ciprian M. 1a, 10j, 18, 20, 43, 47, 62, 68, 89, 97, 98, 112
Cramer, Steve 58
Cribben, Ivor 25
Cristiano, Stephen 4p
Crooks, James L. 118
Crovella, Mark 1c
Cucca, Francesco 75, 130
Cui, Yuehua 47
Cunniff, Chris 76
Dahl, David B. 32
Dai, Hongying 21, 47, 124
Dai, Tian 86
Dale, Anders 25
Danaher, Michelle 73

Daniels, Michael J. 46, 58, 85, 115
Danilova, Ludmila V. 90
Darrow, Lyndsey A. 38
Das, Ritabrata 19
Dasari, Ramachandra 122
Datta, Abhirup 60
Datta, Gauri S. 63
Datta, Susmita 66
Davidian, Marie 44, R7
De Iorio, Maria 56
Deden, Rukmana 9f
DeFor, Todd 114
Degras, David 112
Delaney, Joseph AC. 18
Demerath, Ellen 33
Deng, Ke 83
Derkach, Andriy 55
DeSantis, Stacia M. 72, 74, 116
Devlin, Bernie 1k
Devlin, Sean 88, 102
Dey, Dipak 127
Deyoe, Edgar A. 3k
Diao, Liqun 114
Díaz, Iván 92
Diette, Gregory B. 38
Diez Roux, Ana 45
Diggle, Peter J. 128
Dignam, James J. 88
Diler, Rasim S. 50
Ding, Jun 75, 130
Ding, Wei 9e
Ding, Xianting 102
Ding, Ying 22, 49, 104
DiRienzo, Greg 123
Dobbin, Kevin K. 21
Dominici, Francesca 52, 61, R2
Domthong, Uthumporn 104
Dong, Tuochuan 103
Dong, Xiaoyu 11h, 48
Dore, David D. 39
Doss, Hani 4a
Du, Guangwei 63
Du, Yining 2b
Duan, Leo L. 72
Dudekula, Dawood B. 130
Duerr, Isaac H. 98
Duffin, Bret 4r
Dukic, Vanja 109
Dunn, Graham 87
Dunson, David B. 56, 113
Durkalski, Valerie L. 14, 74
Dyck, Roland 125
Dzemidzic, Mario 25
Eberly, Lynn E. 7c, 86
Edmonson, Michael 90
Egleston, Brian L. 5e
Ellerbe, Caitlyn 74
Elliot, Daniel 10c
Elliott, Lloyd 56
Elliott, Michael R. 3c, 72, 107
Elm, Jordan 74
Eloyan, Ani 89, 112
Emerson, John T5
Emsley, Richard 87
Engelhardt, Barbara 56
Entsuah, Richard 48
Epstein, Michael P. 45, 95
Evani, Bhanu M. 36
Evans, Otis R. 3b
Evans, Scott R. 23
Exner, Natalie 111
Falciani, Francesco 32
Famian, Damian 53
Fan, Jieyu 50
Fan, Qian 21
Fan, Ruzong 43, 62
Fang, Hong-Bin 74, 102
Favaro, Stefano 56
Fazio, Massimo 15
Feingold, Eleanor 4j
Feng, Changyong 114
Feng, Sheng 4q
Feng, Yang 115
Ferguson, Kelly K. 8h
Fernandes, Laura L. 49
Ferrucci, Luigi 18, 127, 130
Fertig, Elana J. 4e, 90, 104
Fiecas, Mark 1j
Fine, Jason 11e, 71, 105
Finley, Andrew O. 60
Fisher, Aaron 24
Fissell, William Henry 11g
Fitzmaurice, Maryann 122
Flournoy, Nancy 11a, 74, 125
Fofana, Demba 23
Foley, Kristen M. 118
Forgor, Abudulai Adams 109
Fortin, Jean-Philippe 4e
Forzani, Liliana 16
Foster, Jared C. 100
Franceschini, Nora 75
Frangakis, Constantine E. 126
Frazee, Alyssa 57
French, Benjamin 72
Fricks, John 78, 94, 109

Fronczyk, Kassie 46
Fu, Haoda 2g, 29, 123
Fuentes, Montse 65
Gail, Mitchell H. 124
Galanter, Joshua 33
Gallagher, Colin M. 71
Gallagher, Jane E 118
Gallop, Robert 34
Ganna, Andrea 1d
Gao, Sujuan 73
Gatsonis, Constantine 29
Gaykalova, Daria A. 90
Gaynor, Sheila 36
Gellar, Jonathan E. 20, 68
Geman, Donald 104
Gennings, Chris 36, 65
George, Brandon J. 7k
George, E. O. 23
George, Varghese 4o, 50, 104
Gerardo-Giorda, Luca 109
Gertheiss, Jan 112
Ghosh, Arpita 33
Ghosh, Debashis 23, 39, 45, 53, 59, 121
Ghosh, Kaushik 32
Ghosh, Pulak 32
Ghosh, Santu 71
Ghosh, Soumitra 24
Gignoux, Chris 33
Gile, Krista J. 113
Gill, Mary K. 50
Gilmore, John H. 7n
Giurcanu, Mihai C. 10i
Glaser, Michelle 18
Gnatenko, Dmitri V. 4c
Goldsmith, Jeff 43, 96, 97, 98, T2
Goldstein, Benjamin 50
Goldstein, Joshua 109
Goldstein, Tina 50
Gönen, Mithat 88, 102
Gorfine, Malka 61
Gou, Jiangtao 23
Goyal, Ravi 46
Graham, Robert R. 24
Gray, Simone 84
Greenwood, Celia M.T. 4e
Greven, Sonja 62
Grineski, Sara E. 8e
Groth, Caroline 63
Gruber, Susan 22
Gruber, Tanja 90
Grubesic, Tony H. 60
Gu, Xiangdong 63, 76
Guan, Weihua 33
Gueorguieva, Ralitza 5d
Guillaume, Bryan 97
Guindani, Michele 32, 46, 83, 88, 108
Gunzler, Douglas 87
Guo, Jing 122
Guo, Wei 4d
Guo, Wenge 108
Guo, Xiuqing 45
Guo, Ying 58, 86, 89
Gur, David 103
Gurvich, Olga 86
Gustafsson, Stefan 1d
Gutman, Roee 39
Hackstadt, Amber J. 38
Hagar, Yolanda 109
Haglund, Michael M. 94
Haibe-Kains, Benjamin 90
Haka, Abigail 122
Hall, Charles B. 18
Hall, Diana 118
Hamasaki, Toshimitsu 23
Han, Fang 22
Han, Junhee 88
Han, Peisong 115
Han, Shengtong 3o
Han, Yu 114
Hancock, William O. 78
Handorf, Elizabeth 82
Hanfelt, John J. 115
Hansen, Kasper D. 4e
Hansen, Niels R. 104
Hao, Han 4k, 62
Haran, Murali 109
Harel, Ofer 127
Harezlak, Jaroslaw 25, 112
Hartge, Patricia 33
Hastings, Nicole 101
Hatfield, Laura A. 3i
Hayden, Mary 109
He, Fanyin 115
He, Jiwei 73
He, Kevin 105, 124
He, Peng 24
He, Qing 7b, 32
He, Tao 47
He, Xin 1k
He, Xuming 30
He, Yulei 79
He, Zangdong 123
He, Zihuai 45
Heagerty, Patrick J. 37, 70, SC5
Hedayat, Samad 64

Heller, Ruth 108
Henderson, Nicholas 66, 128
Hendrichsen, Ditte K. 78
Hernan, Miguel 22
Herrera, Juana M. 8e
Herring, Amy H. 65, 113
Hessel, Engel F. 112
Heyse, Joseph F. 67
Hicks, Gregory 127
Hill, Elizabeth G. 22
Hillis, Stephen L. 103
Hirschhorn, Joel 1d
Ho, Chih-Ming 102
Ho, Yen-Yi 24
Hobbs, Brian P. 122
Hochman, Daryl 94
Hodges, James S. 86
Hodgson, Abraham 109
Hoeschele, Ina 130
Hoffman, Lesa 69
Hoffmann, Raymond G. 3k
Hogan, Joseph H. 113
Hom, Douglas C. 8b
Honaker, John 73
Hong, Chuan 71
Hong, Hwanhee 29, 113, 126
Hooker, Giles 20
Hopson, Tom 109
Hossain, Monir 78
Hou, Jiayi 5h
Hou, Lin 41
Houseman, Andres 1f
Hsu, Jason C. 49
Hsu, Jesse Y. 73
Hsu, Li 26
Hu, Ming 83
Hu, Tao 6c, 59
Hu, Yijuan 1d, 95
Hua, Yi 103
Huang, Chiung-Yu 17, 114
Huang, Erya 4c
Huang, Jian 11k, 124
Huang, Kuan-Chieh 130
Huang, Lei 10j, 89, 96, 112
Huang, Weichun 130
Huang, Whitney 8f
Huang, Xuelin 72, 81
Huang, Xuemei 63
Huang, Yen-Tsung 82, 90
Huang, Yi 117
Huang, Yijian 114
Huang, Ying 100
Huang, Yuan 11k
Hubbard, Alan E. 93
Hudgens, Michael G. 23, 107, 122
Hudson, Thomas J. 4e
Hughes, John 78
Hughes, Michael D. 129
Hunt, Kelly 72
Huo, Zhiguang 53, 102
Hutson, Alan 71, 88
Huynh, Tran 63
Hyrien, Ollivier 36
Hyun, Jung Won 7n
Hyun, Noorie 99
Ibrahim, Joseph G. 34, 67, 89, SC6
Illian, Janine B. 78
Imam, Netsanet 130
Ingelsson, Erik 1d
Ionides, Edward L. 109
Irizarry, Rafael 27, SC4
Irony, Telba Z. 52
Iyengar, Satish 7a, 50
Jaffe, Andrew E. 4m
Janes, Holly 100
Jang, Carey 118
Jang, Woncheol 63
Jarrin, Inmaculada 22
Jarso, Samson 97
Jauch, Edward 74
Jaynes, Jessica 102
Jelsema, Casey M. 101
Jeong, Jong-Hyeon 86, 114
Ji, Hongkai 27, 90
Ji, Pengsheng 108
Ji, Yuan 85
Jia, Jia 22, 75
Jia, Zhenyu 35, 66
Jiang, Bei 72
Jiang, Fei 71
Jiang, Hui 41
Jiang, Qin 2d
Jiang, Wenxin 3d
Jiang, Ying 125
Jiang, Yu 95
Jiang, Yunxuan 45
Jin, Ick Hoon 101
Jin, Jiashun 108
Joffe, Marshall M. 73, 120
Johnson, Brent A. 61, 123
Johnson, Timothy D. 3j, 3l, 8b, 25, 56, 58, 60
Johnson, William D. 8i, 10a, 111
Johnston, Richard 95
Joo, Hyun 32
Joshi, Amit D. 33, 45
Jung, Yoonsung 11d

Kahle, David 3h
Kamboh, M. Ilyas 4f
Kanetsky, Peter 82
Kang, Chaeryon 100
Kang, Hyunseung 73
Kang, Jian 3m, 7b, 97, 113
Kang, Le 104
Kang, Shan 35
Kapur, Kush 37
Kardia, Sharon 45
Kareken, David A. 25
Kasari, Connie 117
Katenka, Natallia 1c
Kattan, Michael W. 81
Kawut, Steve 82
Keiding, Niels 65
Keller, Mark 24
Kelly, Clare 58
Kemmer, Phebe B. 89
Kendziorski, Christina 4r, 24, 102
Kennedy, Edward H. 120
Kenward, Michael G. 44
Kidwell, Kelley M. 117
Kim, Chanmin 46
Kim, Chulmin 116
Kim, Daeyoung 11d
Kim, Eunhee 70
Kim, Ho 34
Kim, Inyoung 34
Kim, Jaejik 104
Kim, Janet S. 20, 96
Kim, Jinheum 102
Kim, Jong-Min 11d
Kim, Namhee 58
Kim, Sehee 6f
Kim, Soyoung 105
Kim, Sujin 9f
Kim, Sungduk 113
Kim, SungHwan 5c, 53
Kim, Youn Nam 102
Kimmel, Stephen E. 4e, 72
Kindo, Bereket P. 22
King, Ruth 78
King, Stuart E. 78
Kirby, Russell 78
Kitago, Tomoko 96
Klassen, Eric 15, 34
Klebnov, Lev 7f
Kleinfeld, David 7a
Kleinman, Ken P. 2i
Knorr, Jack S. 3a
Kodell, Ralph L. 6e
Koestler, Devin C. 1f
Kohn, Nina 111
Kolaczyk, Eric 1c
Kolm, Paul 10c, 61
Kong, Feng-Ming 49
Kong, Lan 72
Kong, Linglong 1e
Kong, Shengchun 99
Kong, Xiangrong 50
Korthauer, Keegan D. 102
Kosorok, Michael R. 10e, 36, 49, 100, 106, R9
Kraft, Peter 33, 45
Krafty, Robert T. 94
Krall, Jenna R. 127
Kransler, Kevin 8a
Krumholz, Harlan M. 31
Kruse, Jane 19
Kryger Jensen, Andreas 43
Kuczek, Thomas 130
Kudela, Maria A. 25
Kulasekera, Kurunarathna B. 71
Kundu, Suprateek 3q
Kurland, Jacquie 117
Kurtek, Sebastian 1b, 15, 46
Kutner, Michael 74
Kwok, Richard 63
Labbe, Aurélie 4e
Laber, Eric 11j, 74
Ladha, Alim 7l
Lai, Hui-Chuan 114
Lai, Ming-Jun 122
Lai, Yinglei 124, 128
Lakshminarayanan, Mani Y. 67
Lan, Kuang-Kuo G. 67
Lan, Shiwei 80
Landau, Sabine 87
Landon, Bruce 61
Landrum, Mary Beth 61
Lane, Adam 74
Langlois, Peter H. 65
Larose, Chantal 127
Larsen, Michael D. 50
Laud, Purushottam 24
Lauer, Stephen A. 2i
LaVange, Lisa M. 28
Lawless, Jerry F. 55
Lawson, Andrew B. 78, SC7
Laxminarayan, Ramanan 111
Lazar, Nicole A. 63
Lee, Adel 38
Lee, Chi Hyun 114
Lee, Ching-Wen 37
Lee, Eun-Joo 6a

Lee, EunYoung 63
Lee, J. Jack 2b, 48
Lee, Juhee 85
Lee, Kuang-Yao 71
Lee, Minjung 88
Lee, Seonjoo 112
Lee, Seung-Hwan 6b
Lee, Seunggeun 45
Leek, Jeffrey T. 4m, 7e, 12, 24, 57, 90
Legrand, Catherine 76
Lehmann, Doug 61
Leisenring, Wendy 128
Lemire, Mathieu 4e
Lenarcic, Alan B. 32
Leng, Ning 4r
Lesser, Martin L. 111
Levin, Bruce R3
Lewis, Mark 98
Lewis, Mechelle 63
Li, Ben 32
Li, Bing 71
Li, Bingshan 75
Li, Cheng 3d
Li, Cong 124
Li, Fan 39, 64
Li, Gen 47, 55
Li, Grace 49
Li, Haocheng 44
Li, Heng 23
Li, Hongzhe 24, 27, 45, 57
Li, Junlong 100
Li, Leping 130
Li, Lerong 20
Li, Lexin 7j
Li, Li 99
Li, Lingling 87
Li, Meijuan 21
Li, Meng 20
Li, Ming-Chung 14
Li, Minming 117
Li, Peng 50
Li, Qin 103
Li, Qiwei 32
Li, Quefeng 100
Li, Qunhua 4l
Li, Runze 11k
Li, Ruosha 71
Li, Shanshan 70, 81
Li, Shi 8h
Li, Shi 26
Li, Shuang 4o
Li, Shu-xia 31
Li, Tan 32
Li, Xiaochun 87
Li, Xiaomao 24
Li, Xiaoshan 7j
Li, Xiaoxue 128
Li, Xinmin 128
Li, Yang 72
Li, Yehua 110
Li, Yi 6f, 61, 105, 124
Li, Yimei 7n
Li, Yuan 4r
Li, Yun 61, 75, 107, 130
Li, Zheng 74
Li, Zhi 19
Liang, Hua 10g, 128
Liao, Fangzi 50
Liao, Ge 22
Liao, Katherine 34
Liao, Peizhou 95
Liao, Serena 7h
Liao, Shu-Min 11d
Lilly, Michael B. 35, 66
Lim, Hyun J. 125
Lin, Chien-Wei 75
Lin, Danyu 1d, 35, 75, 82, 129
Lin, Haiqun 31
Lin, Hongbo 2a
Lin, Hui-Min 126
Lin, Keng-Han 82
Lin, Weili 101
Lin, Xihong 57, 82, 91, 130
Lin, Yan 22
Lindquist, Martin A. 7m, 93, 112
Lindsay, Bruce G. 30, 57
Linero, Antonio 85
Ling, Qiang 101
Ling, Yun 37
Linkletter, Crystal 113
Lipkovich, Ilya 28
Lipsitz, Stuart 114
Lipton, Michael L. 58
Little, Roderick J. 51
Liu, Danping 79, 129
Liu, Guanghan 67
Liu, Guodong 72
Liu, Hai 73
Liu, Han 14, 19, 22, 97
Liu, Hanhua 87
Liu, Jihong 78
Liu, Jin 124
Liu, Jingchen 69
Liu, Jun S. 83
Liu, Ke 76
Liu, Kenneth 48
Liu, Lan 122
Liu, Li 1k

Liu, Minzhao 115
Liu, Peng 78
Liu, Piaomu 76
Liu, Qian 36
Liu, Qing 125
Liu, Shelley 4q
Liu, Shuchang 104
Liu, Shuling 36
Liu, Xiaoxi 99
Liu, Xiaoxue 18
Liu, Yeqian 76
Liu, Ying 115
Liu, Yufeng 11e, 22, 124
Liu, Yulun 126
Liu, Zhuqing 58
Liublinska, Victoria 9a
Lobach, Iryna 62
Lock Morgan, Kari 39
Logan, Roger W. 22
Lok, Judith J. 120, 129
Lombard, Fred 88
Long, D. Leann 9c
Long, Dustin M. 107
Long, Qi 7b, 61
Looney, Stephen W. 21
Lopa, Samia H. 86
Lopez, Adriana 50
Loredo-Osti, J.C. 33, 86
Louis, Thomas A. 126, R4
Lu, Qing 122
Lu, Tao 113
Lu, TingTing 3j, 60
Lu, Wenbin 6d
Lu, Wenjing 37
Lu, Yi 10b
Lu, Zhaohua 7n
Lum, Kristian 60
Lunagomez, Simon 40
Luo, Lola 18
Luo, Sheng 3e, 72, 116
Luo, Xi 80
Luo, Xianghua 114
Luo, Zhehui 92
Lyles, Robert H. 73
Lynch, Miranda L. 63
Lystig, Theodore 54
Ma, Fei 36
Ma, Hua 103
Ma, Junshui 48
Ma, Ling 59
Ma, Rick 105
Ma, Shuangge 11k, 70, 124
Ma, Xiaoye 60
Ma, Yanyuan 71
Maas, Paige 5b
MacMillan, Denise K. 118
Madigan, David 93
Mahmoud, Hamdy 34
Mahshie, James 50
Maier, Verena 112
Mairal, Julien 7p
Maitland, Michael 85
Maity, Arnab 20, 62, 96
Malaisrie, S. Chris 19
Malec, Don 79
Mallick, Bani 3q
Malone, Steve 7c
Manatunga, Amita K. 36, 114, R1
Mandrekar, Vidyadhar 47
Mangold, Elisabeth 24
Manser, Paul T. 4g
Manyam, Ganiraju 62
Mao, Lu 35
Marazita, Mary L. 24
Marchionni, Luigi 104
Marcovitz, Michelle S. 3g
Marcus, Beth H. 46
Markovic, Ana 90
Marron, J. S. 7l, 15
Marsit, Carmen J. 1f
Martinez, Elvis 114
Mateen, Farrah J. 97
Mathew, Thomas 87
Matsui, Elizabeth C. 38
Matuzak, Martha 49
Maxwell, Taylor 45
Mayberg, Helen S. 97
Mazumdar, Sati 115
McCall, Mathew N. 33
McCarthy, Patrick M. 19
McClelland, Robyn L. 18
McClintock, Scott 34
McClure, Leslie A. 2h, 117
McCracken, Courtney E. 21
McCulloch, Charles 44
McDowell, Jennifer E. 63
McGee, Edwin 19
McGready, John 12
Mcintosh, Brian E. 4r
McLean, Mathew W. 20
McMahan, Christopher S. 71
McMurray, Helene 33
Meeden, Glen D. 63
Meeker, John D. 8h
Meirelles, Osorio D. 75, 130
Mejia, Amanda 7m
Mendolia, Franco 125

Menon, Sandeep M. 28
Mercola, Dan A. 35, 66
Mermin, Jonathan 84
Merrill, Peter D. 2h
Meyer, Mark J. 62
Meyer, Nick 74
Miller, David L. 96
Mills, James L. 43, 62
Minsker, Stanislav 100
Mireless, Lynn 4p
Mishra-Kalyani, Pallavi S. 61
Mitchell, Emily M. 73
Mitchell, Shira 60
Mitra, Nandita 82
Mittleman, Murray 38
Molenberghs, Geert 44, 107, SC1
Momin, Amin 3q
Mondal, Shoubhik 59
Monge, Susana 22
Monoghan, Andrew 109
Moonie, Sheniz 35
Moorman, David 80
Morris, Jeffrey S. 15, 62
Morton, Sally C. 51
Mostofsky, Stewart 7m
Motta, Giovanni 94
Mudholkar, Govind 2j
Muehleman, Amber 98
Mueller, Peter 85
Mukherjee, Bhramar 8h, 26, 45
Mukhi, Vandana 23
Müller, Hans-Georg 43
Muller, Keith 119
Müller, Peter T3
Muller, Samuel 4b
Murphy, Susan 11c
Murray, Jeffrey C. 24
Murray, Susan 49
Murray, Thomas A. 122
Muschelli, John 47
Nagaraja, Ramaiah 75
Nahum-Shani, Inbal 117
Nam, Chung Mo 102
Nam, Kijoeng 7o
Nan, Bin 19, 99, 100
Napelenok, Sergey L. 118
Nathoo, Farouk S. 3l
Neas, Lucas M. 118
Neaton, James D. 126
Nebel, Mary Beth 7m, 112
Needham, Dale M. 20
Neelon, Brian 101
Nelson, Jennifer C. 54
Nelson, Sybil L. 7d
Nesvizhskii, Alexey 53
Nettleton, Dan 78, 83
Neugebauer, Romain 92
Neuhaus, John 44
Neumann, Christoph 4n
Newton, Michael A. 66
Neykov, Matey 57
Nguyen, Bao K. 4r
Nguyen, Yet 83
Ni, Ai 73
Nichols, Thomas E. 97
Nicolaie, Mioara Alina 76
Nie, Lei 100
Nightingale, Glenna F. 78
Ning, Jing 21, 81
Ning, Yang 47, 71
Niu, Liang 130
Nobel, Andrew B. 47, 55
Normand, Sharon-Lise T. 3i, T1
North, Kari E. 1d, 75
Nugent, Rebecca 12
Nychka, Doug 18
Oakes, David 125
Oberlin, Brandon G. 25
Obuchowski, Nancy A. 103
Ochs, Michael F. 90
Ogbagaber, Semhar B. 87
Ogburn, Elizabeth L. 39
Ogden, R. Todd 62, 96, T2
Oh, Sam 33
Ohno, Yuko 23
Okosun, Ike 9b
Olson Hunt, Megan J. 127
O'Malley, A. James 61
O'Malley, Stephanie 5d
Ombao, Hernando 58, 80, 89
Orr, Megan 78
Ortmann, Ward 24
Osgood, Nathaniel 125
Ostrovnaya, Irina 88, 102
Ott, Miles Q. 113
Ou, Fang-Shu 59
Ounpraseuth, Songthip T. 6e
Ozonoff, Al 60
Pacifici, Krishna 74
Padmanaban, Shweta 2e
Pagano, Marcello 111
Pal Choudhury, Parichoy 33
Palmas, Walter 45

Pan, Wei 24, 36, 45, 121
Pandya, Raj 109
Pankow, James 33
Pardo, Fernando 32
Park, JuHyun 95
Park, Junyong 126
Park, Sung Kyun 8h
Park, Yongseok 88
Parker, Jennifer D. 84
Parker, Margaret M. 24
Parmigiani, Giovanni 61
Patil, Prasad 90
Patil, Sujata M. 48
Patterson. Andrew D. 121
Pawlikowska, Iwona 90
Payne, Anthony 33
Peddada, Shyamal D. 101
Peña, Edsel A. 22, 59, 76
Peng, Limin 36, 49, 114, 125, T4
Peng, Paul Y. T7
Peng, Roger D. 8d, 38, 127
Pennell, Michael L. 17
Pennello, Gene A. 60
Perkins, Neil J. 73
Pertea, Geo 57
Petersen, Maya 92
Peterson, Derick R. 99
Petkova, Eva 96
Pfeiffer, Ruth M. 17, 124
Pham, Dzung L. 89, 97, 112
Phillips, Daisy 23
Phillips, Sharon B. 118
Pi, Lira 22
Pileggi, Anthony V. 123
Pirracchio, Romain 92
Podolsky, Robert H. 4o, 50
Pomann, Gina-Maria 89
Potgieter, Cornelis J. 88
Pounds, Stan 90
Pourahmadi, Mohsen 16
Powell, Helen L. 8d
Prado, Raquel 58
Pramanik, Santanu 111
Prejean, Joseph 84
Presnell, Brett D. 10i
Prezant, David 18
Price, Dionne L. R6
Price, Elinora 76
Price, Karen L. 29
Proschel, Christoph 7f
Puggioni, Gavino 109
Purcell, David W. 84
Puzhankara, Soman 76
Qaqish, Bahjat F. 23
Qian, Hua 8a
Qian, Lianfen 86
Qian, Min 106
Qin, Jing 17
Qin, Zhaohui S. 32, 53, 83
Qiu, Huitong 22, 89
Qiu, Peihua 1g
Qu, Annie 30, 44, 123, 128
Qu, Long 130
Qu, Simeng 10f
Qu, Yanping 63
Quintana, Fernando 85
Rabe-Hesketh, Sophia 110
Raghavarao, Damaraju 3g
Raghunathan, Trivellore 115
Rahardja, Dewi 46
Rahman, AKM F. 59
Ramachandran, Gurumurthy 63
Ramakrishnan, Viswanathan 7d, 74
Ranjan, Ashutosh 117
Rao, Shangbang 89
Rappold, Ana G. 118
Rathouz, Paul 128
Ray, Meredith 113
Real, Leslie 109
Redden, David T. 50, 61
Regier, Michael D. 73
Reich, Brian J. 38, 74, 85, 108, 118
Reich, Daniel S. 89, 97, 112
Reich, Nicholas G. 2i
Reid, Nancy 47
Reimers, Mark A. 4g, 112
Reiss, Philip T. 58, 96, 112
Reiter, Jerome P. 31, 79
Rema, Manoj T. 9b
Ren, Chunfeng 127
Renfro, Lindsay A. 102
Rice, John D. 129
Rice, Kenneth 26
Richardson, Sylvia T. 53
Rieger, Randall H. 34
Rinaldo, Alessandro 40
Rizopoulos, Dimitris 44
Rodriguez, Stephanie M. 2e
Roeder, Kathryn 1k
Rojas, Natalia 8f

Rom, Dror 23
Romitti, Paul 76
Rose, Sherri 14
Rosenbaum, Paul R. 73
Rosenthal, Michael M. 2f, 14
Rosner, Gary L. 85
Ross, Michelle E. 101
Roth, Lindsey 33
Rothman, Adam J. 16
Roy, Anindya 74
Roy, Jason A. 18, 46
Ruberg, Stephen J. 28, 49
Ruczinski, Ingo 4n, 24
Rudser, Kyle 99
Ruppert, David 20
Rusyn, Ivan 55
Ryu, Duchwan 4o, 50, 104
Sabo, Roy T. 48, 74
Saegusa, Takumi 16
Safo, Sandra 21
Saha Chaudhuri, Paramita 111
Sain, Stephan R. 18
Salzberg, Steven L. 41, 57
Salzman, Julia 41
Samadi, Seyed Yaser 47
Samawi, Hani 103
Sammel, Mary D. 52, 72
Sampene, Emmanuel 35
Sampson, Allan R. 50
Sampson, Joshua N. 4b
Sanchez, Brisa 101
Sanna, Serena 130
Santelli, Rebecca C. 4h
Saracli, Sinan 19
Sargent, Daniel J. 102
Sarkar, Sanat K. 108
Sattar, Abdus 110
Satten, Glen A. 95
Savik, Kay 86
Saville, Benjamin R. 48
Schaid, Daniel J. 24
Scharfstein, Daniel O. 10b, 33, 126
Scharpf, Robert B. 4p
Schaubel, Douglas E. 86, 105
Schenker, Nathaniel 79, 84
Schiffner, Julia 124
Schipper, Matthew 49
Schisterman, Enrique F. 73
Schlessinger, David 75, 130
Schmid, Christopher H. 29
Schnitzer, Mireille E. 120
Schork, Andrew 25
Schork, Nicholas 117
Schrack, Jennifer 18
Schuirmann, Donald J. 88
Schwartzman, Armin 108
Schwender, Holger 4n, 124
Seaman, John W. 3a, 3f, 3g, 3h
Seetharaman, Indu 49
Sen, Saunak 33
Sereika, Susan M. 37
Sewell, Jenny 84
Shabalin, Andrey 55
Shah, Aarti 52, R8
Shahbaba, Babak 80
Shalizi, Cosma 40
Shan, Guogen 35
Shang, Hongwei 102
Shao, Jun 100
Shardell, Michelle 127
Sharif, Abbass 98
Shastry, Shankar 78
Shaubel, Douglas 76
Shen, Changyu 2a, 87
Shen, Haipeng 47, 101
Shen, Jincheng 87
Shen, Juan 30
Shen, Meiyu 11h
Shen, Weining 21
Shen, Xiaotong 30, 36
Shen, Yuanyuan 34
Sheppard, Lianne 38
Sheth-Chandra, Manasi 18
Shi, Haiwen 46, 103
Shi, Huidong 4o
Shi, Peibei 123
Shi, Ran 58
Shi, Xingjie 124
Shi, Yang 41
Shi, Yi 88
Shiee, Navid 97, 112
Shiffman, Saul 128
Shih, Vivian H. 21
Shin, Sunyoung 11e
Shin, Yongyun 127
Shinohara, Russell T. 1a, 89, 97, 112
Shojaie, Ali 16
Shotwell, Matthew Stephen 11g
Shou, Haochang 62, 98, 112
Shu, Xinxin 123
Shu, Xu 86
Shugart, Yin Yao 4d
Siddique, Juned 31
Sidore, Carlo 75
Siegel, Eric R. 6e

Siegmund, David 41
Simon, Noah 14
Simon, Richard 14, 106
Simpson, Charles H. 127
Simsek, Burcin 7a
Sinha, Debajyoti 114
Sinha, Sanjoy 110
Sinnott, Jennifer A. 47
Sitlani, Colleen 26
Skrondal, Anders 110
Slate, Elizabeth H. 22
Small, Dylan S. 18, 73
Smith, Abigail 76
Smith, Jennifer 45
Smith, Luke B. 85
Smith, Paul J. 7o
Snavely, Duane 48
Snyder, Ellen 48
Sobel, Michael E. 93
Sofer, Tamar 33
Song, Minsun 45
Song, Peter X.K 9e, 57, 66
Song, Xiao 21, 70
Soon, Guoxing 100, 117, 126
Sousa, Ines 128
Spiegelman, Donna 6f, 119
Spieker, Andrew J. 18
Srinivasan, Cidambi 122
Srivastava, Anuj 15, 34
Srivastava, Kumar 128
Staicu, Ana-Maria 20, 89, 96, 112
Stamey, James D. 46
Stanek III, Edward J. 50, 111, 117
Staniswalis, Joan 8e
Starr, Jacqueline 18
Staudenmayer, John W. 44, 98
Stefanski, Leonard A. 11i
Stenzel, Mark 63
Sterling, Nicholas 63
Stewart, Patricia 63
Stewart, Paul W. 48
Stewart, Ron 4r
Stewart, Thomas G. 11f
Stone, Nathan 34
Strasser, Sheryl 9b
Stromberg, Arnolod 6g
Stroup, Walter W. 119
Stuart, Elizabeth A. 9d
Styner, Martin 7n
Su, Hai 6g
Su, Haiyan 128
Su, Jingyong 15
Su, Shaoyong 4o
Su, Xiao 72
Su, Ya-Hui 7g, 69
Subramanian, Sundarraman 59
Sugar, Catherine A. 21
Sugimoto, Tomoyuki 23
Sullivan, Danielle M. 127
Sullivan, Meghan 69
Sullivan, Patrick F. 95
Sun, Guang 33
Sun, Han 4i
Sun, Jianguo 6c, 59, 72, 76, 128
Sun, Jiayang 4i
Sun, Lei 55
Sun, Qiang 89
Sun, Wei 22
Sun, Wei 33
Sun, Wenguang 108
Sun, Xiaoqian 3n
Sun, Xiaoyan 114
Sun, Zhaonan 32, 130
Sun, Zhichao 8h
Sundaram, Rajeshwari 65
Surendera Babu, Aruna 84
Sweeney, Elizabeth M. 1a, 47, 89, 97, 112
Sweeney, Patricia 84
Swihart, Bruce J. 43
Symanski, Elaine 8c
Symanzik, Juergen 98
Szatkiewicz, Jin P. 95
Szczesniak, Rhonda D. 72
Tabb, Loni P. 60
Tadesse, Mahlet G. 32
Tamhane, Ajit C. 23
Tan, Kay See 72
Tan, Ming 74, 102
Tanaka, Toshiko 130
Tang, Gong 19, 115, 127
Tang, Jin 110
Tang, Shaowu 22, 126
Tang, Zheng-Zheng 75
Tao, Ge 3p
Tao, Ran 75
Tao, Yebin 8h
Tarpey, Thaddeus 64, 96
Tatsuoka, Curtis 69
Taub, Margaret A. 4n
Taylor, Jeremy M.G 49, 87, 88, 100, 107, 129, T7
Tchetgen Tchetgen, Eric J. 8j, 33
Tcheuko, Lucas 104
Tecson, Kristen M. 3f

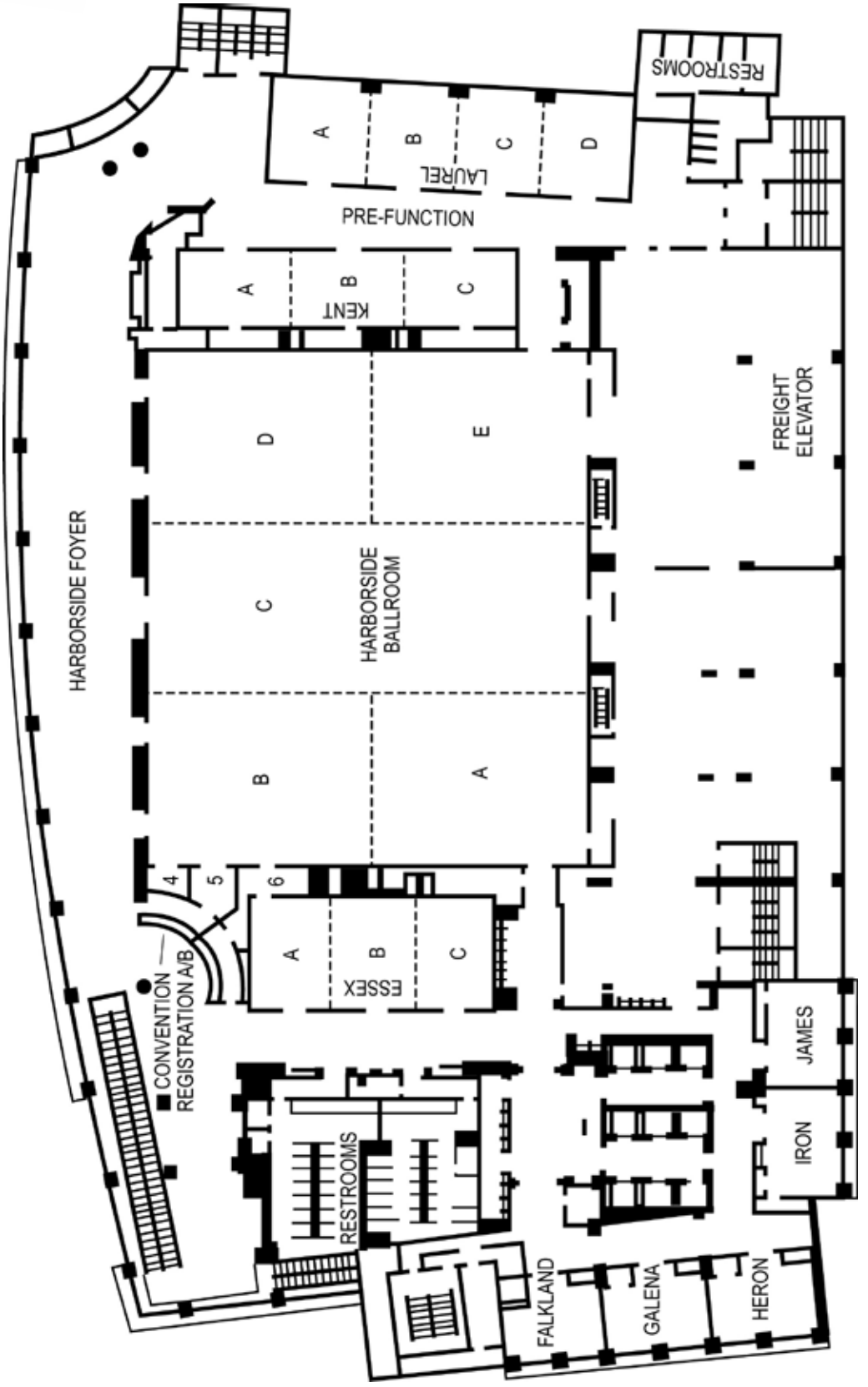
Teh, Yee Whye 56
Templin, Jonathan 69
Teng, Ming 3l
TenHaken, Randy 49
Teran Hidalgo, Sebastian J. 10e
Thall, Peter F. 106
Thomas, Kathleen 7c
Thompson, Laura 60
Thompson, Theodore J. 84
Thompson, Wesley K. 25, 94
Thomson, James A. 4r
Tian, Lili 5a, 103
Tian, Shulan 4r
Tibshirani Robert J. 77
Tiwari, Hemant K. 13
Tiwari, Ram C. 54
Tong, Xin 46
Tong, Xingwei 128
Tran, Van 33
Trikalinos, Thomas A. 29
Troxel, Andrea B. 72
Tsai, Jerry W. 32
Tsai, Wan-Min 5d
Tseng, George C. 4f, 4l, 5c, 7h, 22, 53, 75, 102, 104, 126
Tsiatis, Anastasios A. 28, 44
Tsokos, Chris P. 19
Tsong, Yi 2c, 11h, 48
Tu, Shiyi 3n
Tu, Wanzhu 123
Tu, Xin 114
Turley, Falynn C. 61
Turnbull, Bruce 74
Tzeng, Jung-Ying 95
Umbach, David M. 130
Urbanek, Jacek 25, 112
Urdinola, B. Piedad 8f
Usset, Joseph 20
Uzzo, Robert G. 5e
Valdar, William 32, 124
van der Laan, Mark J. 40, 92, 93, 99
VanderWeele, Tyler 82, T6
Vannucci, Marina 32, 46, 83, 88
Verbeke, Geert 44, SC1
Versace, Francesco 62
Vexler, Albert 3p
Viele, Kert 2k
Vincent, Martin 104
Virnig, Beth A. 126
Viterbi, Andrew 117
Vock, David M. 120
Volberg, Rachel A. 111
Volk, David 50
Volpp, Kevin G. 72
Wacholder, Sholom 33
Wahed, Abdus S. 34, 35, 60, 87
Wakefield, Jon 101
Waldorp, Lourens 97
Wall, Melanie 31, 115
Wallace, Meredith L. 76
Waller, Lance A. 38, 109
Walters, Ryan 69
Wang, Antai 114
Wang, Chenguang 100, 103, 116
Wang, Chenkun 73
Wang, Chi 6g
Wang, Chuan 101
Wang, Dewei 71
Wang, Fei 66
Wang, Haiying 72, 125
Wang, Hao 22
Wang, Haonan 7l
Wang, Huixia J. 72
Wang, Jianxin 62
Wang, Jing 116
Wang, Junhui 64
Wang, Lianming 86
Wang, Lijia 115
Wang, Lily 20, 122
Wang, Lu 66, 87, 115
Wang, Lu 117
Wang, Luojun 117
Wang, Mei-Cheng 18, 70, 81
Wang, Min 3n
Wang, Ming 37, 63
Wang, Naichen 86
Wang, Naisyin 72
Wang, Ningtao 4k, 57, 62
Wang, Pei 57
Wang, Peng 30
Wang, Sijian 123
Wang, Sue-Jane 14
Wang, Tao 24
Wang, Wenting 114
Wang, Wenyi 116
Wang, Xiao 10f
Wang, Xiaoling 4o
Wang, Xiaoshan 18
Wang, Xingbin 4f
Wang, Xujing 24
Wang, Yanpin 117
Wang, Yaping 48
Wang, Yaqun 4k, 57, 62
Wang, Yifan 43, 62
Wang, Yishi 7i
Wang, Yuan 7l
Wang, Yuan 89
Wang, Yuanjia 64, 71, 99, 115

Wang, Zhaoran 19
Wang, Zhong 62
Warren, Joshua L. 13, 38, 65
Watkins, Valerie J. 7i
Webber, Mayris 18
Webb-Vargas, Yenny G. 9d
Weeks, Daniel E. 75
Weerahandi, Samaradasa 10d
Wei, Changshuai 122
Wei, Hua 63
Wei, Lai 71
Wei, Peng 45, 71
Wei, Susan 49
Wei, Yingying 90
Weintraub, William S. 61
Weissfeld, Lisa A. 37
Wellenius, Gregory A. 38
Wen, Xiaoquan 26
Weng, Yu-Ting 34
Wey, Andrew 99
Wiedinmyer, Christine 109
Wiener, R. Constance 9c
Wilding, Gregory 88
Wilkins, Kenneth J. 2e
Williams, Brett 84
Williams, D'Ann L. 38
Williams, Robert J. 111
Wilson, Alexander F. 43
Wilson, Ander 118
Wilson, Janean 50
Wing, Mary Kate 75
Wolf, Bethany J. 7d, 22
Won, Kyoung-Jae 57
Wong, Weng Kee 102
Wong, Yu-Ning 5e
Wright, Fred A. 55
Wu, Changbao 127
Wu, Chong 33
Wu, Colin O. 123
Wu, Gang 90
Wu, Han 83
Wu, Hao SC4
Wu, Hongqian 8l
Wu, Hulin 128
Wu, Jianrong 10g
Wu, Jincao 124
Wu, Jingwei 64
Wu, Michael C. 10e, 11f, 90
Wu, Pan 87
Wu, Qian 57
Wu, Rongling 4k, 57, 62
Wu, Song 90
Wu, Tianshuang 11c
Wu, Wei 34
Wu, Wen-Chi 114
Wu, Wensong 32
Wu, Xiao 58
Wu, Ying 49
Wu, Zhenke 126
Xi, Dong 23
Xi, Mingyu 34
Xia, Changming 10g
Xia, Kai 4h
Xia, Rong 8k
Xia, Xi 3c
Xiao, Luo 10j
Xiao, Tao 17
Xiao, Wei 6d
Xie, Peijin 10d
Xie, Sharon X. 125
Xie, Yuying 124
Xing, Fuyong 6g
Xiong, Momiao 20, 43, 62
Xu, Guangning 11i
Xu, Hongquan 102
Xu, Hongyan 4o, 50, 104
Xu, Hui 76
Xu, Jian-Lun 129
Xu, Mengyuan 116
Xu, Tu 64
Xu, Xiao 31
Xu, Yaoyao 100
Xue, Lan 123
Yabes, Jonathan 59
Yakir, Benjamin 41
Yan, Song 75
Yang, Can 124
Yang, Dan 47
Yang, Hsih-Te 130
Yang, Jie 90
Yang, Jing 125
Yang, Jingjing 32
Yang, Lin 6g
Yang, Rendong 53
Yang, Song 17
Yang, Yang 74
Yang, Yang 101
Yang, Yuchen 6g
Yap, Pew-Thian 89
Ye, Changqing 30
Ye, Lei 37
Ye, Shuyun 24
Yi, Grace 47
Yi, Hui 130
Yi, Min 11a
Yi, Min 72
Yin, Jingjing 5a

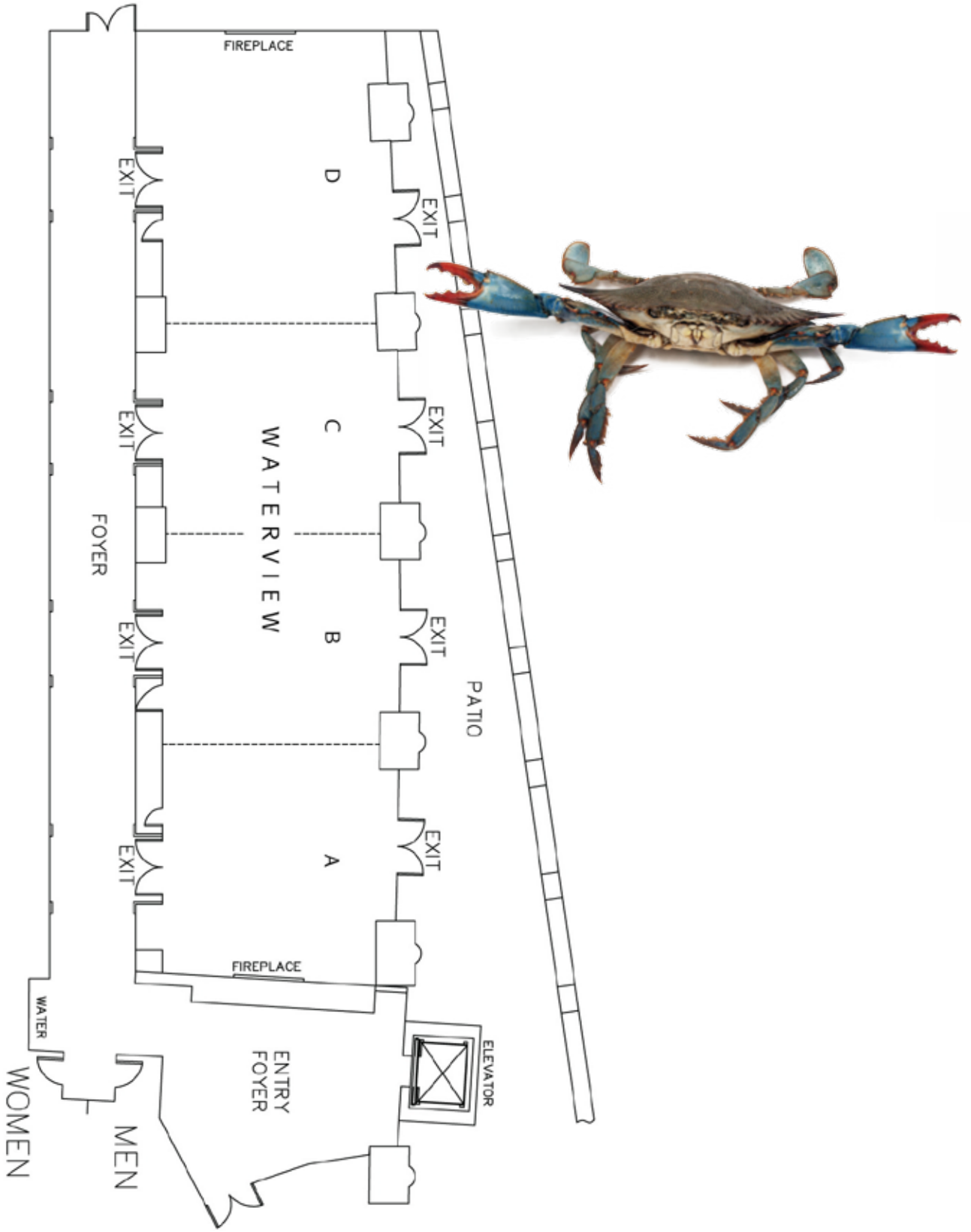
Yin, Zhaoyu 4h
Youk, Ada O. 37, 60
Young, Jessica G. 8j
Young, Nicolas L. 104
Young, Robert 10c
Younkin, Samuel G. 4n, 24
Yu, Bin 7p
Yu, Binbing 10h
Yu, Ching-Ray 10d
Yu, Menggang 100
Yu, Shuli 50
Yu, Tianwei 53
Yu, Zhangsheng 123
Yu, Zhaoxia 80
Yu, Zhe 58
Yu, Ziji 2j
Yuan, Ying 21, 74, 101, 116
Yue, Chen 89
Yung, Godwin 130
Zaleski, Rosemary 8a
Zanke, Brent W. 4e
Zaslavsky, Alan M. 39, 60
Zee, Jarcy 125
Zeig-Owens, Rachel 18
Zeng, Donglin 11f, 59, 64, 70, 75, 99, 100, 129
Zeng, Peng 42
Zeng, Zhen 4j
Zhan, Jia 87
Zhan, Xiang 45, 121
Zhang, Anru 73
Zhang, Daowen 72
Zhang, Fanni 124
Zhang, Guangyu 84
Zhang, Hao 8f
Zhang, Hao Helen 6d, 42
Zhang, Heping 5d
Zhang, Hongmei 3o, 32, 46, 113
Zhang, Jianliang 67
Zhang, Jing 113, 126
Zhang, Jinghui 90
Zhang, Lijun 63
Zhang, Lin 15
Zhang, Linlin 88
Zhang, Min 25, 45
Zhang, Na 11j
Zhang, Nancy R. 41
Zhang, Ruoxin 73
Zhang, Tingting 64
Zhang, Tong 19
Zhang, Wei 86
Zhang, Xuekui 27
Zhang, Yang 19
Zhang, Ying 8l, 37, 76
Zhang, Yiwei 45
Zhang, Yun 50
Zhang, Zhiwei 100
Zhang, Zugui 61
Zhao, Hongyu 41, 71, 124
Zhao, Jinying 43
Zhao, Jiwei 127
Zhao, Ni 90
Zhao, Sihai D. 45
Zhao, Tuo 14
Zhao, Yihong 62
Zhao, Yingqi 100
Zhao, Zhigen 48
Zheng, Jolene 8i
Zheng, Qi 49
Zheng, Wenjing 92
Zheng, Yingye 5g, 81
Zhong, Ping-Shou 47
Zhong, Wenxuan 42
Zhou, Bo 80
Zhou, Feng 47
Zhou, Hua 7j
Zhou, Jin 2g
Zhou, Jing 113
Zhou, Minchun 11g
Zhou, Qingning 6c
Zhou, Xiao-Hua 70, 79
Zhou, Yan 57
Zhou, Yi-Hui 55
Zhou, Yong 76
Zhu, Hongjian 48, 117
Zhu, Hongtu 1e, 7n, 34, 89, 101
Zhu, Hongxiao 32
Zhu, Huirong 116
Zhu, Ji 57, 105, 124
Zhu, Jiawen 90
Zhu, Liang 128
Zhu, Wei 4c
Zhu, Yeying 39
Zhu, Yu 32, 83, 130
Zhu, Yun 43
Zhu, Yunzhang 30
Ziegler, Regina G. 33
Zigler, Corwin 61
Zimmerman, Dale 116
Zink, Richard C. 54
Zipunnikov, Vadim 62, 89, 98, 112
Zoellner, Sebastian 82
Zou, Kelly H. 10d
Zou, Fei 4h
Zubizarreta, Jose 61
Zylbersztejn, Anna 68

GRAND BALLROOM FLOOR PLAN

HARBORSIDE BALLROOM FLOOR PLAN



WATERVIEW BALLROOM FLOOR PLAN



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SPRING MEETING

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