ENAR Spring Meeting
With IMS & Sections of ASA
March 6-9 2016
JW MARRIOTT AUSTIN | AUSTIN, TX

EARLY BIRD DEADLINE
FEBRUARY 1, 2016
Preliminary Program
Welcome! It is my great pleasure to introduce the 2016 ENAR Spring Meeting to be held at the JW Marriott Austin, in Austin, Texas, from March 6–9. The ENAR Spring Meeting brings together researchers and practitioners from academia, industry and government, connected through a common interest in Biometry. It offers a unique opportunity for learning new exciting methods and software, hearing about interesting and impactful applications, meeting new people (including prospective employers and job candidates), and reconnecting with friends, and, this year, getting a break from the cold and snowy winter. The ENAR Spring Meeting only happens through the diligent work of a large number of people who organize and contribute to the program, plan and oversee the meeting logistics, and help with sponsorship — my heartfelt gratitude to all of them.

Scientific Program: Through the leadership of Program Chair Wei Sun, of University of North Carolina at Chapel Hill, and Associate Chair Laura Hatfield, of Harvard University, and with contributions from many of you, the Program Committee (with representatives from 11 ASA sections and 4 ENAR at-large members) has created an outstanding invited program. The sessions cover a wide range of topics of great interest to both researchers and practitioners, such as, data sciences (big data), precision medicine, genomics, clinical trials, neuroimaging, biomarkers, health policy, electronic health records, and epidemiology. The IMS invited program, assembled under the leadership of IMS Program Chair Babak Shahbaba, of the University of California-Irvine, also features an exciting array of sessions that nicely complement and promote synergies with the ENAR invited program.

Poster presentations will, once again, be a vibrant part of the scientific program. In addition to contributed and invited posters, the 2016 ENAR Spring Meeting will continue contributed oral poster sessions (first featured in the 2015 meeting), in which presenters will be able to give a two-minute elevator-speech on the highlights of their posters. The contributed oral sessions, to be held on Monday, will be organized by themes, will feature two invited posters from well-known researchers, and will run parallel to the rest of the sessions in the scientific program. As in previous years, the regular contributed and invited posters will be presented Sunday evening, during the Opening Mixer. The highly popular ENAR Regional Advisory Board (RAB) poster competition will include contributed posters from the Sunday session only.

Educational Program: Be sure to take advantage of the unique and varied learning opportunities that the 2016 ENAR Spring Meeting has to offer through its superb program of short courses, tutorials and roundtables, assembled by the Educational Advisory Committee. Presented by well-known experts in their respective fields, the short courses and tutorials will cover a variety of topics of great interest to meeting attendees, including: statistical analysis of network data, missing data in regression models, introduction to statistical machine learning, statistical genetic and genomic analysis of complex traits with GWAS and next generation sequencing data, Bayesian evidence synthesis in medicine, practical solutions for simple problems with bad consequences in clinical trials, clinical trial designs for validating biomarkers, a new paradigm for finding the subset of patients who benefit from a test treatment, quantile regression for survival analysis, adaptive designs for confirmatory clinical trials, and software applications for high-performance computing, interactive data visualizations, and high throughput DNA sequence data analysis. A favorite of many who come to the meeting, roundtable luncheons, will also be featured in the program. Distinguished statisticians from academia, government, and industry will lead the luncheon discussions on topics ranging from how to publish without perishing to quantitative safety review, big data in healthcare evaluation, and practical considerations for teaching Biostatistics in a hybrid, blended, or online format.

Keynote Lectures: The Presidential Invited Address and the IMS Medallion Lecture are two of the high points of the ENAR Spring Meeting program, delivered by highly accomplished thought leaders in Biometry. I am honored to introduce Dr. Xihong Lin, Henry Pickering Walcott Professor of Biostatistics and Chair of the Department of Biostatistics at the Harvard University, as the 2016 Presidential Invited Speaker. Her lecture will be on “Biostatistics, Biomedical Informatics, and Health Data Science: Research and Training.” Prof. Lin has been an inspirational role model for a long time. She has made significant contribution to development and application of statistical and computational methods for complex data from observational studies and in recent years analysis of massive genetic and genomic, epidemiological, environmental, and medical data. She received the 2002 Mortimer Spiegelman Award from the American Public Health Association and the 2006 COPSS Presidents’ Award. She is an elected fellow of ASA, IMS, and ISI. She received the MERIT Award (R37) (2007-2015) and recently the Outstanding Investigator Award (OIA) (R35) (2015–2022), as
the only awardee who is a statistician, from the National Cancer Institute, which provide long-term research support to experienced investigators with outstanding records of cancer research productivity who propose to conduct exceptional research. She is the contacting PI of the Program Project (PO1) on Statistical Informatics in Cancer Research, and the T32 training grant on interdisciplinary training in statistical genetics and computational biology. She was the former Chair of the COPSS (2010-2012) and a former member of the Committee of Applied and Theoretical Statistics (CATS) of the National Academy of Science. She was the former Coordinating Editor of Biometrics and the founding co-editor of Statistics in Biosciences, and is currently the Associate Editor of Journal of the American Statistical Association and American Journal of Human Genetics. She has served on a large number of statistical society committees, and NIH and NSF review panels.

The IMS Medallion Lecture, entitled “Model-Based Geostatistics for Prevalence Mapping in Low-Resource Settings,” will be presented by Dr. Peter J Diggle, Distinguished University Professor of Statistics in the Faculty of Health and Medicine at Lancaster University. He also holds Adjunct positions at Johns Hopkins, Yale and Columbia Universities, and is president of the Royal Statistical Society (2014-2016). Prof Diggle’s research involves the development of statistical methods for spatial and longitudinal data analysis, motivated by applications in the biomedical, health and environmental sciences. He has published 10 books and more than 200 articles on these topics. He was awarded the Royal Statistical Society’s Guy Medal in Silver in 1997 and is a former editor of the Society’s Journal, Series B. In 2001 he was elected as a Fellow of the American Statistical Association. He was founding co-editor of the journal “Biostatistics” between 1999 and 2009, and is a Trustee for Biometrika.

Additional Meeting Activities: The 2016 ENAR Spring Meeting will feature a host of other activities in addition to the scientific and educational programs. On Sunday, March 6, there will be the Fostering Diversity in Biostatistics Workshop, organized by Simone Gray, of the Centers for Disease Prevention and Control, and Sean Simpson, of Wake Forest School of Medicine.

The Student Mixer on Monday evening and the Tuesday luncheon event organized by the Council of Emerging and New Statisticians (CENS) will provide ample networking opportunities for students and recent graduates. Meeting attendees seeking employment and prospective employers will benefit from the vibrant Career Placement Center. Be sure to visit the exhibitors’ area to browse the latest books and software in your field.

We have arranged an evening of dining, entertainment, and networking at a social event unique to Austin. We’ll begin with dinner at the Iron Cactus, one of Austin’s best-known Mexican restaurants, located on the famous Sixth Street in the music district. After dinner, we will walk a couple of blocks to Esther’s Follies. An Austin tradition and theatric landmark, Esther’s bills itself as “Texas’ premiere magic & musical comedy troupe since 1977.” The show combines elements of political and social satire (a sort of Second City Texas-style), stage magic, musical parody, and old-style burlesque.

Meeting Venue: The conference will be held at newly built JW Marriott Austin hotel, which opened in February 2015. Situated in the heart of the downtown area, this luxury hotel is just a 15-minute drive from Austin International Airport. Located on Congress Avenue between 2nd and 3rd Streets, the hotel is within walking distance of enticing restaurants and bars, 6th Street, the Capitol, and local attractions.

Acknowledgements: This meeting would not happen without the dedication and leadership of Kathy Hoskins, the ENAR Executive Director. Kathy is the institutional memory of ENAR and each year patiently guides incoming presidents-elect, like myself, on the how-to’s of organizing the Spring Meeting. My heartfelt thanks to Kathy and the ENAR team, Katie Earley, and Beatrice Contreras for all the great work they have put into the meeting organization. I am also very grateful to the Local Arrangements Committee, led by Michael Daniels, of the University of Texas at Austin, for their critical work towards the success of the ENAR meeting.

Hope to see you in beautiful Austin for the 2016 ENAR Spring Meeting!

Sincerely,

Jianwen Cai
ENAR 2016 President

Kathy Hoskins
ENAR Executive Director
ENAR 2016 General Information

Location
JW Marriott Austin | Austin, Texas
110 E. 2nd Street | Austin, Texas 78701
Phone: (512)–474-4777
http://www.jwmarriottaustin.com

Registration Hours
Saturday, March 5: 3:00 pm to 5:00 pm
Sunday, March 6: 7:30 am to 6:00 pm

What is included in the Registration Fee?
The meeting registration fee includes all refreshment and beverages during breaks and the opening mixer. The registration fee, less a $100 administrative fee, is refundable if written notice of cancellation is received by February 1, 2016.

Short Courses
The 2016 ENAR meeting will begin with an exciting set of short courses on Sunday, March 6. Please refer to the chart included on this page for the registration fees for these Short Courses. We recommend registering in advance, since the courses close once they are full. Use either the registration form on page 108 or the electronic registration form available on the ENAR website.

Tutorials
Tutorials will be offered on Monday and Tuesday, and are held concurrent with the scientific program. These offerings provide a presentation of a continuing education topic in a briefer time period (1 hour and 45 minutes). Fees for the tutorials are $75 for members ($85 after February 1, 2016) and $85 for non-members ($95 after February 1, 2016). The student registration fee for the tutorials is $40 ($50 after February 1, 2016). Be sure to register in advance, since tutorials will be closed once they are full.

Roundtable Luncheons
This year, the roundtable luncheons will be held on Monday, March 7, from 12:15 to 1:30 pm. Space for each roundtable is limited and pre-registration is recommended. The fee is $40 per person and includes lunch. For full descriptions of the roundtable discussion topics, please refer to pages 103 – 105.

Meeting Registration Fees

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See Pages 94 – 98 for Course Details
Register for Two Half Day Courses and Save!
Savings Information Provided on Page 94
**ENAR 2016 General Information**

**New Member Reception, Opening Mixer, and Poster Session.** A new member reception will be held from 7:30 to 8:00 pm on Sunday, March 6. All new ENAR members are cordially invited to attend. The Opening Mixer and Poster Session (which is included in the meeting registration fee) will take place from 8:00 to 11:00 pm on Sunday, March 6.

**Council for Emerging and New Statisticians (CENS)**

CENS is dedicated to better informing ENAR about the needs of students and recent graduates. The goal at the 2016 Spring Meeting is to improve the networking experience for all attendees. CENS will organize lunches on Tuesday, March 8, 2016 for groups of attendees that share similar interests. The goal is to help attendees meet and network with each other. Although CENS will help to coordinate lunch at local restaurants, please note that lunch is at your own expense and CENS will not be able to cater to special dietary requirements. Closer to the meeting time, CENS will email all attendees interested in this networking event to request information to set up the groups and the lunch reservations. Students and recent graduates are especially encouraged to sign up for this networking event.

**CENS Student Mixer**

All students are invited to attend the CENS student mixer on Monday, March 7, from 5:30 to 6:30 pm. Registration is not required – so please stop by!

**Placement Service**

ENAR will conduct a job placement service at the 2016 Spring Meeting. Additional information regarding the placement center is located on page 106.

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**JW Marriott Austin**

110 E 2nd Street | Austin, TX 78701  
Phone: (512)–474-4777  
http://www.jwmarriottaustin.com

**Room Reservations**

ENAR has negotiated a group hotel room rate of $199.00 for single and double occupancy rooms.  
**Cut-off date:** All reservations must be made by February 12, 2016. To receive this special ENAR meeting rate, you must make your reservations directly with the JW Marriott Austin at (512) -474-4777. Be sure to mention that you are with the ENAR 2016 Spring Meeting when you make your reservations.  
*Please make your reservations early, as all hotel rooms are reserved on a first-come, first-served basis.*

**Parking at the JW Marriott Austin**

The hotel offers on-site self-parking at the rate of $30 per day. Valet parking is also available for a fee of $37 per day. These parking rates are not inclusive of tax.

**Transportation**

**Austin-Bergstrom International Airport (AUS)**

» Approximately 11 miles from the JW Marriott Austin. The hotel does not provide shuttle service.  
» Estimated taxi fare to/from the meeting hotel is $30 USD (one way).  
» SuperShuttle is available to/from the meeting hotel. Reservations are required. Approximate fee is $15 USD (one way).
ENAR 2016 | Spring Meeting | March 6-9 | Preliminary Program

New For the 2016 Spring Meeting!

ENAR is going mobile in 2016 with our Spring Meeting app! We have teamed up with CrowdCompass to build an app that will make this year’s meeting more valuable for our attendees, sponsors, exhibitors, and speakers. The app will provide a new way for you to experience the ENAR Spring Meeting and will be accessible on your iPhone, iPad, or Android! Just a few of the great features on our app include:

» Access to the full program book – including scientific sessions, program schedule, and all abstracts
» Learn more about the exhibitors and locate their booths more easily
» Receive meeting updates as they happen
» See who’s attending the meeting and share contact information

Program Options
At the 2016 Spring Meeting, the full final program will be available on the ENAR meeting website. You will also be able to receive the final program book via the following delivery formats:

» Mobile App – includes access to the full program book, with abstracts (available to all attendees that opt to download the app)
» Small program booklet containing all session and speaker names, session times, and locations (please refer to the registration form on page 108 and select this option when registering)

Note: The large final program & abstract book will no longer be printed and can only be accessed via the ENAR website.

Tuesday Evening Networking & Dinner Event
We have arranged an evening of dining, entertainment, and networking at a social event unique to Austin. We’ll begin with dinner at the Iron Cactus, one of Austin’s best-known Mexican restaurants, located on the famous Sixth Street in the music district. After dinner, we’ll walk a couple of blocks to Esther’s Follies, a long-standing tradition and theatrical landmark, Esther’s bills itself as “Texas’ premiere magic & musical comedy troupe since 1977.”

The show combines elements of political and social satire (sort of Second City Texas-style), stage magic, musical parody, and old-style burlesque. After the show, you can make the short walk back to the Marriott or stay and further explore the Sixth Street bar and music scene. (Please note that there will be a cash bar at both locations and that the registration fee does not include the cost of alcoholic beverages).

SOLD OUT
Welcome to Austin!

Welcome to Austin! Famous for keeping it weird, Austin, Texas, is a hub of creativity and music with a burgeoning restaurant scene and unique culture that makes it easy to see why it ranks high on many lists. What was once a small university town is now one of the fastest-growing cities as the tech boom, good weather, cost of living, and cool factor attract start-ups, accelerators, investors, and job seekers. The self-proclaimed “Live Musical Capital of the World” is so much more – the capital of Texas, Bat City, champions of buy/eat local, and home to festivals year-round – that visitors will have a hard time fitting everything in. Pick up a copy of the Austin Chronicle to find a current calendar of events.

Food
While Texas BBQ wars are legendary, Austin is home to a thriving and diverse food scene where sushi bars and European bistros rub shoulders with traditional Tex-Mex, Southern cooking, and the ubiquitous breakfast taco. Plus with over 1500 food trucks, there is plenty of opportunity to sample a smorgasbord of treats.

Live Music
Country, rock, folk, punk, jazz, classical, bluegrass, hip-hop – you can find it here. With music at the airport, in the coffeehouses, grocery stores, bars, venues, and outdoor spaces, Austin has over 250 venues that feature live music each day and night.

Bats (!)
From March to October, the Ann Richards Congress Avenue Bridge is home to the world’s largest urban colony of Mexican free-tailed bats. People gather every evening around sunset to witness the mass exodus of the bats as they participate in a nightly ritual of controlling our insect population.

Outdoors
A mild, sunny climate with lots of green space for walking, biking and exploring paired with many public swimming pools makes Austin a place to enjoy the outdoors. Take a walk on Town Lake Hike and Bike trail that goes around Lady Bird Lake, go for a swim at Barton Springs or Deep Eddy, or rent a bicycle to explore the city’s quirky neighborhoods.
**Downtown:** Home of the Texas State Capitol, built in 1888, with its pink-granite, soaring dome, and interior mosaic floor honoring the five flags of Texas. Follow a visit to the State Capitol with a quick drink at the Cloak Room — the nearby underground dive bar where legislators gather to make the real deals. Downtown is also home to the infamous 6th Street — a six-block area that is home to more than 50 bars, clubs, restaurants, comedy clubs, the historic Driskill Hotel and Littlefield buildings, the Museum of the Weird, and the Alamo Drafthouse Ritz Theatre.

**Rainey Street:** With its neighborhood roots showing, the Rainey Street district features restaurants and bars tucked away in cozy bungalows, retrofitted shipping containers, and outside patio spaces. Highlights include G’Raj Mahal, Clive, Blackheart, and Banger’s Sausage & Beer Garden. Be warned — there will be dogs.

**East Austin:** One of the fastest-growing areas in town, East Austin is home to some of the city’s oldest blues and jazz clubs, over 250 artist studios, quirky murals, food trucks, and hipster bars. The Texas State Cemetery is the final resting place for such Texas legends as Stephen F. Austin, Darrell Royal, Ann Richards, Barbara Jordan, and Bob Bullock.

**South Austin:** South Austin is what many locals refer to as “old Austin” — quaint neighborhoods, funky shops, long-running restaurants, and a laid-back hippie vibe. A popular bumpersticker reads “South Austin: We’re all here ‘cause we’re not all there.” South Congress (SoCo) offers eclectic shopping at local shops (Uncommon Objects, Allen’s Boots, South Congress Books, Tesoros Trading Company), restaurants, food trailers, and the legendary Continental Club that showcases quality rockabilly, country, and swing bands.

**The University of Texas at Austin:** Located just north of the Texas Capitol, The University of Texas at Austin is a 350-acre campus that includes the UT Tower, the Blanton Museum of Art, the LBJ Library and Museum, the Harry Ransom Center, the Texas Memorial Museum, and of course, Memorial Stadium, home of the Longhorns. Just west of campus is The Drag where you can find restaurants, trendy shops, and the University Co-op where you can buy your burnt-orange memorabilia.

Additional information on Austin is also available from the Austin Convention and Visitors Bureau: [http://www.austintexas.org](http://www.austintexas.org).
Special Thanks!

2016 ENAR Program Committee

Wei Sun, 
Program Chair
University of North Carolina at Chapel Hill

Laura Hatfield, 
Associate Program Chair
Harvard University

Babak Shahbaba, 
IMS Program Chair
University of California, Irvine

ASA Section Representatives
Michael L. Cohen
ASA Statistics in Defense and National Security Section Committee on National Statistics

Michael P. Cohen
ASA Survey Research Methods Section
American Institutes for Research

Sebastien Haneuse
ASA Statistics in Epidemiology Section
Harvard University

Shane Jensen
ASA Bayesian Statistical Science
University of Pennsylvania

Jian Kang
ASA Statistics in Imaging Section
University of Michigan

Seunggeun Lee
ASA Statistics in Genomics and Genetics Section
University of Michigan

Olga Marchenko
ASA Biopharmaceutical Section
Quintiles

Mary D. Sammel
ASA Biometrics Section
University of Pennsylvania

Yuanjia Wang
ASA Section on Mental Health Statistics
Columbia University

Samuel P. Wilcock
ASA Statistical Education Section
Messiah College

Tingting Zhang
ASA Statistical Learning and Data Mining Section
University of Virginia

ENAR At-Large Members
Stacy Lindborg
Biogen Idec

John Scott
US Food and Drug Administration

Guosheng Yin
University of Hong Kong

Mei-Cheng Wang
John Hopkins University

Education Advisory Committee
Jianwen Cai
2016 ENAR President
University of North Carolina at Chapel Hill

Frank Bretz
Novartis Pharmaceuticals

Amita Manatunga
Emory University

Yuanjia Wang
Columbia University

Donglin Zeng
University of North Carolina at Chapel Hill

Fei Zou
University of North Carolina at Chapel Hill

Local Arrangements Chair
Mike Daniels
University of Texas at Austin

ENAR Student Awards 2016
DuBois Bowman
Columbia University

ENAR Diversity Workshop 2016
Simone Gray, Co-Chair
Centers for Disease Control and Prevention

Sean L. Simpson, Co-Chair
Wake Forest School of Medicine

ENAR Executive Team
Kathy Hoskins
Executive Director

Katie Earley
Program Manager

Beatrice Contreras
Administrator

Challee Blackwelder
Graphic Designer
Biostatistics, Biomedical Informatics, and Health Data Science: Research and Training

Biostatistics has played a pivotal role in both the development and success of basic science, public health, and medical research by developing statistical methods for study design and data analysis. Massive ‘ome data, including genome, exposome, and phenome data, are becoming available at an increasing rate with no apparent end in sight. Examples include Whole Genome Sequencing data, large-scale remote-sensing satellite air pollution data, digital phenotyping data, and Electronic Medical Records. The emerging field of Health Data Science (HDS) presents biostatisticians with many research and training opportunities and challenges. It has propelled us to rethink our identity and niche and how we can properly position ourselves as a leader in HDS, especially in promoting and advancing statistical inference in health data science research and training. Success will both for biostatistics and for much of health and biomedical science that we effectively position ourselves together with bio- and medical informaticians, as leading health data scientists. There are countless of examples where the volume of available data requires new, scalable statistical methods and demand an investment in statistical research. These include signal detection, network analysis, integrated analysis of different types and sources of data, and incorporation of domain knowledge in health data science method development. Especially critical is training the next generation of health data scientists, which include not only providing broader training of health and biomedical researchers in sound statistical inference, but also that integrate computer and information science and machine learning into established biostatistical curriculum. Such enhanced training could include both didactic and EdX courses, but will require a careful balance of depth and breadth across areas. In this talk, I discuss some of the challenges and opportunities, and illustrate them using statistical genetics and genomics as examples.
Model-Based Geostatistics for Prevalence Mapping in Low-Resource Settings

In low-resource settings, disease registries do not exist, and prevalence mapping relies on data collected through a finite, often spatially sparse, set of surveys of communities within the region of interest, possibly supplemented by remotely sensed images that can act as proxies for environmental risk factors. A standard geostatistical model for data of this kind is a generalized linear mixed model,

\[ Y_i \sim \text{Bin}(m_i, P(x_i)) \]
\[ \log\left( \frac{P(x_i)}{1-P(x_i)} \right) = z(x_i)' \beta + S(x_i), \]

where \( Y_i \) is the number of positives in a sample of \( m_i \) individuals at location \( x_i \), \( z(x) \) is a vector of spatially referenced explanatory variables and \( S(x) \) is a Gaussian process.

In this talk, I will first review statistical methods and software associated with this standard model, then consider several methodological extensions whose development has been motivated by the requirements of specific applications.

I will focus in particular on prevalence mapping projects that have arisen in connection with pan-African control programs for onchocerciasis (river blindness) and lymphatic filariasis (elephantiasis). These vector-borne diseases are major public health problem in the wet tropical regions of the world, including most of sub-Saharan Africa. Multi-national control programs using mass administration of a protective drug, Mectizan, have been very successful, with more than 60 million treatments to date over 19 countries. However, the programs has been hampered by the recognition that people heavily infected with a third disease, Loa loa (eyeworm) parasite, are at risk of severe, occasionally fatal, adverse reaction to Mectizan. Before the drug is administered in a community, it is relatively easy to estimate the prevalence of eyeworm infection, harder (and more expensive) under field conditions to estimate how many people are "heavily infected," one definition of which is that they as carrying more than 8,000 parasites per ml of blood. To address this problem we develop a joint model for community-level prevalence and the proportion of highly infected individuals in the community.

Biography

Peter J. Diggle, PhD

CHICAS, Medical School, Lancaster University

Peter Diggle is Distinguished University Professor of Statistics in the Faculty of Health and Medicine, Lancaster University. He also holds Adjunct positions at Johns Hopkins, Yale and Columbia Universities, and is president of the Royal Statistical Society (2014-2016).

Between 1974 and 1983 Prof Diggle was a Lecturer, then Reader in Statistics at the University of Newcastle upon Tyne. Between 1984 and 1988 he was Senior, then Principal, then Chief Research Scientist and Chief of the Division of Mathematics and Statistics at CSIRO, Australia. He has worked at Lancaster University since 1988, and held a joint appointment with the University of Liverpool from 2012 to 2015. Between 2004 and 2008 he held a UK Engineering and Physical Sciences Senior Fellowship.

Prof Diggle’s research involves the development of statistical methods for spatial and longitudinal data analysis, motivated by applications in the biomedical, health and environmental sciences. He has published 10 books and more than 200 articles on these topics in the open literature.

He was awarded the Royal Statistical Society’s Guy Medal in Silver in 1997 and is a former editor of the Society’s Journal, Series B. In 2001 he was elected as a Fellow of the American Statistical Association. He was founding co-editor of the journal “Biostatistics” between 1999 and 2009, and is a Trustee for Biometrika. He has served the UK Medical Research Council as a member of their Population and Systems Medicine Research Board, Training and Careers Group and Population Health Group, and the Welcome Trust as a member of their Advisory Group in Sustaining Health.
## Sunday March 6

### 7:30 am - 6:30 pm
- **Conference Registration**

### 8:00 am - 12:00 pm
- **Short Courses**
  - **SC4:** Statistical Genetic and Genomic Analysis of Complex Traits with GWAS and Next Generation Sequencing Data
  - **SC5:** Bayesian Evidence Synthesis in Medicine

### 8:00 am - 5:00 pm
- **Short Courses**
  - **SC1:** Missing Data in Regression Models
  - **SC2:** Statistical Analysis of Network Data
  - **SC3:** Introduction to Statistical Machine Learning

### 12:30 am - 5:30 pm
- **Diversity Workshop**

### 1:00 pm - 5:00 pm
- **Short Courses**
  - **SC6:** Practical Solutions for Simple Problems with Bad Consequences in Clinical Trials

### 3:00 pm - 6:00 pm
- **Exhibits Open**

### 4:30 pm - 7:00 pm
- **ENAR Executive Committee**

### 4:00 pm - 6:30 pm
- **Placement Service**

### 8:00 pm - 11:00 pm
- **Social Mixer and Poster Session**
  1. **Posters:** Latent Variables and Mixture Models
  2. **Posters:** Imaging and Spatiotemporal Applications
  3. **Posters:** Clinical Trials, Adaptive Designs, and Applications
  4. **Posters:** Survival Analysis
  5. **Posters:** Causal Inference
  6. **Posters:** Statistical Genetics, GWAS, and ‘Omics Data
  7. **Posters:** Methodology and Applications in Epidemiology, Environment, and Ecology
  8. **Posters:** Variable Selection and Methods for High Dimensional Data
  9. **Posters:** Bayesian Methods and Computational Algorithms
  10. **Posters:** Semi- and Non-parametric Methods
  11. **Posters:** Censoring, Truncation, and Missingness
  12. **Posters:** Classification, Testing, and Networks
  13. **Posters:** Repeated Measures
  14. **Posters:** Special Topic
**Monday March 7**

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<tr>
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**Scientific Program**

15. Statistical Advances in Functional and Single Cell Genomics
16. Statistical Considerations and Challenges in Evaluating Vaccine Efficacy
17. Recent Advances in Subgroup Identification for Clinical Trial Regulatory Science
18. What I Know Now: Advice on Maximizing Graduate School and Early Career Experience
19. Precision Medicine: Statistical Challenges and Opportunities
20. Innovative Statistical Methodology for Modeling Growth in Fetuses, Children, and Adolescents
21. Recent Advances in Lifetime Data Analysis
22. Analysis of Longitudinally Observed Functional Data
24. Contributed Papers: Clinical Trials
25. Contributed Papers: Clustered Data Methods
26. Contributed Papers: High Dimensional Modeling and Inference
27. Contributed Papers: Prediction and Prognostic Modeling

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<td>10:15 am - 10:30 am</td>
<td>Refreshment Break with Our Exhibitors</td>
</tr>
<tr>
<td>10:30 am - 12:15 pm</td>
<td>Tutorial</td>
</tr>
<tr>
<td>10:32: Interactive Data Visualizations in R with shiny and ggplot2</td>
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</tr>
</tbody>
</table>

**Scientific Program**

28. Statistical Methods for Addressing Challenges in Microbiome and Metagenomic Analysis
29. Recent Advances and Challenges in Adaptive Design for Clinical Trials
30. Health Care Provider Evaluation
31. The Future of Biostatistical Funding Mechanisms
10:30 am - 12:15 pm **Scientific Program** (continued)

32. Computer-intensive Bayesian Techniques and Neurostatistics: A Peaceful Co-existence?
33. Survival Analysis and Genetics
34. Missing Data in Non-inferiority Trials
35. IMS Medallion Lecture
36. Contributed Papers: Analysis of Imaging Data
37. Contributed Papers: Bayesian Clinical Trials
38. Contributed Papers: Diagnostic and Screening Tests
39. Contributed Papers: Longitudinal Data
40. Oral Posters: Machine Learning

12:15 pm - 1:30 pm **Roundtable Luncheons**

12:30 pm - 4:30 pm **Regional Advisory Board (RAB) Luncheon Meeting** (by Invitation Only)

1:45 pm - 3:30 pm **Tutorial**

13: Clinical Trial Designs for Validating Prognostic and Predictive Markers in Oncology

**Scientific Program**

41. High-throughput Expression Landscape: What’s next for Methods?
42. Statistical Issues in Estimating Health Disparities Using Complex Samples
43. Statistical Methods for Neuroscience
44. Recent Advances in Statistical Methods for Genetic Epidemiology
45. Recent Advances in Survival Analysis with High-dimensional Data
46. Dissecting Multiple Imputation from a Multi-phase Inference Perspective
47. Innovative Clinical Trial Design and Analysis Methods
48. Statistical Advances in Evolutionary Dynamics of Infectious Diseases
49. Contributed Papers: Bayesian Semi-Parametric and Non-Parametric Methods
50. Contributed Papers: Bayesian Variable Selection
51. Contributed Papers: Graphical Models
52. Contributed Papers: Multivariate Methods
53. Oral Posters: Clinical Trials

3:30 pm - 3:45 pm **Refreshment Break with Our Exhibitors**

3:45 pm - 5:30 pm **Tutorial**

14: A New Paradigm for Finding the Subset of Patients who Benefit from a Test Treatment

**Scientific Program**

54. New Statistical Methods for Imaging Genetics
3:45 pm - 5:30 pm **Scientific Program (continued)**

- **55.** Recent Advances in Adaptive Model-Based Design of Clinical Trials
- **56.** Statistical Methods for Accelerometry Data: Physical Activity and Health Outcomes
- **57.** Statistical Methods in HIV/AIDS
- **58.** Advances and Challenges in Biomarker Studies
- **59.** Functional Regression Methods and Personalized Medicine
- **60.** Bayesian Methods for Large-Scale non-Gaussian Data
- **61.** Contributed Papers: Cancer Applications
- **62.** Contributed Papers: Heterogeneous Treatment Effects
- **63.** Contributed Papers: High Dimensional Data Applications
- **64.** Contributed Papers: Machine Learning
- **65.** Contributed Papers: Next Generation Sequencing
- **66.** Oral Posters: Genomics

5:30 pm - 6:30 pm **CENS Student Mixer**

6:30 pm - 7:30 pm **President’s Reception** (by Invitation Only)

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**Tuesday March 8**

7:30 am - 5:00 pm **Conference Registration**

7:30 am - 5:00 pm **Speaker Ready Room**

8:30 am - 5:30 pm **Exhibits Open**

9:30 am - 3:30 pm **Placement Service**

8:30 am - 10:15 am **Tutorial**

- **T5:** Introduction to High Throughput DNA Sequence Data Analysis Using R/Bioconductor

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**Scientific Program**

- **67.** New Statistical Developments for Emerging Challenges With Complex Data Structures in Observational Studies
- **68.** Statistical Innovations of Massive Genomic Data Analysis
- **69.** Policy Implications of Scientific Reproducibility - A Panel Discussion
- **70.** Multivariate Models for Spatially Correlated Data
- **71.** Methods for Comparative Effectiveness Research using Electronic Health Records
- **72.** Missing Data Issues in Meta-analysis with Individual Participant Data
- **73.** Modeling High Dimensional Space-Time Data With Applications To Neuroimaging
- **74.** Contributed Papers: Bayesian Hierarchical Modeling
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<th>Scientific Program</th>
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<tr>
<td>8:30 am - 10:15 am</td>
<td>Scientific Program (continued)</td>
<td>75. Contributed Papers: Epidemiologic Methods</td>
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<td></td>
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<td>76. Contributed Papers: GWAS: Applications</td>
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<td>77. Contributed Papers: Missing Data</td>
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<td>78. Contributed Papers: Semi-Parametric and Non-Parametric Survival Analysis</td>
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<td>79. Contributed Papers: Study Design</td>
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<tr>
<td>10:15 am - 10:30 am</td>
<td>Refreshment Break with Our Exhibitors</td>
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<tr>
<td>10:30 am - 12:15 pm</td>
<td>Presidential Invited Address</td>
<td>80. Biostatistics, Biomedical Informatics, and Health Data Science: Research and Training</td>
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<tr>
<td>12:30 pm - 4:30 pm</td>
<td>Regional Committee Luncheon Meeting (by Invitation Only)</td>
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<tr>
<td>1:45 pm - 3:30 pm</td>
<td>Tutorial</td>
<td>16: Adaptive designs for Confirmatory Clinical Trials</td>
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<tr>
<td>3:30 pm - 3:45 pm</td>
<td>Refreshment Break with Our Exhibitors</td>
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<tr>
<td>3:45 pm - 5:30 pm</td>
<td>Tutorial</td>
<td>17: Quantile Regression for Survival Analysis</td>
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<tr>
<td>4:30 pm - 6:00 pm</td>
<td>Tutorial</td>
<td>94: Some New Developments in the Modern Longitudinal Data Analysis</td>
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<td>Time</td>
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<td>3:45 pm - 5:30 pm</td>
<td><strong>Scientific Program</strong> (continued)</td>
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<tr>
<td>95.</td>
<td>Statistical Considerations in Personalized Medicine: Concept and Methodology</td>
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<td>96.</td>
<td>Innovative Techniques Towards Solving the Complexities of Biomarker Discovery</td>
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<tr>
<td>97.</td>
<td>New Developments of Bayesian Methods for Causal Inference</td>
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<td>98.</td>
<td>Integrative Analysis of Multi-Omic Data for Understanding Complex Human Diseases</td>
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<td>99.</td>
<td>Analysis of Next-Generation Sequencing Data: Increasing Accuracy and Novel Applications</td>
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<td>Networks for High Dimensional Time Series</td>
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<td>101.</td>
<td>Contributed Papers: Environmental and Ecological Applications</td>
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<td>102.</td>
<td>Contributed Papers: Genomics</td>
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<td>103.</td>
<td>Contributed Papers: Meta-Analysis</td>
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<td>104.</td>
<td>Contributed Papers: Semi-Parametric and Non-Parametric Methods</td>
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<td>105.</td>
<td>Contributed Papers: Statistical Genetics: Heterogeneity and Hierarchy</td>
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<td>106.</td>
<td>Contributed Papers: Variable Selection</td>
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<tr>
<td>5:30 pm - 6:30 pm</td>
<td><strong>ENAR Business Meeting</strong> – Open to all ENAR Members</td>
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<tr>
<td>6:30 pm - 9:30 pm</td>
<td><strong>Tuesday Night Event</strong> – Dinner at the Iron Cactus and a show at Esther’s Follies</td>
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<td><strong>Wednesday</strong></td>
<td><strong>March 9</strong></td>
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<tr>
<td>7:30 am - 12:00 pm</td>
<td><strong>Speaker Ready Room</strong></td>
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<tr>
<td>7:30 am - 9:00 am</td>
<td><strong>Planning Committee</strong> (by invitation only)</td>
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<tr>
<td>8:00 am - 12:30 pm</td>
<td><strong>Conference Registration</strong></td>
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<tr>
<td>8:00 am - 12:00 pm</td>
<td><strong>Exhibits Open</strong></td>
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<tr>
<td>8:30 am - 10:15 am</td>
<td><strong>Scientific Program</strong></td>
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<tr>
<td>107.</td>
<td>Statistical and Computational Challenges in Omics Data Integration</td>
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<td>108.</td>
<td>Statistical Methods to Handle Treatment Crossover and Switch to an Alternative Therapy in Randomized Controlled Trials</td>
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<td>110.</td>
<td>Statistical Modeling of Data on Health Policy and Cost</td>
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<td>111.</td>
<td>Weight Modification in Sample Surveys</td>
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<td>112.</td>
<td>Generalizing Clinical Data Across Studies/Populations</td>
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<tr>
<td>113.</td>
<td>Novel Statistical Methods for Sequencing Data – From Quality Control to False Positives</td>
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<td>114.</td>
<td>Contributed Papers: Bayesian Causal Inference</td>
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<td>115.</td>
<td>Contributed Papers: Biomarkers</td>
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<tr>
<td>Time</td>
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<tr>
<td>8:30 am - 10:15 am</td>
<td><strong>Scientific Program (continued)</strong></td>
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<tr>
<td>116.</td>
<td>Contributed Papers: Competing Risks</td>
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<td>117.</td>
<td>Contributed Papers: GWAS: Testing</td>
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<tr>
<td>118.</td>
<td>Contributed Papers: Measurement Error</td>
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<tr>
<td>119.</td>
<td>Contributed Papers: Statistical Genetics</td>
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<tr>
<td>10:15 am - 10:30 am</td>
<td><strong>Refreshment Break with Our Exhibitors</strong></td>
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<tr>
<td>10:30 am - 12:15 pm</td>
<td><strong>Scientific Program</strong></td>
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<tr>
<td>120.</td>
<td>Inference for Brain Networks</td>
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<td>121.</td>
<td>Recent Development in Joint Modeling for Longitudinal Data</td>
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<tr>
<td>122.</td>
<td>Model Validation: Its Concept, Statistical Integrity, Regulatory Landscape, and Industry Application</td>
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<td>123.</td>
<td>Missing Data in Longitudinal Clinical Trials: Choice of Primary Estimand and its Relationship to the Statistical Analysis Methods</td>
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<tr>
<td>124.</td>
<td>Bayesian Analysis of Complex Survey Data</td>
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<td>125.</td>
<td>Causal Inference in Social Networks</td>
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<tr>
<td>126.</td>
<td>Optimal Design for Nonlinear Models</td>
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<tr>
<td>127.</td>
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<tr>
<td>128.</td>
<td>Contributed Papers: Causal Inference in Epidemiology and Health Policy</td>
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<tr>
<td>129.</td>
<td>Contributed Papers: Count and Categorical Data Analysis</td>
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<td>130.</td>
<td>Contributed Papers: Joint Models for Longitudinal and Survival Data</td>
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<td>131.</td>
<td>Contributed Papers: Personalized Medicine</td>
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<tr>
<td>132.</td>
<td>Contributed Papers: Survival Analysis</td>
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</table>
### Sunday March 6

#### 8:00 am - 11:00 pm Poster Presentations

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<tr>
<th>1. POSTERS: Latent Variables and Mixture Models</th>
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<tbody>
<tr>
<td><strong>1a. INVITED POSTER:</strong></td>
<td></td>
</tr>
<tr>
<td>The LZIP: A Bayesian Latent Factor Model for Correlated Zero-Inflated Counts</td>
<td></td>
</tr>
<tr>
<td>Brian Neelon* and Dongjun Chung, Medical University of South Carolina</td>
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<tr>
<td><strong>1b. Understanding Gaussian Process Fits Using an Approximate Form of the Restricted Likelihood</strong></td>
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<tr>
<td>Maitreyee Bose* and James S. Hodges, University of Minnesota</td>
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<tr>
<td>Sudipto Banerjee, University of California, Los Angeles</td>
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<tr>
<td><strong>1c. A Joint Distribution for a Time-To-Event Outcome and Recurrent Events</strong></td>
<td></td>
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<tr>
<td>Luojun Wang* and Vernon M Chinchilli, Penn State University</td>
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<tr>
<td><strong>1d. Analysis of PHIS Data for a Zero-Truncated, 1&amp;2 Inflated, and Multi-Level Count Variable</strong></td>
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<tr>
<td>Ji Young Kim* and Benjamin L. Laskin, The Children’s Hospital of Philadelphia</td>
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<td>Tamar Y. Springel, University Hospital</td>
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<tr>
<td>Susan L. Furth, The Children’s Hospital of Philadelphia and University of Pennsylvania</td>
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<tr>
<td>Justine Shults, University of Pennsylvania</td>
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<tr>
<td><strong>1e. A Latent Variable Approach to Elicit Continuous Toxicity Scores and Severity Weights for Multiple Toxicities in Dose-Finding Oncology Trials</strong></td>
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<tr>
<td>Nathaniel S. O’Connell* and Elizabeth Garrett-Mayer, Medical University of South Carolina</td>
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<tr>
<td><strong>1f. Multilevel Binary Principal Component Analysis</strong></td>
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<tr>
<td>Yuting Xu*, Chen Yue, Vadim Zipunnikov, Martin A. Lindquist and Brian S. Caffo, Johns Hopkins Bloomberg School of Public Health</td>
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<tr>
<td><strong>1g. A Score Test for Detecting Publication Bias in Multivariate Random-Effects Meta-Analysis</strong></td>
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<tr>
<td>Chuan Hong*, University of Texas Health Science Center, Houston</td>
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<td>Haitao Chu, University of Minnesota</td>
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<tr>
<td>Yong Chen, University of Pennsylvania Perelman School of Medicine</td>
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<tr>
<td><strong>1h. Measuring Concurrency Using a Joint Multistate and Point Process Model for Retrospective Sexual History Data</strong></td>
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<tr>
<td>Hilary J. Aralis*, Pamina M. Gorbach and Ron Brookmeyer, University of California, Los Angeles</td>
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<tr>
<td><strong>1i. Evaluating Quality of Web Panel Survey Data via Clustering and Latent Classes</strong></td>
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<tr>
<td>Elizabeth Handorf*, Fox Chase Cancer Center, Temple University</td>
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<td>Susan Darlow, National Comprehensive Cancer Network</td>
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<td>Michael Slifker and Carolyn Heckman, Fox Chase Cancer Center, Temple University</td>
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<td>Lee Ritterband, University of Virginia</td>
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<tr>
<td><strong>1j. Joint Modeling of Longitudinal, Recurrent Events and Failure Time Data for Survivor’s Population</strong></td>
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<td>Qing Cai* and Mei-Cheng Wang, Johns Hopkins University</td>
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<td>Gary Chan, University of Washington</td>
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<tr>
<td><strong>1k. Model Diagnostics and Predictive Power Assessment of a Type of Joint Dynamic Models of Recurrent Competing Risks and a Terminal Event</strong></td>
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<tr>
<td>Piaomu Liu*, University of South Carolina, Columbia</td>
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### 2. **POSTERS:** Imaging and Spatiotemporal Applications

**Sponsor:** ENAR

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<td><strong>INVITED POSTER:</strong> Big Data and Neuroimaging: Large-Scale Models for Brain Networks</td>
<td>Xi Luo*, Brown University</td>
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<tr>
<td>2b</td>
<td><strong>Scalar on Image Regression with Application to Multiple Sclerosis MRI Lesion Data</strong></td>
<td>Cui Guo* and Timothy D. Johnson, University of Michigan</td>
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<tr>
<td>2c</td>
<td><strong>Statistical Estimation of White Matter Microstructure from Conventional MRI</strong></td>
<td>Leah H. Suttner*, University of Pennsylvania, Amanda Mejia, Johns Hopkins School of Public Health, Blake Dewey and Pascal Sati, National Institute of Neurological Disease and Stroke, National Institutes of Health, Daniel S. Reich, National Institute of Neurological Disease Disease and Stroke, National Institutes of Health and Johns Hopkins Bloomberg School of Public Health, Russell T. Shinohara, University of Pennsylvania</td>
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<tr>
<td>2d</td>
<td><strong>Spatial Statistical Analysis of Suicidal Behavior in Harris County</strong></td>
<td>Aron M. Trevino*, University of Texas Health Science Center, San Antonio, Dejian Lai, University of Texas Health Science Center, Houston</td>
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<tr>
<td>2e</td>
<td><strong>Penalized Variable Selection for Spatial Binary and Count Data</strong></td>
<td>Abdhi Amitabha Sarkar*, Michigan State University, Chae Young Lim, Seoul National University, Tapabrata Maji, Michigan State University</td>
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<td>2g</td>
<td><strong>A Bayesian Zero-Inflated Multivariate Poisson Model for Identifying Functional Co-Activation Patterns</strong></td>
<td>Caprichia Jeffers*, Emory University, Jian Kang, University of Michigan</td>
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<td>2h</td>
<td><strong>Spatial Approach to Age-Period-Cohort Models</strong></td>
<td>Pavel Chernyavskiy*, Mark P. Little and Philip S. Rosenberg, National Cancer Institute, National Institutes of Health</td>
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<td>2i</td>
<td><strong>Modeling Nonstationarity in Space and Time</strong></td>
<td>Lyndsay Shand* and Bo Li, University of Illinois, Urbana-Champaign</td>
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<td>2j</td>
<td><strong>Statistical Analysis of Trajectories on Riemannian Manifolds</strong></td>
<td>Jingyong Su*, Texas Tech University</td>
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3. **POSTERS: Clinical Trials, Adaptive Designs and Applications**

**Sponsor:** ENAR

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<th>3a.</th>
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<td>C-Learning: A New Classification Framework to Estimate Optimal Dynamic Treatment Regimes</td>
<td>Baqun Zhang, Renmin University</td>
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<td>Min Zhang*, University of Michigan</td>
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| 3c. | A Likelihood Design for Single Arm Phase II Group Sequential Clinical Trials with Time-To-Event Endpoints | Wei Wei* and Elizabeth Garrett-Mayer, Medical University of South Carolina |

| 3d. | Comparing Four Dose Escalation Designs in Phase I Oncology Trials | Zhao Yang*, University of Southern California and Biometrics, Medivation, Inc. |
|---|---|
| Rui Li and Suman Bhattacharya, Biometrics, Medivation, Inc. |

| 3e. | Non-inferiority Studies with Multiple Reference Treatments and Heterogeneous Variances | Li-Ching Huang*, Vanderbilt University |
|---|---|
| Miin-Jye Wen, National Cheng-Kung University, Taiwan |
| Yu Shyr, Vanderbilt University |

| 3f. | Bayesian Clinical Trial Design for a Validation Study of Molecular Alteration Identification | Xiaoxiao Lu* and Sijin Wen, West Virginia University |

| 3g. | AUC Regression for Multiple Comparisons to a Control with Application in Determining the Minimum Effective Dose | Johanna S. Van Zyl* and Jack D. Tubbs, Baylor University |

| 3h. | Bayesian Approach to Sample Size Determination for Multilevel Logistic Regression Models with Misclassified Outcomes | Tyler W. Nelson* and James D. Nelson, Baylor University |

| 3i. | An Evaluation of Constrained Randomization for the Design and Analysis of Group-Randomized Trials | Fan Li* and Yuliya Lokhnygina, Duke University |
|---|---|
| David Murray, National Institutes of Health, Office of Disease Prevention |
| Patrick Heagerty, University of Washington |
| Elizabeth DeLong, Duke University |

| 3j. | Optimal Group Sequential Design | Qi An*, University of Florida |

| 3k. | An Informative Prior Approach to a Bivariate Zero-Inflated Poisson Regression Model | Madeline L. Drevets* and John W. Seaman, Baylor University |

| 3l. | Sensitivity in Prior Elicitation | Somer E. Blair*, David Kahle and John W. Seaman, Jr, Baylor University |

| 3m. | Combining Non-Randomized and Randomized Data in Clinical Trials Using Commensurate Priors | Hong Zhao*, University of Minnesota |
|---|---|
| Brian P. Hobbs, University of Texas MD Anderson Cancer Center |
| Haijun Ma and Qi Jiang, Amgen Inc. |
| Bradley P. Carlin, University of Minnesota |
4. POSTERS: Survival Analysis

Sponsor: ENAR

4a. INVITED POSTER:
Quantile Residual Life Regression with Longitudinal Biomarker Measurements for Dynamic Prediction
Ruoshua Li*, University of Texas Health Science Center, Houston
Xuelin Huang and Jorge Cortes, University of Texas MD Anderson Cancer Center

4b. Evaluating Use of a Cox Regression Model in Landmark Analysis to Approximate an Illness-Death Model
Krithika Suresh*, Jeremy M.G. Taylor and Alex Tsodikov, University of Michigan

4c. Estimating Environmental Modification on Coefficients of Cox Proportional Hazards Model in the Study of Sexual Maturation
Huazhen Lin, Southwestern University of Finance and Economics
Peter Song and Ling Zhou*, University of Michigan

4d. Inference of Transition Probabilities in Multi-State Models Using Adaptive Inverse Probability Censoring Weighting Technique
Ying Zhang* and Meijie Zhang, Medical College of Wisconsin

4e. Measuring the Effects of a Time-Dependent Treatment on Correlated Recurrent and Terminal Events Using Frailty-Based Prognostic Models
Abigail R. Smith* and Douglas E. Schaubel, University of Michigan

4f. Semiparametric Bayesian Estimation of Quantile Function for Survival Data with Cured Fraction
Cherry C.H. Gupta*, Florida State University
Juliana Cobre, Universidade de São Paulo
Andriano Polpo, Universidade Federal de São Carlos
Debjayoti Sinha, Florida State University

4g. Dynamic Prognosis Tool of Acute Graft-Versus-Host Disease Based on Biomarkers
Yumeng Li* and Thomas Braun, University of Michigan

4h. Proportional Hazards Model with a Change Point for Clustered Event Data
Yu Deng* and Donglin Zeng, University of North Carolina, Chapel Hill
Jinying Zhao, Tulane University
Jianwen Cai, University of North Carolina, Chapel Hill

4i. A Class of Two-Sample Tests for Quantile Residual Life Time
Yimeng Liu* and Abdus S. Wahed, University of Pittsburgh

4j. Semiparametric Regression Analysis of Interval-Censored Competing Risks Data
Lu Mao*, Danyu Lin and Donglin Zeng, University of North Carolina, Chapel Hill

4k. Semiparametric Regression Model for Recurrent Bacterial Infections after Hematopoietic Stem Cell Transplantation
Chi Hyun Lee*, University of Texas MD Anderson Cancer Center
Xianghua Luo, University of Minnesota
Chuang-Yu Huang, Johns Hopkins University
Todd E. DeFor, Claudio G. Brunstein and Daniel J. Weisdorf, University of Minnesota

4l. Estimation and Modeling of Sexual Partnership Data
Yared Gurmu*, Harvard University

4m. Estimation and Inference for the Incremental Cost-Effectiveness Ratio for Censored Survival Data
Donna L. Spiegelman*, Polyna Khudyakov and Molin Wang, Harvard School of Public Health

* Presenter  ^ Student Award Winner
### 5. POSTERS: Causal Interference

**Sponsor: ENAR**

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### 6. POSTERS: Statistical Genetics, GWAS, and ‘Omics Data

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Jeea Choi*, University of Wisconsin, Madison  
Ning Leng, Li-Fang Chu, Morgridge Institute for Research  
Christina Kendziorski, University of Wisconsin, Madison

6e. **Corrmeta: Fast Association Analysis for eQTL and GWAS Data with Related Samples and Correlated Phenotypes**

Kai Xia*, University of North Carolina, Chapel Hill  
Andrey A. Shabalin, Virginia Commonwealth University  
Wonil Chung, Zhaoyu Yin, Martin Styner and Patrick F. Sullivan, University of North Carolina, Chapel Hill  
Fred A. Wright, North Carolina State University  
John H. Gilmore, Rebecca C. Santelli and Fei Zou, University of North Carolina, Chapel Hill

6f. **Normalization of Single Cell RNA-Sequencing Data**

Rhonda Bacher* and Keegan Korthaeur, University of Wisconsin, Madison  
Ning Leng, Li-Fang Chu, James A. Thomson and Ron M. Stewart, Morgridge Institute for Research  
Christina Kendziorski, University of Wisconsin, Madison

6g. **A Bayesian Hierarchical Model for RNA-Seq Meta-Analysis and Biomarkers Categorization by Study Heterogeneity**

Tianzhou Ma* and George C. Tseng, University of Pittsburgh

6h. **A Novel Method for Testing Association with Common Variants in Case-Control Studies Using Next-Generation Sequencing Data**

Peizhou Liao* and Yijuan Hu, Emory University  
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6i. **A Novel Random Effect Model for GWAS Meta-analysis and its Application to Trans-ethnic Meta-analysis**

Jingchunzi Shi* and Seunggeun Lee, University of Michigan


Brandon J. Coombes* and Saonli Basu, University of Minnesota

6k. **Incorporating Biological Information in Sparse Principal Component Analysis with Application to Genomic Data**

Ziyi Li*, Sandra Safo and Qi Long, Emory University

6l. **Novel Theory for Mapping and Charting the Genetic Architecture of Gene Expression Profiles on Multiple Tissues**

Kirk Gosik* and Rongling Wu, Penn State College of Medicine

6m. **Estimating Cell Type Specific Associations from Whole Blood Methylation**

Richard T. Barfield* and Xihong Lin, Harvard University

6n. **Application of Sample Quality Weights in Random Effects Meta-Analysis of Gene Expression Studies: Bayesian and Non-Bayesian Approaches**

Uma Siangphoe* and Nitai D. Mukhopadhyay, Virginia Commonwealth University

6o. **Intermittency and Limit Theorems for Superpositions of Ornstein-Uhlenbeck Type Processes**

Danijel Grahovac, University of Osijek  
Nikola Leonenko, Cardiff University  
Alia Sikorskii and Irena Tesnjak*, Michigan State University

6p. **Population Genetic Features of Rare Variants in Finland**

Rosemary Putler* and Sebastian Zoellner, University of Michigan
### 6q. Methods of Inference for Penalized Regression in High-Dimensional Genetic Association Studies
- **Jaron Arbet** and **Saonli Basu**, University of Minnesota

### 6r. A Powerful Approach in Differential Analysis for Time Series Microbial Studies
- **Dan Luo** and **Lingling An**, University of Arizona

### 6s. A Two-Part Mixed Effect Model for Longitudinal Microbiome Data Analysis
- **Eric Z. Chen** and **Hongzhe Li**, University of Pennsylvania

### 6t. A Two-Step Integrated Approach to Detect Differentially Expressed Genes in RNA-Seq Data
- **Naim A. Mahi**, University of Cincinnati
- **Munni Begum**, Ball State University

### 7. POSTERS: Methodology and Applications in Epidemiology, Environment, and Ecology

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* Presenter  ^ Student Award Winner
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   Chongzhi Di, Fred Hutchinson Cancer Research Center
   Luo Xiao, North Carolina State University
   Kelly R. Evenson, University of North Carolina, Chapel Hill
   Andrea Z. LaCroix, University of California, San Diego
   Ciprian M. Crainiceanu, Johns Hopkins University
   David M. Buchner, University of Illinois, Urbana-Champaign

7k. Secondary Response Variable Regression Analysis in a Case-Cohort Study
   Yinghao Pan*, Haibo Zhou and Jianwen Cai, University of North Carolina, Chapel Hill
   Sangmi Kim, Georgia Regents University

7l. The ALERT Algorithm for Detection of Local Onsets of RSV and Influenza
   Alexandria C. Brown* and Nicholas G. Reich, University of Massachusetts, Amherst

8. POSTERS: Variable Selection and Methods for High Dimensional Data
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8a. INVITED POSTER:
   Flexible Modeling and Feature Importance in High Dimensional Problems
   Noah Simon*, University of Washington

8b. Single-Index Varying Coefficient Model for Functional Responses
   Xinchao Luo*, East China Normal University and University of North Carolina, Chapel Hill
   Lixing Zhu, Hong Kong Baptist University
   Hongtu Zhu, University of North Carolina, Chapel Hill

8c. Assessment of DPOAE Test-Retest Difference Curves via Hierarchical Gaussian Processes
   Junshu Bao* and Timothy E. Hanson, University of South Carolina

8d. Variable Selection in Function-On-Scalar Regression
   Yakuan Chen*, Jeff Goldsmith and Todd Ogden, Columbia University

8e. Variable Screening in Multicategory Classification
   Yue Zeng*, Hao Helen Zhang and Ning Hao, University of Arizona

8f. Infer Edge Structure of Mixed Graphic Model
   Suwa Xu*, University of Florida

8g. Bi-Level Variable Selection in an Ordered Probit Regression Model via Maximum Likelihood with Composite Bridge Penalty
   Feiran Jiao* and Kung-sik Chan, University of Iowa

8h. FSEM: Functional Structural Equation Model for Twin Functional Data
   Shikai Luo* and Rui Song, North Carolina State University
   Martin Styner, John Gilmore and Hongtu Zhu, University of North Carolina, Chapel Hill

8i. SIFORM: Shared Informative Factor Models for Integration of Multi-Platform Bioinformatic Data
   Xuebei An*, Jianhua Hu and Kim-Anh Do, University of Texas MD Anderson Cancer Center

8j. Hypothesis Testing for Time-Varying Covariate Effect in Complex Correlated Functional Data
   saehbina Oh* and Ana–Maria Staicu, North Carolina State University

8k. ThrEEboost: Thresholded Boosting for Variable Selection and Prediction Via Estimating Equations
   Benjamin T. Brown*, University of Minnesota
   Christopher J. Miller, 3D Communications
   Julian Wolfson, University of Minnesota
8l. Use of Functional Linear Models to Detect Associations Between Characteristics of Walking and Health Related Outcomes using Accelerometry Data
William F. Fadel* and Jarek Harezlak, Indiana University School of Public Health, Indianapolis
Jacek K. Urbanek, Johns Hopkins Bloomberg School of Public Health
Nancy W. Glynn, University of Pittsburgh

8m. Variable Selection and Covariance Estimation for High Dimensional Data
Runmin Shi*, University of Florida

8n. Scalable Bayesian Variable Selection Using Nonlocal Prior Densities in Ultrahigh-Dimensional Settings
Minsuk Shin*, Anirban Bhattacharya and Valen E. Johnson, Texas A&M University

8o. On Gaussian Comparison Inequality and Its Application to Spectral Analysis of Large Random Matrices
Sheng Xu*, Johns Hopkins University
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Matey Neykov* and Yang Ning, Princeton University
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Han Liu, Princeton University

8q. On the Estimation of Population Eigenvalues and the Asymptotic Properties of PCA in High-Dimensional Data
Rounak Dey* and Seungjeon Lee, University of Michigan

9. POSTERS: Bayesian Methods and Computational Algorithms
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9a. INVITED POSTER: Bayesian Predictive Modeling for Personalized Treatment Selection
Junsheng Ma, Francesco Stingo and Brian Hobbs*, University of Texas MD Anderson Cancer Center

9b. Logistic Regression Model Estimation and Prediction Incorporating Coefficients Information
Wenting Cheng*, Jeremy M.G. Taylor and Bhramar Mukherjee, University of Michigan

9c. A Low Information Prior Specification for a Dirichlet Process Mixture of Gaussian Distributions
Michael Martens* and Purushottam Laud, Medical College of Wisconsin

9d. Some Examples of Bayesian Network Meta-Analysis of Longitudinal Data
Jonathon J. Vallejo*, Baylor University

9e. Frequentist and Bayesian Approaches to the Evaluation of Binary Classifiers
Frithjof Thomas*, University of Tennessee Health Science Center

9f. Spatio-Temporal Bayesian Quantile Regression for Analyzing Weather Data of Us
Priyam Das* and Subhashis Ghosal, North Carolina State University

9g. Simulation-Based Estimation of Mean and Standard Deviation for Meta-Analysis Using Approximate Bayesian Computation (ABC) Coupled with Model Averaging Method
Deukwoo Kwon and Isildinha M. Reis*, University of Miami

9h. A Low Information Prior for Dirichlet Process Mixture of Weibull Distributions
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9i. **MCMC Methods for Bayesian Model Selection for Log-Binomial Regression**  
Wei Zhou* and Siva Sivaganesan, University of Cincinnati

9j. **A Bayesian Hierarchical Summary Receiver Operating Characteristic Model for Network Meta-Analysis of Diagnostic Tests**  
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9k. **Informative Prior Structures for the Covariance in Bivariate Measurement Error Models**  
Courtney N. Weber**, Baylor University  
Melinda M. Holt, Sam Houston State University  
John Seaman, Baylor University

9l. **Prior Elicitation via a Rorschach-Style Graphical Procedure**  
Christopher Casement* and David Kahle, Baylor University

9m. **Bregman Divergence to Generalize Bayesian Influence Measures for Data Analysis**  
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9n. **A Bayesian Screening Approach for Hepatocellular Carcinoma using Two Longitudinal Biomarkers**  
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Xueyi Chen* and Francisco J. Diaz, University of Kansas Medical Center

10b. **Semiparametric Survival Model with Time-Dependent Cure Process**  
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10c. **Semiparametric Models of Bivariate Times to Event Data with a Semicompeting Risk**  
Ran Liao*, Indiana University, Bloomington  
Sujuan Gao, Indiana University, Indianapolis

10d. **Change-Plane Analysis for Subgroup Detection and Sample Size Calculation**  
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10e. **Approximating Small P-Values in Permutation Tests: Using the Structure of the Permutation Space to Speed up Computation**  
Brian D. Segal*, Hui Jiang and Thomas Braun, University of Michigan

10f. **Weighted Semi-Parametric Regression Models for Doubly Truncated Survival Data**  
Lior Rennert* and Sharon X. Xie, University of Pennsylvania

10g. **Non-Parametric Shrinkage Median Estimation**  
Beidi Qiang* and Edsel Pena, University of South Carolina

10h. **Robust Nonparametric Kernel Regression Estimator**  
Ge Zhao* and Yanyuan Ma, University of South Carolina

10i. **A Random Forest of Modified Interaction Trees for Treatment Decision Rules**  
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10j. **A Profile Maximum Pseudolikelihood Estimator for the Proportional Cause-Specific Hazards Model Under Outcome Misclassification**  
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11. POSTERS: Censoring, Truncation, and Missingness

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| Rebecca Ruffin Lehman*, Colleen Jackson-Cook and Kellie Archer, Virginia Commonwealth University |

| 12b. The Optimal Point When Interest is in Only a Portion of the ROC Curve |
| Donna K. McClish*, Virginia Commonwealth University |

| 12c. Automation of Immuno-Oncology Flow Cytometry Assay using Cask-Cyto |
| Shubing Wang*, Junshui Ma, David Alexander, George Skibinski, Jinkai Teo and Janice Hsueh Ling Oh, Merck |

| 12d. A Novel Estimation Technique for A 5-Parameter Bivariate Beta Distribution |
| Lauren G. Perry* and James M. Flegal, University of California, Riverside |

| 12e. Interval Estimation of Ratio of Two Coefficients of Variation for Lognormal Distributions |
| Jun-Mo Nam, National Cancer Institute, National Institutes of Health Deukwoo Kwon*, University of Miami |

| 12f. Evaluating R Packages for Comparing Two Correlated C Indices with a Right-Censored Survival Outcome |
| Brian S. Di Pace* and Le Kang, Virginia Commonwealth University |

| 12g. Comparison of Two Correlated ROC Curves at a Given Specificity Level |
| Leonidas E. Bantis* and Ziding Feng, University of Texas MD Anderson Cancer Center |

| 12h. Locally Relevant Subgraphs Enumeration in Transplant Patient Networks |
| Wen Wang*, Mathieu Bray, Peter Song and John Kalbfleisch, University of Michigan |

| 12i. Statistical Methods to Address Outcome Misclassification in Studies of Alzheimer’s Disease |
| Le Wang* and Rebecca Hubbard, University of Pennsylvania |

| 12j. The Inference Tree System for Accountable Analyses |
| Brian S. Hernandez*, University of Texas Health Science Center, San Antonio Emmy Burnett, Rice University Jonathan A. Gelfond, University of Texas Health Science Center, San Antonio |

| 12k. HIV Incidence Estimation from a Cross-Sectional Survey: An Approach to Calibrate a Biomarker and Derive the MLE of the Incidence |
| Severin Guy Mahiane*, Avenir Health |

| 12l. A Simple Density-Based Empirical Likelihood Ratio Test for Independence |
| Albert Vexler, University of Buffalo, The State University of New York Wan-Min Tsai*, PPD and University of Buffalo, The State University of New York Alan Hutson, University of Buffalo, The State University of New York |

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| 13a. Careful Consideration of Time-Varying Exposures with Possible Repeated Events |
| Andrew D. Althouse*, University of Pittsburgh |

| 13b. Maximum-Likelihood Based Analysis of Kidney Transplant Center Report Cards |
| Shaun D. Bender* and Peter P. Reese, University of Pennsylvania Victoria Gamerman, Boehringer Ingelheim Pharmaceuticals Inc. Justine Shults, University of Pennsylvania |
### 13c. A Flexible Approach for Analyzing Longitudinal Clustered Data: A Generalization of the Difference-In-Difference (DD) Approach
Jason A. Lee*, W. Bruce Vogel, Martin P. Wegman and Keith E. Muller, University of Florida

### 13d. Methods for Evaluating Respondent Attrition in Online Survey Data
Camille J. Hochheimer*, Roy T. Sabo, Alexander Krist, Steven H. Woolf and Teresa Day, Virginia Commonwealth University

### 13e. Predicting Sleep Stages via Gaussian Processes
Xu Gao*, Hernando Ombao and Babak Shahbaba, University of California, Irvine

### 13f. An Extension of Autoregressive and Cross-Lagged Models to Modeling Correlated Bivariate Non-Commensurate Outcomes
Fei He*, Indiana University
Armando Teixeira-Pinto, University of Sydney
Jaroslaw Harezlak, Indiana University School of Public Health

### 13g. Observations or Events Per Variable in Longitudinal Models
Abigail R. Smith and Jarcy Zee*, Arbor Research Collaborative for Health

### 13h. Maximum Likelihood Based Analysis of Equally Spaced Longitudinal Count Data with Specified Marginal Means, First-Order Antedependence, and Linear Conditional Expectations
Victoria Gamerman*, Boehringer-Ingelheim Pharmaceuticals, Inc. & University of Pennsylvania
Matthew Guerra, U.S. Food and Drug Administration
Justine Shults, University of Pennsylvania

### 13i. Parsimonious Regression Models for Associations of Accelerometry-Derived Features of Walking and Performance Measures in the Elderly Population
Jacek K. Urbanek*, and Vadim Zipunnikov, Johns Hopkins Bloomberg School of Public Health
Tamara B. Harris, National Institute on Aging, National Institutes of Health
Nancy W. Glynn, University of Pittsburgh
Ciprian Crainiceanu, Johns Hopkins Bloomberg School of Public Health
Jaroslaw Harezlak, Indiana University School of Public Health

### 13j. Empirical Bayes Shrinkage Estimators for Summary Statistics of Non-Stationary Time Series
Amanda F. Mejia*, Ciprian Crainiceanu and Martin Lindquist, Johns Hopkins Bloomberg School of Public Health

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### 14. POSTERS: Special Topic
**Sponsor:** ENAR

### 14a. INVITED POSTER:
The International Biometric Society
Elizabeth Thompson*, University of Washington, IBS President

---

### Monday  March 7

#### 8:30 am - 10:15 am  Oral Presentations

#### 15. Statistical Advances in Functional and Single Cell Genomics
**Sponsors:** ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics
**Organizer & Chair:** Hongkai Ji, Johns Hopkins University

**8:30** Towards a Global Gene Regulatory Network
Wing Hung Wong* and Yong Wang, Stanford University
Rui Jiang, Tsinghua University
<table>
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<tr>
<th>Time</th>
<th>Session</th>
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</table>
| 8:55   | A Dirichlet Process Mixture Model Approach to Identify Genes Showing Differential Dynamics in Single-Cell RNA-Seq Data  
Keegan Korthauer, Dana-Farber Cancer Institute  
Rhonda Bacher and Jeea Choi, University of Wisconsin, Madison  
Li-Fang Chu, James A. Thomson and Ron Stewart, Morgridge Institute for Research  
Christina Kendzierski*, University of Wisconsin, Madison |
| 9:20   | Statistical Modeling of Dropout Events in Single-Cell RNA Sequencing Data  
Mingyao Li*, Cheng Jia, Yuchao Jiang and Nancy Zhang, University of Pennsylvania |
| 9:45   | A Spectral Approach for the Integration of Functional Genomics Annotations for both Coding and Noncoding Sequence Variants  
Iuliana Ionita-Laza*, Kenneth McCallum and Bin Xu, Columbia University;  
Joseph Buxbaum, Mount Sinai School of Medicine |
| 10:10  | Floor Discussion                                                                          |
| 8:30   | Evaluating Ebola Vaccine Efficacy under Outbreak Conditions using a Ring Vaccination Trial Design  
Natalie E. Dean* and Ira M. Longini, University of Florida  
M. Elizabeth Halloran, Fred Hutchinson Cancer Research Center and University of Washington |
| 9:00   | Inference about Herd Immunity in Observational Vaccine Studies  
Michael G. Hudgens*, University of North Carolina, Chapel Hill |
| 9:30   | Sieve Analysis Using the Number of Infecting Pathogens  
Dean A. Follmann*, National Institute of Allergy and Infectious Diseases, National Institutes of Health  
Ching-Yu Huang, Johns Hopkins University |
| 10:00  | Discussant: Amelia Dale Horne, U.S. Food and Drug Administration                           |
| 8:30   | A Bayesian Credible Subgroups Approach to Identifying Patient Subgroups with Positive Treatment Effects  
Bradley P. Carlin* and Patrick M. Schnell, University of Minnesota  
Qi Tang and Walter W. Offen, AbbVie, Inc. |
| 9:00   | Detection of Predictive Biomarkers Accounting for Sample Heterogeneity  
Jianhua Hu*, University of Texas MD Anderson Cancer Center  
Weining Shen, University of California, Irvine  
Jing Ning and Zideng Feng, University of Texas MD Anderson Cancer Center |
| 9:30   | Evaluating the Impact of Treating the Optimal Subgroup  
Alexander R. Luedtke and Mark J. van der Laan*, University of California, Berkeley |
| 10:00  | Discussant: Lisa LaVange, U.S. Food and Drug Administration                               |
### 18. What I Know Now: Advice on Maximizing Graduate School and Early Career Experience

**Sponsors:** ENAR  
**Organizer:** Michael McIsaac, Queen’s University  
**Chair:** Mark Meyer, Bucknell University

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<thead>
<tr>
<th>Time</th>
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<tbody>
<tr>
<td>8:30</td>
<td>When do we Become Dinosaurs: Life After Grad School</td>
<td>Janet Wittes*, Statistics Collaborative</td>
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<tr>
<td>9:00</td>
<td>Strategic Planning and Management of Your Academic Career in Biostatistics</td>
<td>Richard John Cook*, University of Waterloo</td>
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<tr>
<td>9:30</td>
<td>Statistical Theory, Policy Fact: Preparing for the Role of a Government Statistician</td>
<td>Steven Hoberman*, U.S. Food and Drug Administration</td>
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<tr>
<td>10:00</td>
<td>Floor Discussion</td>
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### 19. Precision Medicine: Statistical Challenges and Opportunities

**Sponsors:** ENAR, ASA Biometrics Section  
**Organizer & Chair:** Bei Jiang, Columbia University & New York University

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<thead>
<tr>
<th>Time</th>
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<th>Presenter(s)</th>
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<tbody>
<tr>
<td>8:30</td>
<td>Machine Learning and Precision Medicine</td>
<td>Michael R. Kosorok*, University of North Carolina, Chapel Hill</td>
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<tr>
<td>8:55</td>
<td>Adaptive Treatment Assignment: Getting Personal in Oncology</td>
<td>Peter F. Thall*, University of Texas MD Anderson Cancer Center</td>
</tr>
</tbody>
</table>
| 9:20 | Identifying Biosignatures for Placebo Response Using High Dimensional Functional Data | Thaddeus Tarpey* and Eva Petkova, New York University  
Todd Ogden, Columbia University  
Jie Vera Tian, Wright State University |
| 9:45 | Optimizing the Personalized Timing for Treatment Initiation with Random Decision Points | Lu Wang* and Yebin Tao, University of Michigan |
| 10:10 | Floor Discussion | |

### 20. Innovative Statistical Methodology for Modeling Growth in Fetuses, Children, and Adolescents

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology  
**Organizer & Chair:** Sung Duk Kim, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

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<th>Time</th>
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<tr>
<td>8:30</td>
<td>Predicting Poor Pregnancy Outcomes from Multivariate Ultrasound Fetal Growth Data</td>
<td>Paul S. Albert*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health</td>
</tr>
</tbody>
</table>
| 9:00 | Modeling Childhood Growth Data with Historical Functional Regression and Landmarking | Jonathan E. Gellar*, Mathematica Policy Research  
Lei Huang, Johns Hopkins Bloomberg School of Public Health  
Luo Xiao, North Carolina State University  
Ciprian M. Crainiceanu, Johns Hopkins Bloomberg School of Public Health |
| 9:30 | SITAR - A Shape Invariant Model for Human Growth in Infancy and Puberty | Tim J. Cole*, University College London Institute of Child Health |
| 10:00 | Discussant: | Amy Herring, University of North Carolina, Chapel Hill |
### 21. Recent Advances in Lifetime Data Analysis
**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology  
**Organizer & Chair:** Mei-Ling Ting Lee, University of Maryland, College Park

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<tr>
<th>Time</th>
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<tbody>
<tr>
<td>8:30</td>
<td>Estimation and Inference for the Incremental Cost-Effectiveness Ratio for Censored Survival Data</td>
<td>Donna L. Spiegelman*, Polyna Khudyakov and Molin Wang, Harvard School of Public Health</td>
</tr>
<tr>
<td>8:55</td>
<td>Statistical Methods for Recurrent Event Data with Missing Event Category</td>
<td>Jianwen Cai*, Feng-Chang Lin and Jason P. Fine, University of North Carolina, Chapel Hill, Huichuan J. Lai, University of Wisconsin, Madison</td>
</tr>
<tr>
<td>9:20</td>
<td>Efficient Design and Analysis of Prevalent Cohort Studies</td>
<td>Yu Shen*, University of Texas MD Anderson Cancer Center, Hao Liu, Baylor College of Medicine, Jing Ning, University of Texas MD Anderson Cancer Center, Jing Qin, National Institute of Allergy and Infectious Disease, National Institutes of Health</td>
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<tr>
<td>9:45</td>
<td>Variable Selection for Penalized Threshold Regression</td>
<td>Xin He* and Mei-Ling Ting Lee, University of Maryland, College Park</td>
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<td>10:10</td>
<td>Floor Discussion</td>
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### 22. Analysis of Longitudinally Observed Functional Data
**Sponsors:** IMS, ENAR  
**Organizer & Chair:** Damla Senturk, University of California, Los Angeles

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<th>Time</th>
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<tr>
<td>8:30</td>
<td>A Functional Data Model for Analyzing Longitudinal Change of Daily Physical Activity</td>
<td>Oliver Chen, Johns Hopkins University, Luo Xiao*, North Carolina State University, Martin Lindquist and Jennifer Schrack, Johns Hopkins University, Luigi Ferrucci, National Institute on Aging, National Institutes of Health, Ciprian Crainiceanu, Johns Hopkins University</td>
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<tr>
<td>9:00</td>
<td>Modern Analysis of Longitudinal Functional Data</td>
<td>So Young Park and Ana-Maria Staicu*, North Carolina State University</td>
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<tr>
<td>9:30</td>
<td>Inferring Brain Signal Synchronicity from a Sample of EEG Readings</td>
<td>Donatello Telesca*, Qian Li, Damla Senturk and Catherine Sugar, University of California, Los Angeles</td>
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<tr>
<td>10:00</td>
<td>Discussant:</td>
<td>Jeffrey Morris, University of Texas MD Anderson Cancer Center</td>
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### 23. CONTRIBUTED PAPERS: Adaptive Designs and Adaptive Randomization
**Sponsor:** ENAR  
**Chair:** Mercedes Bravo, Children’s Environmental Health Initiative

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<th>Time</th>
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<tbody>
<tr>
<td>8:30</td>
<td>Optimal and Lead-In Adaptive Allocation for Binary Outcomes: A Comparison of Bayesian Methodologies</td>
<td>Roy T. Sabo*, Virginia Commonwealth University, Ghalib Bello, Arbor Research Collaborative for Health</td>
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<tr>
<td>8:45</td>
<td>More Efficient Treatment Comparison in Cross-Over Design by Allocating Subject Based on Ranked Auxiliary Variables</td>
<td>Yisong Huang* and Hani Samawi, Georgia Southern University</td>
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<tr>
<td>9:00</td>
<td>A Bayesian Sequential Design with Binary Outcome</td>
<td>Han Zhu*, Qingzhao Yu and Donald Mercante, Louisiana State University</td>
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<tr>
<td>9:15</td>
<td>An Efficient Method to Simulate Bayesian Adaptive Clinical Trials</td>
<td>Zhenning Yu*, Viswanathan Ramakrishnan and Caitlyn Ellerbe, Medical University of South Carolina</td>
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<tr>
<td>9:30</td>
<td>Multi-Stage Dose-Schedule Finding Designs for Pre-Clinical Studies in Stroke</td>
<td>Chunyan Cai*, University of Texas Health Science Center, Houston</td>
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<td>Jing Ning and Xuelin Huang, University of Texas MD Anderson Cancer Center</td>
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<td>9:45</td>
<td>The Most Powerful Test and the Order of Error Probabilities for Response Adaptive Designs</td>
<td>Yanqing Yi*, Memorial University of Newfoundland</td>
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<td>Xuan Li, University of Minnesota, Duluth</td>
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<td>10:00</td>
<td>Floor Discussion</td>
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### 24. CONTRIBUTED PAPERS: Clinical Trials

**Sponsor:** ENAR  
**Chair:** Ritesh Ramchandani, Harvard University

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<tr>
<th>Time</th>
<th>Title</th>
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<tbody>
<tr>
<td>8:30</td>
<td>Stochastic Modeling of Patients Recruitment in Clinical Trials</td>
<td>Nicolas J. Savvy*, Mathematics Institute of Toulouse</td>
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<tr>
<td>8:45</td>
<td>A Multi-State Model for Designing Clinical Trials for Testing Overall Survival Allowing for Crossover after Progression</td>
<td>Fang Xia*, University of Texas MD Anderson Cancer Center</td>
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<td>Stephen L. George and Xiaofei Wang, Duke University</td>
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<td>9:00</td>
<td>Control of False Positives in Randomized Phase III Clinical Trials</td>
<td>Changyu Shen*, Ziyue Liu and Huiping Xu, Indiana University</td>
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<td>Hai Liu, Gilead Sciences, Inc.</td>
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<td>Cynthia Yue, Indiana University</td>
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<td>9:15</td>
<td>One-Sided Global Tests for Multivariate Outcomes in Randomized Trials</td>
<td>Donald Joseph Hebert*, University of Rochester Medical Center</td>
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<td>9:30</td>
<td>Inequality in Treatment Benefits: Can we Determine if a New Treatment Benefits the Many or the Few?</td>
<td>Emily J. Huang**, Johns Hopkins University</td>
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<td>Ethan X. Fang, Princeton University</td>
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<td>Michael A. Rosenblum, Johns Hopkins University</td>
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<td>9:45</td>
<td>Factorial Clinical Trials for Hybrid Research Studies: Design and Analysis of Optimizing Treatment for Complicated Grief</td>
<td>Christine M. Mauro* and Xin Qiu, Columbia University</td>
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<td>Donglin Zeng, University of North Carolina, Chapel Hill</td>
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<td>Naihua Duan and Yuanjia Wang, Columbia University</td>
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<td>10:00</td>
<td>Estimating Individualized Treatment Rules for Ordinal Treatments</td>
<td>Jingxiang Chen**, Yufeng Liu, Michael R. Kosorok, University of North Carolina, Chapel Hill</td>
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<td>Haoda Fu and Xuanyao He, Eli Lilly and Company</td>
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### 25. CONTRIBUTED PAPERS: Clustered Data Methods

**Sponsor:** ENAR  
**Chair:** Grant Brown, University of Iowa

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<tr>
<td>8:30</td>
<td>Learning Parameter Heterogeneity in Data Integration</td>
<td>Lu Tang* and Peter X.K. Song, University of Michigan</td>
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</table>
8:45 Clusters with Random Size: Weighted Estimation for Compound Symmetry and AR(1) Models
Lisa Hermans*, Universiteit Hasselt, Belgium
Vahid Nassiri, Katholieke Universiteit Leuven, Belgium
Geert Molenberghs, Universiteit Hasselt and Katholieke Universiteit Leuven, Belgium
Michael G. Kenward, London School of Hygiene and Tropical Medicine
Wim Van der Elst and Marc Aerts, Universiteit Hasselt, Belgium
Geert Verbeke, Katholieke Universiteit Leuven and Universiteit Hasselt, Belgium

9:00 Goodness of Fit Test for Multinomial Regression Model in NUN Study
Zhiheng Xie* and Richard Kryscio, University of Kentucky

9:15 Sequential Imputation Using Marginal Models
Recai M. Yucel*, State University of New York, Albany
Zeynep I. Kalaylioglu, Middle East Technical University

9:30 A Robust and Flexible Method to Estimate Association for Sparse Clustered Data
Lijia Wang* and John J. Hanfelt, Emory University

9:45 Joint Clustering and Inference in Functional Data Protein Spectroscopic Profiles: Applications in the Eye Lens Protein Crystallin
Miranda L. Lynch*, University of Connecticut Health Center

10:00 Mixture Modeling For Longitudinal Data
Xiwei Tang* and Annie Qu, University of Illinois, Urbana-Champaign

26. CONTRIBUTED PAPERS: High Dimensional Modeling and Inference
Sponsor: ENAR
Chair: Kean Ming Tan, Princeton University

8:30 Provable Smoothing Approach in High Dimensional Generalized Regression Model
Fang Han, Johns Hopkins University
Honglang Wang*, Indiana University-Purdue University, Indianapolis

8:45 Large Covariance Matrix Estimation from Temporally Dependent Observations
Hai Shu* and Bin Nan, University of Michigan

9:00 Confidence Intervals for High-Dimensional Linear Regression: Minimax Rates and Adaptivity
Tony Cai and Zijian Guo*, University of Pennsylvania

9:15 Improved Estimation for High Dimensional Generalized Linear Models
Abhishek Kaul, National Institute of Environmental Health Sciences, National Institutes of Health
Akshita Chawla*, Merck Research Laboratories
Tapabrata Maiti, Michigan State University

9:30 High-Dimensional Inference for Cox Model
Ethan X. Fang**, Yang Ning and Han Liu, Princeton University

9:45 On Longitudinal Gaussian Graphical Models: Estimation and Asymptotic Inference
Quanquan Gu*, University of Virginia
Yuan Cao, Yang Ning and Han Liu, Princeton University

10:00 A General Theory of Hypothesis Tests and Confidence Regions for Sparse High Dimensional Models
Yang Ning* and Han Liu, Princeton University
### 27. CONTRIBUTED PAPERS: Prediction and Prognostic Modeling

**Sponsor:** ENAR  
**Chair:** Yan Yuan, University of Alberta

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<tr>
<td>8:30</td>
<td>Predicting Alzheimer's Disease with Bivariate Mixture Modeling</td>
<td>Frank Appiah*, Erin Abner, David Fardo, Glen Mays and Richard Charnigo, University of Kentucky</td>
</tr>
<tr>
<td>8:45</td>
<td>Time-Dependent Predictive Accuracy Curve Under Marker-Dependent Sampling</td>
<td>Zhaoyin Zhu*, New York University, Xiaofei Wang, Duke University, Paramita Saha Chaudhuri, McGill University</td>
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<td>9:00</td>
<td>Estimating the Impact of Basing Treatment Decisions on Markers that Predict Risk</td>
<td>Marshall D. Brown* and Holly Janes, Fred Hutchinson Cancer Research Center</td>
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<tr>
<td>9:15</td>
<td>Bayesian Inference for Black Hispanic Breast Cancer Survival Data</td>
<td>Hafiz Khan*, Texas Tech University</td>
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<tr>
<td>9:30</td>
<td>Design and Analyses of Two-Phase Studies for Predicting Binary Outcomes</td>
<td>Xinglei Chai* and Jinbo Chen, University of Pennsylvania</td>
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<tr>
<td>9:45</td>
<td>Combining Multiple Biomarkers Linearly to Maximize the Partial Area Under the ROC Curve</td>
<td>Qingxiang Yan*, Leonidas E. Bantis and Ziding Feng, University of Texas MD Anderson Cancer Center</td>
</tr>
<tr>
<td>10:00</td>
<td>Building Better Gene Signatures with Rank-Based Features and Meta-Analysis</td>
<td>Prasad Patil* and Jeffrey T. Leek, Johns Hopkins University</td>
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**10:15 am - 10:30 am**  
**Refreshment Break with Our Exhibitors**

**10:30 am - 12:15 pm**  
**Oral Posters & Presentations**

### 28. Statistical Methods for Addressing Challenges in Microbiome and Metagenomic Analysis

**Sponsors:** ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section  
**Organizer:** Michael Wu, Fred Hutchinson Cancer Research Center  
**Chair:** Ni Zhao, Fred Hutchinson Cancer Research Center

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<tr>
<td>10:30</td>
<td>Statistical Analysis of Data in Metric Space with Applications in Microbiome Studies</td>
<td>Hongzhe Li*, University of Pennsylvania</td>
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<tr>
<td>10:55</td>
<td>High-precision Microbial Community Functional Profiling and Meta’omic Integration</td>
<td>Curtis Huttenhower*, Harvard School of Public Health</td>
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<tr>
<td>11:20</td>
<td>Some Challenges in the Analysis of Microbiome Data: Old Wine in a New Bottle with a Twist!</td>
<td>Abhishek Kaul, National Institute of Environmental Health Sciences, National Institutes of Health, Siddhartha Mandal, Public Health Foundation of India, Gurgaon, India, Shyamal D. Peddada*, National Institute of Environmental Health Sciences, National Institutes of Health</td>
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<tr>
<td>11:45</td>
<td>Flexible Methods for Testing Microbiome by Environment Interactions</td>
<td>Michael C. Wu*, Fred Hutchinson Cancer Research Center</td>
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<td>12:10</td>
<td>Floor Discussion</td>
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<tr>
<td>29</td>
<td>Recent Advances and Challenges in Adaptive Design for Clinical Trials</td>
<td>ENAR, ASA Biopharmaceutical Section</td>
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<tr>
<td>10:30</td>
<td>Continual Reassessment Method with Multiple Toxicity Constraints for Late Onset and Cumulative Toxicities</td>
<td>Shing M. Lee*, Columbia University</td>
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<tr>
<td>10:55</td>
<td>Sequential Design Method for Bioequivalence Test with Serial Sampling Data</td>
<td>Fangrong Yan* and Junling Liu, Pharmaceutical University, China; Xueling Huang, University of Texas MD Anderson Cancer Center</td>
</tr>
<tr>
<td>11:20</td>
<td>Bayesian Optimal Interval (BOIN) Designs for Phase I Clinical Trials</td>
<td>Ying Yuan* and Suyu Liu, University of Texas MD Anderson Cancer Center</td>
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<td>11:45</td>
<td>Phase I-II Clinical Trials with Delayed Outcomes</td>
<td>Joseph S. Koopmeiners*, University of Minnesota</td>
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<td>12:10</td>
<td>Floor Discussion</td>
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<th>Organizer &amp; Chair</th>
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<tr>
<td>30</td>
<td>Health Care Provider Evaluation</td>
<td>ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology</td>
<td>Kevin He, University of Michigan</td>
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<tr>
<td>10:30</td>
<td>A Dirichlet Process Mixture Model for Survival Outcome Data: Assessing Nationwide Kidney Transplant Centers</td>
<td>Lili Zhao, Jing Chunzi Shi, Tempie Shearon and Yi Li*, University of Michigan</td>
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<tr>
<td>10:55</td>
<td>Healthcare Provider Comparisons: Identifying and Meeting Goals</td>
<td>Thomas A. Louis*, Johns Hopkins Bloomberg School of Public Health</td>
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<tr>
<td>11:20</td>
<td>Methods for Profiling Medical Facilities</td>
<td>John D. Kalbfleisch* and Kevin Zhi He, University of Michigan</td>
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<tr>
<td>11:45</td>
<td>On the Accuracy of Classifying Hospitals on Their Performance Measures</td>
<td>Yulei He*, Centers for Disease Control and Prevention; Sharon-lise Normand, Harvard Medical School</td>
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<td>12:10</td>
<td>Floor Discussion</td>
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<tr>
<td>31</td>
<td>The Future of Biostatistical Funding Mechanisms</td>
<td>ENAR</td>
<td>Ciprian Crainiceanu, Johns Hopkins University and Hernando Ombao, University of California, Irvine</td>
<td>Hernando Ombao, University of California, Irvine</td>
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<tr>
<td>10:30</td>
<td>Discussants:</td>
<td>Ciprian M. Crainiceanu, Johns Hopkins University; Francesca Dominici, Harvard University; Debashis Ghosh, Colorado School of Public Health; Lurdes Inoue, University of Washington; Michael R. Kosorok, University of North Carolina, Chapel Hill</td>
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<td>12:00</td>
<td>Floor Discussion</td>
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### 32. Computer-Intensive Bayesian Techniques and Neurostatistics: A Peaceful Co-Existence?

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Imaging  
**Organizer & Chair:** Dipankar Bandyopadhyay, University of Minnesota

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| 10:30  | Bayesian Inference for Cluster-Structured High-Dimensional Ordinary Differential Equations with Applications to Brain Networks | Tingting Zhang*, University of Virginia  
        Brian Caffo, Johns Hopkins University  
        Qiannan Yin, University of Virginia  
        Dana Boatman-Reich, Johns Hopkins University |
| 10:55  | A Novel Distributional ICA Model for Multimodal Neuroimaging Data           | Ying Guo* and Subhadip Pal, Emory University  
        Jian Kang, University of Michigan                                                      |
| 11:20  | A Bayesian Group Sparse Multi-Task Regression Model for Imaging Genomics     | Keelin Greenlaw, University of Waterloo  
        Farouk S. Nathoo* and Mary Lesperance, University of Victoria  
        Elena Szefler and Jinko Graham, Simon Fraser University                                  |
| 11:45  | Analysis of Multiple Sclerosis Lesions via a Bivariate Spatial GLM with Spatially Varying Coefficients | Timothy D. Johnson*, University of Michigan                                                        |

#### 33. Survival Analysis and Genetics

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology, ASA Statistics in Genomics and Genetics Section  
**Organizer:** Ruzong Fan, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health  
**Chair:** Xin Tian, National Heart, Lung and Blood Institute, National Institutes of Health

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<tr>
<th>Time</th>
<th>Session Title</th>
<th>Presenters</th>
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<tbody>
<tr>
<td>10:30</td>
<td>Using Threshold Regression to Analyze Survival Data from Complex Surveys: With Application to NHANES III Phase II Genetic Data</td>
<td>Yan Li, Dandan Liao, and Mei-Ling Ting Lee*, University of Maryland</td>
</tr>
<tr>
<td>10:55</td>
<td>Efficient Tests of Association for Survival Times from Two-Phase Outcome-Dependent Samples</td>
<td>Jerald F. Lawless*, University of Waterloo</td>
</tr>
</tbody>
</table>
| 11:20  | Statistical Issues in Genome-wide Association Studies of Bivariate Survival Outcomes | Ying Ding, Yi Liu and Qi Yan, University of Pittsburgh  
        Lars G. Fritsche and Goncalo G. Abecasis, University of Michigan  
        Anand Swaroop and Emily Y. Chew, National Eye Institute, National Institutes of Health  
        Daniel E. Weeks and Wei Chen*, University of Pittsburgh                                    |
| 11:45  | Gene-based Association Analysis for Censored Traits via Fixed Effect Functional Regressions | Ruzong Fan*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health  
        Yifan Wang, U.S. Food and Drug Administration  
        Yan Qi, Ying Ding, Daniel E. Weeks and Wei Chen, University of Pittsburgh  
        Haobo Ren, Regeneron Pharmaceuticals, Inc.  
        Richard J. Cook, University of Waterloo  
        Momiao Xiong, University of Texas Health Science Center, Houston  
        Emily Y. Chew, National Eye Institute, National Institutes of Health                        |
| 12:10  | Floor Discussion                                                            |                                                                                                      |
34. **Missing Date in Non-Inferiority Trials**
   Sponsors: ENAR, ASA Biopharmaceutical Section
   Organizer: Freda Cooner, U.S. Food and Drug Administration
   Chair: John Scott, U.S. Food and Drug Administration

10:30 The Impact of Missing Data in Historical Placebo-Controlled Trials
   Steven Michael Snapinn*, Amgen Inc.

11:00 Missing Data Considerations for Non-inferiority Trials
   Mark D. Rothmann*, U.S. Food and Drug Administration

11:30 Discussants:
   Scott Emerson, University of Washington
   Peter Mesenbrink, Novartis
   Gerry Gray, U.S. Food and Drug Administration

12:00 Floor Discussion

35. **IMS Medallion Lecture**
   Sponsors: IMS, ENAR
   Organizer & Chair: Babak Shahbaba, University of California, Irvine

10:30 Model-Based Geostatistics for Prevalence Mapping in Low-Resource Settings
   Peter J. Diggle, Ph.D.*, CHICAS, Lancaster University Medical School

36. **CONTRIBUTED PAPERS: Analysis of Imaging Data**
   Sponsor: ENAR
   Chair: Ronald Gangnon, University of Wisconsin

10:30 Mixed Effects Models to Find Differences in Multi-Subject Functional Connectivity
   Manjari Narayan*^ and Genevera I. Allen, Rice University

10:45 Deformation Analysis of Diffusion Tensor Data Using Random Forests
   Neda Sadeghi*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health
   M. Okan Irfanoglu and Amritha Nayak, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health and Henry M. Jackson Foundation
   Cibu Thomas, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health and Center for Neuroscience and Regenerative Medicine
   Carlo Pierpaoli, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

11:00 On Estimating Functional Connectivity for Neuroimaging Data
   Ivor Cribben*, University of Alberta

11:15 Multilinear Principal Components Analysis in Spatially Varying Coefficient Model for Neuroimage Data
   Tianming Zhang* and Yanyuan Ma, University of South Carolina
   Linglong Kong, University of Alberta

11:30 Assessing Uncertainty in Dynamic Functional Connectivity
   Maria Aleksandra Kudela*^ and Jaroslaw Harezlak, Indiana University School of Public Health
   Martin A. Lindquist, John Hopkins Bloomberg School of Public Health

11:45 Modeling Connectivity in High-Dimensional Brain Signals
   Yuxiao Wang*, University of California, Irvine
   Chee-Ming Ting, Universiti Teknologi Malaysia
   Hernando Ombao, University of California, Irvine

* Presenter  ^ Student Award Winner
### 37. CONTRIBUTED PAPERS: Bayesian Clinical Trials

**Sponsor:** ENAR  
**Chair:** Sijin Wen, West Virginia University

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<tr>
<th>Time</th>
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<th>Presenters</th>
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| 10:30 | Credible Subgroup Inference for Bounding the Benefiting Subpopulation for Many Treatments and Multiple Endpoints | Patrick Schnell*, University of Minnesota  
Qi Tang, AbbVie  
Peter Mueller, University of Texas, Austin  
Bradley P. Carlin, University of Minnesota |
| 10:45 | Incorporation of Stochastic Engineering Models as Prior Information in Bayesian Medical Device Trials | Rajesh Nair*, U.S. Food and Drug Administration  
Tarek Haddad and Adam Himes, Medtronic  
Laura Thompson and Telba Irony, U.S. Food and Drug Administration |
| 11:00 | Bayesian Adaptive Dose Finding for Combination Therapy in Phase I Oncology Trials | Chenyi Pan*, University of Virginia  
Yun Shen, Helen Zhou, Parul Gulati, Xiaowei Guan and Katy Simonsen, Bristol-Myers Squibb |
| 11:15 | Using Data Augmentation to Facilitate Conduct of Phase I/II Clinical Trials with Delayed Outcomes | Ick Hoon Jin*, University of Notre Dame  
Suyu Liu, Peter F. Thall and Ying Yuan, University of Texas MD Anderson Cancer Center |
| 11:30 | Control Charts for Monitoring Accumulating Adverse Event Count Frequencies from Single and Multiple Blinded Trials | A. Lawrence Gould*, Merck Research Laboratories |
| 11:45 | Application of Bayesian Methods for Making Go/No-Go Decision in Clinical Trials with an Example | Rodney Croos-Dabrera* and Misun Lee, Astellas Pharma Development |
| 12:00 | Floor Discussion | |

### 38. CONTRIBUTED PAPERS: Diagnostic and Screening Tests

**Sponsor:** ENAR  
**Chair:** Donna McClish, Virginia Commonwealth University

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<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Presenters</th>
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| 10:30 | Comparing Paired Diagnostic Tests Based on Joint Testing of the AUC and the Youden Index | Jingjing Yin*, Georgia Southern University  
Lili Tian, University at Buffalo  
Hani Samawi, Georgia Southern University |
| 10:45 | Modeling Agreement Between Many Raters using an Ordered Classification Scale | Kerrie P. Nelson*, Boston University  
Don Edwards, University of South Carolina |
| 11:00 | On the Use of Min-Max Combination of Biomarkers to Maximize the Partial Area Under the ROC Curve | Hua Ma* and Susan Halabi, Duke University |
11:15  
**Estimation of Discrete Survival Function Through the Modeling of Diagnostic Accuracy for Mismeasured Outcome Data**  
Abidemi K. Adeniji*, Boehringer Ingelheim Pharmaceuticals  
Hee-Koung Joeng, University of Connecticut  
Naitee Ting, Boehringer Ingelheim Pharmaceuticals  
Ming-Hui Chen, University of Connecticut

11:30  
**The Optimal Length of a Sequence of Tests for Classification Tasks**  
Christine M. Schubert Kabbann, Air Force Institute of Technology  
Donna K. McClish, Virginia Commonwealth University

11:45  
**A Placement Value Based Approach to Correlated and Concave ROC Curves with Order Constraints**  
Zhen Chen*, Sung Duk Kim and Beom Seuk Hwang, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

12:00  
**An Application of Factor Analysis in Developing an Abbreviated Questionnaire: Case Study from Neurology**  
Jayawant Mandrekar*, Mayo Clinic

### CONTRIBUTED PAPERS: Longitudinal Data

**Sponsor:** ENAR  
**Chair:** Jarcy Zee, Arbor Research Collaborative for Health

10:30  
**Improving Power with Generalized Estimating Equations in Small-Sample Longitudinal Study Settings**  
Philip M. Westgate* and Woodrow W. Burchett, University of Kentucky

10:45  
**On the Bridge Between Bridge Distributions, Marginalized**  
Geert Molenberghs*, Universiteit Hasselt and Katholieke Universiteit Leuven, Belgium

11:00  
**A Comparison of Three Models in Multivariate Binary Longitudinal Analysis**  
Hissah Alzahrani* and Elizabeth Slate, Florida State University

11:15  
**Discrepancy-Based Parameter Estimation for Balancing Efficiency and Robustness in Fitting State-Space Models**  
Nan Hu* and Joseph Cavanaugh, University of Iowa

11:30  
**Improved Power in Crossover Designs Through Linear Combinations of Baselines**  
Thomas Jemielita* and Mary Putt, University of Pennsylvania  
Devan Mehrotra, Merck Research Laboratories

11:45  
**A Cautionary Note on Using Generalized Estimating Equations to Estimate Transition Models**  
Joe D. Bible*, Paul S. Albert and Danping Liu, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

12:00  
**Some Structured Antedependence Models for Multivariate Longitudinal Data**  
Chulmin Kim*, University of West Georgia

### ORAL POSTERS: Machine Learning

**Sponsor:** ENAR  
**Chair:** Russell Shinohara, University of Pennsylvania

40a.  
**INVITED ORAL POSTER:**  
Regression for Block-missing Multi-modality Data  
Guan Yu, Quefeng Li, Yufeng Liu*, University of North Carolina, Chapel Hill
40b. **INVITED ORAL POSTER:**
A Novel and Efficient Algorithm for De Novo Discovery of Mutated Driver Pathways in Cancer
Binghui Liu, Northeast Normal University, China
Xiaotong Shen and Wei Pan*, University of Minnesota

40c. **Extending the Method, Feature Augmentation Via Nonparametrics and Selection, to the Ordinal Response Setting**
Kyle L. Ferber* and Kellie J. Archer, Virginia Commonwealth University

40d. **Penalized Bayesian Cumulative Logit Model for High-Dimensional Datasets**
Qing Zhou* and Kellie J. Archer, Virginia Commonwealth University

40e. **Sparse Mediation Analysis for High-Dimensional Mediators**
Yi Zhao* and Xi Luo, Brown University

40f. **Inference of Genetic Network from Next Generation Sequencing Data**
Bochao Jia* and Faming Liang, University of Florida

40g. **Interpretable High-Dimensional Inference Via Score Maximization with an Application in Neuroimaging**
Simon N. Vandekar* and Russell T. Shinohara, University of Pennsylvania

40h. **Single Index Latent Factor Model Based on High-Dimensional Features**
Hojin Yang*, Hongtu Zhu and Joseph G. Ibrahim, University of North Carolina, Chapel Hill

40i. **Mixed Models for Ordinal Outcomes in Twin and Sibling Studies with High-Dimensional Covariate Spaces**
Amanda E. Gentry* and Kellie J. Archer, Virginia Commonwealth University

40j. **Evolving Bayesian Networks: Applications to Genomic Pathways and Learning Modules**
Riten Mitra*, University of Louisville
Yuan Ji, NorthShore University Health System
Peter Mueller, University of Texas, Austin

40k. **Sparse Group Lasso and SVM with Overlapping Groups**
David Degras*, DePaul University

12:15 pm - 1:30 pm  **Roundtable Luncheons**

1:45 pm - 3:30 pm  **Oral Posters & Presentations**

41. **High-Throughput Expression Landscape: What’s Next for Methods?**
Sponsors: ENAR, ASA Statistics in Genomics and Genetics Section
Organizer & Chair: Jeffrey Leek, Johns Hopkins University

1:45  **Overcoming Bias and Batch Effects in RNA-Seq Data**
Michael I. Love and Rafael A. Irizarry*, Dana-Faber Cancer Institute and Harvard School of Public Health

2:10  **Integrative Models for Predicting the Regulatory Impact of Rare Non-coding Variation**
Alexis Battle*, Johns Hopkins University

2:35  **Annotation-agnostic Differential Expression Analysis**
Leonardo Collado-Torres* and Alyssa Frazee, Johns Hopkins University
Michael I. Love and Rafael A. Irizarry, Dana-Faber Cancer Institute and Harvard School of Public Health
Andrew Jaffe, Lieber Institute for Brain Development
Jeffrey Leek, Johns Hopkins University
3:00  Detecting Differential Usage of Exons using RNA-Seq Data
Alejandro Reyes*, European Molecular Biology Laboratory
Simon Anders, Institute for Molecular Medicine Finland
Wolfgang Huber, European Molecular Biology Laboratory

3:25  Floor Discussion

42.  Statistical Issues in Estimating Health Disparities Using Complex Samples
Sponsors: ENAR, ASA Survey Research and Methodology Section
Organizer: Mandi Yu, National Cancer Institute, National Institutes of Health
Chair: Fang-Shu Ou, Mayo Clinic

1:45  Comparing Methods of Healthcare Disparity Estimation in the Presence of Complex Survey Design
Benjamin Cook* and Alan Zaslavsky, Harvard Medical School

2:10  Covariance Enhanced Screening for Ultrahigh-Dimensional Classification
Yanming Li*, Kevin Ke, Ji Zhu and Yi Li, University of Michigan

2:35  Examining Socioeconomic Health Disparities Using a Rank-Dependent Rényi Index
Makram Talih*, Centers for Disease Control and Prevention

3:00  Estimating the Relative Concentration Index from Complex Survey Samples
Mandi Yu* and Benmei Liu, National Cancer Institute, National Institutes of Health
Yan Li, University of Maryland, College Park

3:25  Floor Discussion

43.  Statistical Methods for Neuroscience
Sponsors: ENAR, ASA Biometrics Section, ASA Mental Health Statistics Section, ASA Section on Statistics in Imaging
Organizer & Chair: Russell Shinohara, University of Pennsylvania

1:45  Multi-scale Factor Analysis of High Dimensional Time Series Data with Applications to fMRI
Hernando Ombao* and Yuxiao Wang, University of California, Irvine
Chee-Ming Ting, Universiti Teknologi Malaysia

2:10  Kinematic Data in Motor Control Experiments
Jeff Goldsmith*, Columbia University
Tomoko Kitago, Columbia University Medical Center

2:35  Multivariate Pattern Analysis and Confounding in Neuroimaging
Kristin Linn*, Bilwaj Gaonkar, Jimit Doshi, Christos Davatzikos and Russell Shinohara, University of Pennsylvania

3:00  A Bayesian Approach to the Study of Dynamic Functional Connectivity Networks in fMRI Data
Michele Guindani*, University of Texas MD Anderson Cancer Center
Ryan Warnick and Marina Vannucci, Rice University
Erik Erhardt, University of New Mexico
Elena Allen and Vince Calhoun, MRN Mind Research Network and University of New Mexico

3:25  Floor Discussion
### 44. Recent Advances in Statistical Methods for Genetic Epidemiology

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology, ASA Statistics in Genomics and Genetics Section  
**Organizer & Chair:** Swati Biswas, University of Texas at Dallas

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<tr>
<th>Time</th>
<th>Session Title</th>
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<tbody>
<tr>
<td>1:45</td>
<td>Rare Variant Association Tests with Longitudinal Outcome Data</td>
<td>Zihuai He, Seungeung Lee, Min Zhang and Bhramar Mukherjee*, University of Michigan</td>
</tr>
</tbody>
</table>
| 2:10  | Detecting Associations of Rare Variants with Common Diseases Using SNP Data on Families | Shili Lin*, The Ohio State University  
Meng Wang, Nationwide Children’s Hospital |
| 2:35  | Detection of Set-based Gene-Environment Interactions in Families               | Saonli Basu* and Brandon Coombes, University of Minnesota                 |
| 3:00  | Additive Models for Evaluating Predictive Biomarkers in Cancer Epidemiology Studies | Jaya M. Satagopan*, Memorial Sloan Kettering Cancer Center |
| 3:25  | Floor Discussion                                                              |                                                                            |

### 45. Recent Advances in Survival Analysis with High-Dimensional Data

**Sponsor:** ENAR  
**Organizer:** Gang Li, University of California, Los Angeles  
**Chair:** Donatello Telesca, University of California, Los Angeles

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<th>Time</th>
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</table>
| 1:45  | Feature Screening in Ultrahigh Dimensional Cox’s Model                         | Guangren Yang, Jinan University  
Ye Yu, Wells Fargo Bank  
Runze Li*, The Pennsylvania State University  
Anne Buu, University of Michigan |
| 2:15  | Integrating Multidimensional Omics Data for Cancer Prognosis                   | Shuangge Ma*, Yale University                                             |
| 2:45  | Survival Prediction from Large-scale Data using Metric Learning                | Daniel Conn and Christina Ramirez, University of California, Los Angeles  
Zhenqiu Liu, Cedars-Sinai Medical Center  
Gang Li*, University of California, Los Angeles |
| 3:15  | Discussant:                                                                   | Yingying Fan, University of Southern California                          |

### 46. Dissecting Multiple Imputation from a Multi-Phase Inference Perspective

**Sponsor:** ENAR  
**Organizers:** Zhiliang Ying, Columbia University, Hsin-Cheng Huang, Academia Sinica and Ruey S. Tsay, University of Chicago  
**Chair:** Zhiliang Ying, Columbia University

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<thead>
<tr>
<th>Time</th>
<th>Session Title</th>
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| 1:45  | Dissecting Multiple Imputation from a Multi-phase Inference Perspective: What Happens When God’s, Imputer’s and Analyst’s Models Are Uncongenial? | Xianchao Xie, Two Sigma  
Xiaoli Meng*, Harvard University |
| 2:15  | Discussants:                                                                  | Trivellore E. Raghunathan, University of Michigan  
Jerry Reiter, Duke University  
Tony Desmond, University of Guelph |
| 3:25  | Floor Discussion                                                              |                                                                            |
### Innovative Clinical Trial Design and Analysis Methods

**Sponsors:** ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section  
**Organizer:** Haitao Chu, University of Minnesota  
**Chair:** Jing Zhang, University of Maryland  

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<th>Time</th>
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| 1:45  | Bayesian Design of Superiority Clinical Trials for Recurrent Events Data with Applications to Bleeding and Transfusion Events in Myelodyplastic Syndrome | Joseph G. Ibrahim*, University of North Carolina, Chapel Hill  
Ming-Hui Chen, University of Connecticut  
Donglin Zeng, University of North Carolina, Chapel Hill  
Kuo Lung Hu and Catherine Jia, Amgen, Inc. |

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<th>Time</th>
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<th>Presenters</th>
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| 2:10  | Statistical Methods for Conditional Survival Analysis                | Sin-Ho Jung*, Duke University  
Sunkyu Choi and Ho Yun Lee, Samsung Medical Center                                           |

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<th>Time</th>
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<tr>
<td>2:35</td>
<td>Multi-arm Platform Designs for Screening Effective Treatments via Predictive Probability</td>
<td>J. Jack Lee*, Brian P. Hobbs and Nan Chen, University of Texas MD Anderson Cancer Center</td>
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<tr>
<td>3:00</td>
<td>Optimal Flexible Sample Size Design with Robust Power</td>
<td>Lu Cui*, Lanju Zhang and Bo Yang, AbbVie Inc.</td>
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<td>3:25</td>
<td>Floor Discussion</td>
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### Statistical Advances in Evolutionary Dynamics of Infectious Diseases

**Sponsors:** IMS, ENAR  
**Organizer:** Vladimir Minin, University of Washington  
**Chair:** Ali Shojaie, University of Washington  

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<th>Time</th>
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<th>Presenters</th>
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</table>
| 1:45  | Algorithms Linking Phylogenetic and Transmission Trees for Molecular Infectious Disease Epidemiology | Eben Kenah*, University of Florida  
Tom Britton, Stockholm University  
M. Elizabeth Halloran, Fred Hutchinson Cancer Research Center and University of Washington  
Ira M. Longini, Jr., University of Florida |

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<th>Time</th>
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</table>
| 2:10  | Phylogenetic Analysis with Limited Data: Emergence and Epidemiological Impact of Transmissible Dengue Viruses | Ruian Ke*, North Carolina State University  
John Aaskov, Queensland University of Technology  
Edward C. Holmes, University of Sydney  
James O. Lloyd-Smith, University of California, Los Angeles |

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<th>Time</th>
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</table>
| 2:35  | An Efficient Bayesian Inference Framework for Coalescent-based Nonparametric Phylogenetics | Shiwei Lan*, University of Warwick  
Julia A. Palacios, Harvard University and Brown University  
Michael Karcher and Vladimir N. Minin, University of Washington  
Babak Shahbaba, University of California, Irvine |

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<tr>
<td>3:00</td>
<td>Effects of Ignoring Recombination in Phylogenetics of Infectious Diseases</td>
<td>Julia A. Palacios*, Harvard University and Brown University</td>
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<td>3:25</td>
<td>Floor Discussion</td>
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<tr>
<td>49. CONTRIBUTED PAPERS: Bayesian Semi-Parametric and Non-Parametric Methods</td>
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| Sponsor: ENAR  
Chair: A. Lawrence Gould, Merck Research Laboratories |

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<tr>
<th>1:45 Flexible Bayesian Survival Modeling with Semiparametric Time-Dependent and Shape-Restricted Covariate Effects</th>
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<tbody>
<tr>
<td>Thomas A. Murray* and Brian P. Hobbs, University of Texas MD Anderson Cancer Center</td>
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<td>Daniel J. Sargent, Mayo Clinic</td>
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<td>Bradley P. Carlin, University of Minnesota</td>
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<tr>
<th>2:00 A Bayesian Semiparametric Approach for Panel Count Data</th>
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<td>Jianhong Wang* and Xiaoyan Lin, University of South Carolina</td>
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<tr>
<th>2:15 Nonparametric Smoothing Estimation of Fecundability from a Conception Model</th>
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<td>Mohammed R. Chowdhury*, Kennesaw State University</td>
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<tr>
<th>2:30 Marginal Bayesian Hierarchical Model for Multivariate Binary Data to Estimate the Etiology of Childhood Pneumonia</th>
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<tr>
<td>Detian Deng* and Scott Zeger, Johns Hopkins University</td>
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<tr>
<th>2:45 A Semiparametric Bayesian Approach to Borrow Information from Historical Control Data in Two Arm Clinical Trials.</th>
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<tr>
<td>Arpita Chatterjee*, Georgia Southern University</td>
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<tr>
<th>3:00 Bayesian Multivariate Nonlinear Mixed Effects Models with a Matrix Stick-Breaking Process Prior</th>
</tr>
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| Xiao Wu*, University of Florida  
Michael J. Daniels, University of Texas, Austin |

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<tr>
<th>3:15 Bayesian Additive Partial Linear Models with Measurement Error and Heteroscedastic Regression Error Variance</th>
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<tr>
<td>Chang Liu and Sally W. Thurston*, University of Rochester</td>
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<th>50. CONTRIBUTED PAPERS: Bayesian Variable Selection</th>
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| Sponsor: ENAR  
Chair: Rajesh Nair, U.S. Food and Drug Administration |

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<tr>
<th>1:45 Altered Singular Bayesian Information Criteria for Bivariate Mixture Models</th>
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</table>
| Richard Charnigo*, University of Kentucky  
Qian Fan, Wells Fargo  
Ruriko Yoshida, University of Kentucky  
Mathias Drton, University of Washington  
Hongying Dai, Children’s Mercy Hospital |

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<tr>
<th>2:00 Bayesian Bi-Level Variable Selection</th>
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<tr>
<td>Eunjee Lee*, Hongtu Zhu and Joseph G. Ibrahim, University of North Carolina, Chapel Hill</td>
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<tr>
<th>2:15 Bayesian Variable Selection for Skewed Heteroscedastic Response</th>
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| Libo Wang**, Florida State University  
Yuanyuan Tang, AbbiVie  
Debajyoti Sinha and Debdeep Pati, Florida State University  
Stuart Lipsitz, Brigham and Women’s Hospital |

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<tr>
<th>2:30 Bayesian Ranking and Selection with Application to Identification of Risk Genes</th>
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| Xiaojian Sun* and Feng Luo, Clemson University  
Anand K. Srivastava, Greenwood Genetic Center |

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<tr>
<th>2:45 Bayesian Variable Selection in Additive Partial Linear Models with Error in Variables</th>
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<tr>
<td>Chang Liu*, Hongqi Xue and Sally W. Thurston, University of Rochester</td>
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### 51. CONTRIBUTED PAPERS: Graphical Models

**Sponsor:** ENAR  
**Chair:** Ivor Cribben, Alberta School of Business

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<tbody>
<tr>
<td>1:45</td>
<td>Estimation of High-Dimensional Graphical Models Using Regularized Score Matching</td>
<td>Lina Lin*, Mathias Drton and Ali Shojaie, University of Washington</td>
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<tr>
<td>2:00</td>
<td>High-Dimensional Robust Precision Matrix Estimation: Cellwise Corruption Under Epsilon-Contamination</td>
<td>Po-Ling Loh and Xin Lu Tan*, University of Pennsylvania</td>
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</tbody>
</table>
Runze Li and Rongling Wu, The Pennsylvania State University  |
| 2:30  | Detecting Hidden Characteristics for Network Data Within Latent Space | Shiwen Shen* and Edsel Pena, University of South Carolina                   |
| 2:45  | Structured Sparse Multiple Co-Inertia Analysis with Applications to Genomics and Metabolomics Data | Eun Jeong Min* and Qi Long, Emory University Rollins School of Public Health |
| 3:00  | Nonparametric Mixture of Gaussian Graphical Models, with Applications in Brain Functional Connectivity Estimation | Kevin Haeseung Lee* and Lingzhou Xue, The Pennsylvania State University       |
Peter Song, University of Michigan                                             |

### 52. CONTRIBUTED PAPERS: Multivariate Methods

**Sponsor:** ENAR  
**Chair:** Geert Molenberghs, Universiteit Hasselt and Katholieke Universiteit Leuven, Belgium

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Presenter(s)</th>
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</thead>
</table>
| 1:45  | Groupwise Envelope Model for Efficient Estimation and Response Variable Selection | Yeonhee Park*, University of Texas MD Anderson Cancer Center  
Zhihua Su, University of Florida |
| 2:00  | Consistent Estimation in Partially Linear Models with Correlated Observations | Liangdong Fan*, Cidambi Srinivasan and Richard Charnigo, University of Kentucky |
| 2:15  | Multivariate Mean Estimation Under Efficient Sampling Designs         | Daniel F. Linder, Haresh D. Rochani*, Hani M. Samawi and Viral V. Panchal, Georgia Southern University |
| 2:30  | Global Rank Tests for Multiple Ordinal and Failure Outcomes          | Ritesh Ramchandani*, Harvard School of Public Health  
David A. Schoenfeld and Dianne M. Finkelstein, Massachusetts General Hospital |
| 2:45  | Envelope Models for Efficient Multivariate Binary Regression         | Emil A. Cornea*, Joseph G. Ibrahim and Hongtu Zhu, University of North Carolina, Chapel Hill |
3:00  A Geometric Perspective on the Powers of Principal Component Association Tests in Multiple Phenotype Studies  
Zhonghua Liu* and Xihong Lin, Harvard University

3:15  Multilevel Matrix-Variate Analysis and its Application to Long-Term Remote Patient Monitoring  
Lei Huang*, Johns Hopkins University  
Tamara Harris, National Institute of Aging, National Institutes of Health  
Mathew Maurer and Philip Green, Columbia University Medical Center  
Andrada Ivanescu, Montclair State University  
Vadim Zipunnikov, Johns Hopkins University

53. **ORAL POSTERS: Clinical Trials**  
Sponsor: ENAR  
Chair: Bradley P. Carlin, University of Minnesota

53a. **INVITED ORAL POSTER:**  
Adaptive Platform Trials: The Future of Clinical Research  
Donald A. Berry*, University of Texas MD Anderson Cancer Center

53b. **INVITED ORAL POSTER:**  
Statistical Design and Issues in a Scientific Breakthrough Trial for HIV Prevention  
Ying Qing Chen*, Fred Hutchinson Cancer Research Center

53c.  Estimation of Dosage Frequency of Pre-Exposure Prophylaxis Needed to Protect Against HIV Infection  
Claire F. Ruberman*, Johns Hopkins University

53d.  A Mixture of Mixed Logistic Regression Model for Dynamic Treatment Regime with Application to Prostate Cancer Trial  
Bing Yu*, Bruce Craig and Yu Zhu, Purdue University

53e.  Understanding the Operating Characteristics of Different Bayesian Adaptive Allocations in Two Arm Confirmatory Trial with A Dichotomous Outcome  
Yunyun Jiang*, Wenle Zhao and Valerie L. Durkalski, Medical University of South Carolina

53f.  Using Event Counts in Phase I Clinical Trials  
Daniel G. Muenz*, Thomas M. Braun, Jeremy M. G. Taylor, University of Michigan

53g.  Meta-Analysis of Clinical Trials with Sparse Binary Outcomes Using Zero-Inflated Binomial (ZIB) Models  
Cheng Dong*, University of Missouri  
Yueqin Zhao and Ram Tiwari, U.S. Food and Drug Administration

53h.  Response Adaptive Randomization Using Surrogate and Primary Endpoints  
Hui Wang* and Nitai Mukhopadhyay, Virginia Commonwealth University

53i.  Efficient Double Robust Estimation for Two-Stage Dynamic Treatment Regimes  
Andrew S. Topp*, Geoff S. Johnson and Abdus S. Wahed, University of Pittsburgh

53j.  Choosing Covariates for Adjustment in Non-Inferiority Trials Based on Influence and Disparity  
Katherine S. Nicholas*, Viswanathan Ramakrishnan and Valerie L. Durkalski-Mauldin, Medical University of South Carolina

53k.  Bayesian Modeling and Prediction of Accrual Using Gaussian Process  
Yi Deng*, Qing He and Qi Long, Emory University

53l.  Stepped Wedge Cluster Randomized Controlled Trials with Two Layers of Clustering: Designs and Comparisons of Power  
Ranran Dong* and Abigail Shoben, The Ohio State University
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<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>3:30 pm - 3:45 pm</td>
<td>Refreshment Break with Our Exhibitors</td>
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<tr>
<td>3:45 pm - 5:30 pm</td>
<td>Oral Posters &amp; Presentations</td>
</tr>
</tbody>
</table>

54. **New Statistical Methods for Imaging Genetics**
   - **Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Imaging, ASA Statistics in Genomics and Genetics Section
   - **Organizer & Chair:** Jianhua Hu, University of Texas MD Anderson Cancer Center

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<tr>
<th>Time</th>
<th>Title</th>
<th>Presenters</th>
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<tbody>
<tr>
<td>3:45</td>
<td>Testing for Association Between Genetic Variants and Brain Networks</td>
<td>Junghi Kim and Wei Pan*, University of Minnesota</td>
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<tr>
<td>4:10</td>
<td>Integrating Genomic and Imaging Data: An Atomic Approach</td>
<td>Debashis Ghosh*, Colorado School of Public Health</td>
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<tr>
<td>4:35</td>
<td>Joint Mediation Analysis of Imaging and Genetic Data in Genetic Association Studies of Complex Diseases</td>
<td>Hongtu Zhu*, University of North Carolina, Chapel Hill</td>
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<tr>
<td>5:00</td>
<td>Heritability-based Prioritization of Structural Neuroimaging Phenotypes</td>
<td>Tian Ge*, Harvard Medical School, Thomas E. Nichols, University of Warwick, Martin Reuter, Harvard Medical School, Anderson M. Winkler, University of Oxford, Avram J. Holmes, Yale University, Phil H. Lee and Joshua L. Roffman, Harvard Medical School, Randy L. Buckner, Harvard University, Jordan W. Smoller and Mert R. Sabuncu, Harvard Medical School</td>
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<tr>
<td>5:25</td>
<td>Floor Discussion</td>
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</table>

55. **Recent Advances in Adaptive Model-Based Design of Clinical Trials**
   - **Sponsors:** ENAR, ASA Biopharmaceutical Section
   - **Organizer & Chair:** Sergei Leonov, ICON Clinical Research

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<tr>
<th>Time</th>
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<tr>
<td>3:45</td>
<td>Adaptive Dose Escalation Methods in Phase I Oncology Trials: A Case Study</td>
<td>Inna Perevozskaya*, Roberto Bugarini and Mani Lakshminarayanan, Pfizer Inc.</td>
</tr>
<tr>
<td>4:15</td>
<td>Early-phase Design for a Combination of Targeted Therapies in Oncology</td>
<td>Nolan A. Wages*, Craig A. Portell and Gina R. Petroni, University of Virginia</td>
</tr>
<tr>
<td>4:45</td>
<td>Inference in Experiments with Pilot Data</td>
<td>Nancy Flournoy*, University of Missouri</td>
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<tr>
<td>5:15</td>
<td>Discussant:</td>
<td>Valerii Fedorov, ICON Clinical Research</td>
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</tbody>
</table>

56. **Statistical Methods for Accelerometry Data: Physical Activity and Health Outcomes**
   - **Sponsor:** ENAR
   - **Organizer:** Jaroslaw Harezlak, Indiana University
   - **Chair:** Jacek Urbanek, Johns Hopkins Bloomberg School of Public Health

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<th>Time</th>
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<th>Presenters</th>
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<tr>
<td>3:45</td>
<td>Quantifying Physical Activity in Mid-to-Late Life</td>
<td>Jennifer A. Schrack* and Vadim Zipunnikov, Johns Hopkins University</td>
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<td>Luo Xiao, North Carolina State University</td>
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<td>Ciprian Crainiceanu, Johns Hopkins University</td>
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<td>Luigi Ferrucci, National Institute on Aging, National Institutes of Health</td>
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</tbody>
</table>
4:10  **Multilevel Models for Analysis of Actigraphy Data**  
Vadim Zipunnikov*, Johns Hopkins University  
Jeff Goldsmith, Columbia University  
Junrui Di, Andrew Leroux and Jacek Urbanek, Johns Hopkins University

4:35  **Three-Part Joint Modeling Methods for Complex Functional Data in Physical Activity Studies**  
Haocheng Li*, University of Calgary  
John Staudenmayer, University of Massachusetts  
Tianying Wang and Raymond J. Carroll, Texas A&M University

5:00  **Accelerometers, Physical Activity, and Conditional Random Fields**  
Evan Ray and John W Staudenmayer*, University of Massachusetts, Amherst

5:25  Floor Discussion

57. **Statistical Methods in HIV/AIDS**  
**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology  
**Organizer & Chair:** Michael Hudgens, University of North Carolina, Chapel Hill

3:45  **Integration of Dynamic Gene Regulatory Networks for HIV Infection in the Big Data Era**  
Hulin Wu*, University of Texas Health Science Center, Houston

4:05  **Estimating the Association of Bivariate Survival Data Through Copula Models: An Application to a Study of AIDS-related Non-Hodgkin’s Lymphoma in East Africa**  
Pingfu Fu* and Xiaozhen Han, Case Western Reserve University  
Scot Remick, Mary Babb Randolph Cancer Center

4:25  **A Dirichlet Process Mixture Model for Non-Ignorable Dropout**  
Camille Marie Moore*, Samantha MaWhinney and Nichole E. Carlson, University of Colorado Denver

4:45  **A State Space Framework for Patient-Level Modeling of the HIV Care Cascade using Longitudinal Cohort Data**  
Hana Lee*, Joseph W. Hogan and Becky L. Genberg, Brown University  
Paula Braitsstein, Indiana University

5:05  **A Structural Equation Modeling Approach to Understanding the Cardiovascular Effects of Antiretroviral Therapy (ART) Initiation: Results from a Phase III Clinical Trial**  
Carlee B. Moser*, Harvard School of Public Health  
Judith S. Currier, University of California, Los Angeles  
James H. Stein, University of Wisconsin School of Medicine and Public Health  
Howard N. Hodis and Michael P. Dube, University of Southern California  
Todd T. Brown, Johns Hopkins University School of Medicine  
Grace A. McComsey, Case Western Reserve University School of Medicine

5:25  Floor Discussion

58. **Advances and Challenges in Biomarker Studies**  
**Sponsors:** ENAR, ASA Biometrics  
**Organizer & Chair:** Zheyu Wang, Johns Hopkins University

3:45  **A Paradigm for Center Effects in Biomarker Studies**  
Kathleen F. Kerr* and Allision Meisner, University of Washington

4:10  **An Efficient Procedure to Combine Biomarkers with Limits of Detection for Risk Prediction**  
Ruth Pfeiffer*, National Cancer Institute, National Institutes of Health  
Diego Tomassi, Instituto de Matemática Aplicada del Litoral, Argentina  
Efstathia Bura, George Washington University  
Liliana Forzani, Universidad Nacional del Litoral, Argentina
### 59. Functional Regression Methods and Personalized Medicine

**Sponsors:** ENAR, ASA Biometrics Section
**Organizer & Chair:** Ana-Maria Staicu, North Carolina State University

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<tr>
<th>Time</th>
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<tr>
<td>3:45</td>
<td>Functional Regression Methods for Densely-Sampled Biomarkers in the ICU</td>
<td>Ciprian Crainiceanu*, Johns Hopkins University</td>
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<tr>
<td>4:10</td>
<td>Functional Feature Construction for Personalized Treatment Regimes</td>
<td>Eric B. Laber*, Robert Pehlman and Ana-Maria Staicu, North Carolina State University</td>
</tr>
<tr>
<td>4:35</td>
<td>Estimation of Optimal Treatment Policies and Marginal Screening of Functional Predictors</td>
<td>Ian W. McKeague*, Columbia University</td>
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<tr>
<td>5:00</td>
<td>Developing Biomarkers for Brain Lesion Trajectories in Longitudinal MRI</td>
<td>Elizabeth M. Sweeney, Johns Hopkins University, Russell T. Shihora*, University of Pennsylvania, Blake E. Dewey and Matthew K. Schindler, National Institute of Neurological Disorders and Stroke, National Institutes of Health, John Muschelli, Johns Hopkins University, Daniel S. Reich, National Institute of Neurological Disorders and Stroke, National Institutes of Health, Ciprian M. Crainiceanu, Johns Hopkins University, Ani Eloyan, Brown University</td>
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<td>5:25</td>
<td>Floor Discussion</td>
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### 60. Bayesian Methods for Large-Scale Non-Gaussian Data

**Sponsors:** IMS, ENAR
**Organizer & Chair:** Michele Guindani, University of Texas MD Anderson Cancer Center

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<th>Time</th>
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<tr>
<td>3:45</td>
<td>Bayesian Modeling of Huge Tables and Discrete Data</td>
<td>David B. Dunson*, Duke University</td>
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<tr>
<td>4:10</td>
<td>Bayesian Models of High-Dimensional Count Data</td>
<td>Marina Vannucci*, Rice University, Michele Guindani, University of Texas MD Anderson Cancer Center</td>
</tr>
<tr>
<td>4:35</td>
<td>Valid Statistical Analyses and Reproducible Science in the Era of High-throughput</td>
<td>Edoardo M. Airoldi*, Harvard University</td>
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<td>5:00</td>
<td>Floor Discussion</td>
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### 61. CONTRIBUTED PAPERS: Cancer Applications

**Sponsor:** ENAR
**Chair:** Kerrie Nelson, Boston University

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<tr>
<th>Time</th>
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<tr>
<td>3:45</td>
<td>P53-Based Strategy to Reduce Hematological Toxicity of Chemotherapy: A Pilot Study</td>
<td>Chul S. Ha, Joel Michalek*, Richard Elledge, Kevin R. Kelley, Suthakar Ganapathy, Su Hang, Carol A. Jenkins, Athanassios Argiris, Ronan Swords and Tony Y. Eng, University of Texas Health Science Center, San Antonio</td>
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<tr>
<td>4:00</td>
<td>Using IMRE and ANOVA to Select MicroRNAs for Predicting Prostate Cancer Recurrence</td>
<td>Qi Wang*, Bin Guo and Yarong Yang, North Dakota State University</td>
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<tr>
<td>4:15</td>
<td>Implementation of a 2-Stage Crossover Correction in Analysis of Overall Survival (OS):</td>
<td>Ruifeng Xu*, Jingshu Wang and James M. Pellissier, Merck &amp; Co., Inc.</td>
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<td></td>
<td>An Example in Oncology</td>
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<td>4:30</td>
<td>Modeling Multiple Primary Cancers Over Time Using Non-Homogeneous Poisson Process</td>
<td>Jialu Li*, University of Texas MD Anderson Cancer Center</td>
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<td>Seung Jun Shin, Korea University</td>
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<td>Wenyi Wang, University of Texas MD Anderson Cancer Center</td>
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<td>4:45</td>
<td>Assessing Intra-Tumor Heterogeneity and Tracking Longitudinal and Spatial Clonal</td>
<td>Yuchao Jiang*, Andy J. Minn and Nancy R. Zhang, University of Pennsylvania</td>
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<td>Evolution by Next-Generation Sequencing</td>
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<td>5:00</td>
<td>Pathway-Based Differential Network Analysis in Cancer</td>
<td>Min Jin Ha*, Veerabhadran Baladandayuthapani and Kim-Anh Do, University of Texas MD</td>
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<td>Anderson Cancer Center</td>
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<td>5:15</td>
<td>Cell Type-Specific Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration</td>
<td>Zeya Wang*, Rice University</td>
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<td>Using Expression Data</td>
<td>Jeffrey S. Morris, University of Texas MD Anderson Cancer Center</td>
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<td>Jaeli Ahn, Georgetown University</td>
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<td>Bo Li, Harvard University</td>
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<td>Wei Lu, Xiaoming Tang and Ignacio I. Wistuba, University of Texas MD Anderson Cancer</td>
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<td>Chris C. Holmes, University of Oxford</td>
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<td>Wenyi Wang, University of Texas MD Anderson Cancer Center</td>
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<td>Chris C. Holmes, University of Oxford</td>
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<td>3:45</td>
<td>On Clinical Trials with a High Placebo Response Rate</td>
<td>George Chi and Pilar Lim*, Janssen Research &amp; Development, LLC</td>
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<td>4:00</td>
<td>Using IMRE and Dual KS to Select MicroRNAs for Predicting Prostate Cancer Recurrence</td>
<td>Yarong Yang* and Qi Wang, North Dakota State University</td>
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<td>4:15</td>
<td>Estimating Treatment Effect in Time to Relapse When Patients Switch Treatment</td>
<td>Miao Lu*, University of Virginia</td>
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<td>Jian Han, Genentech, Inc.</td>
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<td>4:30</td>
<td>Inference on Subgroups and All-Comers Cognizant of Logical Relationships Among</td>
<td>Szu-Yu Tang*, Ventana Medical Systems, Inc. (Roche Group)</td>
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<td>Efficacy Parameters</td>
<td>Yi Liu, Millennium: The Takeda Oncology Company</td>
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<td>Jason Hsu, Eli Lilly &amp; Company and The Ohio State University</td>
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<td>4:45</td>
<td>Logical Inference on Treatment Efficacy in Subgroups and Their Mixtures</td>
<td>Ying Ding*, University of Pittsburgh</td>
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<td>Hui-Min Lin, Takeda Pharmaceuticals</td>
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<td>Jason C. Hsu, Eli Lilly &amp; Company and The Ohio State University</td>
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<td>5:00</td>
<td>Confident Effect of a SNP on the Efficacy of a Drug</td>
<td>Jason C. Hsu*, Eli Lilly &amp; Company and The Ohio State University</td>
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<td>Ying Ding, University of Pittsburgh</td>
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<td>Ying Grace Li and Stephen J. Ruberg, Eli Lilly &amp; Company</td>
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</table>
5:15  **A Predictive Enrichment Procedure to Identify Potential Responders to a New Therapy for Randomized, Comparative Controlled Clinical Studies**
Junlong Li, Harvard University
Lihui Zhao*, Northwestern University
Lu Tian, Stanford University
Tianxi Cai, Harvard University
Brian Claggett, Brigham and Women’s Hospital
Andrea Callegaro, Benjamin Dizier, Bart Spiessens and Fernando Ulloa-Montoya, GlaxoSmi...
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<th>Time</th>
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<th>Title</th>
<th>Authors</th>
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<tr>
<td>3:45</td>
<td><strong>CONTRIBUTED PAPERS: Machine Learning</strong></td>
<td>Lagged Kernel Machine Regression for Identifying Time Windows of Susceptibility to Complex Metal Mixtures</td>
<td>Shelley H. Liu*, Harvard University, Jennifer F. Bobb and Kyu Ha Lee, Harvard School of Public Health, Chris Gennings, Mount Sinai Hospital, Birgit Claus Henn, Boston University School of Public Health, Robert O. Wright, Mount Sinai Hospital, Lourdes Schnaas and Martha Tellez Rojo, Instituto Nacional De Salud Publica, Mexico, Manish Arora, Mount Sinai Hospital, Brent Coull, Harvard School of Public Health</td>
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<td>4:00</td>
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<td>A Group-Specific Recommender System</td>
<td>Xuan Bi* and Annie Qu, University of Illinois, Urbana-Champaign, Junhui Wang, City University of Hong Kong, Xiaotong Shen, University of Minnesota</td>
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<tr>
<td>4:15</td>
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<td>A General Unimodal Null Distribution with Applications to Cluster Significance Testing</td>
<td>Erika Helgeson and Eric Bair*, University of North Carolina, Chapel Hill</td>
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<td>4:45</td>
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<td>Robust Learning for Optimal Treatment Decision with NP-Dimensionality</td>
<td>Chengchun Shi*, Rui Song and Wenbin Lu, North Carolina State University</td>
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<td>5:00</td>
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<td>Region Based Mediation Test of DNA Methylation Using Kernel Machine Regression</td>
<td>Jincheng Shen* and Xihong Lin, Harvard School of Public Health</td>
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<td>5:15</td>
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<td>Adaptive Contrast Weighted Learning for Multi-Stage Multi-Treatment Decision-Making</td>
<td>Yebin Tao* and Lu Wang, University of Michigan</td>
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<tr>
<td>3:45</td>
<td><strong>CONTRIBUTED PAPERS: Next Generation Sequencing</strong></td>
<td>Shrinkage of Dispersion Parameters in the Binomial Family, with Application to Differential Exon Skipping</td>
<td>Sean Ruddy*, Marla Johnson and Elizabeth Purdom, University of California, Berkeley</td>
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<td>4:00</td>
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<td>Accounting for Stochastic Dropout Events in Detecting Differential Gene Expression Using Single-Cell RNA-Seq Data</td>
<td>Cheng Jia*, Mingyao Li and Nancy Zhang, University of Pennsylvania</td>
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<tr>
<td>4:15</td>
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<td>NEXT-Peak: A Per-Base Regression Model for ChIP-Seq Peak Calling</td>
<td>Nak-Kyeong Kim*, Virginia Commonwealth University</td>
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<td>4:30</td>
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<td>Gene-Set Analysis Via Combining P-Values in RNA-Seq Data</td>
<td>Yu-Chung Wei*, Ching-Wei Chang and Nysia I. George, U.S. Food and Drug Administration</td>
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<tr>
<td>4:45</td>
<td></td>
<td>A Model for Paired-Multinomial Data and its Application to Analysis of Data on a Taxonomic Tree</td>
<td>Pixu Shi* and Hongzhe Li, University of Pennsylvania</td>
</tr>
<tr>
<td>5:00</td>
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<td>A Novel Normalization Method for Time Series Metagenomic Count Data</td>
<td>Lingling An*, Zhenqiang Lu, Meng Lu and Dan Luo, University of Arizona</td>
</tr>
</tbody>
</table>
5:15 Homology Cluster Differential Expression Analysis for Interspecies mRNA-Seq Experiments
Jonathan A. Gelfond*, University of Texas Health Science Center, San Antonio
Joseph G. Ibrahim, University of North Carolina, Chapel Hill
Ming-Hiu Chen, University of Connecticut
Sun Wei, Fred Hutchinson Cancer Center
Kaitlyn Lewis, University of Texas Health Science Center, San Antonio
Sean Kinahan and Matthew Hibbs, Trinity University
Rochelle Buffenstein, Calico Labs

66. ORAL POSTERS: Genomics
Sponsor: ENAR
Chair: Tanya Garcia, Texas A&M University

66a. INVITED ORAL POSTER:
Statistical Methods for Single-Cell RNA-Seq
Rhonda Bacher and Jeea Choi, University of Wisconsin
Keegan Korthauer, Dana-Farber Cancer Institute
Ning Leng, Li-Fang Chu, James A. Thomson and Ron Stewart,
Morgridge Institute for Research
Christina Kendziorski*, University of Wisconsin

66b. INVITED ORAL POSTER:
The Widespread and Critical Impact of Systematic Bias and Batch Effects in Single-Cell RNA-Seq Data
Stephanie C. Hicks and Mingxiang Teng, Harvard University
Rafael A. Irizarry*, Dana-Farber Cancer Institute and Harvard University

66c. Change in Variance of IGF2 Gene Methylation is Associated with Three Metabolites
Emily C. Hector*, Jaclyn M. Goodrich, Lu Tang, Wei Peng and Dana C. Dolinoy,
University of Michigan
Adriana Mercado-Garcia, National Institute of Public Health, Mexico
Howard Hu, University of Toronto
Martha Maria Tellez-Rojo, National Institute of Public Health, Mexico
Karen E. Peterson, University of Michigan and Harvard School of Public Health
Peter X.K. Song, University of Michigan

66d. Prioritizing Genes Based on Bayes Factor
Hongyan Xu* and Fengjiao Hu, Georgia Regents University
Duchwan Ryu, Northern Illinois University
Varghese George*, Georgia Regents University

66e. RefCNV: Identification of Gene-Based Copy Number Variants Using Whole Exome Sequencing
Lun-Ching Chang*, National Cancer Institute, National Institutes of Health
Biswajit Das, Chih-Jian Lih, Corrine Camalier and Paul McGregor,
Leidos Biomedical Research Inc.
Eric Polley, National Cancer Institute, National Institutes of Health

66f. A Generalized Functional Model for Association Analysis of Family-Based Sequencing Data
Sneha Jadhav* and Qing Lu, Michigan State University

66g. Bayesian Hierarchical Modeling and Shrinkage Priors for GWAS
LiJin Joo* and Cheongeun Oh, New York University

66h. Statistical Methods for Compositional Data Analysis with Application in Metagenomics
Hongmei Jiang*, Northwestern University
66i. Pathway-based Integrative Bayesian Modeling of Multi-platform Genomics Data
Elizabeth J. McGuffey*, United States Naval Academy
Jeffrey S. Morris and Ganiraju C. Manyam, University of Texas MD Anderson Cancer Center
Raymond J. Carroll, Texas A&M University
Veerabhadran Baladandayuthapani, University of Texas MD Anderson Cancer Center

66j. Incorporating Functional Information into SNP-Based Phenotype Prediction
Yue-Ming Chen* and Peng Wei, University of Texas School of Public Health, Houston

66k. Detection of Genetic Interactions Through Meta-Analysis and Effect Size Heterogeneity
Yulun Liu*, University of Texas MD Anderson Cancer Center
Yong Chen, University of Pennsylvania School of Medicine
Paul Scheet, University of Texas MD Anderson Cancer Center

66l. Assessing Mitochondrial DNA Variation and Copy Number Using Tailored Sequencing Analysis Tools
Jun Ding*, National Institute on Aging, National Institutes of Health
Carlo Sidore and Francesco Cucca, Istituto di Ricerca Genetica e Biomedica, Consiglio Nazionale delle Ricerche, Italy
Goncalo R. Abecasis, University of Michigan
David Schlessinger, National Institute on Aging, National Institutes of Health

66m. Bayesian Latent Hierarchical Model for Transcriptomic Meta-Analysis to Detect Biomarkers with Clustered Meta-Patterns of Differential Expression Signals
Zhiguang Huo, University of Pittsburgh
Chi Song*, The Ohio State University
George Tseng, University of Pittsburgh

Tuesday March 8

8:30 - 10:15 am Oral Presentations

67. New Statistical Developments for Emerging Challenges with Complex Data Structures in Observational Studies
Sponsors: ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology
Organizer & Chair: Lu Wang, University of Michigan

8:30 Joint Modeling of Longitudinal Health Predictors and Cross-sectional Health Outcomes via Mean and Variance Trajectories
Michael R. Elliott*, University of Michigan
Bei Jiang, University of Alberta
Naisyn Wang, University of Michigan
Mary Sammel, University of Pennsylvania

8:55 Spatial Measurement Error and Correction by Spatial SIMEX in Linear Regression Models when Using Predicted Air Pollution Exposures
Stacey E. Alexeeff, Kaiser Permanente
Raymond J. Carroll, Texas A&M University
Brent A. Coull*, Harvard University

9:20 Intrinsic Efficiency and Multiple Robustness in Longitudinal Data Analysis with Dropout
Peisong Han*, University of Waterloo

9:45 Multiple Robust Fitting of a Log-linear Model
Andrea Rotnitzky*, Di Tella University
Thomas Richardson, University of Washington, Seattle

10:10 Floor Discussion
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<th>Session</th>
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<td>68.</td>
<td>Statistical Innovations of Massive Genomic Data Analysis</td>
<td>ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section</td>
<td>Yuping Zhang, University of Connecticut and Zhaohui (Steve) Qin, Emory University</td>
<td>Zhaohui (Steve) Qin, Emory University</td>
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<tr>
<td>8:55</td>
<td>Leveraging Algorithms for Logistic Regression with Massive Data</td>
<td>Ping Ma*, University of Georgia</td>
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<tr>
<td>9:20</td>
<td>Statistical Modeling of High-Throughput RNA Structure Probing Data</td>
<td>Zhengqing Ouyang*, The Jackson Laboratory for Genomic Medicine</td>
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<tr>
<td>9:45</td>
<td>Expansion of Biological Pathways by Integrating Enormous mRNA Expression Datasets</td>
<td>Yang Li and Jun Liu*, Harvard University</td>
<td>Vamsi Mootha, Harvard Medical School</td>
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| 69.     | Policy Implications of Scientific Reproducibility - A Panel Discussion | ENAR | Michelle Schwalbe, National Research Council |
| 8:30    | Discussants: | Constantine Gatsonis, Brown University | Marcia McNutt, Science (Editor-in-Chief) | Lawrence Tabak, National Institutes of Health (Principal Deputy Director) | Steven Goodman, Stanford University |
| 10:00   | Floor Discussion |

| 70.     | Multivariate Models for Spatially Correlated Data | ENAR, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Section on Statistics and the Environment | Mahlet Tadesse, Georgetown University |
| 8:30    | Bayesian Matrix Models for Multivariate Disease Mapping | Miguel A. Martinez-Beneito, Public Health Research Center of Valencia | Paloma Botella-Rocamora, CEU Cardinal Herrera University, Spain | Sudipto Banerjee*, University of California, Los Angeles |
| 8:55    | Multivariate Generalized Linear Models for Space-Time Disease Mapping | Marie Denis* and Sebastien Tisne, CIRAD, France | Indra Syahputra, PT Socfino, Indonesia | Hubert de Franqueville and Benoit Cochard, PalmElit SAS |
| 9:20    | Multivariate Latent Structure in Bayesian Spatio-temporal Health Models | Andrew B. Lawson and Rachel Carroll*, Medical University of South Carolina |
| 9:45    | A Hierarchical Bayesian Model for Prediction of Multivariate Non-Gaussian Random Fields | Frederic Mortier*, CIRAD, France | Pierrette Chagneau, INSA de Rennes, France | Nicolas Picard, Food and Agriculture Organization of the United Nations |
| 10:10   | Floor Discussion |
### 71. Methods for Comparative Effectiveness Research Using Electronic Health Records

**Sponsors:** ENAR, ASA Biometrics Section, ASA Statistical Learning and Data Mining Section  
**Organizer:** Yingqi Zhao, University of Wisconsin, Madison  
**Chair:** Chaeryon Kang, University of Pittsburgh

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<th>Time</th>
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| 8:30  | Comparing Comparative Effectiveness Studies Using Electronic Health Record (EHR) Data | Ruth Etzioni*, Fred Hutchinson Cancer Research Center  
Lurdes Inoue, University of Washington |
| 8:55  | Comparative Effectiveness of Dynamic Treatment Strategies: The Renaissance of the Parametric g-Formula | Miguel Hernan*, Harvard University |
| 9:20  | Electronic Health Records as Evidence Generation Tools for Medical Decision Making | Marianghi Markatou*, University at Buffalo |
| 9:45  | Methods for Misclassified Time to Event Outcomes in Studies Using EHR-derived Endpoints | Rebecca A. Hubbard*, University of Pennsylvania  
Weiwei Zhu and Jessica Chubak, Group Health Research Institute |
| 10:10 | Floor Discussion                                                      |                                                                            |

### 72. Missing Data Issues in Meta-Analysis with Individual Participant Data

**Sponsors:** ENAR, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Survey Research and Methodology Section  
**Organizer & Chair:** Yajuan Si, University of Wisconsin, Madison

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<th>Time</th>
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| 8:30  | Missing Confounder Data in Observational Meta-Analysis with Systematically Missing Data | Ian R. White*, MRC Biostatistics Unit, Cambridge, UK  
Matthieu Resche-Rigon, Universite Paris Diderot |
| 8:55  | Allowing for Uncertainty Due to Missing Outcome Data in Pairwise and Network Meta-analysis | Dimitris Mavridis*, University of Ioannina, Greece  
Ian R. White, MRC Biostatistics Unit, Cambridge, UK  
Julian PT. Higgins, University of Bristol, UK  
Andrea Cipriani, University of Oxford, UK  
Anna Chaimani and Georgia Salanti, University of Ioannina, Greece |
| 9:20  | Multiple Imputation for Harmonizing Longitudinal Non-Commensurate Measures in Individual Participant Data Meta-Analysis | Juned Siddique*, Northwestern University  
Jerome P. Reiter, Duke University  
Ahnalee Brincks, University of Miami  
Robert D. Gibbons, University of Chicago  
Catherine M. Crespi, University of California, Los Angeles  
C. H. Brown, Northwestern University |
| 9:45  | Bayesian Inference for Multivariate Meta-regression with a Partially Observed Within-Study Sample Covariance Matrix | Hui Yao, Ernst & Young  
Sungduk Kim*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health  
Ming-Hui Chen, University of Connecticut  
Joseph G. Ibrahim, University of North Carolina, Chapel Hill  
Arvind Shah and Jianxin Lin, Merck |
| 10:10 | Floor Discussion                                                      |                                                                            |
## Modeling High Dimensional Space-Time Data with Applications to Neuroimaging

**Sponsor:** IMS, ENAR  
**Organizer:** Hernando Ombao, University of California, Irvine  
**Chair:** Ciprian Crainiceanu, Johns Hopkins University

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<tr>
<th>Time</th>
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| 8:30   | **Estimating Information Flow in Large Brain Networks via Convex Optimization**  
         | Xi Luo* and Yi Zhao, Brown University                                      |
| 8:55   | **A Scalable Multi-resolution Model for Activation and Brain Connectivity in fMRI Data**  
         | Stefano Castruccio*, Newcastle University  
         | Hernando Ombao, University of California, Irvine  
         | Marc Genton, King Abdullah University of Science and Technology, Saudi Arabia |
| 9:20   | **A Novel Multiscale Methodology for Multimodal Data Integration**  
         | John Aston and Jean-Marc Freyermuth*, University of Cambridge  
         | Hernando Ombao, University of California, Irvine                          |
| 9:45   | **Robust Clustering Methods for Time-Evolving Brain Signals**  
         | Tianbo Chen and Ying Sun*, King Abdullah University of Science and Technology, Saudi Arabia  
         | Hernando Ombao, University of California, Irvine  
         | Carolina Euan, Centro de Investigación en Matemáticas, Mexico               |

### 74. CONTRIBUTED PAPERS: Bayesian Hierarchical Modeling

**Sponsor:** ENAR  
**Chair:** Sally Thurston, University of Rochester

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<th>Time</th>
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| 8:30   | **Bayesian Mixed-Effects Varying-Coefficient Joint Models for Skewed Longitudinal Data with Application to AIDS Clinical Studies**  
         | Tao Lu*, State University of New York, Albany                             |
| 8:45   | **Modelling Pulsatile Hormone Associations with Cox Cluster Models**  
         | Huayu Liu*, Nichole E. Carlson and Alex J. Polotsky, University of Colorado, Anschutz Medical Campus |
| 9:00   | **A Bayesian Formulation for Capturing Population Heterogeneity**  
         | Junxian Geng* and Elizabeth Slate, Florida State University               |
| 9:15   | **Bayesian Hierarchical Modeling to Determine Substate Reporting Areas**  
         | Tianyi Cai* and Francesca Dominici, Harvard School of Public Health  
         | Alan Zaslavsky, Harvard Medical School                                     |
| 9:30   | **Spatial-Temporal Survival Analysis on Prostate Cancer in Pennsylvania Using Bayesian Accelerated Failure Time Models**  
         | Zheng Li* and Ming Wang, Penn State College of Medicine  
         | Stephen A. Matthews, Penn State Hershey Cancer Institute  
         | Khaled Iskandarani, Penn State College of Medicine  
         | Yimei Li, University of Pennsylvania  
         | Vernon M. Chinchilli, Penn State College of Medicine                      |
| 9:45   | **Hierarchical Multivariate Space-Time Methods for Modeling Counts with an Application to Stroke Mortality Data**  
         | Harrison Quick*, Centers for Disease Control and Prevention  
         | Lance A. Waller, Emory University  
         | Michele Casper, Centers for Disease Control and Prevention                |
| 10:00  | Floor Discussion                                                        |
### 75. CONTRIBUTED PAPERS: Epidemiologic Methods

**Sponsor:** ENAR  
**Chair:** Ran Tao, University of North Carolina, Chapel Hill

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<tr>
<th>Time</th>
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<tbody>
<tr>
<td>8:30</td>
<td>Accounting for Informed Presence in the Analysis of Electronic Health Records</td>
<td>Benjamin A. Goldstein*, Nrupen Bhavsar, Duke University</td>
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<td>Matthew Phelan, Duke Clinical Research Institute</td>
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<td>Michael J. Pencina, Duke University</td>
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<td>8:45</td>
<td>Spatial Patterning of Diabetes in Durham, North Carolina: A Bayesian Analysis of</td>
<td>Mercedes A. Bravo*, Rebecca Anthopolos, Children’s Environmental Health Initiative, University of Michigan</td>
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<td>Associations with Individual and Neighborhood Characteristics</td>
<td>Marie Lynn Miranda, Rice University</td>
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<td>9:00</td>
<td>The Associations of Drugs with Acute Myocardial Infarction: Bias Correction, Global</td>
<td>Changyu Shen, Xiao Chun Li and Jia Zhan*, Indiana University School of Medicine and</td>
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<td>Profiling and Inference on Individual Drug</td>
<td>School of Public Health</td>
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<td>9:15</td>
<td>Approximate Bayesian Computation for Compartamental Epidemic Models - Methods and Software</td>
<td>Grant D. Brown*, University of Iowa</td>
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<td>Aaron T. Porter, Colorado School of Mines</td>
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<td>Jacob J. Oleson, University of Iowa</td>
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<td>9:30</td>
<td>Proportional Hazards Regression for Interval-Censored Failure Time Data in Case-Cohort</td>
<td>Qingning Zhou*, Haibo Zhou and Jianwen Cai, University of North Carolina, Chapel Hill</td>
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<td>9:45</td>
<td>Bias and Artifact Trade-Off in Modeling Temporal Trend of Archived Data with Applications</td>
<td>Martina Fu, Stanford University</td>
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<td>to Public Health Studies, Demography, Marketing Research and Sociology</td>
<td>David Todem, Michigan State University</td>
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<td>Wenjiang Fu*, University of Houston</td>
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<td>Shuangge Ma, Yale University</td>
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<td>10:00</td>
<td>Floor Discussion</td>
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### 76. CONTRIBUTED PAPERS: GWAS: Applications

**Sponsor:** ENAR  
**Chair:** Naomi Brownstein, Florida State University

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<tbody>
<tr>
<td>8:30</td>
<td>Shrinkage-Based Genome Wide Association Analyses Based on Sparse Versus Gaussian Priors</td>
<td>Chunyu Chen*, Juan P. Steibel and Robert J. Tempelman, Michigan State University</td>
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<td>8:45</td>
<td>An Exposure-Weighted Score Test for Genetic Associations Integrating Environmental</td>
<td>Summer S. Han*, Stanford University</td>
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<td>Risk Factors</td>
<td>Philip S. Rosenberg, National Cancer Institute, National Institutes of Health</td>
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<td>Arpita Ghosh, Public Health Foundation of India</td>
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<td>Maria Teresa Landi and Neil E. Caporaso, National Cancer Institute, National Institutes of Health</td>
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<td>Nilanjan Chatterjee, Johns Hopkins University</td>
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<tr>
<td>9:00</td>
<td>Detecting Shared Genetic Variants Between Two Diseases with Dependent SNPs</td>
<td>Wanjie Wang*, Tony Cai, and Hongzhe Li, University of Pennsylvania</td>
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</table>
9:15  Detection of Signal Regions in Whole Genome Association Studies  
Zilin Li*, Tsinghua University and Harvard School of Public Health  
Xihong Lin, Harvard School of Public Health

9:30  A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits  
Chi-Yang Chiu* and Ruzong Fan, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health  
Jeesun Jung, National Institute on Alcohol Abuse and Alcoholism, National Institutes of Health  
Daniel E. Weeks, University of Pittsburgh  
Alexander F. Wilson, National Human Genome Research Institute, National Institutes of Health  
Joan E. Bailey-Wilson, National Human Genome Research Institute, National Institutes of Health  
James L. Mills, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

9:45  The Correction of Cell-Type Composition in Epigenome-Wide Association Studies  
Shaoyu Li*, University of North Carolina, Charlotte

10:00  Floor Discussion

77. CONTRIBUTED PAPERS: Missing Data  
Sponsor: ENAR  
Chair: Recai Yucel, State University of New York, Albany

8:30  Estimating the Marginal Effect of Interventions to Reduce Spread of Communicable Diseases: What Can be Gained from Contact Network Information?  
Melanie Prague*, Patrick Staples, JP Onnela, Eric Tchetgen Tchetgen and Victor De Gruttola, Harvard School of Public Health

8:45  A Double Robust Semiparametric Method to Account for Missing Confounder Data  
Katherine L. Evans*, Harvard University  
Eric Tchetgen Tchetgen, Harvard School of Public Health

9:00  On Inverse Probability Weighting for Nonmonotone Missing at Random Data  
BaoLuo Sun* and Eric Tchetgen Tchetgen, Harvard School of Public Health

9:15  Maximum Likelihood Estimation in a Semicontinuous Regression Model with a Covariate Subject to a Detection Limit  
Paul W. Bernhardt*, Villanova University

9:30  Feasibility of Variable-By-Variable Imputation in Clustered Data with Multiple Membership  
Tugba Akkaya-Hocagil* and Recai M. Yucel, State University of New York, Albany

9:45  Mixed-Effects Models for Multivariate Clustered Data with Nonignorable Missing Outcomes  
Jiebiao Wang*, University of Chicago  
Pei Wang, Icahn Medical School at Mount Sinai  
Lin S. Chen, University of Chicago

10:00  A Simple Method of Estimating the Odds Ratio with Incomplete Data in 1:N Matched Case-Control Studies  
Chan Jin and Stephen W. Looney*, Augusta University
### 78. CONTRIBUTED PAPERS: Semi-Parametric and Non-Parametric Survival

**Sponsor:** ENAR  
**Chair:** Thomas Murray, University of Texas MD Anderson Cancer Center

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<tr>
<td>8:30</td>
<td>Regression Analysis of Current Status Data with Generalized Odds-Rate Hazards Models</td>
<td>Bin Yao* and Lianming Wang, University of South Carolina</td>
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<td>8:45</td>
<td>A Joint Model of Cancer Incidence, Metastasis, and Mortality</td>
<td>Qui Tran*, Kelley M. Kidwell and Alex Tsodikov, University of Michigan</td>
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</table>
| 9:00  | Proportional Subdistribution Hazards Regression with Interval-Censored Competing Risks Data | Yi Ren*, U.S. Food and Drug Administration  
Chung-Chou Chang, University of Pittsburgh  
Ruoshua Li, University of Texas Health Science Center, Houston |
| 9:15  | Tuning Parameter Selection in Cox Proportional Hazards Model with a Diverging Number of Parameters | Ai Ni*, Memorial Sloan Kettering Cancer Center  
Jianwen Cai, University of North Carolina, Chapel Hill                                        |
| 9:30  | Permutation Test for General Dependent Truncation                    | Sy Han Chiu*, Harvard School of Public Health  
Jing Qian, University of Massachusetts, Amherst  
Rebecca Betensky, Harvard School of Public Health                                               |
| 9:45  | Semiparametric Modeling and Analysis of Paired Longitudinal Method Comparison Data | Lasitha N. Rathnayake* and Pankaj K. Choudhary, University of Texas, Dallas                   |
| 10:00 | Semiparametric Estimation of the Accelerated Failure Time Model with Partly Interval-Censored Data | Fei Gao*, Donglin Zeng and Danyu Lin, University of North Carolina, Chapel Hill               |

### 79. CONTRIBUTED PAPERS: Study Design

**Sponsor:** ENAR  
**Chair:** Xavier De Luna, Umeå University

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| 8:30  | Value-Driven Optimization of Study Design and Go/No Go Decision at POC Stage: A Program Level Simulation Approach | Masanori Ito*, Astellas Pharma Global Development Inc.  
Nitin Patel, Cytel Inc.                                                                 |
| 8:45  | A Revisit to Two-Way Factorial ANOVA for Unbalanced Data             | Tao Wang*, Medical College of Wisconsin                                                        |
| 9:00  | Exposure Enriched Case-Control (EECC) Design for the Assessment of Gene-Environment Interaction | Md Hamidul Huque*, University of Technology Sydney, Australia  
Raymond J. Carroll, Texas A&M University  
Nancy Diao and David C. Christiani, Harvard School of Public Health  
Louise M. Ryan, University of Technology Sydney, Australia |
<p>| 9:15  | Sample Size Calculations for Stratified Micro-Randomized Trials in mHealth | Walter Dempsey*, Peng Liao and Susan Murphy, University of Michigan                         |
| 9:30  | Compound Criteria for Constructing Efficient and Flexible Designs | Luzia A. Trinca*, Universidade Estadual Paulista, Brasil (UNESP)                             |</p>
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<tr>
<td>9:45</td>
<td>SeqDesign: A Framework for RNA-Seq Genome-Wide Power Calculation and</td>
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<td>Experimental Design Issues</td>
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<td>Chien-Wei Lin*^, Serena G. Liao and George C. Tseng, University of</td>
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<td>Pittsburgh</td>
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<td>10:00</td>
<td>Statistical Considerations in Designing Precision Study for Optical</td>
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<td>Coherence Tomography Device</td>
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<td>Haiwen Shi*, U.S. Food and Drug Administration</td>
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<td>10:15 - 10:30 am</td>
<td>Refreshment Break with Our Exhibitors</td>
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<td>10:30 am - 12:15 pm</td>
<td>Presidential Invited Address</td>
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<td>80.</td>
<td>Biostatistics, Biomedical Informatics, and Health Data Science: Research</td>
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<td>Sponsor: ENAR</td>
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<td>Organizer &amp; Chair: Jianwen Cai, University of North Carolina, Chapel</td>
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<td>Hill</td>
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<td>Biostatistics, Biomedical Informatics, and Health Data Science: Research</td>
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<td>Xihong Lin, Ph.D., Chair and Henry Pickering Walcott Professor,</td>
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<td>Department of Biostatistics, Harvard University</td>
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<td>1:45 - 3:30 pm</td>
<td>Oral Presentations</td>
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<td>81.</td>
<td>New Developments for Individualized Medical Decision Making in Real</td>
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<td>Sponsors: ENAR, ASA Biometrics Section, ASA Mental Health Statistics</td>
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<td>Organizer: Yuanjia Wang, Columbia University</td>
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<td>Chair: Bei Jiang, University of Alberta</td>
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<td>1:45</td>
<td>Dynamic Systems for Identifying Biomarkers Predicting Landmarks of</td>
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<td>Disease Degeneration</td>
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<td>Yuanjia Wang*, Columbia University</td>
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<td>2:10</td>
<td>Model Validation and Selection in G-estimation of Dynamic Treatment</td>
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<td>Erica E. M. Moodie*, Michael P. Wallace and David A. Stephens, McGill</td>
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<td>2:35</td>
<td>Learning Optimal Personalized Treatment Rules in Benefit-Risk Analysis</td>
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<td>Yuanjia Wang, Columbia University</td>
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<td>Haoda Fu, Eli Lilly and Company</td>
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<td>Donglin Zeng*, University of North Carolina, Chapel Hill</td>
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<tr>
<td>3:00</td>
<td>Building Personalized Treatment Strategy with Binary Outcomes</td>
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<td>Min Qian*, Columbia University</td>
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<td>Eric Laber, North Carolina State University</td>
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<td>3:25</td>
<td>Floor Discussion</td>
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82. Emerging Issues in Clinical Trials with Time-to-Event Data in the Presence of Competing Risks

**Sponsors:** ENAR, ASA Biopharmaceutical Section

**Organizer:** Qingxia Chen, Vanderbilt University

**Chair:** Julie Cong, Boehringer Ingelheim Pharmaceuticals, Inc.

1:45 A Bayesian Cure Rate Frailty Model for Survival Data in Presence of Semi-competing and Competing Risks

Mario de Castro, Universidade de Sao Paulo, Brasil

Ming-Hui Chen*, University of Connecticut

Anthony V. D’Amico, Harvard University and Brigham and Women’s Hospital

2:10 Treatment Effect Estimate and Model Diagnostics with Time-Varying Treatment Switching

Qingxia Chen*, Vanderbilt University

Fan Zhang and Ming-Hui Chen, University of Connecticut

Xiuyu Julie Cong, Boehringer Ingelheim Pharmaceuticals, Inc.

2:35 Regression Analysis for Cumulative Incidence Function under Two-stage Randomization

Idil Yavuz, Dokuz Eylul University, Turkey

Ling-Wan Chen, Yu Cheng* and Abdus Wahed, University of Pittsburgh

3:00 Penalized Variable Selection in Competing Risks Regression

Zhixuan Fu and Chirag Parikh, Yale University

Bingqing Zhou*, Novartis and Yale University

3:25 Floor Discussion

83. New Development of Statistical Methods for Family-Based Sequencing Studies

**Sponsors:** ENAR, ASA Statistics in Genomics and Genetics

**Organizers:** Wei Chen, Children’s Hospital of Pittsburgh of the University of Pittsburgh Medical Center and Bingshan Li, Vanderbilt University

**Chair:** Wei Chen, Children’s Hospital of Pittsburgh, University of Pittsburgh Medical Center

1:45 Rare-variant Association Testing of Complex Disease in Pedigrees Using Identity-by-Descent Information

Michael P. Epstein*, Emory University School of Medicine

Glen A. Satten, Centers for Disease Control and Prevention

2:10 Searching Rare Variants under Complex Traits Leveraging on Linkage Evidence

Xiaofeng Zhu*, Case Western Reserve University

2:35 Gene-Based Association Testing of Dichotomous Traits Using Generalized Functional Linear Mixed Models for Family Data

Yingda Jiang*, University of Pittsburgh

Chi-Yang Chiu and Ruzong Fan, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

Qi Yan and Wei Chen, Children’s Hospital of Pittsburgh of the University of Pittsburgh Medical Center

Michael B. Gorin, University of California, Los Angeles

Yvette P. Conley and Daniel E. Weeks, University of Pittsburgh

3:00 A Bayesian Framework for de novo Mutation Calling in Family Sequencing Data

Qiang Wei, Rui Chen and Xue Zhong, Vanderbilt University

Yongzhuang Liu, Harbin Institute of Technology

Xiaowei Zhan, University of Texas Southwestern

Wei Chen, University of Pittsburgh

Bingshan Li*, Vanderbilt University

3:25 Floor Discussion
### New Developments of Quantile Regression for Complex Data Analysis: Theories and Applications

**Sponsors:** ENAR, ASA Statistics in Genomics and Genetics  
**Organizers:** Linglong Kong, University of Alberta and Peisong Han, University of Waterloo  
**Chair:** Linglong Kong, University of Alberta

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Presenters</th>
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| 1:45  | Partially Linear Additive Quantile Regression in Ultra-high Dimension | Ben Sherwood, John Hopkins University  
Lan Wang*, University of Minnesota |
| 2:10  | Model Selection for Quantile Regression with Varying Covariate Effects | Qi Zheng, University of Louisville  
Limin Peng*, Emory University |
| 2:35  | Regularized Quantile Regression under Heterogeneous Sparsity with Application to Quantitative Genetic Traits | Chad He*, Fred Hutchinson Cancer Research Center  
Linglong Kong, University of Alberta  
Yanhua Wang, Beijing Institute of Technology  
Sijian Wang, University of Wisconsin, Madison  
Timothy Chan, Memorial Sloan-Kettering Cancer Center  
Eric Holland, Fred Hutchinson Cancer Research Center |
| 3:00  | Some Aspects of Regularization in Quantile Regression                | Ivan Mizera*, University of Alberta |
| 3:25  | Floor Discussion                                                     |                                                                            |

### Current Developments and Issues for Meta-Analysis

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology  
**Organizer:** Yong Chen, University of Texas School of Public Health  
**Chair:** Haitao Chu, University of Minnesota

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<th>Time</th>
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<tr>
<td>1:45</td>
<td>Some Recent Theoretical Results on Meta-Analysis</td>
<td>Danyu Lin*, University of North Carolina, Chapel Hill</td>
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<tr>
<td>2:10</td>
<td>Adaptively Weighted Meta-analysis in-omics Applications</td>
<td>Zhiguang Huo, Yongseok Park and George Tseng*, University of Pittsburgh</td>
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<tr>
<td>2:35</td>
<td>Network Meta-Analysis for Diagnostic Accuracy</td>
<td>Thomas Trikalinos*, Wei Cheng, Constantine Gatsonis and Christopher Schmid, Brown University</td>
</tr>
</tbody>
</table>
| 3:00  | A Novel Method for Correcting Publication Bias in Multivariate Meta-analysis | Yong Chen*, University of Pennsylvania  
Chuan Hong, University of Texas Health Science Center, Houston  
Haitao Chu, University of Minnesota |
| 3:25  | Floor Discussion                                                     |                                                                            |

### Survival Prediction Models for Medical Decision Making

**Sponsors:** ENAR, ASA Biometrics Section  
**Organizer & Chair:** Jing Ning, University of Texas MD Anderson Cancer Center

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<th>Time</th>
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<tr>
<td>1:45</td>
<td>Evaluation of Biomarkers for Prediction of Clinical Events: Connection to Information Theory</td>
<td>Patrick J. Heagerty*, University of Washington</td>
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* Presenter  
^ Student Award Winner
2:10  **Dynamic Prediction of Time-to-Event Distributions**  
Xuelin Huang*, University of Texas MD Anderson Cancer Center  
Fangrong Yan,  
China Pharmaceutical University & University of Texas MD Anderson Cancer Center  
Jing Ning and Ziding Feng, University of Texas MD Anderson Cancer Center

2:35  **Robust Learning of Optimal Treatment Regimes for Survival Endpoints**  
Runchao Jiang, Facebook  
Wenbin Lu* and Rui Song, North Carolina State University  
Michael Hudgens and Sonia Napravnik, University of North Carolina, Chapel Hill

3:00  **An Analytical Framework for Building and Evaluating Landmark Models for Dynamic Prediction of Survival Using Longitudinal Data**  
Liang Li*, University of Texas MD Anderson Cancer Center  
Sheng Luo, University of Texas Health Science Center, Houston  
Bo Hu, Cleveland Clinic  
Tom Greene, University of Utah

3:25  **Floor Discussion**

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87.  **Statistical Machine Learning for Big-Bio-Data**  
**Sponsors:** IMS, ENAR  
**Organizer & Chair:** Genevra Allen, Rice University

1:45  **Estimation of Directed Acyclic Graphs using BIC under Path Restrictions**  
George Michailidis*, University of Florida

2:10  **Spatially Relating Developmental Transcription Factors Using Drosophila Embryonic Gene Expression Images**  
Karl Kumbier*, Siqi Wu and Antony Joseph, University of California, Berkeley  
Ann Hammonds, William Fisher, Richard Weiszmann and Sue Celniker, Lawrence Berkeley National Laboratory  
Bin Yu, University of California, Berkeley  
Erwin Frise, Lawrence Berkeley National Laboratory

2:35  **Estimating False Inclusion Rates in Penalized Regression Models**  
Patrick Breheny*, University of Iowa

3:00  **Toward Personalized Pan-Omic Association Analysis under Complex Structures**  
Eric P. Xing*, Carnegie Mellon University

3:15  **Floor Discussion**

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88.  **CONTRIBUTED PAPERS: Causal Inference**  
**Sponsor:** ENAR  
**Chair:** Adam King, California State Polytechnic University, Pomona

1:45  **A Cautionary Tale: Mediation Analysis Applied to Censored Survival Data**  
Isabel R. Fulcher*, Eric J. Tchetgen Tchetgen and Paige L. Williams, Harvard University

2:00  **Simpler Approach for Mediation Analysis for Dichotomous Mediators in Logistic Regression**  
Hani Samawi, Jingxian Cai*, Harash Rochani and Daniel Linder, Georgia Southern University

2:15  **Propensity Score and Doubly Robust Methods for Estimating the Effect of Treatment on Censored Cost**  
Jiaqi Li* and Nandita Mitra, University of Pennsylvania
### 89. CONTRIBUTED PAPERS: Functional Data Analysis

**Sponsor:** ENAR  
**Chair:** Adam Ciarleglio, New York University

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<tr>
<td>1:45</td>
<td>Single-Index Models for Function-On-Function Regression</td>
<td>Guanqun Cao*, Auburn University, Lily Wang, Iowa State University</td>
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<td>2:00</td>
<td>Multivariate Multiscale Functional Data Analysis</td>
<td>Andrew N. Potter* and Stewart J. Anderson, University of Pittsburgh</td>
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<tr>
<td>2:15</td>
<td>Ordinal Probit Wavelet-Based Functional Models for eQTL Analysis</td>
<td>Mark J. Meyer*, Bucknell University, Jeffrey S Morris, University of Texas MD Anderson Cancer Center, Craig P. Hersh and Jarrett D. Morrow, Brigham and Women’s Hospital, Christoph Lange and Brent A. Coull, Harvard School of Public Health</td>
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<tr>
<td>2:30</td>
<td>Optimal Design for Sparse Functional Data</td>
<td>So Young Park* and Luo Xiao, North Carolina State University, Jayson Wilbur, Metrum Research Group LLC, Ana-Maria Staicu, North Carolina State University</td>
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<tr>
<td>2:45</td>
<td>Detecting Outliers in Images of DNA Molecules Using Functional Data Depth and Morphological Features</td>
<td>Subhrangshu Nandi*, University of Wisconsin, Madison, Alicia Nieto-Reyes, Universidad de Cantabria, Chengyue Wu, University of Science and Technology of China, Michael A. Newton, University of Wisconsin, Madison</td>
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<tr>
<td>3:00</td>
<td>A Bayesian Wavelet Based Analysis of Longitudinally Observed Skewed Heteroscedastic Response</td>
<td>Danisha S. Baker*, Eric Chicken, Debajyoti Sinha and Debdeep Pati, Florida State University</td>
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<tr>
<td>3:15</td>
<td>Floor Discussion</td>
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### 90. CONTRIBUTED PAPERS: High Dimensional Variable Selection

**Sponsor:** ENAR  
**Chair:** Andy Ni, Memorial Sloan Kettering Cancer Center

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<th>Time</th>
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<tbody>
<tr>
<td>1:45</td>
<td>An Efficient Method for Variable Selection in Linear and Nonlinear Models</td>
<td>Arnab K. Maity* and Sanjib Basu, Northern Illinois University</td>
</tr>
</tbody>
</table>
2:00 Covariance-Insured Screening Methods for Ultrahigh Dimensional Variable Selection
Kevin He*, Yi Li and Ji Zhu, University of Michigan
Jiashun Jin, Carnegie Mellon University
Yanming Li and Jian Kang, University of Michigan
Hyokyoung (Grace) Hong, Michigan State University

2:15 A Data-Driven Approach to Conditional Screening of High Dimensional Variables
Hyokyoung (Grace) Hong*, Michigan State University
Lan Wang, University of Minnesota
Xuming He, University of Michigan

2:30 Selection-Assisted Smoothed Partial Regression Estimation and Inference for High-Dimensional Linear Model
Zhe Fei*, Yi Li and Ji Zhu, University of Michigan

2:45 On High Dimensional Inference
Qiang Sun* and Heping Zhang. Yale University

3:00 A New Class of Measures for Testing Independence
Xiangrong Yin and Qingcong Yuan*, University of Kentucky

3:15 Distributed Inference for High Dimensional Semi-Parametric Elliptical Graphical Models
Lu Tian*, Pan Xu and Quanquan Gu, University of Virginia

91. CONTRIBUTED PAPERS: Nonparametric Methods
Sponsor: ENAR
Chair: Mohammed Chowdhury, Kennesaw State University

1:45 Notes on Kernel Based Mode Estimation Using More Efficient Sampling Designs
Hani Samawi*, Haresh Rochani, JingJing Yin, Daniel Linder and Robert Vogel, Georgia Southern University

2:00 An Exact Test of Fit for the Gaussian Linear Model Using Optimal Nonbipartite Matching
Samuel D. Pimentel*, Dylan S. Small and Paul R. Rosenbaum, University of Pennsylvania

2:15 Non-Inferiority Test Based on Transformations for Non-Normal Distributions
Santu Ghosh*, Georgia Regents University
Arpita Chatterjee, Georgia Southern University
Samiran Ghosh, Wayne State University

2:30 Nonparametric Multivariate Change-Point: Estimation and Testing of Existence
Sebastian J. Teran Hidalgo* and Michael R. Kosorok, University of North Carolina, Chapel Hill
Michael C. Wu, Fred Hutchinson Cancer Research Center

2:45 Adjusted Empirical Likelihood Method for Treatment Comparisons in Linear Models
Haiyan Su* and Xi Kang, Montclair State University
Wei Ning, Bowling Green State University

3:00 Penalised Spline Estimation for Generalised Partially Linear Single-Index Models
Yuankun Zhang* and Yan Yu, University of Cincinnati
Chaojiang Wu, Drexel University

3:15 Floor Discussion
92. CONTRIBUTED PAPERS: Spatiotemporal Modeling  
Sponsor: ENAR  
Chair: Michael Regier, West Virginia University

1:45  Modelling Nonlinear Lagged Effects with Spatial Heterogeneity  
Lung-Chang Chien*, University of Texas School of Public Health, San Antonio  
Kai Zhang, University of Texas School of Public Health, Houston  
Yuming Guo, University of Queensland School of Public Health  
Hwa-Lung Yu, National Taiwan University

2:00  Stepwise And Stagewise Approaches for Spatial Cluster Detection  
Jiale Xu and Ronald Gangnon*, University of Wisconsin

2:15  A Spatio-Temporal Approach for Modeling the Effects of Weather and Climate on Malaria Distributions in West Africa  
Ali Arab*, Georgetown University  
Monica Jackson, American University  
Cezar Kongoli, University of Maryland, and National Oceanic and Atmospheric Administration (NOAA), National Environmental Satellite Data and Information Service (NESDIS)

2:30  An Uncertainty Quantification Approach for Deterministic Spatial Interpolations  
Robert J. Waken*, Baylor University  
Soohyun Kwon and GyuWon Lee, Kyungpook National University  
Joon Song, Baylor University

2:45  Modeling High Dimensional Multichannel Electroencephalograms  
Lechuan Hu* and Hernando Ombao, University of California, Irvine

3:00  Non-Separable Dynamic Nearest-Neighbor Gaussian Process Models for Large Spatio-Temporal Data with an Application to Particulate Matter Analysis  
Abhirup Datta**, University of Minnesota  
Sudipto Banerjee, University of California, Los Angeles  
Andrew O. Finley, Michigan State University  
Nicholas A.S. Hamm, University of Twente  
Martijn Schaap, TNO Built Environment and Geosciences

3:15  An Exploratory Coherence Analysis of Electroencephalograms using the Functional Boxplots Approach  
Duy Ngo** and Hernando Ombao, University of California, Irvine

93. CONTRIBUTED PAPERS: Survival Analysis: Multivariate and Hierarchical  
Sponsor: ENAR  
Chair: Paul Bernhardt, Villanova University

1:45  Circulatory Disease Mortality in a Pooled Analysis of the Massachusetts and Canadian Tuberculosiis Fluoroscopy Cohorts  
Van Tran*, National Cancer Institute, National Institutes of Health  
Lydia B. Zablotska, University of California, San Francisco  
Alina V. Brenner and Mark P. Little, National Cancer Institute, National Institutes of Health

2:00  A Joint Frailty Model for Zero-Inflated Recurrent Events and a Terminal Event in a Matched Study  
Cong Xu*, Ming Wang and Vernon Chinchilli, The Pennsylvania State University

2:15  A Three-State Markov Frailty Model for Interval Censored Caries Life History Data  
Daewoo Pak*, Chenxi Li and David Todem, Michigan State University

2:30  A Score Test for Copula-Based Bivariate Survival Model, with an Application to Genome-Wide Analysis for Progression of Age-Related Macular Degeneration  
Yi Liu*, Ying Ding and Wei Chen, University of Pittsburgh
2:45 Mixture Models for Left-Censored and Irregularly-Censored Data: Applications to a Cancer Screening Cohort Assembled from Electronic Health Records
Li C. Cheung* and Qing Pan, George Washington University
Noorie Hyun, National Cancer Institute, National Institutes of Health
Barbara Fetterman, Kaiser Permanente, Northern California
Philip E. Castle, Albert Einstein School of Medicine
Hormuzd A. Katki, National Cancer Institute, National Institutes of Health

3:00 Regression Analysis of Interval Censored Data in the Presence of Cured Subgroup and Mismeasured Covariates
Yeqian Liu*, University of Missouri, Columbia
Tao Hu, Capital Normal University
Jianguo Sun, University of Missouri, Columbia

3:15 Accounting for Heterogeneity When Evaluating Surrogate Endpoints in a Discrete-Time Survival Model
Andrew J. Spieker*, University of Washington
Ying Huang, Fred Hutchinson Cancer Research Center

3:30 - 3:45 pm Refreshment Break with Our Exhibitors

3:45 - 5:30 pm Oral Presentations

94. Some New Developments in the Modern Longitudinal Data Analysis
Sponsors: ENAR, ASA Biometrics Section
Organizer & Chair: Shengchun Kong, Purdue University

3:45 Marginal Regression Model for Longitudinal Network Data
Yan Zhou, Merck & Co.
Peter X.K. Song*, University of Michigan

4:10 Multivariate Semi-continuous Two Part Fixed Effects Models
Yaoguo Xie*, Zhengjun Zhang*, Paul Rathouz and Bruce Barrett, University of Wisconsin, Madison

4:35 Generalized Additive Partial Linear Models for Clustered Data with Diverging Number of Covariates Using GEE
Hua Liang*, George Washington University
Heng Lian, University of New South Wales, Australia
Lan Wang, University of Minnesota

5:00 The Modeling of Medical Expenditure Data from a Longitudinal Survey using the Generalized Method of Moments (GMM) Approach
Zachary Hass and Michael Levine*, Purdue University
Laura P. Sands, Virginia Tech
Jeffrey C.-Y. Ting, American Credit Acceptance
Huiping Xu, Indiana University Purdue University, Indianapolis

5:25 Floor Discussion

95. Statistical Considerations in Personalized Medicine: Concept and Methodology
Sponsors: ENAR, ASA Biometrics Section
Organizers: Jincao Wu, Yaji Xu and Haiwen Shi, U.S. Food and Drug Administration
Chair: Jincao Wu, U.S. Food and Drug Administration

3:45 The Impact of Companion Diagnostic Device Measurement Performance on Clinical Validation of Personalized Medicine
Meijuan Li*, Tinghui Yu and Yun-Fu Hu, U.S. Food and Drug Administration
4:10 Personalized Oncology in 2015: New Paradigms in Clinical Trial Methodology
Richard Macey Simon*, National Cancer Institute, National Institutes of Health

4:35 Bias Correction in Estimating the Heterogeneous Treatment Effect in Subgroup Analysis
Lu Tian*, Stanford University
Lee-Jen Wei, Harvard School of Public Health

5:00 The Brave New World of Cancer Clinical Trials: Learning Who Benefits from What?
Donald Berry*, University of Texas MD Anderson Cancer Center

5:25 Floor Discussion

**96. Innovative Techniques Towards Solving the Complexities of Biomarker Discovery**
Sponsor: ENAR
Organizer: Tanya Garcia, Texas A&M University
Chair: Siying Li, University of North Carolina, Chapel Hill

3:45 Designing Disease Elimination Strategies using Models and Data from Multiple Sources
John M. Marshall*, University of California, Berkeley

4:10 Analysis of Proportional Hazards Model with Sparse Time-Dependent Covariates
Jason Fine*, University of North Carolina, Chapel Hill

4:35 A Multi-Step Classifier Identifies Cohort Heterogeneity in Cancers Leading to Improved Accuracy of Prognostic Biomarkers
Samuel Mueller*, University of Sydney
Ellis Patrick, Harvard Medical School
Jean Yang, University of Sydney

5:00 Cox Regression with Exclusion Frequency-based Weights to Identify Neuroimaging Markers Relevant to Huntington’s Disease Onset
Tanya P. Garcia*, Texas A&M University
Samuel Mueller, University of Sydney

5:25 Floor Discussion

**97. New Developments of Bayesian Methods for Causal Inference**
Sponsors: ENAR, ASA Bayesian Statistical Science Section, ASA Section on Statistics in Epidemiology
Organizer & Chair: Bo Lu, The Ohio State University

3:45 A Nonparametric Bayesian Approach for Estimating the Average Causal Effect
Bo Lu, Steven N. MacEachern* and Ling Wang, The Ohio State University

4:15 Bayesian Inference about Causal Effects in the Presence of Unmeasured Confounding
Joseph W. Hogan* and Allison K. DeLong, Brown University
Michael J. Daniels, University of Texas, Austin

4:45 A Bayesian Nonparametric Approach to Marginal Structural Models for Point Treatments and a Continuous or Survival Outcome
Jason Roy* and Kirsten Lum, University of Pennsylvania
Michael J. Daniels, University of Texas, Austin

5:15 Discussant:
Michael Rosenblum, Johns Hopkins University
| 98. | **Integrative Analysis of Multi-OMIC Data for Understanding Complex Human Diseases**  
**Sponsors:** ENAR, ASA Statistics in Genomics and Genetics  
**Organizer & Chair:** Yijuan Hu, Emory University |
|---|---|
| **3:45** | **Longitudinal Gaussian Graphical Models Integrate Gene Expression and Sequencing Data for Autism Risk Gene Detection**  
Kevin Lin, Carnegie Mellon University  
Han Liu, Princeton University  
Kathryn Roeder*, Carnegie Mellon University |
| **4:10** | **Prioritization of Disease-Causing Genetic Variants Through Integrated Analysis of Association Signals and Genomic Functional Annotation**  
Qiongshi Lu, Ryan Powles, Xinwei Yao, Yiming Hu, Jiehuan Sun, Yuwei Cheng, Kei Cheung, Qian Wang, Beixin He and Hongyu Zhao*, Yale University |
| **4:35** | **Integrated Analysis of DNA Methylation, Genetic Variation, and Gene Expression Data in Human Aging**  
Karen N. Conneely*, Elizabeth M. Kennedy, Lynn M. Almli and Alicia K. Smith, Emory University School of Medicine  
Elisabeth B. Binder, Max Planck Institute of Psychiatry and Emory University School of Medicine  
Kerry J. Ressler, Harvard Medical School and Emory University School of Medicine |
| **5:00** | **Integrative Multi-omic Analysis of X Chromosome Inactivation in Epithelial Ovarian Cancer**  
Nicholas B. Larson*, Stacey J. Winham, Zach Fogarty and Melissa C. Larson, Mayo Clinic  
Brooke L. Fridley, University of Kansas Medical Center  
Ellen L. Goode, Mayo Clinic |
| **5:25** | **Floor Discussion** |

| 99. | **Analysis of Next-Generation Sequencing Data: Increasing Accuracy and Novel Applications**  
**Sponsors:** ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetic  
**Organizer & Chair:** Sujay Datta, University of Akron |
|---|---|
| **3:45** | **The Next Generation of (Epi-) Genomic Data: Single Cells**  
Faye Zheng and Rebecca W. Doerge*, Purdue University |
| **4:05** | **Dispensing with the Bioinformatics Pipeline: State Space Models for NGS Base-calling and Error Correction**  
Karin S. Dorman*, Xin Yin and Aditya Ramamoorthy, Iowa State University |
| **4:25** | **Can Epigenetic Profiles Predict Genetic Risk for Blood Disorders?**  
Paul Auer**, University of Wisconsin, Milwaukee  
Alex Reiner, Fred Hutchinson Cancer Research Center |
| **4:45** | **Deconvolving Copy Number Profiles of Cancer Genomes using NGS Data**  
Xuefeng Wang*, Stony Brook University |
| **5:05** | **Discussant:**  
Susmita Datta, University of Florida |
### 100. Networks for High Dimensional Time Series

**Sponsors:** IMS, ENAR  
**Organizer:** Ali Shojaie, University of Washington  
**Chair:** Min Jin Ha, University of Texas MD Anderson Cancer Center

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<tr>
<td>3:45</td>
<td>Lag Structured Modeling for High Dimensional Vector Autoregression</td>
<td>William Nicholson, Jacob Bien* and David Matteson, Cornell University</td>
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<td>4:15</td>
<td>Non-Gaussian Estimation for Time Series Sampled at Mixed Frequencies</td>
<td>Alex Tank, Emily Fox* and Ali Shojaie, University of Washington</td>
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<tr>
<td>4:45</td>
<td>Network Reconstruction from High Dimensional Ordinary Differential Equations</td>
<td>Shizhe Chen, Ali Shojaie*, Daniela Witten, University of Washington</td>
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**Discussant:** George Michailidis, University of Florida

### 101. CONTRIBUTED PAPERS: Environmental and Ecological Applications

**Sponsor:** ENAR  
**Chair:** Emily Leary, University of Missouri

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<tr>
<td>3:45</td>
<td>An Adaptive Association Test for Microbiome Data</td>
<td>Chong Wu*, Junghi Kim and Wei Pan, University of Minnesota</td>
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| 4:00  | A Class of Distance Tests for Comparing Environmental Exposure Distributions in Presence of Detection Limits | Yuchen Yang*, Brent Shelton, Richard Kryscio and Tom Tucker, University of Kentucky  
Li Li, Case Western Reserve University  
Li Chen, University of Kentucky |
| 4:15  | Dietary Patterns and Determinants of Mercury and Omega-3 Exposure in Pregnant Women Living in the Seychelles | Tanzy Love*, University of Rochester  
Maria Mulhern, Ulster University  
Sally Thurston, University of Rochester  
Alison Yeates, Ulster University  
Katie Evans, Du Pont  
Maxine Bonham and Emeir McSorley, Ulster University  
Conrad F. Shamlaye, Seychelles  
J. J. Strain, Ulster University  
Philip W. Davidson, University of Rochester |
| 4:30  | Spatial Prediction of Naturally Occurring Indoor Gamma Radiation in Great Britain | Pavel Chernyavskiy, National Cancer Institute, National Institutes of Health  
Gerald M. Kendall, University of Oxford  
Philip S. Rosenberg, National Cancer Institute, National Institutes of Health  
Richard Wakeford, University of Manchester  
Mark P. Little*, National Cancer Institute, National Institutes of Health |
| 4:45  | Bayesian Distributed Lag Interaction Models | Ander Wilson*, Harvard School of Public Health  
Yueh-Hsui Mathilda Chiu and Rosalind Wright, Icahn School of Medicine at Mount Sinai  
Brent Coull, Harvard School of Public Health |
| 5:00  | Estimation of the Effectiveness of Influenza Vaccination from Household Studies | Kylie Ainslie* and Michael Haber, Emory University |
| 5:15  | A Stochastic Epidemic Model to Identify Unobserved Urban Insect Infestations | Erica M.W. Billig*, Jason A. Roy and Michael Z. Levy, University of Pennsylvania |
### 102. CONTRIBUTED PAPERS: Genomics

**Sponsor:** ENAR  
**Chair:** Shaoyu Li, University of North Carolina, Charlotte

#### 3:45 Detecting eQTLs in Megakaryocytes (MKs) Derived from Induced Pluripotent Stem Cells (iPSCs)

Kai Kammers*, Jeffrey T. Leek and Ingo Ruczinski, Johns Hopkins Bloomberg School of Public Health  
Joshua Martin, The GeneSTAR Program, Johns Hopkins School of Medicine  
Margaret A. Taub, Johns Hopkins Bloomberg School of Public Health  
Lisa R Yanek, The GeneSTAR Program, Johns Hopkins School of Medicine  
Linzhao Cheng and Zack Z. Wang, Johns Hopkins School of Medicine  
Rasika A. Mathias and Lewis Becker, The GeneSTAR Program, Johns Hopkins School of Medicine

#### 4:00 Detecting Rare Haplotype-Environment Interaction Under Uncertainty of Gene-Environment Independence Assumption

Yuan Zhang*, University of Texas, Dallas  
Shili Lin, The Ohio State University  
Swati Biswas, University of Texas, Dallas

#### 4:15 A Numerical Method for Likelihood Estimation of Species Trees from Large Genomic Data Using the Coalescent Process

Arindam RoyChoudhury*, Columbia University

#### 4:30 A Statistical Framework for Predictive Modeling of Microbiome Data Integrating the Phylogenetic Tree

Jun Chen* and Jian Xiao, Mayo Clinic

#### 4:45 Promise-Me: A Robust Method for Integrated Analysis of DNA Methylation, Gene Expression, and Multiple Biologically Related Clinical and Pharmacological Outcomes

Xueyuan Cao, Stanley B. Pounds* and Tong Lin, St. Jude Children’s Research Hospital

#### 5:00 Integrated Analysis of Multidimensional (Epi)Genetic Data on Cutaneous Melanoma Prognosis

Yu Jiang*, University of Memphis  
Xingjie Shi, Nanjing University of Finance and Economics, China  
Qing Zhao and Shuangge Ma, Yale University

#### 5:15 Detection of Shared Common Genetic Variants Between Complex Disease Pairs

Julie Kobie**, University of Pennsylvania  
Sihai D. Zhao, University of Illinois, Urbana-Champaign  
Yun R. Li and Hakon Hakonarson, The Children’s Hospital of Philadelphia  
Hongzhe Li, University of Pennsylvania

### 103. CONTRIBUTED PAPERS: Meta-Analysis

**Sponsor:** ENAR  
**Chair:** Santu Ghosh, Georgia Regents University

#### 3:45 Integrative Analysis for Pathway Selection Using Individual Patient Data

Quefeng Li*, University of North Carolina, Chapel Hill  
Menggang Yu and Sijian Wang, University of Wisconsin, Madison

#### 4:00 Alternative Measures of Between-Study Heterogeneity in Meta-Analysis: Reducing the Impact of Outlying Studies

Lifeng Lin**, Haitao Chu and James S. Hodges, University of Minnesota
4:15  Testing for Publication Bias Under the Copas Selection Model in Meta-Analysis  
Yong Chen, University of Pennsylvania  
Jing Ning, University of Texas MD Anderson Cancer Center  
Jin Piao*, University of Texas Health Science Center, Houston

4:30  Parametric Bootstrap to Construct Confidence Intervals for Event Rates or Differences in Rates in Meta-Analyses  
Gaohong Dong*, Novartis Pharmaceuticals Corporation  
Roland Fisch, Novartis Pharma AG  
Jennifer Ng, Novartis Pharmaceuticals Corporation  
Steffen Ballerstedt and Marc Vandemeulebroecke*, Novartis Pharma AG

4:45  Using Meta-Analytic Approaches for Analyzing Non-Converging Clustered Dependent Binary Data  
Aobo Wang* and Roy T. Sabo, Virginia Commonwealth University

5:00  A Lineup Protocol for Funnel Plot Assessment in Meta-Analysis  
Michael P. LaValley*, Boston University School of Public Health

5:15  Floor Discussion

104. CONTRIBUTED PAPERS: Semi-Parametric and Non-Parametric Methods  
Sponsor: ENAR  
Chair: Olli Saarela, University of Toronto

3:45  Single Index Modeling and Estimation in Secondary Analysis of Case-Control Studies  
Liang Liang* and Raymond J. Carroll, Texas A&M University  
Yanyuan Ma, University of South Carolina

4:00  Marginal Mean Models for Zero-Inflated Count Data with Spline-Based Semiparametric Estimation  
David Todem* and Yifan Yang, Michigan State University  
Wei-Wen Hsu, Kansas State University  
KyungMann Kim, University of Wisconsin, Madison

4:15  Nonparametrically Assisted Parametric Regression Analysis for Multiple-Infection Group Testing Data  
Dewei Wang* and Peijie Hou, University of South Carolina

4:30  Nonparanormal Graphical Model Estimation with False Discovery Rate Control: A Score Test Approach  
Ritwik Mitra*, Yang Ning and Han Liu, Princeton University

4:45  Testing for Association in a Heterogeneous Sample  
Fangyuan Zhang*, Texas Tech University  
Jie Ding, Stanford University  
Shili Lin, The Ohio State University

5:00  A Maximum Alternative to the Cochran-Mantel-Haenszel Analysis  
Bernhard Klingenberg*, Williams College

5:15  Floor Discussion

105. CONTRIBUTED PAPERS: Statistical Genetics: Heterogeneity and Hierarchy  
Sponsor: ENAR  
Chair: Minsun Song, University of Nevada, Reno

3:45  Aggregated Quantitative Multifactor Dimensionality Reduction  
Rebecca E. Crouch*, Katherine L. Thompson and Richard J. Charnigo, University of Kentucky

4:00  The Influence of Population Stratification on Genomic Heritability  
Gota Morota*, University of Nebraska, Lincoln
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<tbody>
<tr>
<td>4:15</td>
<td>An Adaptive Testing Approach for Meta-Analysis of Gene Set Enrichment Studies</td>
<td>Wentao Lu* and Xinlei Wang, Southern Methodist University</td>
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<tr>
<td>4:30</td>
<td>Modeling Secondary Phenotypes Conditional on Genotypes in Case-Control Studies</td>
<td>Naomi C. Brownstein*, Florida State University, Wei Xue, Jianwen Cai and Eric Bair, University of North Carolina, Chapel Hill</td>
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<tr>
<td>4:45</td>
<td>The Parametric t-test's Latent Weakness</td>
<td>Daniel P. Gaile* and Jeffrey C. Miecznikowski, University at Buffalo</td>
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<tr>
<td>5:00</td>
<td>NanoStringDiff: A Novel Statistical Method for Differential Expression Analysis Based on NanoString nCounter Data</td>
<td>Hong Wang*, University of Kentucky, Craig Horbinski, Northwestern University, Hao Wu, Emory University, Yin Xing Liu, University of Kentucky, Shao Yi Sheng, Paul Laurence Dunbar High School, Arnold J. Stromberg and Chi Wang, University of Kentucky</td>
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### 106. CONTRIBUTED PAPERS: Variable Selection

**Sponsor:** ENAR  
**Chair:** Hyokyoung Hong, Michigan State University

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<tr>
<td>3:45</td>
<td>Data-Driven Confounder Selection Via Markov and Bayesian Networks</td>
<td>Jenny Haggstrom*, Umea University</td>
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<td>4:00</td>
<td>Feature Selection for Complex Metabolite Network</td>
<td>Qingpo Cai*, Emory University, Jian Kang, University of Michigan, Tianwei Yu, Emory University</td>
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<td>4:15</td>
<td>Variable Selection in the Presence of Nonignorable Missing Data</td>
<td>Jiwei Zhao*, State University of New York at Buffalo</td>
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<td>4:30</td>
<td>Sequential Multiple Testing for Variable Selection</td>
<td>Xinping Cui* and Hailu Chen, University of California, Riverside</td>
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<tr>
<td>4:45</td>
<td>Variable Selection for Model-Based Clustering of Functional Data</td>
<td>Kyra Singh* and Tanzy Love, University of Rochester</td>
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<tr>
<td>5:00</td>
<td>Bayesian Variable Selection Incorporating Biological Pathway Information Using Dependent Shrinkage Priors</td>
<td>Changgee Chang*, Suprateek Kundu and Qi Long, Emory University</td>
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<tr>
<td>5:15</td>
<td>Bayesian Spatial Feature Selection for Massive Neuroimaging Data Via Thresholded Gaussian Processes</td>
<td>Ran Shi*, Emory University, Jian Kang, University of Michigan</td>
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**Wednesday March 9**  
8:30 - 10:15 am  
**Oral Presentations**

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<th>Session</th>
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| 107     | **Statistical and Computational Challenges in OMICS Data Integration** | Sponsors: ENAR, ASA Statistics in Genomics and Genetics  
Organizer: Ronglai Shen, Memorial Sloan-Kettering Cancer Center  
Chair: Veera Baladandayuthapani, University of Texas MD Anderson Cancer Center | Katerina Kechris*, Dominik Reinhold, Junxiao Hu and Debashis Ghosh, University of Colorado, Denver |
| 8:50    | Discovery of Novel Loci Associated with COPD by Pooling Information from Related Clinical Feature and Functional Annotation | Jiehuan Sun* and Qiongshi Lu, Yale School of Public Health  
Russell P. Bowler, National Jewish Health  
Katerina J. Kechris, University of Colorado, Denver  
Hongyu Zhao, Yale School of Public Health |
| 9:10    | Bayesian Multivariate Modeling of the Sphingolipid Pathway           | Christine B. Peterson*, Stanford University  
Elin B. Sellers, Rice University  
Francesco C. Stingo, University of Texas MD Anderson Cancer Center  
Marina Vannucci, Rice University |
| 9:30    | Leveraging Multiple Omics Data to Infer Pathway Disturbance in Complex Diseases | Yuping Zhang*, SAMSI TCGA Data Integration Working Group, University of Connecticut |
| 9:50    | Integrating Clinical and Molecular Data for Survival Prediction in TCGA | Bin Zhu*, National Cancer Institute, National Institutes of Health  
Nan Song, NSABP Foundation  
Ronglai Shen, Memorial Sloan Kettering Cancer Center  
Veera Baladandayuthapani, University of Texas MD Anderson Cancer Center  
Katerina Kechris, University of Colorado, Denver  
Hongyu Zhao, Yale University |

| 108     | **Statistical Methods to Handle Treatment Crossover and Switch to an Alternative Therapy in Randomized Controlled Trials** | Sponsors: ENAR, ASA Biopharmaceutical Section  
Organizer: Shijie Tang, Biostatistics Infinity Pharmaceuticals, Inc.  
Chair: Jingxiang Chen, University of North Carolina, Chapel Hill | Chengqing Wu*, Xiaolong Luo, Mingyu Li, Qiang Xu, Guang Chen, Bruce E. Dornseif and Markus F. Renschler, Celgene  
Gary Koch, University of North Carolina, Chapel Hill |
| 8:30    | Regression Based Imputation Analysis Adjusting for Subsequent Therapy | Chengqing Wu*, Xiaolong Luo, Mingyu Li, Qiang Xu, Guang Chen, Bruce E. Dornseif and Markus F. Renschler, Celgene  
Gary Koch, University of North Carolina, Chapel Hill |
| 8:55    | Weighted Logrank Tests for Treatment Effects in Clinical Trials with Crossover | Rajeev Ayyagari*, Analysis Group, Inc.  
James M. Robins, Harvard School of Public Health |
| 9:20    | On the Use of Rank-Preserving Structural Failure Time Model to Account for both Treatment Crossover and Switch to Alternative Therapies | Liewen Jiang*, Shijie Tang, Biostatistics, Infinity Pharmaceuticals, Inc.  
Lingling Li, Harvard University |

* Presenter  
^ Student Award Winner
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<tr>
<td>9:45</td>
<td><strong>Biology, Causal Models, and Cross-over in Cancer Trials</strong></td>
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<td><em>James M. Robins</em>, Harvard School of Public Health</td>
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<td>10:10</td>
<td><strong>Floor Discussion</strong></td>
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<td>109.</td>
<td><strong>Sentinel Statistical Methods Working Groups, Challenges With Using</strong></td>
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<td><strong>Claims Data for Public Health</strong></td>
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<td><strong>Sponsors:</strong> ENAR, ASA Biopharmaceutical Section, ASA Section on Statistics in Epidemiology</td>
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<td><strong>Organizer &amp; Chair:</strong> Rima Izem, U.S. Food and Drug Administration</td>
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<tr>
<td>8:30</td>
<td><strong>Introduction to Sentinel Distributed Data System and Selected Methods Work</strong></td>
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<td><em>Judith C. Maro</em>, Harvard Medical School and Harvard Pilgrim Health Care Institute</td>
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<td>9:00</td>
<td><strong>Lessons Learned from Two Sentinel Sequential Surveillance Activities:</strong></td>
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<td><strong>Saxagliptin and Rivaroxaban</strong></td>
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<td><em>Bruce Fireman</em>, Kaiser Permanente Division of Research</td>
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<td>9:30</td>
<td><strong>Survival Methods for Postmarketing Medical Product Surveillance in a Distributed Network</strong></td>
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<td><em>Andrea J. Cook</em>, Robert Wellman, Group Health Research Institute</td>
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<td>*Rima Izem, Azadeh Shoaibi, and Ram Tiwari, U.S. Food and Drug Administration</td>
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<td>*Susan Heckbert, University of Washington</td>
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<td><em>Lingling Li, Harvard University</em></td>
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<td><em>Rongmei Zhang, U.S. Food and Drug Administration</em></td>
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<td>Jennifer Nelson, Group Health Research Institute</td>
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<td>10:00</td>
<td><strong>Discussant:</strong></td>
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<td><em>Mark Levenson</em>, U.S. Food and Drug Administration</td>
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<td>110.</td>
<td><strong>Statistical Modeling of Data on Heath Policy and Cost</strong></td>
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<td><strong>Sponsor:</strong> ENAR</td>
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<td><strong>Organizer:</strong> Zhezhen Jin, Columbia University</td>
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<td><strong>Chair:</strong> Yu Deng, University of North Carolina, Chapel Hill</td>
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<td>8:30</td>
<td><strong>On Statistical Modeling of National Surveys to Assess the Impact of State Specific Medical Marijuana Policies</strong></td>
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<td><em>Christine Mauro</em>, Columbia University</td>
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<td><em>Melanie M. Wall</em>, Columbia University and New York State Psychiatric Institute</td>
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<td>8:55</td>
<td><strong>An Improved Survival Estimator for Medical Costs with Censored Data Using Kernel Methods</strong></td>
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<td><em>Shuai Chen</em>, University of Wisconsin, Madison</td>
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<td><em>Wenbin Lu</em>, North Carolina State University</td>
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<td><em>Hongwei Zhao</em>, Texas A&amp;M Health Science Center</td>
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<td>9:20</td>
<td><strong>Comparison in Medical Cost between a Cancer Survivor Cohort and the General Population Using Longitudinal Physician Claims</strong></td>
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<td><em>Huijing Wang</em>, X. Joan Hu, Simon Fraser University</td>
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<td>9:45</td>
<td><strong>&quot;Nonparametric&quot; Meta Analysis with Unknown Study-specific Parameters and with an Application to Health Policy Data</strong></td>
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<td><em>Min-ge Xie</em>, Rutgers University</td>
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<tr>
<td>10:10</td>
<td><strong>Floor Discussion</strong></td>
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### 111. Weight Modification in Sample Surveys

**Sponsors:** ENAR, ASA Survey Research and Methodology Section  
**Organizer:** Michael Elliott, University of Michigan  
**Chair:** Lei Huang, Johns Hopkins University

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<tr>
<td>8:30</td>
<td>Weight Trimming and Weight Smoothing Procedures for Survey Data</td>
<td>David Haziza*</td>
<td>Université de Montréal</td>
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<tr>
<td>8:55</td>
<td>Weight Modification in Sample Surveys: An Overview</td>
<td>Malay Ghosh*</td>
<td>University of Florida</td>
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<tr>
<td>9:20</td>
<td>Weight Modification in Sample Surveys: Using Regression Models</td>
<td>Qixuan Chen*</td>
<td>Columbia University</td>
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<tr>
<td>9:45</td>
<td>Weight Modification in Sample Surveys: Results from a Simulation Study</td>
<td>Joe Sedransk*</td>
<td>University of Maryland</td>
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<td>10:10</td>
<td>Floor Discussion</td>
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### 112. Generalizing Clinical Data Across Studies/Populations

**Sponsors:** ENAR, ASA Biometrics Section  
**Organizers:** Jingjing Ye and Haiwen Shi, U.S. Food and Drug Administration  
**Chair:** Haiwen Shi, U.S. Food and Drug Administration

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<td>8:30</td>
<td>Adjusted Comparisons to External Controls Using Both Individual Patient Data and Published Summary Statistics</td>
<td>James E. Signorovitch*, David Cheng</td>
<td>Analysis Group Inc., Harvard University</td>
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<td>8:55</td>
<td>Robust Methods for Treatment Effect Calibration, with Application to Non-Inferiority Trials</td>
<td>Zhiwei Zhang*, Lei Nie and Guoxing Soon, Zonghui Hu</td>
<td>U.S. Food and Drug Administration, National Institute of Allergy and Infectious Diseases, National Institutes of Health</td>
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<td>9:45</td>
<td>Bayesian Network Meta-analyses of Multiple Diagnostic Tests</td>
<td>Haitao Chu*, Xiaoye Ma, Qinshu Lian, Yong Chen, Joseph G. Ibrahim</td>
<td>University of Minnesota, Amgen Inc., University of Pennsylvania, University of North Carolina, Chapel Hill</td>
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<td>10:10</td>
<td>Floor Discussion</td>
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### 113. Novel Statistical Methods for Sequencing Data - From Quality Control to False Positives

**Sponsors:** IMS, ENAR  
**Organizer:** Zhaoxia Yu, University of California, Irvine  
**Chair:** Chad He, Fred Hutchson Cancer Research Center

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<tr>
<td>8:30</td>
<td>A Generalized Similarity U Test for Multivariate Analysis of Sequencing Data</td>
<td>Changshuai Wei, Qing Lu*</td>
<td>University of North Texas Health Science Center, Michigan State University</td>
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8:55 Statistical and Computational Aspects in the Analysis of Genomic Data from Family Based Designs
Ingo Ruczinski*, Johns Hopkins Bloomberg School of Public Health

9:20 Empirical Estimation of Sequencing Error Rates Using Smoothing Splines
Xuan Zhu, Jian Wang, Bo Peng and Sanjay Shete*, University of Texas MD Anderson Cancer Center

9:45 Rare Variants Association Analysis in Large-Scale Sequencing Studies at the Single Locus Level
X. Jessie Jeng, North Carolina State University
Z. John Daye, University of Arizona
Wenbin Lu and Jung-Ying Tzeng*, North Carolina State University

10:10 Floor Discussion

114. CONTRIBUTED PAPERS: Bayesian Causal Inference
Sponsor: ENAR
Chair: Rhonda Bacher, University of Wisconsin, Madison

8:30 Utilizing Validation Data: A Bayesian Variable Selection Approach to Adjust for Confounding
Joseph Antonelli* and Francesca Dominici, Harvard School of Public Health

8:45 A Causal Inference Approach for Estimating an Exposure Response Curve: Estimating Health Effects at Low Pollution Levels
Georgia Papadogeorgou*, Harvard University
Francesca Dominici, Harvard School of Public Health

9:00 A Semi-Parametric Double Robust Bayesian’s Approach to Casual Inference
Bin Huang* and Chen Chen, Cincinnati Children’s Hospital Medical Center

9:15 Addressing Unmeasured Confounding Using External Validation Data: Improving BayesPS Approach
Negar Jaberasari* and Bin Huang, Cincinnati Children’s Hospital Medical Center

9:30 Bayesian Methods for Multiple Mediators: Principal Stratification and Causal Mediation Analysis of Power Plant Emission Controls
Chanmin Kim*, Harvard University
Michael Daniels, University of Texas, Austin
Joseph Hogan, Brown University
Christine Choirat and Corwin Zigler, Harvard University

9:45 Floor Discussion

115. CONTRIBUTED PAPERS: Biomarkers
Sponsor: ENAR
Chair: Nan Jia, Eli Lilly and Company

8:30 Estimating the Receiver Operating Characteristic Curve for Paired Family Data in a Case-Control Design
Yalda Zarnegarnia* and Shari Messinger Cayetano, University of Miami

8:45 Evaluating Longitudinal Biomarkers
Rosa Oliveira, Instituto Politecnico do Porto, Portugal
Raymond Carroll, Texas A&M University
Armando Teixeira-Pinto*, University of Sydney
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<td>Evaluation of Biomarkers for Treatment Selection Using Individual Participant Data Meta-Analysis</td>
<td>Chaeryon Kang*, University of Pittsburgh</td>
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<td>Holly Janes, Fred Hutchinson Cancer Research Center</td>
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<td>9:15</td>
<td>Comparing the Surrogacy of Multiple Vaccine-Induced Immune Response Biomarkers in HIV Prevention</td>
<td>Sayan Dasgupta* and Ying Huang, Fred Hutchinson Cancer Research Center</td>
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<td>9:30</td>
<td>Comparison of Methods for Updating Risk Prediction Models</td>
<td>Sonja Grill*, Technical University Munich, Germany</td>
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<td>Donna P. Ankerst, Technical University Munich, Germany and University of Texas Health Science Center, San Antonio</td>
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<td>Ruth M. Pfeiffer, National Cancer Institute, National Institutes of Health</td>
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<td>9:45</td>
<td>Evaluation of Biomarker Identification Through Likelihood Ratio Test</td>
<td>Yu-Chuan Chen* and James J. Chen, U.S. Food and Drug Administration</td>
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<td>10:00</td>
<td>Meta-Analysis of Predictive Values of Biomarkers</td>
<td>Mun Sang Yue* and Constantine A. Gatsonis, Brown University</td>
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116. CONTRIBUTED PAPERS: Competing Risks
Sponsor: ENAR
Chair: Olive Buhlule, National Institutes of Health

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<td>Checking Fine and Gray Model with Cumulative Sums of Residuals: Theory and Implementation</td>
<td>Jianing Li*, Merck</td>
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<td>Mei-Jie Zhang, Medical College of Wisconsin</td>
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<td>Thomas H. Scheike, University of Copenhagen</td>
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<td>8:45</td>
<td>Competing Risks Model of Screening and Symptoms Diagnosis</td>
<td>Sheng Qiu* and Alexander Tsodikov, University of Michigan</td>
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<td>9:00</td>
<td>Cause-Specific Hazard Regression for Competing Risks Data Under Interval Censoring and Left Truncation</td>
<td>Chenxi Li*, Michigan State University</td>
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<td>9:15</td>
<td>Evaluating Center Performance on Competing Outcomes</td>
<td>Sai Hurrish Dharmarajan* and Douglas E. Schaubel, University of Michigan</td>
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<td>9:30</td>
<td>Adaptive Group Bridge for Competing Risks Data</td>
<td>Natasha A. Sahr*, Kwang Woo Ahn and Anjishnu Banerjee, Medical College of Wisconsin</td>
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<td>9:45</td>
<td>Evaluating Utility Measurement from Recurrent Marker Processes in the Presence of Competing Terminal Events</td>
<td>Yifei Sun* and Mei-Cheng Wang, Johns Hopkins University</td>
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<td>10:00</td>
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117. CONTRIBUTED PAPERS: GWAS: Testing
Sponsor: ENAR
Chair: Luis Leon Novelo, University of Texas School of Public Health

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<td>Measuring and Testing Dependence by Kernelized RV Coefficient</td>
<td>Xiang Zhan**, Ni Zhao and Michael C. Wu, Fred Hutchinson Cancer Research Center</td>
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<td>8:45</td>
<td>Adaptive Gene- and Pathway-Trait Association Testing with GWAS Summary Statistics</td>
<td>Il-Youp Kwak* and Wei Pan, University of Minnesota</td>
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### 9:00 SNP-Set Tests Using Generalized Berk-Jones Statistics in Genetic Association Studies
Ryan Sun* and Xihong Lin, Harvard University

### 9:15 Testing for Genetic Associations in Arbitrarily Structured Populations
Minsun Song*, University of Nevada Reno
Wei Hao and John D. Storey, Princeton University

### 9:30 Novel Statistical Test for Genetic Pleiotropy
Daniel J. Schaid*, Mayo Clinic

### 9:45 An Adaptive Multivariate Test in Applications to Multiple Trait-Multiple Genetic Variant Associations for GWAS and Sequence Data
Junghi Kim* and Wei Pan, University of Minnesota

### 10:00 Floor Discussion

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#### 118. CONTRIBUTED PAPERS: Measurement Error
**Sponsor:** ENAR  
**Chair:** Qingning Zhou, University of North Carolina, Chapel Hill

### 8:30 The Orthogonally Partitioned EM Algorithm: Extending the EM Algorithm for Algorithmic Stability for Bias Correction Due to Imperfect Data
Michael Regier*, West Virginia University  
Erica Moodie, McGill University

### 8:45 A Simulation Study of Nonparametric Total Deviation Index as a Measure of Agreement Based on Quantile Regression
Yi Pan*, Centers for Disease Control and Prevention  
Lawrence Lin, JBS Consulting Services Company  
A.S. Hedayat, University of Illinois, Chicago  
Huiman Barnhart, Duke Clinical Research Institute, Duke University  
Michael Haber, Emory University

### 9:00 There is no Impact of Exposure Measurement Error on Latency Estimation in Linear Models
Sarah B. Peskoe*, Molin Wang and Donna Spiegelman, Harvard School of Public Health

### 9:15 Improved Estimation for High Dimensional Measurement Error Models
Abhishek Kaul*, National Institute of Environmental Health Sciences, National Institutes of Health

### 9:30 Identifying Heat Waves in Florida: The Impact of Missing Exposure Data and Thresholds on Missingness
Emily Leary*, University of Missouri, Columbia  
Linda J. Young, University of Florida

### 9:45 Optimal Design Strategy to Achieve a Pre-Specified Power when the Biomarker is Subject to Measurement Error
Matthew T. White*, Boston Children’s Hospital  
Sharon X. Xie, University of Pennsylvania

### 10:00 The Estimation of Misclassification Via Continuous-Time Hidden Markov Model
Liqiong Fan* and Sharon Yeatts, Medical University of South Carolina

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#### 119. CONTRIBUTED PAPERS: Statistical Genetics
**Sponsor:** ENAR  
**Chair:** Babette Brumback, University of Florida

### 8:30 A Functional Weighted U Test for Detecting Gene-Gene Interactions
Pei Geng* and Qing Lu, Michigan State University
8:45  Time-Course Gene Set Analysis of Longitudinal RNA-Seq Data  
Boris P. Hejblum*, Harvard School of Public Health  
Denis M. Agniel, Harvard Medical School
9:00  A Powerful and Data-Adaptive Test for Rare Variant-Based GxE Analysis  
Tianzhong Yang* and Peng Wei, University of Texas School of Public Health
9:15  Mediation Methods for Case-Control Settings with Applications to Genomics  
Sheila M. Gaynor* and Xihong Lin, Harvard School of Public Health
9:30  A Random Field Method for Genetic Association Analysis of Correlated Phenotypes Derived from Electronic Medical Records  
Xue Zhong* and Nancy J. Cox, Vanderbilt University
9:45  Statistical Considerations in Analytical Validations for Sequencing Based Genetic Tests  
Jincao Wu* and Mei Juan Li, U.S. Food and Drug Administration
10:00  Floor Discussion

10:15 - 10:30 am  Refreshment Break with Our Exhibitors
10:30 am - 12:15 pm  Oral Presentations

120.  Inference for Brain Networks  
Sponsors: ENAR, ASA Section on Statistics in Imaging  
Organizer: Lei Huang, Johns Hopkins University  
Chair: Michael Elliott, University of Michigan
10:30  Population Inference for Functional Brain Connectivity  
Manjari Narayan, Rice University  
Genevera I. Allen*, Rice University and Baylor College of Medicine
10:55  Robust Brain Structural Connectivity Analysis Using HCP Data  
Zhengwu Zhang*, SAMSI and University of North Carolina at Chapel Hill  
Antonio Canale, University of Turin  
David B. Dunson, Duke University
11:20  Node-wise Inference for Groups of Connectivity Graphs  
Philip T. Reiss*, New York University School of Medicine
11:45  Disentangling Brain Graphs: The Conflation of Network and Connectivity Inference  
Sean L. Simpson* and Paul J. Laurienti, Wake Forest School of Medicine
12:10  Floor Discussion

121.  Recent Development in Joint Modeling for Longitudinal Data  
Sponsors: ENAR, ASA Biometrics Section  
Organizer: Cheng Yong Tang, Temple University  
Chair: Zhaoxia Yu, University of California, Irvine
10:30  Bayesian Methods for Non-ignorable Dropout in Joint Models in Smoking Cessation Studies  
Jeremy Gaskins, University of Louisville  
Michael J. Daniels*, University of Texas, Austin
11:00  Mean-Correlation Regression for Discrete Longitudinal Responses  
Cheng Yong Tang*, Temple University  
Weiping Zhang, University of Science and Technology of China  
Chenlei Leng, University of Warwick
### 11:30 Simultaneous Mean and Covariance Modeling of Chronic Kidney Disease

Xiaoyue Niu*, The Pennsylvania State University  
Peter Hoff, University of Washington

### 12:00 Discussant:

Mohsen Pourahmadi, Texas A&M University

### 122. Model Validation: Its Concept, Statistical Integrity, Regulatory Landscape, and Industry Application

**Sponsor:** ENAR  
**Organizers:** Victoria Petrides, Abbott Diagnostics, Norberto Pantoja-Galicia and Haiwen Shi, U.S. Food and Drug Administration  
**Chair:** Victoria Petrides, Abbott Diagnostics

- 10:30 Issues with Training, Testing and Validation Datasets in the Development of Diagnostic Devices  
  R. Lakshmi Vishnuvajjala*, U.S. Food and Drug Administration

- 10:55 Establishing Clinical Usefulness of a Diagnostic Test Intended to Guide Therapy Decisions  
  Lisa M. McShane*, National Cancer Institute, National Institutes of Health

- 11:20 Guidelines for Reporting Studies that Develop or Validate a Multivariable Risk Prediction Model  
  Doug Altman and Gary Collins*, University of Oxford

- 11:45 Model Validation: An Industry Case Study  
  Susan H. Gawel*, Abbott Labs

### 12:10 Floor Discussion

### 123. Missing Data in Longitudinal Clinical Trials: Choice of Primary Estimand and It’s Relationship to the Statistical Analysis Methods

**Sponsor:** ENAR  
**Organizers:** Elena Polverejan and Cristiana Mayer, Janssen R&D  
**Chair:** Elena Polverejan, Janssen R&D

- 10:30 Choice of Estimand and Missing Data in Clinical Trials  
  Roderick J. Little*, University of Michigan

- 11:00 Role of Simulations in the Selection of the Primary Estimand and Statistical Methods for Handling Missing Data in Longitudinal Trials  
  Elena Polverejan*, Janssen R&D

- 11:30 Choosing Estimands in Clinical Trials with Missing Data  
  Craig H. Mallinckrodt*, Eli Lilly and Company

### 12:00 Discussant:

Thomas Permutt, U.S. Food and Drug Administration

### 124. Bayesian Analysis of Complex Survey Data

**Sponsors:** ENAR, ASA Survey Research and Methodology Section  
**Organizer:** Sahar Zangeneh, Fred Hutchinson Cancer Research Center  
**Chair:** Qixuan Chen, Columbia University

- 10:30 Cluster Like You Do: When to Avoid Traditional Clustering Approaches in the Presence of Sparse Data  
  Rebecca C. Steorts*, Duke University

- 10:55 Spatial Smoothing of Complex Survey Data for Small Area Estimation  
  Jon Wakefield*, University of Washington
### 11:20 Multilevel Regression and Poststratification for Survey Weighted Inference
Yajuan Si*, University of Wisconsin, Madison
Andrew Gelman, Columbia University

### 11:45 Robust Bayesian Models for Surveys with Missing Data and External Information
Sahar Z. Zangeneh*, Fred Hutchinson Cancer Research Center
Roderick J.A. Little, University of Michigan

### 12:10 Floor Discussion

#### 125. Causal Inference in Social Networks
**Sponsors:** ENAR, ASA Biometrics Section  
**Organizer:** Lan Liu, Harvard University  
**Chair:** Hana Lee, Brown University

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<th>Time</th>
<th>Title</th>
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| 10:30 | Causal Estimation of Peer Effects in Longitudinal Dyadic Data Using Instrumental Variables  | A. James O’Malley*, Geisel School of Medicine at Dartmouth  
Felix Elwert, University of Wisconsin, Madison  
J. Niels Rosenquist, Massachusetts General Hospital  
Alan M. Zaslavsky, Harvard Medical School  
Nicholas A. Christakis, Yale University |
| 11:20 | Indirect Adjustment for Homophily Bias with a Negative Control Variable in Peer Effect Analysis | Lan Liu* and Eric Tchetgen Tchetgen, Harvard University                                        |
| 11:45 | Segregated Graphs and Marginals of Chain Graph Models                                       | Ilya Shpitser*, Johns Hopkins University                                                        |
| 12:10 | Floor Discussion                                                                            |                                                                                                |

#### 126. Optimal Design for Nonlinear Models
**Sponsors:** IMS, ENAR  
**Organizer:** Dan Gillen, University of California, Irvine  
**Chair:** Matt Shotwell, Vanderbilt University

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<th>Time</th>
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| 10:30 | A Bayesian Decision Theoretic Approach to Experimental Designs for Hormesis                 | Steven B. Kim*, California State University, Monterey Bay  
Scott M. Bartell and Daniel L. Gillen, University of California, Irvine |
| 11:00 | Optimal Design for Dose-finding Study with Delayed Responses                               | Tian Tian, University of Illinois, Chicago  
Lei Nie, U.S. Food and Drug Administration  
Min Yang*, University of Illinois, Chicago |
| 12:00 | Floor Discussion                                                                            |                                                                                                |

#### 127. CONTRIBUTED PAPERS: Bayesian Methods
**Sponsor:** ENAR  
**Chair:** Arpita Chatterjee, Georgia Southern University

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<tr>
<td>10:30</td>
<td>Bayesian Regression Analysis for Estimating Disease Etiology</td>
<td>Zhenke Wu* and Scott L. Zeger, Johns Hopkins Bloomberg School of Public Health</td>
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10:45  Controlling for Systematic Bias in Allelic Imbalance Estimation Using a Negative Binomial Bayesian Model
Luis G. Leon Novelo*, University of Texas School of Public Health
Lauren M. McIntyre, Alison R. Gerken and Alison M. Morse, University of Florida College of Medicine
Justin M. Fear, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health
Sergey Nuzhdin, University of Southern California

11:00  Patient-Specific Prediction of Abdominal Aortic Aneurysm Expansion Using Bayesian Calibration
Liang Liang Zhang*, Justin Mrkva, Sajjad Seyedsalehi and Jongeun Choi, Michigan State University
Chae Young Lim, Seoul National University
Tapabrata Maiti and Seungik Baek, Michigan State University

11:15  Spatial Skew-Normal/Independent Models for Clustered Periodontal Data with Non-Random Missingness
Dipankar Bandyopadhyay*, Virginia Commonwealth University
Victor H. Lachos, University of Campinas, Brazil
Marcos Prates, Universidade Federal de Minas Gerais, Brazil
Xioayue Zhao, University of Minnesota

11:30  Bayesian Approach for Clustered Interval-Censored Data with Time-Varying Covariate Effects
Yue Zhang* and Xia Wang, University of Cincinnati
Bin Zhang, Cincinnati Children’s Hospital Medical Center

11:45  Repulsive Priors for Meaningful Inferences in Biomedical Applications
Yanxun Xu*, Johns Hopkins University
Peter Mueller, University of Texas, Austin
Donatello Telesca, University of California, Los Angeles

12:00  A Model and R Package for Bayesian Survival and Multistate Analysis
Adam King*, California State Polytechnic University, Pomona

128. CONTRIBUTED PAPERS: Causal Inference in Epidemiology and Health Policy
Sponsor: ENAR
Chair: Bin Huang, Cincinnati Children’s Hospital Medical Center

10:30  Defining and Estimating Causal Direct and Indirect Effects when Setting the Mediator to Specific Values is not Feasible
Judith J. Lok*, Harvard School of Public Health

10:45  Using Structural-Nested Models to Estimate the Effect of Cluster-Level Adherence on Individual-Level Outcomes with a Three-Armed Cluster-Randomized Trial
Babette A. Brumback*, University of Florida
Zhulin He, Iowa State University
Shanjun Helian, University of Florida
Matthew Freeman, Emory University
Richard Rheingans, University of Florida

11:00  A Multiple-Imputation Based Doubly Robust Estimation of Treatment Effects in Longitudinal Studies
Tingting Zhou*, Michael Elliott and Roderick Little, University of Michigan

11:15  A General Approach on Causal Mediation Analysis
Pan Wu*, Christiana Care Health System
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<td>Improving Covariate Balancing Propensity Score for Continuous Treatment Regimes</td>
<td>Samantha Noreen* and Qi Long, Emory University</td>
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<td>11:45</td>
<td>Calibrate Measurement Errors and Misclassifications in Mendelian Randomization Studies</td>
<td>Cheng Zheng*, University of Wisconsin, Milwaukee</td>
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<td>12:00</td>
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<td>11:30</td>
<td>129. CONTRIBUTED PAPERS: Count and Categorical Data Analysis</td>
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<td>Chair: Matthew White, Boston Children’s Hospital</td>
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<td>10:30</td>
<td>A New Compound Class of Exponentiated Power Lindley-Logarithmic Distribution: Model, Properties and Applications</td>
<td>Mavis Pararai*, Indiana University of Pennsylvania</td>
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<td>Jacinth A. Maynard, Lock Haven University of Pennsylvania</td>
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<td>Gayan W. Liyanage, Central Michigan University</td>
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<td>10:45</td>
<td>A Bayesian Approach in Estimating Odds Ratios for Rare or Zero Events</td>
<td>Mehmet Kocak*, University of Tennessee Health Science Center</td>
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<td>11:00</td>
<td>Analysis of Inflated Bivariate Count Data that Occur in Health Care Studies Using Poisson Regression Models</td>
<td>N. Rao Chaganty*, Old Dominion University</td>
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<td>Pooja Sengupta, International Management Institute</td>
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<td>11:15</td>
<td>A Bayesian Test of Independence in a Two-Way Contingency Table with Covariates Under Cluster Sampling</td>
<td>Dilli Bhatta*, University of South Carolina Upstate</td>
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<td>Balgobin Nandram, Worcester Polytechnic Institute</td>
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<td>11:30</td>
<td>Simulating Longer Vectors of Correlated Binary Random Variables Via Multinomial Sampling</td>
<td>Justine Shults*, University of Pennsylvania Perelman School of Medicine</td>
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<td>11:45</td>
<td>Testing for Trend with a Nominal Outcome</td>
<td>Aniko Szabo*, Medical College of Wisconsin</td>
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<td>12:00</td>
<td>Estimation of the Optimal ROC in Complex Classification Settings</td>
<td>Daniel B. Shin*, University of Pennsylvania</td>
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<td>Farrah J. Mateen, Massachusetts General Hospital and Harvard Medical School</td>
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<td>Jaroslaw Haeslik, Indiana University, Indianapolis</td>
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<td>Joel M. Gelfand and Russell T. Shinohara, University of Pennsylvania</td>
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<td>130.</td>
<td>130. CONTRIBUTED PAPERS: Joint Models for Longitudinal and Survival Data</td>
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<td>Chair: Armando Teixeira-Pinto, University of Sydney</td>
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<td>10:30</td>
<td>Weighted ZIP Mixed Model with an Application to Medicaid Data</td>
<td>Sang Mee Lee* and Theodore Karrison, University of Chicago</td>
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<td>10:45</td>
<td>A Semiparametric Joint Model for Longitudinal Data and Survival in End-Of-Life Studies</td>
<td>Zhigang Li* and H. R. Frost, Dartmouth College</td>
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<td>Lihui Zhao and Lei Liu, Northwestern University</td>
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<td>Kathleen D. Lyons, Dartmouth College</td>
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<td>Huaihou Chen, University of Florida</td>
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<td>Bernard Cole, University of Vermont</td>
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<td>David Currow, Flinders University, Australia</td>
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<td>Marie Bakitas, University of Alabama</td>
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<td>Tor D. Tosteson, Dartmouth College</td>
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11:00  Dynamic Prediction for Multiple Repeated Measures and Event Time Data: An Application to Parkinson’s Disease
Jue Wang*, Sheng Luo, University of Texas Health Science Center, Houston
Liang Li, University of Texas MD Anderson Cancer Center

11:15  Flexible Link Functions in a Joint Model of Binary and Longitudinal Data
Dan Li*, Xia Wang and Seongho Song, University of Cincinnati
Nanhua Zhang, Cincinnati Children’s Hospital Medical Center
Dipak K. Dey, University of Connecticut

11:30  Joint Modeling of Functional Data and Time to Event: An Application to Fecundity Studies
Ling Ma*, Rajeshwari Sundaram, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health
Animikh Biswas, University of Maryland Baltimore County

11:45  A Joint Model Approach for Longitudinal Data with no Time Zero and Time-To-Event with a Competing Risk
Olive D. Buhule* and Paul S. Albert, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

12:00  Floor Discussion

131. CONTRIBUTED PAPERS: Personalized Medicine
Sponsor: ENAR
Chair: Corwin Zigler, Harvard University

10:30  Comparing Mobile Health Treatment Policies
Peng Liao*, Pedja Klasjna and Susan A. Murphy, University of Michigan

10:45  A Bayesian Approach for Exploring Heterogeneous Treatment Effects and Individualized Treatment Decisions
Nicholas C. Henderson*, Thomas A. Louis and Ravi Varadhan, Johns Hopkins University

11:00  Early Phase Designs for Targeted and Immunotherapeutic Agents: Preparing for Precision Medicine
Cody Chiuzan*, Columbia University

11:15  Estimating Optimal Treatment Recommendation in Observation Studies
Haoda Fu and Nan Jia*, Eli Lilly and Company

11:30  Combining Functional Additive Models and Advantage Learning for Estimating a Treatment Decision Rule
Adam Ciarleglio* and Eva Petkova, New York University School of Medicine
R. Todd Ogden, Columbia University
Thaddeus Tarpey, Wright State University

11:45  Companion Diagnostic Device Partial Bridging Study in Precision Medicine - Challenges and Methods
Meijuan Li and Yaji Xu*, U.S. Food and Drug Administration

12:00  Identifying Predictive Markers for Personalized Treatment Selection
Yuanyuan Shen* and Tianxi Cai, Harvard School of Public Health
### 132. CONTRIBUTED PAPERS: Survival Analysis

**Sponsor:** ENAR  
**Chair:** Daniel Schaid, Mayo Clinic

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<tr>
<td>10:30</td>
<td>A Unified Slice Sampler for Regression Analysis of Current Status Data Under Linear Transformation Models</td>
<td>Sheng-Yang (Sean) Wang* and Lianming Wang, University of South Carolina</td>
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<td>10:45</td>
<td>An Extended Kaplan-Meier Estimator for Time to Success with Informative Censoring</td>
<td>Wei Li* and Misun Lee, Astellas Pharma Development</td>
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| 11:00  | Survival Data for Multiple Diseases from Stratified Case-Cohort Design  | Soyoun Kim*, Medical College of Wisconsin  
Jianwen Cai, Donglin Zeng and David J. Couper, University of North Carolina at Chapel Hill, Chapel Hill |
| 11:15  | Improved Estimation of Relative Risk Under Small Samples Using a Generalized Log-Rank Statistic | Rengyi Xu* and Pamela A. Shaw, University of Pennsylvania  
Devan V. Mehrotra, Merck                                                                 |
| 11:30  | Life Expectancy Estimation Based on Gompertz Function                | Zugui Zhang* and Paul Kolm, Christiana Care Health System                                 |
| 11:45  | Detecting Associations Between Microbiome Composition and Time-To-Event Outcomes | Anna Plantinga*, University of Washington  
Ni Zhao and Michael C. Wu, Fred Hutchinson Cancer Research Center                           |
| 12:00  | Semiparametric Structural Equation Models with Latent Variables for Right-Censored Data | Kin Yau Wong*, Danyu Lin and Donglin Zeng, University of North Carolina, Chapel Hill       |
SC1: Missing Data in Regression Models

**FULL DAY: 8:00 am to 5:00 pm**

**Joe Ibrahim**
University of North Carolina at Chapel Hill

**Overview:** Missing data is a major issue in many applied problems, especially in the biomedical sciences. In this short course, we present a detailed account of the four common paradigms for inference in missing data problems. These are i) Maximum Likelihood (ML), ii) Multiple Imputation (MI), iii) Fully Bayesian (FB), and Weighted Estimating Equations (WEE). There is considerable interest as to how these four methodologies are related, the properties of each approach, the advantages and disadvantages of each methodology, and their computational implementation. We also discuss the various assumptions and definitions of missing data mechanisms, present several examples, and examine data that are missing at random (MAR) and/or nonignorably missing (MNAR), as well as missing covariate and/or response data. We will also discuss methods and applications for several types of models including generalized linear models, models for longitudinal data, and survival models. For each paradigm (ML, MI, FB, WEE) and model, we will present detailed case studies and software implementation in SAS, WinBUGS, and Cytel Studio’s XMISS package.

**Instructor Biography:** Dr. Joseph Ibrahim is Alumni Distinguished Professor, Director of Graduate Studies, and Program Director of the Cancer Genomics Training grant, in the Department of Biostatistics at UNC. His areas of research focus are Bayesian inference, missing data problems, clinical trials, and cancer genomics. He has directed or co-directed 25 doctoral students and 8 post-doctoral fellows. He has taught courses in Bayesian statistics, Advanced Statistical Inference, Generalized Linear Models, and Missing Data in the Department of Biostatistics at UNC. He is currently the Editor for the Journal of the American Statistical Association – Applications and Case Studies. Dr. Ibrahim has published over 265 research papers, mostly in top statistical journals. He also has published two advanced graduate-level books on Bayesian survival analysis and Monte Carlo methods in Bayesian computation. Dr. Ibrahim has a long standing history of teaching half day and full day short courses at ENAR, JSM, and at pharmaceutical companies. He has done full day short courses in Meta-analysis and Network Meta-analysis, Bayesian Methods for Computation, Bayesian Survival Analysis, Missing Data in Regression Models, Bayesian Methods in SAS, Bayesian Methods in Clinical Trials, Joint Modeling of Longitudinal and Survival Data, Introduction to Longitudinal Data Modeling, Introduction to Bayesian Methods, and Informative Prior Elicitation. He is an elected fellow of the American Statistical Association and the Institute of Mathematical Statistics, and an elected member of the International Statistical Institute.
**SC2: Statistical Analysis of Network Data**

**FULL DAY: 8:00 am to 5:00 pm**

**Eric Kolaczyk**  
Boston University

**Overview:** Networks have permeated everyday life through everyday realities like the Internet, social networks, and viral marketing. Their use has become especially prevalent in the biological and life sciences, particularly in computational biology and neuroscience. Accordingly, network analysis is an important growth area in the quantitative sciences, with roots in social network analysis going back to the 1930s and graph theory going back centuries. Measurement and analysis are integral components of network research, and statistical methods therefore play a critical role in network analysis. This course will provide a broad treatment of foundational topics relevant to statistical analysis of network data across the disciplines. Material will be organized according to a statistical taxonomy, with presentation entailing a conscious balance of conceptual and technical aspects. Additionally, practical application of network analysis will be demonstrated in the context of the R software environment. Topics for the morning will include manipulation, visualization, and descriptive analysis of network data. In the afternoon, we will focus on network sampling and inference, and the modeling of networks and network-indexed processes. Specific examples of network analysis will be drawn from a variety of domain areas, with emphasis on computational biology and neuroscience and on social networks.

**Instructor Biography:** Eric Kolaczyk is Professor of Statistics, and Director of the Program in Statistics, in the Department of Mathematics and Statistics at Boston University, where he also is an affiliated faculty member in the Program in Bioinformatics, the Program in Computational Neuroscience, and the Division of Systems Engineering. Prof. Kolaczyk’s main research interests currently revolve around the statistical analysis of network-indexed data, and include both the development of basic methodology and interdisciplinary work with collaborators in bioinformatics, computer science, geography, neuroscience, and sociology. Besides various research articles on these topics, he has also authored two books in this area—Statistical Analysis of Network Data: Methods and Models (Springer, 2009) and Statistical Analysis of Network Data with R (Springer, 2014), joint with Gabor Csardi. He has given various short courses on material from his book in recent years, including for the Center for Disease Control (CDC) and the Statistical and Applied Mathematical Sciences Institute (SAMSI) in the US, as well as similar venues in Belgium, England, and France. Prof. Kolaczyk has served as associate editor on several journals, including currently the Journal of the American Statistical Association and the IEEE Transactions on Network Science and Engineering. He has also served as (co) organizer for workshops focused on networks and network data, including as lead organizer for a year-long program at SAMSI in 2010-11. He is an elected fellow of the American Statistical Association (ASA), an elected senior member of the Institute for Electrical and Electronics Engineers (IEEE), and an elected member of the International Statistical Institute (ISI).

**SC3: Introduction to Statistical Machine Learning**

**FULL DAY: 8:00 am to 5:00 pm**

**Yufeng Liu**  
University of North Carolina at Chapel Hill

**Genevera Allen**  
Rice University

**Overview:** This full day short course will provide an overview of statistical machine learning techniques with applications to the analysis of big biomedical data. Both supervised and unsupervised techniques will be covered. Supervised learning techniques include penalized regression such as LASSO and its variants, support vector machines, Boosting, and tree-based methods. Unsupervised learning techniques include dimension reduction methods such as principal components analysis and non-negative matrix factorization, clustering analysis, and network analysis with graphical models. The main emphasis will be on the analysis of real high-dimensional data sets from various scientific fields, including genomics and biomedical imaging. The techniques discussed will be demonstrated in R.

**Instructors Biography:** Yufeng Liu is professor in Department of Statistics and Operations Research, Department of Biostatistics, and Department of...
Genetics at UNC-Chapel Hill. His current research interests include statistical machine learning, high dimensional data analysis, and bioinformatics. He has taught statistical machine learning courses multiple times at UNC, as well as short courses on this subject at Joint Statistical Meetings and Biostatistics Summer Institutes at University of Washington. Dr. Liu received the CAREER Award from National Science Foundation in 2008, and Ruth and Phillip Hettleman Prize for Artistic and Scholarly Achievement in 2010. He is a fellow at American Statistical Association and an elected member of International Statistical Institute.

Genevera Allen is the Dobelman Family Junior Chair and Assistant Professor in Statistics and Electrical and Computer Engineering at Rice University. She also holds a joint appointment at the Jan and Dan Duncan Neurological Research Institute at Baylor College of Medicine. Dr. Allen’s research focuses on developing statistical methods to help scientists make sense of their ‘big data’ in applications such as high-throughput genomics and neuroimaging. Her work lies in the areas of modern multivariate analysis, graphical models, statistical machine learning, and data integration or data fusion. She has taught statistical machine learning courses for many years at Rice University as well as short courses on this subject at the Biostatistics Summer Institutes at University of Washington and the Data Science Summer Institute at Rice University. Dr. Allen has represented the American Statistical Association in the “This is Statistics” public relations campaign and is the recipient of several honors including the David P. Byar Young Investigator travel award and the International Biometric Society’s Young Statistician Showcase award. Current emerging area is genomics and modern genetics (GWAS and sequencing data).

SC4: Statistical Genetic and Genomic Analysis of Complex Traits with GWAS and Next Generation Sequencing Data

HALF DAY: 8:00 am to 12:00 noon

Hongyu Zhao
Yale University

Fei Zou
University of North Carolina at Chapel Hill

Overview: Recent advances in genotyping and sequencing technologies have revolutionized biological and biomedical research. Great efforts have been taken to uncover genetic factors of many complex human disorders and traits with genome-wide association and next generation sequencing studies. An unprecedented wealth of data generated from these studies has created great opportunities and challenges for statisticians and biomedical researchers. In this short course, we will cover genotyping and sequencing technologies, and state-of-the-art statistical approaches to analyzing and interpreting GWAS and Next Generation Sequencing data. Topics to be covered include:

» Introduction to genetics, and genomic analysis technologies and software
» Introduction to GWAS data processing and analysis
» Introduction to next generation sequencing data and analysis
» Real data examples on psychiatric diseases, autoimmune disorders, cancer, and anthropological traits.

Instructors Biography: Dr. Hongyu Zhao is the Ira V. Hiscock Professor of Biostatistics and Professor of Statistics and Genetics, Chair of the Biostatistics Department and the Co-Director of Graduate Studies of the Inter-Departmental Program in Computational Biology and Bioinformatics at Yale University. His research interests are the applications of statistical methods in molecular biology, genetics, drug developments, and personalized medicine. Some of his recent projects include large scale genome wide studies to identify genetic variants underlying complex diseases (schizophrenia, bipolar, autism, and substance abuse), biological network modeling and analysis, disease biomarker identification through proteomics, genome annotations, microbiome analysis and systems biology study of herbal medicine. Dr. Zhao has been teaching statistical genetics and bioinformatics at Yale since 1996 and has offered multiple short courses on statistical genetics and genomics at JSM, ENAR, Deming Conference, and other statistical and genomics conferences.

Dr. Fei Zou is Professor in Department of Biostatistics and Department of Genetics at UNC-Chapel Hill. She is also the director of the Biostatistics/Bioinformatics core of UNC Neuroscience Center Research Cores. Her research interests include genome-wide association mapping with emphasis on assessing population stratification, and bias correction; QTL mapping with...
experimental mouse data; integrated statistical analysis of high-dimensional genetics and genomics data, and differential gene expression and methylation analysis of next generation sequencing data. Dr. Zou is a co-investigator on multiple association studies on schizophrenia, early child brain development, and cystic fibrosis. She has taught statistical genetics and genomic courses multiple times at UNC and SAMSI.

SC5: Bayesian Evidence Synthesis in Medicine

HALF DAY: 8:00 am to 12:00 noon

Heinz Schmidli
Novartis, Basel, Switzerland

David Ohlssen
Novartis, New Jersey

Overview: In the past decade, evidence synthesis has become an indispensable approach in many areas of medicine. Using combined information from several clinical studies, the effectiveness and safety of available treatments can be compared, providing guidance on how to best treat patients. Evidence synthesis approaches are also important in the design and analysis of clinical studies, for example when planning to use historical placebo information, or in non-inferiority studies. Bayesian methods are ideally suited to combine information from various sources. This course will describe the main meta-analytic models for evidence synthesis of clinical trials. These models take into account differences among studies by use of covariate information and random-effects. Applications and examples will motivate and illustrate the methods, covering topics such as comparative effectiveness research, clinical trials with historical controls, non-inferiority and biosimilar clinical trials, subgroup meta-analyses, and safety meta-analyses. The course will cover:

» Evidence synthesis in medicine
» Brief introduction to Bayesian inference and computation
» Evidence synthesis tools: Meta-analysis, Network meta-analysis, Meta-regression.
» Prediction based on meta-analytic models
» Assessing and dealing with conflicting information

Instructors Biography: Dr. Heinz Schmidli is a Biometrical Fellow within the Novartis Statistical Methodology group, based in Basel, Switzerland. He studied Mathematics at the University of Basel, and received his PhD in Statistics in 1994. In 2012 he received the Paul-Martini-Prize of the GMDS (jointly with Tim Friede), and in 2013 the Novartis leading scientist award. He has authored or co-authored more than 50 articles in peer-reviewed journals, and is author of a book.

Dr. David Ohlssen is currently a Biometrical Fellow and Bayesian focus team lead, within the Novartis statistical methodology group, based in East Hanover New Jersey. Since joining Novartis in 2007, he has developed a broad range of experience in applying novel statistical approaches within a drug development setting. Previously, after completing his PhD in Biostatistics at the University of Cambridge, he worked as a research fellow at the MRC Biostatistics Unit (Cambridge UK), where his interests included: diagnostics for Bayesian models, novel clinical trial design and statistical methods for the profiling of health-care providers. His professional activities include serving as a member of the Bayesian DIA Working Group and within the group acting as the chair of the safety meta-analysis sub-team.

SC6: Practical Solutions for Simple Problems with Bad Consequences in Clinical Trials

HALF DAY: 1:00 pm to 5:00 pm

Peter Thall
University of Texas, M.D. Anderson Cancer Center

Overview: Many conventional methods used for clinical trial design or analysis have undesirable properties that are not obvious and often are not well understood. In many cases, the problem may have very undesirable consequences if it is ignored. This half day short course will describe a variety of such problems, and provide a practical alternative for each. Topics will include (1) consequences of ignoring treatment efficacy in dose-finding trials, (2) misinterpreting hypothesis test-based designs, (3) dealing with late onset toxicities, (4) futility or safety monitoring rules that may not work well in practice, (5) consequences of ignoring patient heterogeneity (6) scientific and ethical problems with adaptive randomization in comparative trials, (7) estimation bias, (8) some counterintuitive relationships between early response rate and mean survival time, (9) decision making for multi-stage dynamic treatment regimes, and (10) SMART (Sequential Multiple Assignment

Continued on following page....
Randomized Trial) designs. The examples will include very little mathematical detail, but attendees should have some knowledge of elementary probability and statistics. The course is appropriate for anyone involved in clinical trial design, conduct, or analysis, including statisticians, physicians, research nurses, administrators, professionals in the pharmaceutical industry, or federal employees in the NIH or FDA.

**Instructor Biography:** Peter Thall has been a Science Faculty member at M.D. Anderson Cancer Center since 1990, where he holds the Anise J. Sorrell Endowed Professorship. He is a Fellow of the American Statistical Association (ASA) and the Society of Clinical Trials, and received the Don Owen award from the San Antonio chapter of the ASA in 2014. Dr. Thall has pioneered application of Bayesian methods in medical research, designed hundreds of clinical trials, published over 200 papers and book chapters in the statistical and medical literature, and presented 28 short courses and over 190 invited talks. His current research interests include Bayesian utility-based clinical trial design, nonparametric Bayesian methods, bias correction, and dynamic treatment regimes. He is an Associate Editor for the journals Clinical Trials and Statistics in Biosciences, an ASA Media Expert, a member of the International Biometric Society ENAR Regional Advisory Board, and is Principal Investigator of the NIH/NCI R01 grant “Statistical Methods for Complex Cancer Trials.”
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**T1: Topics in High-Performance Computing with R**

**Monday, March 7 | 8:30 am to 10:15 am**

**John W. Emerson**

Yale University

**Description:** This tutorial will introduce you to topics in high-performance computing with R. We will touch upon a few important language fundamentals relating to memory management and algorithmic efficiency. We will quickly explore the parallel package (containing snow and multicore), but will concentrate on the elegant framework for parallel programming offered by packages for each and the associated parallel backends. We will conclude with basic examples of handling larger-than-RAM numeric matrices and use of shared memory. Take-away material will include a concise example authoring an R package that includes C/C++ code, uses Rcpp, and roxygen2 for efficient documentation.

**Instructor Biography:** John W. Emerson (Jay) is Director of Graduate Studies in the Department of Statistics at Yale University. He teaches a range of graduate and undergraduate courses as well as workshops, tutorials, and short courses at all levels around the world. His interests are in computational statistics and graphics, and his applied work ranges from topics in sports statistics to bioinformatics, environmental statistics, and Big Data challenges. He is the author of several R packages including bcp (for Bayesian change point analysis), bigmemory and sister packages (towards a scalable solution for statistical computing with massive data), and gpairs (for generalized pairs plots). His teaching style is engaging and his workshops are active, hands-on learning experiences.

**T2: Interactive Data Visualizations in R with shiny and ggplot2**

**Monday, March 7 | 10:30 am to 12:15 pm**

**Garrett Grolemund**

RStudio

**Description:** Data visualizations are one of the most useful tools for scientific discovery and communication. They become even more useful when they are enhanced with interactive techniques like linked brushing, hover effects, and zooming. However, interactive visualizations typically require specialized or proprietary software that cannot be easily installed or extended. As a result this valuable technique often goes underused. This tutorial will teach you an easy workflow for creating both static and interactive data visualizations with R, a free and open source computer language that is widely used by biostatisticians. You will learn how to make static plots with the grammar of graphics, an easy to use system for building plots. With the grammar of graphics, you can describe---and build---any plot by describing three components: a data set to visualize, a geometric object to use to represent individual observations, and a set of mappings between variables in the data set and visual properties of the geometric objects (like location, size, and color). We will use the popular ggplot2 package to implement the grammar of graphics. We will then look at how to add interactivity to your plots with Shiny, an R package that builds interactive data displays. We will focus on the newest features of Shiny, which enable interactive graphics. Participants will finish the tutorial by building their own visualizations that use linked brushing and hover effects.

**Instructor Biography:** Garrett Grolemund is a Data Scientist and Master Instructor at RStudio. He holds a...
Ph.D. in Statistics and specializes in teaching others how to do data science with open source tools. He is a long time user and advocate of R; he wrote the popular lubridate package for working with dates and times in R, and is the editor of the Shiny development center at shiny.rstudio.com, which is the primary resource for learning how to build interactive web applications with R. Garrett designed and delivered the highly rated video series “Introduction to Data Science with R” by O’Reilly media, and he is the author of Hands-On Programming with R, as well as the co-author, with Hadley Wickham, of R for Data Science, a forthcoming book by O’Reilly media.

**T3: Clinical Trial Designs for Validating Prognostic and Predictive Markers in Oncology**

**Monday, March 7 | 1:45 pm – 3:30 pm**

**Daniel J. Sargent**

**Mayo Clinic**

**Description:** Increasing scientific knowledge is creating both substantial opportunities and challenges in oncology drug development. As diseases are sub-stratified into bio-marker-based groups, usual paradigms for phase II and III disease may no longer apply. In some circumstances, carefully conducted retrospective-prospective analysis may provide sufficient evidence of a predictive biomarker for clinical use. Prospectively, enrichment designs are appropriate when preliminary evidence suggest that patients with/without that marker profile do not benefit from treatments in question; however this may leave questions unanswered regarding the activity of an agent in a larger but still relevant population. An unselected design is optimal where preliminary evidence regarding treatment benefit and assay reproducibility is uncertain. The biomarker-based strategy design may be useful when there is a choice between many treatment options. Adaptive analysis designs allow for pre-specified marker defined subgroup analyses of data from a RCT. Umbrella or basket trials enroll large groups of patients with subsequent assignment to either individual randomized trials or single arm investigations. These trials may be disease specific, or may include patients from multiple sites who share a common biomarker status. We discuss features of these various novel design strategies in the context of multiple ongoing and planned real trials. Emphasis will be placed on practical considerations that may impact an academically optimal design.

**Instructor Biography:** Daniel J. Sargent, Ph.D. is the Ralph S. and Beverly E. Caulkins Professor of Cancer Research at the Mayo Clinic. He is the Group Statistician for the Alliance for Clinical Trials in Oncology and the Director of Biostatistics Shared Resource at the Mayo Clinic Comprehensive Cancer Center. Dr. Sargent co-chaired a joint NCI-EORTC committee on methodology for tumor marker studies, was a member of the FDA panel on endpoints for colon cancer clinical trials, and from 2007 - 2013 was a member of the US NCI Clinical Trials Advisory Committee, which oversees all NSI funded cancer clinical trials in the United States. He presently serves on the Clinical Trial Design Task force of the NCI’s Investigational Drug Steering Committee. He has published extensively in colorectal cancer treatment in the elderly, optimal clinical trial endpoints, and prognostic and predictive biomarkers. He has authored over 290 peer-reviewed manuscripts, book chapters, editorials, and letters.

**T4: A New Paradigm for Finding the Subset of Patients who Benefit from a Test Treatment**

**Monday, March 7 | 3:45 pm – 5:30 pm**

**Richard Simon**

**National Cancer Institute**

**Noah Simon**

**University of Washington**

**Description:** Conventionally defined diseases are often heterogeneous in biology, natural course and response to treatment. The traditional paradigm of conducting broad eligibility randomized clinical trials followed by post-hoc subset analysis does not provide a reliable or efficient basis for precision/personalized medicine. Broad eligibility clinical trials often lead to subsequent over-treatment of patient populations and conventional post-hoc subset analysis often does not provide reliable or actionable findings. In this tutorial we describe an alternative paradigm for finding and evaluating the subset of patients who benefit from a test treatment relative to a control. The paradigm re-formulates the problem as one of developing a predictive classifier and obtaining valid estimates of the properties of the classifier such as the treatment effect in the population predicted to benefit from the test treatment. We describe two contexts for the application of this paradigm. One context involves prospective

*Continued on following page....*
application using an Adaptive Enrichment Design. The other context involves retrospective application using the principles of the Prospective/Retrospective Design. We describe the development of predictive classifiers for binary outcome and time-to-event data. Several types of predictive classifiers are described. The approaches are applicable to settings with a small number of candidate features are available and settings with high-dimensional feature sets. We describe how the approach provides an intended use population and describe use of re-sampling and permutation techniques to obtain valid estimates of treatment effect for that population. Recent results by us and related work by others will be described.

Instructors Biography: Richard Simon is Chief of the Biometric Research Program at the National Cancer Institute and head of the Computational and Systems Oncology Branch. He is a fellow of the American Statistical Association and a former member of the Oncologic Drug Advisory Committee of the FDA. He is the architect of BRB Array Tools software and author of Using Genomics in Clinical Trials and Predictive Medicine (Cambridge U. Press 2013). He is the recipient of the 2013 Karl Peace award of the American Statistical Association “for contributions that have played a pivotal role in bridging the gap among statistics, clinical research, and translational medicine to improve human health”.

Noah Simon (Ph.D. in Statistics from Stanford University) is an Assistant Professor in the Department of Biostatistics at the University of Washington. He works on problems at the intersection of statistics, biology and computer science, developing algorithms to build scientific knowledge from modern high-throughput technologies. His interests include high dimensional modeling and inference, selection-bias in high-throughput experiments, biomarker development, and adaptive clinical trial design. He was a Weiland Fellow and currently holds the Genentech Endowed Professorship in Biostatistics at the University of Washington.

Instructors Biography: Dr. Martin Morgan leads the successful open source, open development Bioconductor project (http://bioconductor.org) for the analysis and comprehension of high throughput genomic data. Dr. Morgan’s interests include statistical computation, integrative analysis of multiple ‘omics data sets, and effective data comprehension.

T6: Adaptive designs for Confirmatory Clinical Trials

Tuesday, March 8 | 1:45 pm – 3:30 pm
Franz König
Medical University of Vienna

Description: Since the first methodological papers on adaptive designs, some published more than 25 years ago, adaptive designs have gained increasing attention in drug development. Especially in pivotal phase III trials, their use is subject to enhanced scrutiny by regulators as the increased complexity of flexible study designs also increases the risk of operational and statistical biases and hidden fallacies. Broad enthusiasm about potential applications of such designs faced critical positions regarding their statistical efficiency. Despite, or possibly because of, this controversy, the methodology and its areas of applications grew steadily over the years, with significant contributions from statisticians working in academia, industry and agencies around the world. In the meantime, such types of adaptive designs have become the subject of three major regulatory guidance documents in the US and Europe and the field is still evolving. The main goal of this tutorial is to give an introduction to the key principles and statistical methodologies of adaptive designs for confirmatory clinical trials. Important applications of Continued on following page....
adaptive designs include sample size reassessment, treatment selection procedures, and population enrichment designs. The change of design parameters at an adaptive interim analysis may depend on any internal and external data available. Using adaptive multiple test procedures the type I error rate can be controlled even if the selection rule, the number of selected treatments or the final sample sizes are not prefixed. The tutorial shall provide an overview of methods from the published literature including the most recent developments. Special emphasis is put on sample size reassessment and multiple hypotheses testing with adaptive designs. Regulatory issues and case studies will be discussed.

Instructor Biography: Franz König is an Associate Professor at the Section of Medical Statistics at the Medical University of Vienna, Austria. He serves on several data safety monitoring boards (DSMB) as independent statistical expert. From 2008 till 2010 he was seconded to the European Medicines Agency (London, UK) as statistical expert in the Unit Human Medicines Development and Evaluation. At the EMA he held the Scientific Secretariat of the then newly founded Biostatistics Working Party (BSWP). He was involved in the development of guidelines and assessment of statistical methods and clinical trial protocols. His main research interests are multiple testing, adaptive/flexible designs, interim analyses and data safety monitoring boards. Franz has served as Guest Editor for Special Issues in Biometrical Journal and Statistics in Medicine. He is currently the work package leader of the work package “adaptive designs” in the EU FP7-funded research project IDEAL and deputy coordinator of an EU Horizon 2020 funded Marie Curie ITN network IDEAS on early drug development studies.

T7: Quantile Regression for Survival Analysis
Tuesday, March 8 | 3:45 pm – 5:30 pm
Limin Peng
Emory University

Description: Quantile regression offers a useful alternative strategy for analyzing survival data. It formulates covariate effects on the quantile(s) of an event time of interest. Such a modeling perspective entails easy interpretations of covariate effects, and allows for a comprehensive and flexible evaluation of the association between covariates and the survival outcome. Moreover, many existing quantile regression methods for survival analysis enjoy simple and stable computation. By these nice features, quantile regression has emerged as a valuable practical tool that can provide in-depth investigations of survival studies. In this tutorial, I plan to introduce the fundamentals of quantile regression (including basic concepts, modeling strategies, computing features and interpretations). Through reviewing and comparing with traditional regression methods for survival data, I will elaborate the benefits of conducting quantile regression analysis in survival settings. I will provide an overview of currently available methods for quantile regression with survival data, with a particular focus on a few popular approaches developed for randomly censored data. Available computing resources will be discussed. Examples will be presented to illustrate method applications and implementation.

Instructor Biography: Dr. Limin Peng is an Associate Professor in the Department of Biostatistics and Bioinformatics at the Emory University. She has been an active researcher in the areas of survival analysis and quantile regression. She has published a series of work in major statistical journals on quantile regression methods (or extensions) for various types of survival data, including randomly censored data, competing risks data, semicompeting risks data, truncated data, censored longitudinal data, and recurrent events data. Dr. Peng has disseminated novel applications of quantile regressions to research communities in Neurology, Dialysis, and Cystic Fibrosis. Dr. Peng has extensive teaching experiences on topics related to this tutorial. She has taught courses, “Survival Analysis Methods” and “Quantile Regression” at Emory University and taught a tutorial on quantile regression for survival analysis at 2014 ENAR Spring meeting and a short course on the same topic at Centers for Disease Control and Prevention.
### R1: Challenges in Cancer Epidemiology in the Era of Genomic Medicine

**Colin Begg**  
Sloan Kettering Cancer Center

**Description:** For decades cancer epidemiologists have investigated cancer risk and outcomes using studies in which the disease has been defined with the anatomic site of origin. This continues to be the organizing framework for much of our current research arena. The advent of powerful tools for examining tumors at the molecular level is altering the landscape of cancer investigation to one in which cancers are increasingly being classified on the basis of somatic mutations and other tumor characteristics. In this session we will discuss the implications of these trends for the design and analysis of epidemiologic studies of cancer risk.

### R2: Statistical Issues in the Analysis of Electronic Health Record Data

**Sebastain Haneuse**  
Harvard University

**Description:** Electronic health record (EHR) data present an incredibly appealing opportunity for public health and medical research. Relative to study designs that use dedicated databases, EHR data can provide information on a broad range of patients over longer timeframes and in real-world settings. Furthermore, they are typically relatively cheap to obtain. Nevertheless, the use of EHR data for research purposes is subject to many challenges including: (i) accurate extraction of text-based information; (ii) missing data; (iii) measurement error and misclassification and (iv) the control of confounding. While these issues arise in other contexts, the complexity and high-dimensional nature of EHR data poses additional challenges for statisticians. The purpose of this roundtable is to provide a forum for statisticians and analysts to discuss these issues, in general as well as in their own contexts, and also to discuss recent methodologic developments in the area.

### R3: Precision Medicine

**Michael Kosorok**  
University of North Carolina at Chapel Hill

**Description:** We will discuss research in precision medicine and key roles that biostatistics play, including important aspects of both discovery and evaluation. We will examine the multi-disciplinary character of the research and how recent developments in machine learning are being driven by biostatistical considerations.

### R4: Big Data in Healthcare Evaluation: The Role for Biostatistics

**David Ohlssen**  
Novartis

**Description:** Traditionally, big data has been defined as a dataset too large to be efficiently collected, stored, organized, and analyzed using currently available software. This complexity can be characterized by a combination of volume, velocity and variety. It has been suggested that the use of big data has enormous potential in the healthcare sector. For example, the aggregation and analysis of large real-world datasets adds power, allows trends and associations to be more readily observed, and overcomes some of the limitations associated with randomized clinical trials. The growing area of big data provides enormous potential for contributions by biostatisticians. However, so far our profession and ENAR have not been highly involved in big data activities. Within the context of healthcare evaluation this roundtable aims to discuss big data and the role for biostatistics. Possible topics for discussion include:

1. The skills we need to be involved with big data
2. Combining scientific knowledge (e.g. knowledge about pharmacology or design) with big data
3. Is big data just for prediction or can we make progress with causal inference

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4. Trials of the future will utilize censors and gadgets that potentially provide much richer more complex data from clinical research.

5. Data transparency initiatives have led to most pharmaceutical companies providing access to their individual patient clinical trial. What can be done to explore this new abundance of clinical data.

6. Computation developments such as Hamilton Monte Carlo and STAN.

R5: Quantitative Safety Review at FDA’s Center for Drug Evaluation and Research (CDER)

Mark Levenson
Food and Drug Administration

Description: This round table will discuss recent examples and future directions of the quantitative safety review at FDA’s Center for Drug Evaluation and Research (CDER). The following topics will be the bases of the discussion:

» Examples of quantitative safety review including meta-analyses, large safety trials, and observational studies conducted by drug companies or the FDA to address important drug safety issues.

» Implications of recent and proposed legislation and guidances and new data sources.

» Statistical careers at the FDA/CDER, particularly those involving drug safety.

R6: Leadership in Statistics

Dubois Bowman
Columbia University

Description: Statistical leadership is critical given the growing demand for analytical skills in society, coupled with the emergence of new areas from varied quantitative disciplines. In this roundtable, we will discuss leadership opportunities for statisticians. We will examine the role of being an effective leader, both within and outside in interdisciplinary settings. We will also cover ways that statisticians can prepare for leadership roles during various stages of their careers and tips for identifying leadership positions.

R7: Balancing Responsibilities in Academia: Methodological and Collaborative Research, Teaching, and Service

Amy Herring
University of North Carolina at Chapel Hill

Description: Faculty positions in biostatistics provide many interesting opportunities to engage in methodological and collaborative health science research, collaborate with students and junior scholars, and improve the home institution and profession more broadly through service activities. During this roundtable, we will share goals and formulate strategies for success (and recipes for stress) in exploring the sample space of academic opportunities. Amy Herring is Professor and Associate Chair of Biostatistics at UNC-Chapel Hill. She is a former ENAR President and recently completed a term as Chair of UNC’s Committee on Appointment, Promotion, and Tenure.

R8: Publishing Without Perishing: Strategies for Success in Publishing in Biostatistical 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 requires that it will be widely read and cited. In this roundtable, we will discuss 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.
R9: Practical Considerations for Teaching Biostatistics in a Hybrid, Blended, or Online Format

Jane Monaco
University of North Carolina at Chapel Hill

Todd Schwartz
University of North Carolina at Chapel Hill

Description: Whether you are considering updating an existing biostatistics course or tasked with developing a new one, numerous options exist for delivering the content. Many courses are moving away from traditional classroom lecturing. While some courses are taught completely online, debate surrounding the effectiveness of this format continues. Meanwhile, gaining in popularity are “Hybrid” or “Blended” formats, in which students are expected to view pre-recorded lectures before coming to class; class-time is devoted to active learning strategies and hands-on practice. This roundtable will provide an opportunity to discuss practical considerations, best practices and lessons learned in teaching biostatistics as classroom technology, online resources and student expectations continue to evolve. Discussion topics will include:

» What technologies are most effective? Considerations include ease of use, compatibility, and cost. Technology to be discussed may include desktop recording software, grading options, and classroom technology.

» What resources are available? Rather than “reinventing the wheel,” what existing options are helpful and available online?

» How can you avoid a “flipped classroom” flop? What strategies are effective for delivering content and administering the course?

» Roadblocks – what happens when students or administrators are reluctant to embrace an innovative classroom model?

» What is the time commitment for developing or updating a course with a hybrid, blended or online format?

Participate in Student-Focused Elements of the Scientific Program

The Sunday night mixer presents an ideal opportunity to obtain feedback on your work in our Annual ENAR Poster session. This year we will conduct our fifth Poster Competition for the session. Prizes will be announced within topical areas in the Tuesday morning Presidential Invited Address session. A student winner will be selected within each topical area. Watch for details on entering the competition on the website when the meeting registration becomes available.

Educational and Professional Development Opportunities

Be sure to take advantage of the educational offerings to be held during the meeting – short courses, tutorials, and roundtable discussions (see pages 94 - 105).

Network with Your Fellow Students

Back by popular demand, a CENS mixer will be held the evening of Monday, March 7, 2016. This is a great way to meet and greet your students from other graduate programs. Don’t miss this opportunity to begin building connections with your future colleagues and friends.
**ENAR 2016 Career Placement Services**

**Hours of Operation**

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**General Information**

The ENAR 2016 Career Placement Service helps match applicants seeking employment and employers. The service includes online registration and electronic uploading and distribution of applicant and employer materials through a password-protected online web-based facility. Visit the ENAR website at http://www.enar.org/meetings2016/career_center to register for the placement center.

Job announcements and applicant information can be readily accessed electronically, applicant information will be opened prior to the meeting, and materials will remain available online after the meeting. ENAR provides separate large reading/planning rooms for employers and applicants to review materials, dedicated placement center personnel onsite, and optional private interview rooms available for employers. Employer and applicant reading/planning rooms are equipped with a small number of computers with internet connections, and printers. However, to make the most efficient use of the Placement Center, we recommend that participants register listings in advance of the meeting to maximize visibility, explore the database before the meeting, and, if attending, have a laptop computer on-site.

**Employers**

Each year numerous qualified applicants, many approaching graduation, look to the ENAR Placement Center to begin or further their careers. Organizations including government agencies, academic institutions, and private pharmaceutical firms all utilize the ENAR Career Placement Service. ENAR recognizes the value the Career Placement Service provides to members and, to make it more efficient and effective for both employers and applicants, uses an electronic registration process and an online database of applicant resumes. All registered employers will receive full access to the placement center for up to 3 company representatives, up to 4 job postings, pre-meeting access to the online applicant database of resumes, full conference registration for up to 3 representatives, and access to the employer placement center room. ENAR is also offering those organizations seeking private interview space the option to reserve a private room for interviews in 4-hour increments.

**Employer Registration**

The registration fee for employers includes full access for up to four position postings and up to 3 representatives, pre-meeting access to the online applicant database of resumes, up to 3 full conference registrations, and access to the employer placement center room.

**Employer Resource Area**

ENAR will provide internet access, laptops, and printers available in the employer resource room for viewing the applicant resume database. However, for most efficient use of the resource room, we recommend employers have on-site access to a personal laptop computer.

**Interview Suites**

For an additional fee, employers may reserve private interview suites each day on a first-come, first-served basis.
Applicants
If you have an interest in a career in biometrics, you can utilize the ENAR Career Placement Center to get started or get ahead. Many employers attend the ENAR Spring Meeting each year seeking qualified applicants. All registered applicants may register for up to three job classification types, and receive full access to the placement center applicant room and the online employer job posting database. Please note that to fully utilize the online database, we recommend applicants register in advance to maximize visibility, explore the database shortly before the meeting and, if attending, have a laptop computer on-site. If you are planning to interview and participate on-site you must also register for the conference and pay the meeting registration fee.

Applicant Registration
The ENAR Career Placement Center provides opportunities for qualified applicants to meet employers and learn about organizations employing biostatisticians.

Visibility to Employers
The Online Applicant database is made available to all employers prior to the opening of the placement center.

Applicant Resource Area
ENAR will have internet access, three laptops, and printers in the applicant room for viewing the employer job posting database. However, for most efficient use we recommend applicants have on-site access to a personal laptop computer.

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Applicants
PLEASE NOTE: If you are planning to interview and participate on-site you must also register for the conference and pay the meeting registration fee.
The tutorials will be held on Monday, March 7 & Tuesday, March 8.

**Meeting Fees**
(To be paid by all applicants)
Registration fees, less a $100 administrative fee, will be refunded if written notice is received by February 1, 2016. Requests for refunds will not be honored after February 1, 2016. **No refunds will be issued for cancellation of short courses, tutorials, roundtables or the social event.**

**Meeting Registration Fees**

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* Includes membership in ENAR through December 31, 2016

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<th>Student (With letter from major professor verifying status.)</th>
<th>$165 ($175 after 2/1)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nonmember Student (With letter from major professor verifying status.)</td>
<td>$200 ($210 after 2/1)</td>
</tr>
<tr>
<td>Guest</td>
<td>$85 ($95 after 2/1)</td>
</tr>
</tbody>
</table>

**Short Courses**
The short courses will be held on Sunday, March 6. (Indicate short course number.)

<table>
<thead>
<tr>
<th>Member (participating society)</th>
<th>Fee:</th>
</tr>
</thead>
<tbody>
<tr>
<td>SC</td>
<td>$325 ($350 after 2/1)</td>
</tr>
<tr>
<td>SC</td>
<td>$225 ($250 after 2/1)</td>
</tr>
<tr>
<td>SC</td>
<td>$190 ($215 after 2/1)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Nonmember*</th>
<th>Fee:</th>
</tr>
</thead>
<tbody>
<tr>
<td>SC</td>
<td>$375 ($400 after 2/1)</td>
</tr>
<tr>
<td>SC</td>
<td>$275 ($300 after 2/1)</td>
</tr>
<tr>
<td>SC</td>
<td>$240 ($265 after 2/1)</td>
</tr>
</tbody>
</table>

**Tutorials**
The tutorials will be held on Monday, March 7 & Tuesday, March 8.

<table>
<thead>
<tr>
<th>Member</th>
<th>Nonmember</th>
<th>Student</th>
</tr>
</thead>
<tbody>
<tr>
<td>T1</td>
<td>$75 ($85 after 2/1)</td>
<td>$85 ($95 after 2/1)</td>
</tr>
<tr>
<td>T2</td>
<td>$75 ($85 after 2/1)</td>
<td>$85 ($95 after 2/1)</td>
</tr>
<tr>
<td>T3</td>
<td>$75 ($85 after 2/1)</td>
<td>$85 ($95 after 2/1)</td>
</tr>
<tr>
<td>T4</td>
<td>$75 ($85 after 2/1)</td>
<td>$85 ($95 after 2/1)</td>
</tr>
<tr>
<td>T5</td>
<td>$75 ($85 after 2/1)</td>
<td>$85 ($95 after 2/1)</td>
</tr>
<tr>
<td>T6</td>
<td>$75 ($85 after 2/1)</td>
<td>$85 ($95 after 2/1)</td>
</tr>
<tr>
<td>T7</td>
<td>$75 ($85 after 2/1)</td>
<td>$85 ($95 after 2/1)</td>
</tr>
</tbody>
</table>

**Council for Emerging and New Statisticians (CENS) Lunch, Tuesday, March 8**
I would like to join a group of attendees for a Tuesday networking lunch (at my own expense). **YES NO**

**Final Program Format**
I would like to receive the Final Abstract Book (you MUST check one)
- Mobile App Only
- Small Program Book – (no additional charge)
(Note that the full Final Program & Abstract book will be available on the ENAR website)

**Tuesday Night Dinner, Entertainment, and Networking Event**

<table>
<thead>
<tr>
<th>Event</th>
<th>Fee:</th>
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</thead>
<tbody>
<tr>
<td>Regular</td>
<td>$95</td>
</tr>
<tr>
<td>Student</td>
<td>$50</td>
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**Membership**

<table>
<thead>
<tr>
<th>Membership</th>
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</tr>
</thead>
<tbody>
<tr>
<td>Regular Member</td>
<td>$140</td>
</tr>
<tr>
<td>Includes electronic access to the Biometrics Journal, JABES Journal and Biometric Bulletin Newsletter</td>
<td></td>
</tr>
<tr>
<td>Regular Member</td>
<td>$150</td>
</tr>
<tr>
<td>Includes print subscription of one journal</td>
<td></td>
</tr>
<tr>
<td>either</td>
<td>Biometrics Journal or JABES Journal, and Biometric Bulletin newsletter</td>
</tr>
<tr>
<td>Regular Member</td>
<td>$160</td>
</tr>
<tr>
<td>Includes print subscriptions to Biometrics Journal, JABES Journal, and Biometric Bulletin newsletter</td>
<td></td>
</tr>
<tr>
<td>Student Member</td>
<td>$20</td>
</tr>
<tr>
<td>Includes electronic access to the Biometrics Journal, JABES Journal and Biometric Bulletin Newsletter</td>
<td></td>
</tr>
</tbody>
</table>

**TOTAL PAYMENT**

$__________

**FORM OF PAYMENT**

<table>
<thead>
<tr>
<th>Payment Method</th>
<th>YES NO</th>
</tr>
</thead>
<tbody>
<tr>
<td>Check*</td>
<td></td>
</tr>
<tr>
<td>Money Order*</td>
<td></td>
</tr>
<tr>
<td>MasterCard</td>
<td></td>
</tr>
<tr>
<td>Visa</td>
<td></td>
</tr>
<tr>
<td>AmEx</td>
<td></td>
</tr>
</tbody>
</table>

*The check or money order should be in U.S. currency, payable to ENAR.

**Credit Card Information**

<table>
<thead>
<tr>
<th>Credit Card Information</th>
<th>YES NO</th>
</tr>
</thead>
<tbody>
<tr>
<td>CARD NO.</td>
<td></td>
</tr>
<tr>
<td>EXP. DATE</td>
<td></td>
</tr>
<tr>
<td>NAME ON CARD</td>
<td>SIGNATURE</td>
</tr>
</tbody>
</table>
Membership Application

The International Biometric Society

Eastern North American Region (ENAR) | 12100 Sunset Hills Road, Suite 130 | Reston, VA 20190
Tel: 703–437–4377 | Fax: 703–435–4390 | E-mail: enar@enar.org

Please Print or Type

FIRST NAME       MIDDLE INITIAL   LAST NAME
DEGREE      TITLE
MAILING ADDRESS
CITY         STATE    ZIP CODE  COUNTRY
DAYTIME PHONE    FAX     E-MAIL

MEMBERSHIP TYPE

☐ Regular Member: $140
  Includes electronic access to the Biometrics Journal, JABES Journal and Biometric Bulletin Newsletter

☐ Regular Member: $150
  Includes print subscription of one journal, either ☐ Biometrics Journal or ☐ JABES Journal, and Biometric Bulletin newsletter

☐ Regular Member: $160
  Includes print subscriptions to Biometrics Journal, JABES Journal, and Biometric Bulletin newsletter

☐ Supporting Member: $30

☐ Student Member: $20
  Includes electronic access to the Biometrics Journal, JABES Journal and Biometric Bulletin Newsletter

I certify that ___________________________________________________________ is a full-time student.

Signature: ___________________________________________ Title: __________________________________________________

A Regular Member who is a member of a Region/National Group, termed Region/Group [R], may elect to become a Supporting Member in another Region/National Group, termed Region/National Group [S], Supporting Members will pay the International portion of the dues once and pay the additional Regional dues only to Region/National Group [S]. A Regular Member may become a Supporting Member of more than one Region or National Group. A Regular Member At-large may also become a Supporting Member in a Region/National Group of their choice. Supporting Members may not vote or hold any office in Regions/National Groups they support.

PLEASE INDICATE TWO AREAS OF INTEREST

☐ Agriculture (01)  ☐ Genetics and Heredity (05)
☐ Animal and Veterinary Science (02)  ☐ Molecular Biology and Biotechnology (06)
☐ Clinical Trials (03)  ☐ Toxicology (07)
☐ Epidemiology (04)  ☐ Entomology (08)

PAYMENT INFORMATION

☐ Enclosed is my Check, payable to ENAR (Remittance accepted only in US currency)

☐ Please charge my membership dues to: ☐ Visa ☐ MasterCard ☐ AmEx

CARD NO.      EXP. DATE
NAME ON CARD     SIGNATURE

NATURAL RESOURCES

☐ Ecology (08)  ☐ Forestry (11)
☐ Entomology (09)  ☐ Wildlife (12)
☐ Fisheries (10)

MAIL TO:
Wachovia Bank/ENAR
P.O. Box 758929
Baltimore, MD 21275–8929