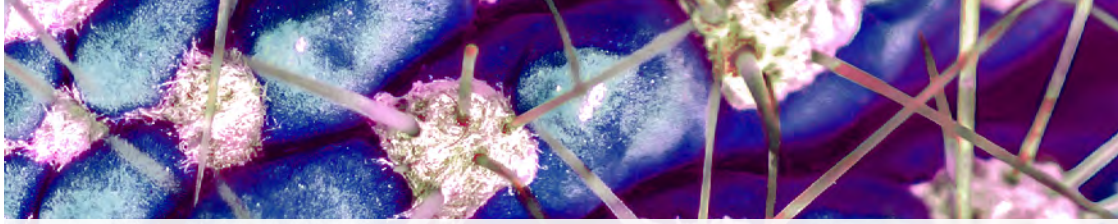
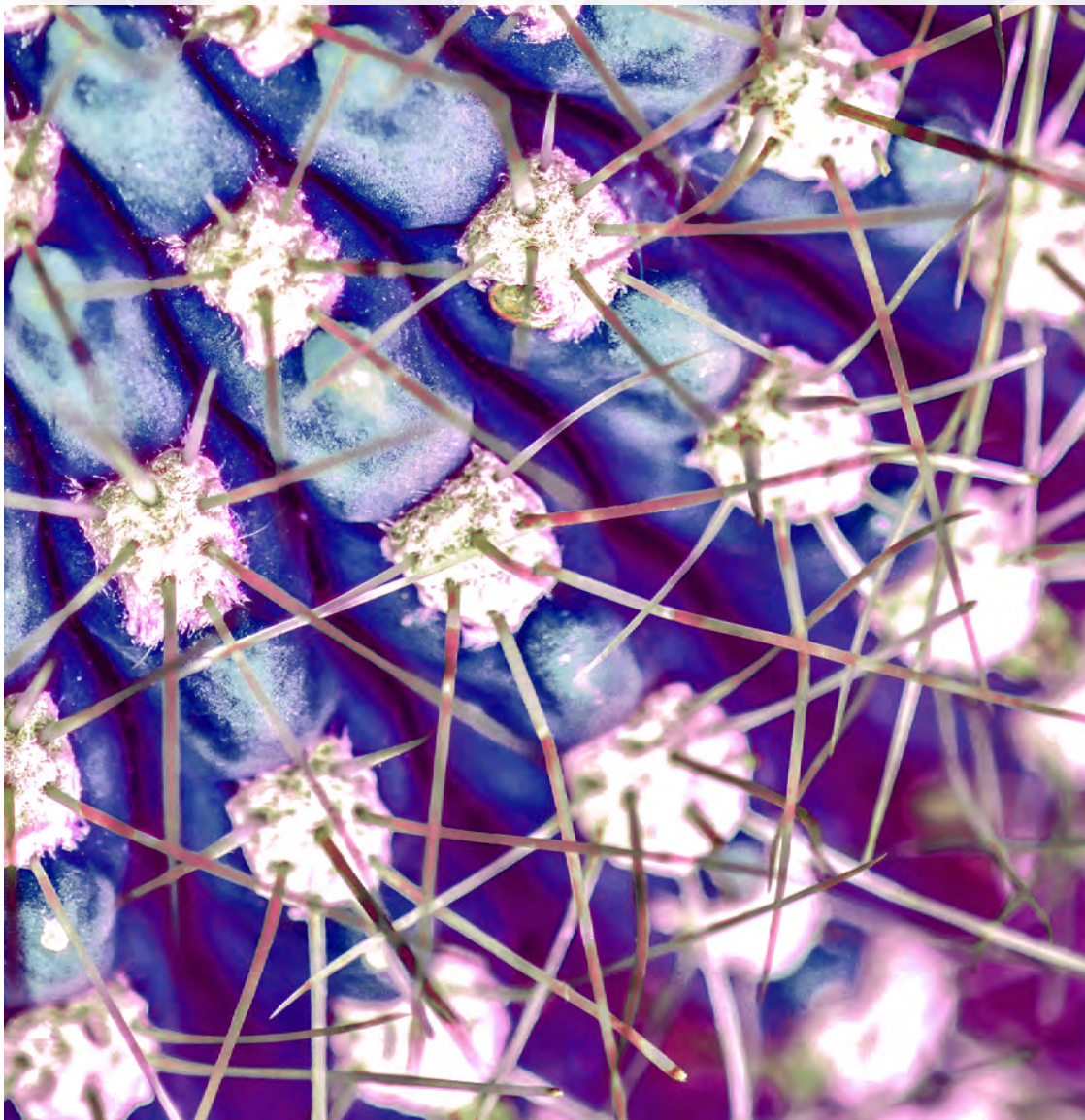


ENAR Spring Meeting

With IMS & Sections of ASA

March 6–9 2016

JW MARRIOTT AUSTIN | AUSTIN, TX



EARLY BIRD DEADLINE
FEBRUARY 1, 2016

Preliminary Program

ENAR

Welcome

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 Spring Meeting

March 6–9 | JW Marriott Austin | Austin, TX

With IMS and Sections of ASA

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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.

ENAR

Meeting Registration Fees

	By Feb.1	After Feb.1
ENAR/ WNAR/ IBS Member	$400	$475
ASA Member *(Not a member of ENAR/ WNAR/ IBS)*	$540	$615
IMS Member *(Note a Member of ENAR/ WNAR/ IBS) ($420 – $20 IMS contribution: $400)*	$400	$475
Student Member	$165	$175
Guest Fee	$85	$95
Non-member *(of any participating society)*	$590	$665
Student Non-member	$200	$210

Short Course Registration Fees

	By Feb.1		After Feb.1	
	Half Day	Full Day	Half Day	Full Day
Member	$225	$325	$250	$350
Non-Member	$275	$375	$300	$400

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.

Hotel & Transportation

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.*

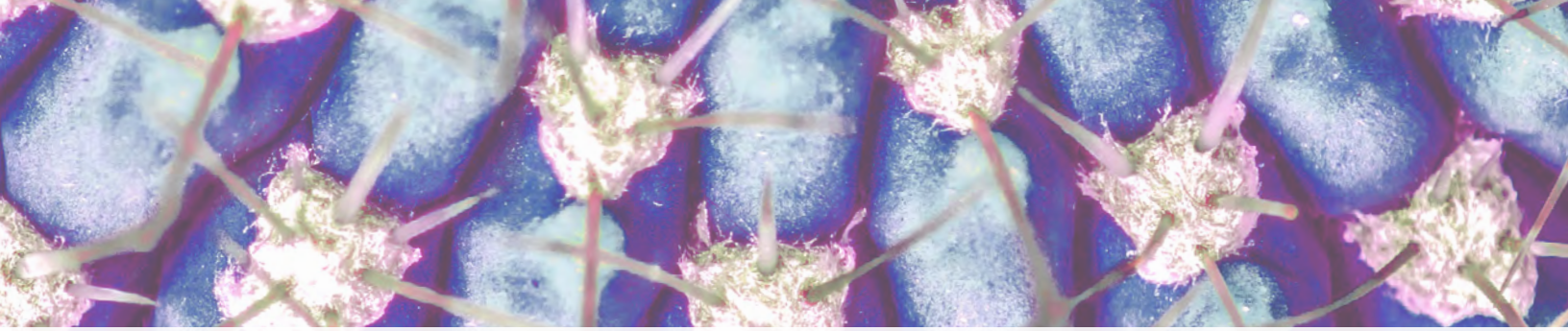
Parking at the JW Marriott Austin

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).



New For the 2016 Spring Meeting!

ENAR Meeting Mobile App

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

SOLD OUT

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 (sort of Second City Texas-style), singing, 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).*

Welcome to Austin!

Welome 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.

Entertainment Districts

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.

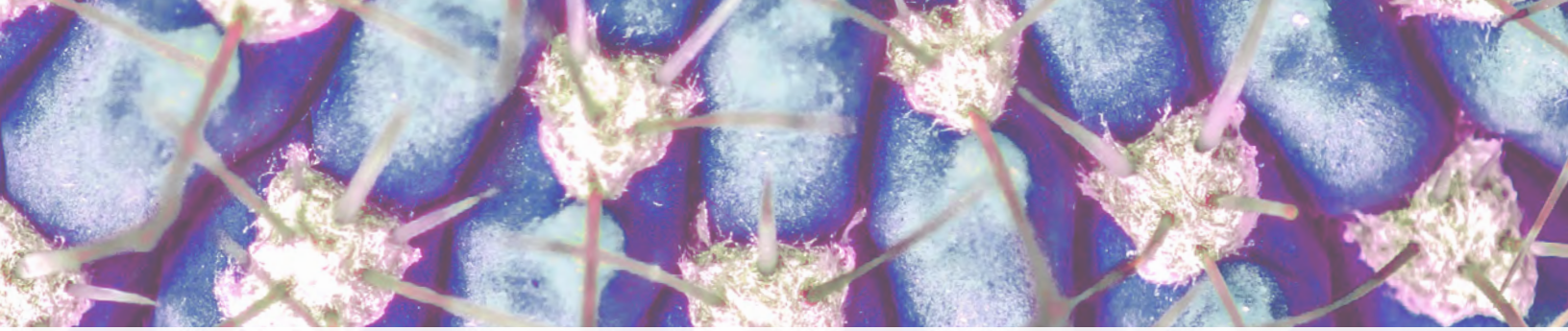
Rainey Street: With its neighborhood roots showing, the Rainey Street district features restaurants and bars tucked away in cozy bungalows, retrofitted shipping containers, and outside patio spaces. Highlights include G'Raj Mahal, Clive, Blackheart, and Banger's Sausage & Beer Garden. Be warned – there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



Special Thanks!

2016 ENAR Program Committee

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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

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ASA Statistics in Defense and National Security Section
Committee on National Statistics

Michael P. Cohen
ASA Survey Research Methods Section
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Sebastien Haneuse
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ASA Bayesian Statistical Science
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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

ENAR 2016 Presidential Invited Speaker

Xihong Lin, PhD

ENAR President Invited Talk

Chair and Henry Pickering Walcott Professor
Department of Biostatistics | Harvard University

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.

Biography

Xihong Lin is Chair and Henry Pickering Walcott Professor of Department of Biostatistics and Coordinating Director of the Program of Quantitative Genomics at the Harvard T. H. Chan School of Public Health. She received BS in Applied Mathematics from Tsinghua University, China and PhD in Biostatistics from University of Washington. Dr. Lin's research interests lie in development and application of statistical and computational methods for analysis of massive genetic and genomic, epidemiological, environmental, and medical data. She currently works on whole genome sequencing association studies, genes and environment, analysis of integrated data, and statistical methods for massive health science data.

Dr. Lin 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. Dr. Lin received the MERIT Award (R37) (2007-2015), and recently the Outstanding Investigator Award (OIA) (R35) (2015-2022) from the National Cancer Institute, which provides "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 (P01) on Statistical Informatics in Cancer Research, and the T32 training grant on interdisciplinary training in statistical genetics and computational biology.

Dr. Lin 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 is the Chair of the new ASA Section of Statistical Genetics and Genomics. 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.

ENAR 2016 IMS Medallion Lecture

Peter J. Diggle, PhD

CHICAS, Medical School, Lancaster University

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,

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

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, Mecitzan, 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 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

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

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

9:00 am - 5:00 pm **Placement Service**

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

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

T1: Topics in High-Performance Computing with R

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
23. Contributed Papers: Adaptive Designs and Adaptive Randomization
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

9:30 am - 4:30 pm **Placement Service**

10:15 am - 10:30 am **Refreshment Break with Our Exhibitors**

10:30 am - 12:15 pm **Tutorial**

T2: Interactive Data Visualizations in R with shiny and ggplot2

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**

T3: 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**

T4: 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)

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
	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

8:30 am - 10:15 am	**Scientific Program** (continued)
75.	Contributed Papers: Epidemiologic Methods
76.	Contributed Papers: GWAS: Applications
77.	Contributed Papers: Missing Data
78.	Contributed Papers: Semi-Parametric and Non-Parametric Survival Analysis
79.	Contributed Papers: Study Design
10:15 am - 10:30 am	**Refreshment Break with Our Exhibitors**
10:30 am - 12:15 pm	**Presidential Invited Address**
80.	Biostatistics, Biomedical Informatics, and Health Data Science: Research and Training
12:30 pm - 4:30 pm	**Regional Committee Luncheon Meeting (by Invitation Only)**
1:45 pm - 3:30 pm	**Tutorial**
T6:	Adaptive designs for Confirmatory Clinical Trials
	Scientific Program
81.	New Developments for Individualized Medical Decision Making in Real World Settings
82.	Emerging Issues in Clinical Trials with Time-to-Event Data in the Presence of Competing Risks
83.	New Development of Statistical Methods for Family-Based Sequencing Studies
84.	New Developments of Quantile Regression for Complex Data Analysis: Theories and Applications
85.	Current Developments and Issues for Meta-Analysis
86.	Survival Prediction Models for Medical Decision Making
87.	Statistical Machine Learning for Big-Bio-Data
88.	Contributed Papers: Causal Inference
89.	Contributed Papers: Functional Data Analysis
90.	Contributed Papers: High Dimensional Variable Selection
91.	Contributed Papers: Nonparametric Methods
92.	Contributed Papers: Spatiotemporal Modeling
93.	Contributed Papers: Survival Analysis: Multivariate and Hierarchical
3:30 pm - 3:45 pm	**Refreshment Break with Our Exhibitors**
3:45 pm - 5:30 pm	**Tutorial**
T7:	Quantile Regression for Survival Analysis
	Scientific Program
94.	Some New Developments in the Modern Longitudinal Data Analysis

3:45 pm - 5:30 pm	**Scientific Program** (continued)
95.	Statistical Considerations in Personalized Medicine: Concept and Methodology
96.	Innovative Techniques Towards Solving the Complexities of Biomarker Discovery
97.	New Developments of Bayesian Methods for Causal Inference
98.	Integrative Analysis of Multi-Omic Data for Understanding Complex Human Diseases
99.	Analysis of Next-Generation Sequencing Data: Increasing Accuracy and Novel Applications
100.	Networks for High Dimensional Time Series
101.	Contributed Papers: Environmental and Ecological Applications
102.	Contributed Papers: Genomics
103.	Contributed Papers: Meta-Analysis
104.	Contributed Papers: Semi-Parametric and Non-Parametric Methods
105.	Contributed Papers: Statistical Genetics: Heterogeneity and Hierarchy
106.	Contributed Papers: Variable Selection
5:30 pm - 6:30 pm	**ENAR Business Meeting** – Open to all ENAR Members
6:30 pm - 9:30 pm	**Tuesday Night Event** – Dinner at the Iron Cactus and a show at Esther's Follies

Wednesday March 9

7:30 am - 12:00 pm	**Speaker Ready Room**
7:30 am - 9:00 am	**Planning Committee** (by Invitation Only)
8:00 am - 12:30 pm	**Conference Registration**
8:00 am - 12:00 pm	**Exhibits Open**
8:30 am - 10:15 am	**Scientific Program**
107.	Statistical and Computational Challenges in Omics Data Integration
108.	Statistical Methods to Handle Treatment Crossover and Switch to an Alternative Therapy in Randomized Controlled Trials
109.	Sentinel Statistical Methods Working Groups, Challenges with Using Claims Data for Public Health
110.	Statistical Modeling of Data on Health Policy and Cost
111.	Weight Modification in Sample Surveys
112.	Generalizing Clinical Data Across Studies/Populations
113.	Novel Statistical Methods for Sequencing Data – From Quality Control to False Positives
114.	Contributed Papers: Bayesian Causal Inference
115.	Contributed Papers: Biomarkers

8:30 am - 10:15 am	**Scientific Program** (continued)
116.	Contributed Papers: Competing Risks
117.	Contributed Papers: GWAS: Testing
118.	Contributed Papers: Measurement Error
119.	Contributed Papers: Statistical Genetics
10:15 am - 10:30 am	**Refreshment Break with Our Exhibitors**
10:30 am - 12:15 pm	**Scientific Program**
120.	Inference for Brain Networks
121.	Recent Development in Joint Modeling for Longitudinal Data
122.	Model Validation: Its Concept, Statistical Integrity, Regulatory Landscape, and Industry Application
123.	Missing Data in Longitudinal Clinical Trials: Choice of Primary Estimand and its Relationship to the Statistical Analysis Methods
124.	Bayesian Analysis of Complex Survey Data
125.	Causal Inference in Social Networks
126.	Optimal Design for Nonlinear Models
127.	Contributed Papers: Bayesian Methods
128.	Contributed Papers: Causal Inference in Epidemiology and Health Policy
129.	Contributed Papers: Count and Categorical Data Analysis
130.	Contributed Papers: Joint Models for Longitudinal and Survival Data
131.	Contributed Papers: Personalized Medicine
132.	Contributed Papers: Survival Analysis

Sunday March 6

8:00 am - 11:00 pm Poster Presentations

1. POSTERS: Latent Variables and Mixture Models

Sponsor: ENAR

1a. INVITED POSTER:
The LZIP: A Bayesian Latent Factor Model for Correlated Zero-Inflated Counts

Brian Neelon* and **Dongjun Chung**, Medical University of South Carolina

1b. Understanding Gaussian Process Fits Using an Approximate Form of the Restricted Likelihood

Maitreyee Bose* and **James S. Hodges**, University of Minnesota
Sudipto Banerjee, University of California, Los Angeles

1c. A Joint Distribution for a Time-To-Event Outcome and Recurrent Events

Luojun Wang* and **Vernon M Chinchilli**, Penn State University

1d. Analysis of PHIS Data for a Zero-Truncated, 1&2 Inflated, and Multi-Level Count Variable

Ji Young Kim* and **Benjamin L. Laskin**, The Children's Hospital of Philadelphia
Tamar Y. Springel, University Hospital
Susan L. Furth, The Children's Hospital of Philadelphia and University of Pennsylvania
Justine Shults, University of Pennsylvania

1e. A Latent Variable Approach to Elicit Continuous Toxicity Scores and Severity Weights for Multiple Toxicities in Dose-Finding Oncology Trials

Nathaniel S. O'Connell* and **Elizabeth Garrett-Mayer**,
Medical University of South Carolina

1f. Multilevel Binary Principal Component Analysis

Yuting Xu*, **Chen Yue**, **Vadim Zipunnikov**, **Martin A. Lindquist** and **Brian S. Caffo**,
Johns Hopkins Bloomberg School of Public Health

1g. A Score Test for Detecting Publication Bias in Multivariate Random-Effects Meta-Analysis

Chuan Hong*, University of Texas Health Science Center, Houston
Haitao Chu, University of Minnesota
Yong Chen, University of Pennsylvania Perelman School of Medicine

1h. Measuring Concurrency Using a Joint Multistate and Point Process Model for Retrospective Sexual History Data

Hilary J. Aralis*, **Pamina M. Gorbach** and **Ron Brookmeyer**,
University of California, Los Angeles

1i. Evaluating Quality of Web Panel Survey Data via Clustering and Latent Classes

Elizabeth Handorf*, Fox Chase Cancer Center, Temple University
Susan Darlow, National Comprehensive Cancer Network
Michael Slifker and **Carolyn Heckman**, Fox Chase Cancer Center, Temple University
Lee Ritterband, University of Virginia

1j. Joint Modeling of Longitudinal, Recurrent Events and Failure Time Data for Survivor's Population

Qing Cai* and **Mei-Cheng Wang**, Johns Hopkins University
Gary Chan, University of Washington

1k. Model Diagnostics and Predictive Power Assessment of a Type of Joint Dynamic Models of Recurrent Competing Risks and a Terminal Event

Piaomu Liu*, University of South Carolina, Columbia

2. POSTERS: Imaging and Spatiotemporal Applications

Sponsor: ENAR

2a. INVITED POSTER:
Big Data and Neuroimaging: Large-Scale Models for Brain Networks

Xi Luo*, Brown University

2b. Scalar on Image Regression with Application to Multiple Sclerosis MRI Lesion Data

Cui Guo* and **Timothy D. Johnson**, University of Michigan

2c. Statistical Estimation of White Matter Microstructure from Conventional MRI

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

2d. Spatial Statistical Analysis of Suicidal Behavior in Harris County

Aron M. Trevino*, University of Texas Health Science Center, San Antonio
Dejian Lai, University of Texas Health Science Center, Houston

2e. Penalized Variable Selection for Spatial Binary and Count Data

Abdhi Amitabha Sarkar*, Michigan State University
Chae Young Lim, Seoul National University
Tapabrata Maiti, Michigan State University

2f. Relating Multi-Sequence Longitudinal Intensity Profiles and Clinical Covariates in Incident Multiple Sclerosis Lesions

Elizabeth M. Sweeney*, Johns Hopkins Bloomberg School of Public Health
Russell T. Shinohara, University of Pennsylvania
Blake E. Dewey and **Matthew K. Schindler**, National Institute of Neurological Disease and Stroke, National Institutes of Health
John Muschelli, Johns Hopkins Bloomberg School of Public Health
Daniel S. Reich, National Institute of Neurological Disease and Stroke, National Institutes of Health
Ciprian M. Crainiceanu, Johns Hopkins Bloomberg School of Public Health
Ani Eloyan, Brown University

2g. A Bayesian Zero-Inflated Multivariate Poisson Model for Identifying Functional Co-Activation Patterns

Caprichia Jeffers*, Emory University
Jian Kang , University of Michigan

2h. Spatial Approach to Age-Period-Cohort Models

Pavel Chernyavskiy*, **Mark P. Little** and **Philip S. Rosenberg**, National Cancer Institute, National Institutes of Health

2i. Modeling Nonstationarity in Space and Time

Lyndsay Shand* and **Bo Li**, University of Illinois, Urbana-Champaign

2j. Statistical Analysis of Trajectories on Riemannian Manifolds

Jingyong Su*, Texas Tech University

3. POSTERS: Clinical Trials, Adaptive Designs and Applications

Sponsor: ENAR

3a. INVITED POSTER:
C-Learning: A New Classification Framework to Estimate Optimal Dynamic Treatment Regimes

Baqun Zhang, Renmin University
Min Zhang*, University of Michigan

3b. An Extension of the Closure Principle for the Identification of Individual Efficacious Endpoints when Using Composite Endpoints in Clinical Trials

Jaclyn A. McTague*, **Dror Rom** and **Chen Chen**, Prosoft Clinical

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: Survivial Analysis

Sponsor: ENAR

4a. INVITED POSTER:
Quantile Residual Life Regression with Longitudinal Biomarker Measurements for Dynamic Prediction

Ruosha 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
Chiung-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

4n. **A Threshold-Free Prospective Prediction Accuracy Measure for Censored Time to Event Data**

Yan Yuan*, University of Alberta
Bingying Li and **Qian Zhou**, Simon Fraser University

5. POSTERS: Causal Interference

Sponsor: ENAR

5a. **INVITED POSTER:**
Estimating Causal Effects of Power Plant Regulations: Bipartite Causal Inference with Interference

Corwin M. Zigler* and **Chanmin Kim**, Harvard School of Public Health

5b. **On Justifying the Use of Summary Comorbidity Measures for Health Services Research**

Elizabeth A. Gilbert*, Temple University
Robert T. Krafty, Temple University and University of Pittsburgh
Richard J. Bleicher and **Brian L. Egleston**, Fox Chase Cancer Center

Nonparametric Estimation of Complier Effects with Continuous Instrumental Variables

Edward H. Kennedy* and **Dylan S. Small**, University of Pennsylvania

5d. **Propensity Score Matching for Clustered Data**

Mi-Ok Kim, Cincinnati Children's Hospital Medical Center
Bo Lu, The Ohio State University
Yu Wang*, **Chunyan Liu**, **Edward Nehus** and **Maurizio Macaluso**, Cincinnati Children's Hospital Medical Center

5e. **Machine Learning for Characterization of Developing Neuronal Cultures**

Diana R. Hall*, Columbia University
Ellese Cotterill, Cambridge University
Kathleen Wallace and **William Mundy**, United States Environmental Protection Agency
Stephen J. Eglen, Cambridge University
Timothy J. Shafer, United States Environmental Protection Agency

5f. **GLiDeR: Doubly Robust Estimation of Causal Treatment Effects with the Group Lasso**

Brandon Lee D. Koch*, **David M. Vock** and **Julian Wolfson**, University of Minnesota

5g. **The Validation Average Predictive Effect (VAPE) for Evaluating Risk Prediction Tools**

Andreas N. Strobl*, Technical University Munich, Germany
Donna P. Ankerst, Technical University Munich, Germany and University of Texas Health Science Center, San Antonio

6. POSTERS: Statistical Genetics, GWAS, and 'Omics Data

Sponsor: ENAR

6a. **INVITED POSTER:**
Bayesian Functional Graphical Regression: Application to Smoking Cessation Studies

Lin Zhang*, University of Minnesota
Veera Baladandayuthapani, **Francesco Versace** and **Jeffrey Morris**, University of Texas MD Anderson Cancer Center

6b. **INVITED POSTER:**
TSCAN: Pseudo-Time Reconstruction and Evaluation in Single-Cell RNA-Seq Analysis

Zhicheng Ji and **Hongkai Ji***, Johns Hopkins Bloomberg School of Public Health

6c. **Efficient Semiparametric Inference Under Two-Phase, Outcome-Dependent Sampling**

Ran Tao*, **Donglin Zeng** and **Dan-Yu Lin**, University of North Carolina, Chapel Hill

6d. **A Statistical Approach to Remove Nuisance Variation in Single Cell RNA-Seq Experiments**

Jeea Choi*, University of Wisconsin, Madison
Ning Leng and **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
Glen A. Satten, Centers for Disease Control and Prevention

6i. **A Novel Random Effect Model for GWAS Meta-analysis and its Application to Trans-ethic Meta-analysis**

Jingchunzi Shi* and **Seunggeun Lee**, University of Michigan

6j. **Novel Tests for Detection of Gene-Environment Interaction in Family Studies**

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
Nikolai Leonenko, Cardiff University
Alla 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 Longitudial 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

Sponsor: ENAR

7a. **INVITED POSTER: False Discovery Rate Smoothing**

James G. Scott* and **Wesley Tansey**, University of Texas, Austin

7b. **Asymptotic Behaviors of the Mantel-Haenszel Estimators and Their Robust Variance Estimators When the Common Effect Assumptions are Violated**

Hisashi Noma*, The Institute of Statistical Mathematics
Kengo Nagashima, Chiba University

7c. **StatStart, Harvard University Biostatistics Department**

Octavious Talbot*, **Sam Tracy** and **Alex Ocampo**, Harvard University

7d. **A Bayesian Approach to Account for Misclassification and Overdispersion in Count Data**

Wenqi Wu*, **James Stamey** and **David Kahle**, Baylor University

7e. **Improving the Dynamics of Data-Driven Discovery at Academic Health Centers**

Jonathan Gelfond and **Martin W. Goros***,
University of Texas Health Science Center, San Antonio

7f. **Simultaneous Prediction of Anticancer Activity and Toxicity in Aliphatic Nitrosoureas Using Quantitative Structure Activity Relationship (QSAR) Methods**

Soyi Sarkar*, **Isabel Alland** and **Solomon H. Jacobson**, Newark Academy

7g. **Incorporating Candidates with Multiple Associated Incompatible Donors in Kidney Paired-Donation**

Mathieu Bray*, **Wen Wang**, **Peter X-K. Song** and **John D. Kalbfleisch**,
University of Michigan

7h. **Estimating Neighborhood Socioeconomic Status Indexes in Cancer Risk Models**

David C. Wheeler* and **Jenna Czarnota**, Virginia Commonwealth University
Mary H. Ward, National Cancer Institute, National Institutes of Health

7i. **Comparison of Linear, Quadratic, and Linear Spline Regression Models to Examine the Relationship Between Birth-Weight and Systolic Blood Pressure in Children**

Amna Umer, **Candice Hamilton**, **Cris Britton**, **Lee Pyles**, **William Neal**, **Collin John** and **Christa Lilly***, West Virginia University

7j. **An Activity Index for Raw Accelerometry Data and its Comparison with Activity Counts**

Jiawei Bai*, Johns Hopkins University
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

Sponsor: ENAR

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**

Saebitna 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 **Jaroslaw 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
Wenxin Zhou, University of Melbourne
Fang Han, Johns Hopkins University

8p. **A Unified Theory of Confidence Regions and Testing for High Dimensional Estimating Equations**

Matey Neykov* and **Yang Ning**, Princeton University
Jun S. Liu, Harvard University
Han Liu, Princeton University

8q. **On the Estimation of Population Eigenvalues and the Asymptotic Properties of PCA in High-Dimensional Data**

Rounak Dey* and **Seunggeun Lee**, University of Michigan

9. POSTERS: Bayesian Methods and Computational Algorithms

Sponsor: ENAR

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**

Fridtjof Thomas*, University of Tennessee Health Science Center

9f. **Spatio-Temporal Bayesian Quantile Regression for Analyzing Weather Data of Us**

Priyam Das* and **Subhashis Ghoshal**, 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**

Yushu Shi* and **Purushottam Laud**, Medical College of Wisconsin

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**

Qinshu Lian* and **Haitao Chu**, University of Minnesota

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**

Matthew M. Weber* and **Debajyoti Sinha**, Florida State University
Dipak K. Dey, University of Connecticut

9n. **A Bayesian Screening Approach for Hepatocellular Carcinoma using Two Longitudinal Biomarkers**

Nabihah Tayob*, **Francesco Stingo**, **Kim-Anh Do** and **Ziding Feng**,
University of Texas MD Anderson Cancer Center

10. POSTERS: Semi-and Non-Parametric Methods

Sponsor: ENAR

10a. **On the Asymptotic Distribution of the Wilcoxon Signed Rank Test Statistic**

Xueyi Chen* and **Francisco J. Diaz**, University of Kansas Medical Center

10b. **Semiparametric Survival Model with Time-Dependent Cure Process**

Sophie Yu-Pu Chen* and **Alexander Tsodikov**, University of Michigan

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**

Ailin Fan*, **Rui Song** and **Wenbin Lu**, North Carolina State University

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-Parameric 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**

Zhen Zeng*, Merck
Wei Zheng and **Yuefeng Lu**, Sanofi

10j. **A Profile Maximum Pseudolikelihood Estimator for the Proportional Cause-Specific Hazards Model Under Outcome Misclassification**

Giorgos Bakoyannis*, **Ying Zhang** and **Constantin T. Yiannoutsos**,
Indiana University School of Medicine and Richard M. Fairbanks School of Public Health

10k. **Likelihood Ratio Testing in Functional Additive Models**

Merve Yasemin Tekbudak*, **Marcela Alfaro-Cordoba**, **Ana-Maria Staicu** and **Arnab Maity**, North Carolina State University

10l. **Nonparametric Change Point Detection Methods for Profile Variability**

Vladimir J. Geneus*, Florida State University

10m. **Covariate Adjusted Spearman's Rank Correlation with Probability-Scale Residuals**

Qi Liu* and **Bryan Shepherd,** Vanderbilt University
Valentine Wanga, Institute for Health Metrics and Evaluation
Chun Li, Case Western Reserve University

11. POSTERS: Censoring, Truncation, and Missingness

Sponsor: ENAR

11a. **Truncation-Based Nearest Neighbors Imputation for High Dimensional Data with Detection Limit Thresholds**

Jasmit S. Shah*, **Guy N. Brock, Shesh N. Rai** and **Aruni Bhatnagar**, University of Louisville

11b. **Multiple Imputation of Missing Covariates for the Cox Proportional Hazards Cure Model**

Lauren J. Beesley*, University of Michigan
Jonathan W. Bartlett, London School of Hygiene & Tropical Medicine
Jeremy M. G. Taylor, University of Michigan

11c. **Sequential BART for Imputation of Missing Covariates**

Dandan Xu*, University of Florida
Michael J. Daniels, University of Texas, Austin
Almut G. Winterstein, University of Florida

11d. **Combining Item Response Theory with Multiple Imputation to Equate Health Assessment Questionnaires**

Chenyang Gu*, **Roee Gutman** and **Vincent Mor**, Brown University

11e. **Hot Deck Multiple Imputation for Handling Accelerometer Missing Data**

Siying Li* and **Amy Herring**, University of North Carolina, Chapel Hill

11f. **Sampling Methods to Improve the Efficiency of Two-Phase Estimators for a Continuous Outcome**

Paul M. Imbriano* and **Trivellore E. Raghunathan**, University of Michigan

11g. **Bayesian Nonparametric Feature Selection Over Large-Scale Gene Networks with Missing Values**

Zhuxuan Jin*, Emory University
Zhou Lan, North Carolina State University
Jian Kang, University of Michigan
Tianwei Yu, Emory University

11h. **Binary Exposure and Longitudinal Cognition Outcomes in the Presence of Non-Ingorable Dropout and Death**

Maria Josefsson* and **Xavier de Luna**, Umea University
Michael J. Daniels, University of Texas, Austin
Lars Nyberg, Umea University

11i. **A Scalable Approach and R Package to Measure the Impact of Nonignorable Missing Data**

Weihua Gao* and **Baodong Xing**, University of Illinois, Chicago
Donald Hedeker, University of Chicago
Robin Mermelstin, University of Illinois, Chicago
Hui Xie, University of Illinois, Chicago and Simon Fraser University

11j. **Nonparametric Imputation for Nonignorable Missing Data**

Domonique Watson Hodge* and **Qi Long**, Emory University

12. POSTERS: Classification, Testing and Networks

Sponsor: ENAR

12a. Modeling Overdispersed Nuclear Bud Count Data Using the Generalized Monotone Incremental Forward Stagewise Method

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

13. POSTERS: Repeated Measures

Sponsor: ENAR

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 Pharmacueticals, 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

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

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 Kendziorski*, 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**

16. Statistical Considerations and Challenges in Evaluating Vaccine Efficacy

Sponsors: ENAR, ASA Biometrics Section
Organizer: Chiung-Yu Huang, Johns Hopkins University
Chair: Ying Qing Chen, Fred Hutchinson Cancer Research Center

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

17. Recent Advances in Subgroup Identification for Clinical Trial Regulatory Science

Sponsors: ENAR
Organizer: Bradley P. Carlin, University of Minnesota
Chair: Peter Muller, University of Texas at Austin

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 Experienve

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

8:30 **When do we Become Dinosaurs: Life After Grad School**
Janet Wittes*, Statistics Collaborative

9:00 **Strategic Planning and Management of Your Academic Career in Biostatistics**
Richard John Cook*, Universitiy of Waterloo

9:30 **Statistical Theory, Policy Fact: Preparing for the Role of a Government Statistician**
Steven Hoberman*, U.S. Food and Drug Administration

10:00 **Floor Discussion**

19. Precision Medicine: Statistical Challenges and Opportunities

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

8:30 **Machine Learning and Precision Medicine**
Michael R. Kosorok*, University of North Carolina, Chapel Hill

8:55 Adaptive Treatment Assignment: Getting Personal in Oncology
Peter F. Thall*, University of Texas MD Anderson Cancer Center

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

8:30 **Predicting Poor Pregnancy Outcomes from Multivariate Ultrasound Fetal Growth Data**
Paul S. Albert*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

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

8:30 **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

8:55 **Statistical Methods for Recurrent Event Data with Missing Event Category**

Jianwen Cai*, **Feng-Chang Lin** and **Jason P. Fine**, University of North Carolina, Chapel Hill
Huichuan J. Lai, University of Wisconsin, Madison

9:20 **Efficient Design and Analysis of Prevalent Cohort Studies**

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

9:45 **Variable Selection for Penalized Threshold Regression**

Xin He* and **Mei-Ling Ting Lee**, University of Maryland, College Park

10:10 **Floor Discussion**

22. Analysis of Longitudinally Observed Functional Data

Sponsors: IMS, ENAR
Organizer & Chair: Damla Senturk, University of California, Los Angeles

8:30 **A Functional Data Model for Analyzing Longitudinal Change of Daily Physical Activity**

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

9:00 **Modern Analysis of Longitudinal Functional Data**

So Young Park and **Ana-Maria Staicu***, North Carolina State University

9:30 **Inferring Brain Signal Synchronicity from a Sample of EEG Readings**

Donatello Telesca*, **Qian Li**, **Damla Senturk** and **Catherine Sugar**, University of California, Los Angeles

10:00 **Discussant:**

Jeffrey Morris, University of Texas MD Anderson Cancer Center

23. CONTRIBUTED PAPERS: Adaptive Designs and Adaptive Randomization

Sponsor: ENAR
Chair: Mercedes Bravo, Children's Environmental Health Initiative

8:30 **Optimal and Lead-In Adaptive Allocation for Binary Outcomes: A Comparison of Bayesian Methodologies**

Roy T. Sabo*, Virginia Commonwealth University
Ghalib Bello, Arbor Research Collaborative for Health

8:45 **More Efficient Treatment Comparison in Cross-Over Design by Allocating Subject Based on Ranked Auxiliary Variables**

Yisong Huang* and **Hani Samawi**, Georgia Southern University

9:00 **A Bayesian Sequential Design with Binary Outcome**

Han Zhu*, **Qingzhao Yu** and **Donald Mercante**, Louisiana State University

9:15 **An Efficient Method to Simulate Bayesian Adaptive Clinical Trials**
Zhenning Yu*, **Viswanathan Ramakrishnan** and C**aitlyn Ellerbe**, Medical University of South Carolina

9:30 **Multi-Stage Dose-Schedule Finding Designs for Pre-Clinical Studies in Stroke**
Chunyan Cai*, University of Texas Health Science Center, Houston
Jing Ning and **Xuelin Huang**, University of Texas MD Anderson Cancer Center

9:45 **The Most Powerful Test and the Order of Error Probabilities for Response Adaptive Designs**
Yanqing Yi*, Memorial University of Newfoundland
Xuan Li, University of Minnesota, Duluth

10:00 **Floor Discussion**

24. CONTRIBUTED PAPERS: Clinical Trials

Sponsor: ENAR
Chair: Ritesh Ramchandani, Harvard University

8:30 **Stochastic Modeling of Patients Recruitment in Clinical Trials**
Nicolas J. Savy*, Mathematics Institute of Toulouse

8:45 **A Multi-State Model for Designing Clinical Trials for Testing Overall Survival Allowing for Crossover after Progression**
Fang Xia*, University of Texas MD Anderson Cancer Center
Stephen L. George and **Xiaofei Wang**, Duke University

9:00 **Control of False Positives in Randomized Phase III Clinical Trials**
Changyu Shen*, **Ziyue Liu** and **Huiping Xu,** Indiana University
Hai Liu, Gilead Sciences, Inc.
Cynthia Yue, Indiana University

9:15 **One-Sided Global Tests for Multivariate Outcomes in Randomized Trials**
Donald Joseph Hebert*, University of Rochester Medical Center

9:30 **Inequality in Treatment Benefits: Can we Determine if a New Treatment Benefits the Many or the Few?**
Emily J. Huang*^, Johns Hopkins University
Ethan X. Fang, Princeton University
Michael A. Rosenblum, Johns Hopkins University

9:45 **Factorial Clinical Trials for Hybrid Research Studies: Design and Analysis of Optimizing Treatment for Complicated Grief**
Christine M. Mauro* and Xin Qiu, Columbia University
Donglin Zeng, University of North Carolina, Chapel Hill
Naihua Duan and **Yuanjia Wang**, Columbia University

10:00 **Estimating Individualized Treatment Rules for Ordinal Treatments**
Jingxiang Chen*^, **Yufeng Liu**, **Michael R. Kosorok**, University of North Carolina, Chapel Hill
Haoda Fu and **Xuanyao He**, Eli Lilly and Company

25. CONTRIBUTED PAPERS: Clustered Data Methods

Sponsor: ENAR
Chair: Grant Brown, University of Iowa

8:30 **Learning Parameter Heterogeneity in Data Integration**
Lu Tang* and **Peter X.K. Song**, University of Michigan

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

8:30 Predicting Alzheimer's Disease with Bivariate Mixture Modeling

Frank Appiah*, **Erin Abner**, **David Fardo**, **Glen Mays** and **Richard Charnigo**, University of Kentucky

8:45 Time-Dependent Predictive Accuracy Curve Under Marker-Dependent Sampling

Zhaoyin Zhu*, New York University
Xiaofei Wang, Duke University
Paramita Saha Chaudhuri, McGill University

9:00 Estimating the Impact of Basing Treatment Decisions on Markers that Predict Risk

Marshall D. Brown* and **Holly Janes**, Fred Hutchinson Cancer Research Center

9:15 Bayesian Inference for Black Hispanic Breast Cancer Survival Data

Hafiz Khan*, Texas Tech University

9:30 Design and Analyses of Two-Phase Studies for Predicting Binary Outcomes

Xinglei Chai* and **Jinbo Chen**, University of Pennsylvania

9:45 Combining Multiple Biomarkers Linearly to Maximize the Partial Area Under the ROC Curve

Qingxiang Yan*, **Leonidas E. Bantis** and **Ziding Feng**, University of Texas MD Anderson Cancer Center

10:00 Building Better Gene Signatures with Rank-Based Features and Meta-Analysis

Prasad Patil* and **Jeffrey T. Leek**, Johns Hopkins University

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

10:30 Statistical Analysis of Data in Metric Space with Applications in Microbiome Studies

Hongzhe Li*, University of Pennsylvania

10:55 High-precision Microbial Community Functional Profiling and Meta'omic Integration

Curtis Huttenhower*, Harvard School of Public Health

11:20 Some Challenges in the Analysis of Microbiome Data: Old Wine in a New Bottle with a Twist!

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

11:45 Flexible Methods for Testing Microbiome by Environment Interactions

Michael C. Wu*, Fred Hutchinson Cancer Research Center

12:10 Floor Discussion

29. Recent Advances and Challenges in Adaptive Design for Clinical Trials

Sponsors: ENAR, ASA Biopharmaceutical Section
Organizer: Ying Yuan, University of Texas MD Anderson Cancer Center
Chair: Haitao Pan, University of Texas MD Anderson Cancer Center

10:30 **Continual Reassessment Method with Multiple Toxicity Constraints for Late Onset and Cumulative Toxicities**
Shing M. Lee*, Columbia University

10:55 **Sequential Design Method for Bioequivalence Test with Serial Sampling Data**
Fangrong Yan* and **Junling Liu**, Pharmaceutical University, China
Xueling Huang, University of Texas MD Anderson Cancer Center

11:20 **Bayesian Optimal Interval (BOIN) Designs for Phase I Clinical Trials**
Ying Yuan* and **Suyu Liu**, University of Texas MD Anderson Cancer Center

11:45 **Phase I-II Clinical Trials with Delayed Outcomes**
Joseph S. Koopmeiners*, University of Minnesota

12:10 **Floor Discussion**

30. Health Care Provider Evaluation

Sponsors: ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology
Organizer & Chair: Kevin He, University of Michigan

10:30 **A Dirichlet Process Mixture Model for Survival Outcome Data: Assessing Nationwide Kidney Transplant Centers**
Lili Zhao, **Jing Chunzi Shi**, **Tempie Shearon** and **Yi Li***, University of Michigan

10:55 **Healthcare Provider Comparisons: Identifying and Meeting Goals**
Thomas A. Louis*, Johns Hopkins Bloomberg School of Public Health

11:20 **Methods for Profiling Medical Facilities**
John D. Kalbfleisch* and **Kevin Zhi He**, University of Michgan

11:45 **On the Accuracy of Classifying Hospitals on Their Performance Measures**
Yulei He*, Centers for Disease Control and Prevention
Sharon-lise Normand, Harvard Medical School

12:10 **Floor Discussion**

31. The Future of Biostatistical Funding Mechanisms

Sponsor: ENAR
Organizers: Ciprian Crainiceanu, Johns Hopkins University and Hernando Ombao, University of California, Irvine
Chair: Hernando Ombao, University of California, Irvine

10:30 **Discussants:**
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

12:00 **Floor Discussion**

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

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 Szefer 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

12:00 **Floor Discussion**

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

10:30 **Using Threshold Regression to Analyze Survival Data from Complex Surveys: With Application to NHANES III Phase II Genetic Data**

Yan Li , **Dandan Liao**, and **Mei-Ling Ting Lee***, University of Maryland

10:55 **Efficient Tests of Association for Survival Times from Two-Phase Outcome-Dependent Samples**

Jerald F. Lawless*, University of Waterloo

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

12:00 **Statistical Approaches for Exploring Brain Connectivity with Multi-Modal Neuroimaging Data**

Phebe B. Kemmer* and **Ying Guo**, Emory University
DuBois Bowman, Columbia University

37. CONTRIBUTED PAPERS: Bayesian Clinical Trials

Sponsor: ENAR

Chair: Sijin Wen, West Virginia University

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

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 Kabban, 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

39. 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

40. 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 am - 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-Torrres* and **Alyssa Frazee**, Johns Hopkins University
Michael I. Love and **Rafael A. Irizarry**,
Dana-Farber 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

1:45 Rare Variant Association Tests with Longitudinal Outcome Data

Zihuai He, **Seungeung Lee**, **Min Zhang** and **Bhramar Mukherjee***, University of Michigan

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

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

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

47. 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

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
Kuolung Hu and **Catherine Jia**, Amgen, Inc.

2:10 **Statistical Methods for Conditional Survival Analysis**

Sin-Ho Jung*, Duke University
Sunkyu Choi and **Ho Yun Lee**, Samsung Medical Center

2:35 **Multi-arm Platform Designs for Screening Effective Treatments via Predictive Probability**

J. Jack Lee*, **Brian P. Hobbs** and **Nan Chen**, University of Texas MD Anderson Cancer Center

3:00 **Optimal Flexible Sample Size Design with Robust Power**

Lu Cui*, **Lanju Zhang** and **Bo Yang**, AbbVie Inc.

3:25 **Floor Discussion**

48. Statistical Advances in Evolutionary Dynamics of Infectious Diseases

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

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

2:10 **Phylodynamic Analysis with Limited Data: Emergence and Epidemiological Impact of Transmissible Defective 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

2:35 **An Efficient Bayesian Inference Framework for Coalescent-based Nonparametric Phylodynamics**

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

3:00 **Effects of Ignoring Recombination in Phylodynamics of Infectious Diseases**

Julia A. Palacios*, Harvard University and Brown University

3:25 **Floor Discussion**

49. CONTRIBUTED PAPERS: Bayesian Semi-Parametric and Non-Parametric Methods

Sponsor: ENAR

Chair: A. Lawrence Gould, Merck Research Laboratories

1:45 Flexible Bayesian Survival Modeling with Semiparametric Time-Dependent and Shape-Restricted Covariate Effects

Thomas A. Murray* and **Brian P. Hobbs**, University of Texas MD Anderson Cancer Center
Daniel J. Sargent, Mayo Clinic
Bradley P. Carlin, University of Minnesota

2:00 A Bayesian Semiparametric Approach for Panel Count Data

Jianhong Wang* and **Xiaoyan Lin**, University of South Carolina, Columbia

2:15 Nonparametric Smoothing Estimation of Fecundability from a Conception Model

Mohammed R. Chowdhury*, Kennesaw State University

2:30 Marginal Bayesian Hierarchical Model for Multivariate Binary Data to Estimate the Etiology of Childhood Pneumonia

Detian Deng* and **Scott Zeger**, Johns Hopkins University

2:45 A Semiparametric Bayesian Approach to Borrow Information from Historical Control Data in Two Arm Clinical Trials.

Arpita Chatterjee*, Georgia Southern University

3:00 Bayesian Multivariate Nonlinear Mixed Effects Models with a Matrix Stick-Breaking Process Prior

Xiao Wu*, University of Florida
Michael J. Daniels, University of Texas, Austin

3:15 Bayesian Additive Partial Linear Models with Measurement Error and Heteroscedastic Regression Error Variance

Chang Liu and **Sally W. Thurston***, University of Rochester

50. CONTRIBUTED PAPERS: Bayesian Variable Selection

Sponsor: ENAR

Chair: Rajesh Nair, U.S. Food and Drug Administration

1:45 Altered Singular Bayesian Information Criteria for Bivariate Mixture Models

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

2:00 Bayesian Bi-Level Variable Selection

Eunjee Lee*, **Hongtu Zhu** and **Joseph G. Ibrahim**, University of North Carolina, Chapel Hill

2:15 Bayesian Variable Selection for Skewed Heteroscedastic Response

Libo Wang*^, Florida State University
Yuanyuan Tang, AbbVie
Debajyoti Sinha and **Debdeep Pati**, Florida State University
Stuart Lipsitz, Brigham and Women's Hospital

2:30 Bayesian Ranking and Selection with Application to Identification of Risk Genes

Xiaoqian Sun* and **Feng Luo**, Clemson University
Anand K. Srivastava, Greenwood Genetic Center

2:45 Bayesian Variable Selection in Additive Partial Linear Models with Error in Variables

Chang Liu*, **Hongqi Xue** and **Sally W. Thurston,** University of Rochester

3:00 **Bayesian Feature Screening for Big Neuroimaging Data Via Massively Parallel Computing**
Jian Kang*, University of Michigan

3:15 **The Bayesian Multivariate Regression for High Dimensional Longitudinal Data with Heavy-Tailed Errors**
Viral V. Panchal*, **Daniel Linder** and **Hani Samawi**, Georgia Southern University

51. CONTRIBUTED PAPERS: Graphical Models

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

1:45 **Estimation of High-Dimensional Graphical Models Using Regularized Score Matching**
Lina Lin*, **Mathias Drton** and **Ali Shojaie**, University of Washington

2:00 **High-Dimensional Robust Precision Matrix Estimation: Cellwise Corruption Under Epsilon-Contamination**
Po-Ling Loh and **Xin Lu Tan***, University of Pennsylvania

2:15 **A New Ordinary Differential Equation Model for Reconstruction of Gene Regulatory Network**
Yaqun Wang*, Rutgers, The State University of New Jersey
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

3:15 **A Joint Modeling Approach for Directed Acyclic Network Data**
Yan Zhou*, Merck & Co.
Peter Song, University of Michigan

52. CONTRIBUTED PAPERS: Multivariate Methods

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

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. Durkals**ki, 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

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

3:45 pm - 5:30 pm **Oral Posters & Presentations**

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

3:45 Testing for Association Between Genetic Variants and Brain Networks

Junghi Kim and **Wei Pan***, University of Minnesota

4:10 Integrating Genomic and Imaging Data: An Atomic Approach

Debashis Ghosh*, Colorado School of Public Health

4:35 Joint Mediation Analysis of Imaging and Genetic Data in Genetic Association Studies of Complex Diseases

Hongtu Zhu*, University of North Carolina, Chapel Hill

5:00 Heritability-based Prioritization of Structural Neuroimaging Phenotypes

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

5:25 Floor Discussion

55. Recent Advances in Adaptive Model-Based Design of Clinical Trials

Sponsors: ENAR, ASA Biopharmaceutical Section

Organizer & Chair: Sergei Leonov, ICON Clinical Research

3:45 Adaptive Dose Escalation Methods in Phase I Oncology Trials: A Case Study

Inna Perevozskaya*, **Roberto Bugarini** and **Mani Lakshminarayanan**, Pfizer Inc.

4:15 Early-phase Design for a Combination of Targeted Therapies in Oncology

Nolan A. Wages*, **Craig A. Portell** and **Gina R. Petroni**, University of Virginia

4:45 Inference in Experiments with Pilot Data

Nancy Flournoy*, University of Missouri

5:15 Discussant:

Valerii Fedorov, ICON Clinical Research

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

3:45 Quantifying Physical Activity in Mid-to-Late Life

Jennifer A. Schrack* and **Vadim Zipunnikov**, Johns Hopkins University
Luo Xiao, North Carolina State University
Ciprian Crainiceanu, Johns Hopkins University
Luigi Ferrucci, National Institute on Aging, National Institutes of Health

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 Braitstein, 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

4:35 **Validation of Reclassification Measures-the Role of Calibration**
Nancy R. Cook*, Brigham and Women's Hospital

5:00 **Correcting for Over-optimism in Metrics of Prognostic Model Improvement**
Megan L. Neely* and **Michael J. Pencina**, Duke University and Duke Clinical Research Institute

5:25 **Floor Discussion**

59. Functional Regression Methods and Personalized Medicine

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

3:45 **Functional Regression Methods for Densely-Sampled Biomarkers in the ICU**
Ciprian Crainiceanu*, Johns Hopkins University

4:10 **Functional Feature Construction for Personalized Treatment Regimes**
Eric B. Laber*, **Robert Pehlman** and **Ana-Maria Staicu**, North Carolina State University

4:35 **Estimation of Optimal Treatment Policies and Marginal Screening of Functional Predictors**
Ian W. McKeague*, Columbia University

5:00 **Developing Biomarkers for Brain Lesion Trajectories in Longitudinal MRI**
Elizabeth M. Sweeney, Johns Hopkins University
Russell T. Shinohara*, 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

5:25 **Floor Discussion**

60. Bayesian Methods for Large-Scale Non-Guassian Data

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

3:45 **Bayesian Modeling of Huge Tables and Discrete Data**
David B. Dunson*, Duke University

4:10 **Bayesian Models of High-Dimensional Count Data**
Marina Vannucci*, Rice University
Michele Guindani, University of Texas MD Anderson Cancer Center

4:35 **Valid Statistical Analyses and Reproducible Science in the Era of High-throughput**
Edoardo M. Airoldi*, Harvard University

5:00 **Floor Discussion**

61. CONTRIBUTED PAPERS: Cancer Applications

Sponsor: ENAR
Chair: Kerrie Nelson, Boston University

3:45 **P53-Based Strategy to Reduce Hematological Toxicity of Chemotherapy: A Pilot Study**
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

4:00 **Using IMRE and ANOVA to Select MicroRNAs for Predicting Prostate Cancer Recurrence**
Qi Wang*, **Bin Guo** and Y**arong Yang**, North Dakota State University

4:15 **Implementation of a 2-Stage Crossover Correction in Analysis of Overall Survival (OS): An Example in Oncology**

Ruifeng Xu*, **Jingshu Wang** and **James M. Pellissier**, Merck & Co., Inc.

4:30 **Modeling Multiple Primary Cancers Over Time Using Non-Homogeneous Poisson Process**

Jialu Li*, University of Texas MD Anderson Cancer Center
Seung Jun Shin, Korea University
Wenyi Wang, University of Texas MD Anderson Cancer Center

4:45 **Assessing Intra-Tumor Heterogeneity and Tracking Longitudinal and Spatial Clonal Evolution by Next-Generation Sequencing**

Yuchao Jiang*, **Andy J. Minn** and **Nancy R. Zhang**, University of Pennsylvania

5:00 **Pathway-Based Differential Network Analysis in Cancer**

M**in Jin Ha***, **Veerabhadran Baladandayuthapani** and **Kim-Anh Do**, University of Texas MD Anderson Cancer Center

5:15 **Cell Type-Specific Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration Using Expression Data**

Zeya Wang*, Rice University
Jeffrey S. Morris, University of Texas MD Anderson Cancer Center
Jaeil Ahn, Georgetown University
Bo Li, Harvard University
Wei Lu, **Ximing Tang** and **Ignacio I. Wistuba**, University of Texas MD Anderson Cancer Center
Chris C. Holmes, University of Oxford
Wenyi Wang, University of Texas MD Anderson Cancer Center

62. CONTRIBUTED PAPERS: Heterogeneous Treatment Effects

Sponsor: ENAR

Chair: David Wheeler, Virginia Commonwealth University

3:45 **On Clinical Trials with a High Placebo Response Rate**

George Chi and **Pilar Lim***, Janssen Research & Development, LLC

4:00 **Using IMRE and Dual KS to Select MicroRNAs for Predicting Prostate Cancer Recurrence**

Yarong Yang* and **Qi Wang**, North Dakota State University

4:15 **Estimating Treatment Effect in Time to Relapse When Patients Switch Treatment**

Miao Lu*, University of Virginia
Jian Han, Genentech, Inc.

4:30 **Inference on Subgroups and All-Comers Cognizant of Logical Relationships Among Efficacy Parameters**

Szu-Yu Tang*, Ventana Medical Systems, Inc. (Roche Group)
Yi Liu, Millennium: The Takeda Oncology Company
Jason Hsu, Eli Lilly & Company and The Ohio State University

4:45 **Logical Inference on Treatment Efficacy in Subgroups and Their Mixtures**

Ying Ding*, University of Pittsburgh
Hui-Min Lin, Takeda Pharmaceuticals
Jason C. Hsu, Eli Lilly & Company and The Ohio State University

5:00 **Confident Effect of a SNP on the Efficacy of a Drug**

Jason C. Hsu*, Eli Lilly & Company and The Ohio State University
Ying Ding, University of Pittsburgh
Ying Grace Li and **Stephen J. Ruberg**, Eli Lilly & Company

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**, GlaxoSmithKline Vaccines
L. J. Wei, Harvard University

63. CONTRIBUTED PAPERS: High Dimensional Data Applications

Sponsor: ENAR

Chair: Quanquan Gu, University of Virginia

3:45 **Linear Shrinkage Revisited: Positive-Definite Modification of Large-dimensional Covariance Matrix Estimators with Applications to Rehabilitative Speech Treatment of Patients with Parkinson's Disease**

Young-Geun Choi*^ and **Johan Lim**, Seoul National University

4:00 **Multivariate Test for High Dimensional Compositional Changes in Paired Microbiome Studies**

Ni Zhao*, **Xiang Zhan** and **Michael Wu**, Fred Hutchinson Cancer Research Center

4:15 **Kernel-Based Nonparametric Testing in High-Dimensional Data with Applications to Gene Set Analysis**

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

4:30 **Covariance Enhanced Screening for Ultrahigh-Dimensional Classification**

Yanming Li*, **Kevin Ke**, **Ji Zhu** and **Yi Li**, University of Michigan

4:45 **Dissecting the Gene-Environment Interactions: A Robust Penalization Approach Accounting for Hierarchical Structures**

Cen Wu*, Kansas State University and Yale University
Yu Jiang, University of Memphis
Shuangge Ma, Yale University

5:00 **Do-Over: Replicates in High Dimensions, with Applications to Latent Variable Graphical Models**

Kean Ming Tan* and **Yang Ning**, Princeton University
Daniela Witten, University of Washington
Han Liu, Princeton University

5:15 **Sparse Linear Discriminant Analysis in Structured Covariates Space**

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

64. CONTRIBUTED PAPERS: Machine Learning

Sponsor: ENAR

Chair: Haresh Rochani, Georgia Southern University

3:45 **Lagged Kernel Machine Regression for Identifying Time Windows of Susceptibility to Complex Metal Mixtures**

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

4:00 **A Group-Specific Recommender System**

Xuan Bi* and **Annie Qu**, University of Illinois, Urbana-Champaign
Junhui Wang, City University of Hong Kong
Xiaotong Shen, University of Minnesota

4:15 **A General Unimodal Null Distribution with Applications to Cluster Significance Testing**

Erika Helgeson and **Eric Bair***, University of North Carolina, Chapel Hill

4:30 **Random Forests: How a Chance Driven Learning Machine Does So Spectacularly Well**

Dan Steinberg*, Salford Systems
Adele Cutler, Utah State University

4:45 **Robust Learning for Optimal Treatment Decision with NP-Dimensionality**

Chengchun Shi*, **Rui Song** and **Wenbin Lu**, North Carolina State University

5:00 **Region Based Mediation Test of DNA Methylation Using Kernel Machine Regression**

Jincheng Shen* and **Xihong Lin**, Harvard School of Public Health

5:15 **Adaptive Contrast Weighted Learning for Multi-Stage Multi-Treatment Decision-Making**

Yebin Tao*^ and **Lu Wang**, University of Michigan

65. CONTRIBUTED PAPERS: Next Generation Sequencing

Sponsor: ENAR

Chair: Yaqun Wang, Rutgers University

3:45 **Shrinkage of Dispersion Parameters in the Binomial Family, with Application to Differential Exon Skipping**

Sean Ruddy*, **Marla Johnson** and **Elizabeth Purdom**, University of California, Berkeley

4:00 **Accounting for Stochastic Dropout Events in Detecting Differential Gene Expression Using Single-Cell RNA-Seq Data**

Cheng Jia*, **Mingyao Li** and **Nancy Zhang**, University of Pennsylvania

4:15 **NEXT-Peak: A Per-Base Regression Model for ChIP-Seq Peak Calling**

Nak-Kyeong Kim*, Virginia Commonwealth University

4:30 **Gene-Set Analysis Via Combining P-Values in RNA-Seq Data**

Yu-Chung Wei*, **Ching-Wei Chang** and **Nysia I. George**, U.S. Food and Drug Administration

4:45 **A Model for Paired-Multinomial Data and its Application to Analysis of Data on a Taxonomic Tree**

Pixu Shi* and **Hongzhe Li**, University of Pennsylvania

5:00 **A Novel Normalization Method for Time Series Metagenomic Count Data**

Lingling An*, **Zhenqiang Lu**, **Meng Lu** and **Dan Luo**, University of Arizona

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, L**i-Fang Chu**, J**ames 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**

68. Statistical Innovations of Massive Genomic Data Analysis

Sponsors: ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section
Organizers: Yuping Zhang, University of Connecticut and Zhaohui (Steve) Qin, Emory University
Chair: Zhaohui (Steve) Qin, Emory University

8:30 The Generalized Higher Criticism for Testing SNP-set Effects in Genetic Association Studies
Ian Barnett, Harvard School of Public Health
Rajarshi Mukherjee, Stanford University
Xihong Lin*, Harvard School of Public Health

8:55 Leveraging Algorithms for Logistic Regression with Massive Data
Ping Ma*, University of Georgia

9:20 Statistical Modeling of High-Throughput RNA Structure Probing Data
Zhengqing Ouyang*, The Jackson Laboratory for Genomic Medicine

9:45 Expansion of Biological Pathways by Integrating Enormous mRNA Expression Datasets
Yang Li and **Jun Liu***, Harvard University
Vamsi Mootha, Harvard Medical School

10:10 Floor Discussion

69. Policy Implications of Scientific Reproducibility - A Panel Discussion

Sponsor: ENAR
Organizer & Chair: 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

Sponsors: ENAR, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Section on Statistics and the Environment
Organizer & Chair: 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 **Sabastien Tisne**, CIRAD, France
Indra Syahputra, PT Socfindo, 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

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**
Marianthi 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

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**

73. 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

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

10:10 **Floor Discussion**

74. CONTRIBUTED PAPERS: Bayesian Hierarchical Modeling

Sponsor: ENAR

Chair: Sally Thurston, University of Rochester

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

8:30 Accounting for Informed Presence in the Analysis of Electronic Health Records

Benjamin A. Goldstein* and **Nrupen Bhavsar**, Duke University
Matthew Phelan, Duke Clinical Research Institute
Michael J. Pencina, Duke University

8:45 Spatial Pattern ing of Diabetes in Durham, North Carolina: A Bayesian Analysis of Associations with Individual and Neighborhood Characteristics

Mercedes A. Bravo* and **Rebecca Anthopolos**, Children's Environmental Health Initiative, University of Michigan
Marie Lynn Miranda, Rice University

9:00 The Associations of Drugs with Acute Myocardial Infarction: Bias Correction, Global Profiling and Inference on Individual Drug

Changyu Shen, **Xiaochun Li** and **Jia Zhan***, Indiana University School of Medicine and School of Public Health

9:15 Approximate Bayesian Computation for Compartmental Epidemic Models - Methods and Software

Grant D. Brown*, University of Iowa
Aaron T. Porter, Colorado School of Mines
Jacob J. Oleson, University of Iowa

9:30 Proportional Hazards Regression for Interval-Censored Failure Time Data in Case-Cohort Studies

Qingning Zhou*, **Haibo Zhou** and **Jianwen Cai**, University of North Carolina, Chapel Hill

9:45 Bias and Artifact Trade-Off in Modeling Temporal Trend of Archived Data with Applications to Public Health Studies, Demography, Marketing Research and Sociology

Martina Fu, Stanford University
David Todem, Michigan State University
Wenjiang Fu*, University of Houston
Shuangge Ma, Yale University

10:00 Floor Discussion

76. CONTRIBUTED PAPERS: GWAS: Applications

Sponsor: ENAR

Chair: Naomi Brownstein, Florida State University

8:30 Shrinkage-Based Genome Wide Association Analyses Based on Sparse Versus Gaussian Priors

Chunyu Chen*, **Juan P. Steibel** and **Robert J. Tempelman**, Michigan State University

8:45 An Exposure-Weighted Score Test for Genetic Associations Integrating Environmental Risk Factors

Summer S. Han*, Stanford University
Philip S. Rosenberg, National Cancer Institute, National Institutes of Health
Arpita Ghosh, Public Health Foundation of India
Maria Teresa Landi and **Neil E. Caporaso**, National Cancer Institute, National Institutes of Health
Nilanjan Chatterjee, Johns Hopkins University

9:00 Detecting Shared Genetic Variants Between Two Diseases with Dependent SNPs

Wanjie Wang*, **Tony Cai**, and **Hongzhe Li,** University of Pennsylvania

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 Helath

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
Christopher I. Amos, Dartmouth Medical School
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

8:30 Regression Analysis of Current Status Data with Generalized Odds-Rate Hazards Models

Bin Yao* and **Lianming Wang**, University of South Carolina

8:45 A Joint Model of Cancer Incidence, Metastasis, and Mortality

Qui Tran*, **Kelley M. Kidwell** and **Alex Tsodikov**, University of Michigan

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
Ruosha 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 Chiou*, 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

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

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)

9:45 **SeqDesign: A Framework for RNA-Seq Genome-Wide Power Calculation and Experimental Design Issues**
Chien-Wei Lin*^, **Serena G. Liao** and **George C. Tseng**, University of Pittsburgh

10:00 **Statistical Considerations in Designing Precision Study for Optical Coherence Tomography Device**
Haiwen Shi*, U.S. Food and Drug Administration

10:15 - 10:30 am Refreshment Break with Our Exhibitors

10:30 am - 12:15 pm Presidential Invited Address

80. Biostatistics, Biomedical Informatics, and Health Data Science: Research and Training

Sponsor: ENAR
Organizer & Chair: Jianwen Cai, University of North Carolina, Chapel Hill

10:30 **Introduction**

10:35 **Distinguished Student Paper Awards**

10:45 **Biostatistics, Biomedical Informatics, and Health Data Science: Research and Training**
Xihong Lin, Ph.D., Chair and Henry Pickering Walcott Professor, Department of Biostatistics, Harvard University

1:45 - 3:30 pm Oral Presentations

81. New Developments for Individualized Medical Decision Making in Real World Settings

Sponsors: ENAR, ASA Biometrics Section, ASA Mental Health Statistics Section, ASA Statistical Learning and Data Mining Section
Organizer: Yuanjia Wang, Columbia University
Chair: Bei Jiang, University of Alberta

1:45 **Dynamic Systems for Identifying Biomarkers Predicting Landmarks of Disease Degeneration**
Yuanjia Wang*, Columbia University

2:10 **Model Validation and Selection in G-estimation of Dynamic Treatment Regimes**
Erica E. M. Moodie*, **Michael P. Wallace** and **David A. Stephens**, McGill University

2:35 **Learning Optimal Personalized Treatment Rules in Benefit-Risk Analysis**
Yuanjia Wang, Columbia University
Haoda Fu, Eli Lilly and Company
Donglin Zeng*, University of North Carolina, Chapel Hill

3:00 **Building Personalized Treatment Strategy with Binary Outcomes**
Min Qian*, Columbia University
Eric Laber, North Carolina State University

3:25 **Floor Discussion**

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**

84. 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

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

85. Curent 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

1:45 Some Recent Theoretical Results on Meta-Analysis
Danyu Lin*, University of North Carolina, Chapel Hill

2:10 Adaptively Weighted Meta-analysis in-omics Applications
Zhiguang Huo, **Yongseok Park** and **George Tseng***, University of Pittsburgh

2:35 Network Meta-Analysis for Diagnostic Accuracy
Thomas Trikalinos*, **Wei Cheng**, **Constantine Gatsonis** and **Christopher Schmid**, Brown University

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

86. Survival Prediction Models for Medical Decision Making

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

1:45 Evaluation of Biomarkers for Prediction of Clinical Events: Connection to Information Theory
Patrick J. Heagerty*, University of Washington

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 Naprvavnik**, 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**

87. Statistical Machine Learning for Big-Bio-Data

Sponsors: IMS, ENAR

Organizer & Chair: Genevera 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**

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

2:30 **Semiparametric Efficient Estimation of Coarse Structural Nested Mean Models in the Presence of Informative Censoring with Application to the Effect of One-Year of HAART**
Shu Yang* and **Judith Lok**, Harvard University

2:45 **A New Weighted Partial Likelihood Method for Estimating Marginal Structural Hazard Models**
Olli Saarela*, University of Toronto
Zhihui Liu, Cancer Care Ontario and University of Toronto

3:00 **Is the Double Robust Estimator Really Robust?**
Xavier de Luna*, Umeå University
Eva Cantoni, University of Geneva

3:15 **Covariate Balancing in Propensity Score-Based Methods for Observational Studies**
Adin-Cristian Andrei*, Northwestern University

89. CONTRIBUTED PAPERS: Functional Data Analysis

Sponsor: ENAR
Chair: Adam Ciarleglio, New York University

1:45 **Single-Index Models for Function-On-Function Regression**
Guanqun Cao*, Auburn University
Lily Wang, Iowa State University

2:00 **Multivariate Multiscale Functional Data Analysis**
Andrew N. Potter* and **Stewart J. Anderson**, University of Pittsburgh

2:15 **Ordinal Probit Wavelet-Based Functional Models for eQTL Analysis**
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

2:30 **Optimal Design for Sparse Functional Data**
So Young Park* and **Luo Xiao**, North Carolina State University
Jayson Wilbur, Metrum Research Group LLC
Ana-Maria Staicu, North Carolina State University

2:45 **Detecting Outliers in Images of DNA Molecules Using Functional Data Depth and Morphological Features**
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

3:00 **A Bayesian Wavelet Based Analysis of Longitudinally Observed Skewed Heteroscedastic Response**
Danisha S. Baker*, **Eric Chicken**, **Debajyoti Sinha** and **Debdeep Pati**, Florida State University

3:15 **Floor Discussion**

90. CONTRIBUTED PAPERS: High Dimensional Variable Selection

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

1:45 **An Efficient Method for Variable Selection in Linear and Nonlinear Models**
Arnab K. Maity* and **Sanjib Basu**, Northern Illinois University

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 Tuberculosis 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 Personlized 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 Pennslyvania
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

3:45 **Lag Structured Modeling for High Dimensional Vector Autoregression**
William Nicholson, **Jacob Bien*** and **David Matteson**, Cornell University

4:15 **Non-Gaussian Estimation for Time Series Sampled at Mixed Frequencies**
Alex Tank, **Emily Fox*** and **Ali Shojaie**, University of Washington

4:45 **Network Reconstruction from High Dimensional Ordinary Differential Equations**
Shizhe Chen, **Ali Shojaie***, **Daniela Witten**, University of Washington

5:15 **Discussant:**
George Michailidis, University of Florida

101. CONTRIBUTED PAPERS: Environmental and Ecological Applications

Sponsor: ENAR
Chair: Emily Leary, University of Missouri

3:45 **An Adaptive Association Test for Microbiome Data**
Chong Wu*, Junghi Kim and Wei Pan, University of Minnesota

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, Dupont
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-Hsiu 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

4:15 **An Adaptive Testing Approach for Meta-Analysis of Gene Set Enrichment Studies**
Wentao Lu* and **Xinlei Wang**, Southern Methodist University

4:30 **Modeling Secondary Phenotypes Conditional on Genotypes in Case-Control Studies**
Naomi C. Brownstein*, Florida State University
Wei Xue, **Jianwen Cai** and **Eric Bair**, University of North Carolina, Chapel Hill

4:45 **The Parametric t-test's Latent Weakness**
Daniel P. Gaile* and **Jeffrey C. Miecznikowski**, University at Buffalo

5:00 **NanoStringDiff: A Novel Statistical Method for Differential Expression Analysis Based on NanoString nCounter Data**
Hong Wang*^, University of Kentucky
Craig Horbinski, Northwestern University
Hao Wu, Emory University
Yinxing Liu, University of Kentucky
Shaoyi Sheng, Paul Laurence Dunbar High School
Arnold J. Stromberg and **Chi Wang**, University of Kentucky

5:15 **Measurement Error in Tests for Gene-Environment Interactions: Implications of Gene-Environment Dependence**
Stacey Alexeeff*, Kaiser Permanente Division of Research
Xihong Lin, Harvard School of Public Health

106. CONTRIBUTED PAPERS: Variable Selection

Sponsor: ENAR
Chair: Hyokyoung Hong, Michigan State University

3:45 **Data-Driven Confounder Selection Via Markov and Bayesian Networks**
Jenny Haggstrom*, Umea University

4:00 **Feature Selection for Complex Metabolite Network**
Qingpo Cai*, Emory University
Jian Kang, University of Michigan
Tianwei Yu, Emory University

4:15 **Variable Selection in the Presence of Nonignorable Missing Data**
Jiwei Zhao*, State University of New York at Buffalo

4:30 **Sequential Multiple Testing for Variable Selection**
Xinping Cui* and **Hailu Chen**, University of California, Riverside

4:45 **Variable Selection for Model-Based Clustering of Functional Data**
Kyra Singh* and **Tanzy Love**, University of Rochester

5:00 **Bayesian Variable Selection Incorporating Biological Pathway Information Using Dependent Shrinkage Priors**
Changgee Chang*, **Suprateek Kundu** and **Qi Long**, Emory University

5:15 **Bayesian Spatial Feature Selection for Massive Neuroimaging Data Via Thresholded Gaussian Processes**
Ran Shi*^, Emory University
Jian Kang, University of Michigan

Wednesday March 9

8:30 - 10:15 am Oral Presentations

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

8:30 **Data Integration Using Network Analysis and Kernel Machine Methods**

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

10:10 **Floor Discussion**

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

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

9:45 **Biology, Causal Models, and Cross-over in Cancer Trials**
James M. Robins*, Harvard School of Public Health

10:10 **Floor Discussion**

109. Sentinel Statistical Methods Working Groups, Challenges With Using Claims Data for Public Health

Sponsors: ENAR, ASA Biopharmaceutical Section, ASA Section on Statistics in Epidemiology
Organizer & Chair: Rima Izem, U.S. Food and Drug Administration

8:30 **Introduction to Sentinel Distributed Data System and Selected Methods Work**
Judith C. Maro*, Harvard Medical School and Harvard Pilgrim Health Care Institute

9:00 **Lessons Learned from Two Sentinel Sequential Surveillance Activities: Saxagliptin and Rivaroxaban**
Bruce Fireman*, Kaiser Permanente Division of Research

9:30 **Survival Methods for Postmarketing Medical Product Surveillance in a Distributed Network**
Andrea J. Cook* and **Robert Wellman**, Group Health Research Institute
Rima Izem, **Azadeh Shoaibi** and **Ram Tiwari**, U.S. Food and Drug Administration
Susan Heckbert, University of Washington
Lingling Li, Harvard University
Rongmei Zhang, U.S. Food and Drug Administration
Jennifer Nelson, Group Health Research Institute

10:00 **Discussant:**
Mark Levenson, U.S. Food and Drug Administration

110. Statistical Modeling of Data on Heath Policy and Cost

Sponsor: ENAR
Organizer: Zhezhen Jin, Columbia University
Chair: Yu Deng, University of North Carolina, Chapel Hill

8:30 **On Statistical Modeling of National Surveys to Assess the Impact of State Specific Medical Marijuana Policies**
Christine Mauro, Columbia University
Melanie M. Wall*, Columbia University and New York State Psychiatric Institute

8:55 **An Improved Survival Estimator for Medical Costs with Censored Data Using Kernel Methods**
Shuai Chen*, University of Wisconsin, Madison
Wenbin Lu, North Carolina State University
Hongwei Zhao, Texas A&M Health Science Center

9:20 **Comparison in Medical Cost between a Cancer Survivor Cohort and the General Population Using Longitudinal Physician Claims**
Huijing Wang* and **X. Joan Hu**, Simon Fraser University

9:45 **"Nonparametric" Meta Analysis with Unknown Study-specific Parameters and with an Application to Health Policy Data**
Min-ge Xie*, Rutgers University

10:10 **Floor Discussion**

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

8:30 **Weight Trimming and Weight Smoothing Procedures for Survey Data**
David Haziza*, Université de Montréal

8:55 **Weight Modification in Sample Surveys: An Overview**
Malay Ghosh*, University of Florida

9:20 **Weight Modification in Sample Surveys: Using Regression Models**
Qixuan Chen*, Columbia University

9:45 **Weight Modification in Sample Surveys: Results from a Simulation Study**
Joe Sedransk*, University of Maryland

10:10 **Floor Discussion**

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

8:30 **Adjusted Comparisons to External Controls Using Both Individual Patient Data and Published Summary Statistics**
James E. Signorovitch*, Analysis Group Inc.
David Cheng, Harvard University

8:55 **Robust Methods for Treatment Effect Calibration, with Application to Non-Inferiority Trials**
Zhiwei Zhang*, **Lei Nie** and **Guoxing Soon**, U.S. Food and Drug Administration
Zonghui Hu, National Institute of Allergy and Infectious Diseases, National Institutes of Health

9:20 **Sensitivity Analysis for an Unobserved Moderator in RCT-to-Target Population Generalization of Treatment Effect**
Trang Q. Nguyen* and **Cyrus Ebnesajjad**, Johns Hopkins Bloomberg School of Public Health
Stephen R. Cole, University of North Carolina, Chapel Hill
Elizabeth A. Stuart, Johns Hopkins Bloomberg School of Public Health

9:45 **Bayesian Network Meta-analyses of Multiple Diagnostic Tests**
Haitao Chu*, University of Minnesota
Xiaoye Ma, Amgen Inc.
Qinshu Lian, University of Minnesota
Yong Chen, University of Pennsylvania
Joseph G. Ibrahim, University of North Carolina, Chapel Hill

10:10 **Floor Discussion**

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

8:30 **A Generalized Similarity U Test for Multivariate Analysis of Sequencing Data**
Changshuai Wei, University of North Texas Health Science Center
Qing Lu*, Michigan State University

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

9:00 **Evaluation of Biomarkers for Treatment Selection Using Individual Participant Data Meta-Analysis**
Chaeryon Kang*, University of Pittsburgh
Holly Janes, Fred Hutchinson Cancer Research Center

9:15 **Comparing the Surrogacy of Multiple Vaccine-Induced Immune Response Biomarkers in HIV Prevention**
Sayan Dasgupta* and **Ying Huang**, Fred Hutchinson Cancer Research Center

9:30 **Comparison of Methods for Updating Risk Prediction Models**
Sonja Grill*, Technical University Munich, Germany
Donna P. Ankerst, Technical University Munich, Germany and University of Texas Health Science Center, San Antonio
Ruth M. Pfeiffer, National Cancer Institute, National Institutes of Health

9:45 **Evaluation of Biomarker Identification Through Likelihood Ratio Test**
Yu-Chuan Chen* and James J. Chen, U.S. Food and Drug Administration

10:00 **Meta-Analysis of Predictive Values of Biomarkers**
Mun Sang Yue* and **Constantine A. Gatsonis**, Brown University

116. CONTRIBUTED PAPERS: Competing Risks

Sponsor: ENAR
Chair: Olive Buhule, National Institutes of Health

8:30 **Checking Fine and Gray Model with Cumulative Sums of Residuals: Theory and Implementation**
Jianing Li*, Merck
Mei-Jie Zhang, Medical College of Wisconsin
Thomas H. Scheike, University of Copenhagen

8:45 **Competing Risks Model of Screening and Symptoms Diagnosis**
Sheng Qiu* and **Alexander Tsodikov**, University of Michigan

9:00 **Cause-Specific Hazard Regression for Competing Risks Data Under Interval Censoring and Left Truncation**
Chenxi Li*, Michigan State University

9:15 **Evaluating Center Performance on Competing Outcomes**
Sai Hurrish Dharmarajan* and **Douglas E. Schaubel**, University of Michigan

9:30 **Adaptive Group Bridge for Competing Risks Data**
Natasha A. Sahr*, **Kwang Woo Ahn** and **Anjishnu Banerjee**, Medical College of Wisconsin

9:45 **Evaluating Utility Measurement from Recurrent Marker Processes in the Presence of Competing Terminal Events**
Yifei Sun* and **Mei-Cheng Wang**, Johns Hopkins University

10:00 **Floor Discussion**

117. CONTRIBUTED PAPERS: GWAS: Testing

Sponsor: ENAR
Chair: Luis Leon Novelo, University of Texas School of Public Health

8:30 **Measuring and Testing Dependence by Kernelized RV Coefficient**
Xiang Zhan*^, **Ni Zhao** and **Michael C. Wu**, Fred Hutchinson Cancer Research Center

8:45 **Adaptive Gene- and Pathway-Trait Association Testing with GWAS Summary Statistics**
Il-Youp Kwak* and **Wei Pan**, University of Minnesota

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**

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

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 **Meijuan 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

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

10:55 **Observational Causal Inference in Community-Structured Social Networks**
Cosma R. Shalizi*, Carnegie Mellon 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

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

11:30 **Nature-inspired Meta-heuristic Algorithms for Generating Optimal Designs for Nonlinear Models**
Weng Kee Wong*, University of California, Los Angeles

12:00 **Floor Discussion**

127. CONTRIBUTED PAPERS: Bayesian Methods

Sponsor: ENAR
Chair: Arpita Chatterjee, Georgia Southern University

10:30 **Bayesian Regression Analysis for Estimating Disease Etiology**
Zhenke Wu* and **Scott L. Zeger**, Johns Hopkins Bloomberg School of Public Health

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

11:30 **Improving Covariate Balancing Propensity Score for Continuous Treatment Regimes**
Samantha Noreen* and **Qi Long**, Emory University

11:45 **Calibrate Measurement Errors and Misclassifications in Mendelian Randomization Studies**
Cheng Zheng*, University of Wisconsin, Milwaukee

12:00 **Floor Discussion**

129. CONTRIBUTED PAPERS: Count and Categorical Data Analysis

Sponsor: ENAR
Chair: Matthew White, Boston Children's Hospital

10:30 **A New Compound Class of Exponentiated Power Lindley-Logarithmic Distribution: Model, Properties and Applications**
Mavis Pararai*, Indiana University of Pennsylvania
Jacinth A. Maynard, Lock Haven University of Pennsylvania
Gayan W. Liyanage, Central Michigan University

10:45 **A Bayesian Approach in Estimating Odds Ratios for Rare or Zero Events**
Mehmet Kocak*, University of Tennessee Health Science Center

11:00 **Analysis of Inflated Bivariate Count Data that Occur in Health Care Studies Using Poisson Regression Models**
N. Rao Chaganty*, Old Dominion University
Pooja Sengupta, International Management Institute

11:15 **A Bayesian Test of Independence in a Two-Way Contingency Table with Covariates Under Cluster Sampling**
Dilli Bhatta*, University of South Carolina Upstate
Balgobin Nandram, Worcester Polytechnic Institute

11:30 **Simulating Longer Vectors of Correlated Binary Random Variables Via Multinomial Sampling**
Justine Shults*, University of Pennsylvania Perelman School of Medicine

11:45 **Testing for Trend with a Nominal Outcome**
Aniko Szabo*, Medical College of Wisconsin

12:00 **Estimation of the Optimal ROC in Complex Classification Settings**
Daniel B. Shin*, University of Pennsylvania
Farrah J. Mateen, Massachusetts General Hospital and Harvard Medical School
Jaroslaw Hareslak, Indiana University, Indianapolis
Joel M. Gelfand and **Russell T. Shinohara**, University of Pennsylvania

130. CONTRIBUTED PAPERS: Joint Models for Longitudinal and Survival Data

Sponsor: ENAR
Chair: Armando Teixeira-Pinto, University of Sydney

10:30 **Weighted ZIP Mixed Model with an Application to Medicaid Data**
Sang Mee Lee* and **Theodore Karrison**, University of Chicago

10:45 **A Semiparametric Joint Model for Longitudinal Data and Survival in End-Of-Life Studies**
Zhigang Li* and **H. R. Frost**, Dartmouth College
Lihui Zhao and **Lei Liu**, Northwestern University
Kathleen D. Lyons, Dartmouth College
Huaihou Chen, University of Florida
Bernard Cole, University of Vermont
David Currow, Flinders University, Australia
Marie Bakitas, University of Alabama
Tor D. Tosteson, Dartmouth College

11:00 **Dynamic Prediction for Multiple Repeated Measures and Event Time Data: An Application to Parkinson's Disease**

Jue Wang*^ and **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* and **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

10:30 **A Unified Slice Sampler for Regression Analysis of Current Status Data Under Linear Transformation Models**

Sheng-Yang (Sean) Wang* and **Lianming Wang**, University of South Carolina

10:45 **An Extended Kaplan-Meier Estimator for Time to Success with Informative Censoring**

Wei Li* and **Misun Lee**, Astellas Pharma Development

11:00 **Survival Data for Multiple Diseases from Stratified Case-Cohort Design**

Soyoung 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

ENAR 2016 Short Courses

	REGISTRATION RECEIVED					
	By Feb.1			After Feb.1		
	Half Day	Second Half Day	Full Day	Half Day	Second Half Day	Full Day
Member	$225	$190	$325	$250	$215	$350
Non-Member	$275	$240	$375	$300	$265	$400

Sunday March 6

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 inter- disciplinary 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 it variants, support vector machines, Boosting, and tree-based methods. Unsupervervised 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

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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

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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

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"Greetings From Austin - Capitol of Texas" *postcard mural, at the Roadhouse Relics building*

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 RO1 grant "Statistical Methods for Complex Cancer Trials."

	REGISTRATION RECEIVED	
	By Feb.1	After Feb.1
Member	$75	$85
Non-Member	$85	$95
Student	$40	$50

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

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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 develop. As diseases are sub-stratified into often biomarker-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

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

Tuesday, March 8 | 8:30 am – 10:15 am

Martin Morgan
Roswell Park Cancer Institute

Description: Modern methods of high-throughput genomic data generate large primary data sets that require significant data manipulation and statistical summary before arriving at biological insight. This workshop starts by outlining basic DNA sequence analysis work flows, from primary data generation to biological interpretation. We use this outline, and especially the 'RNA-seq known gene differential expression' work flow, to identify relevant data management and statistical issues. The workshop then steps through R and Bioconductor code to implement essential stages in data management and statistical analysis. We conclude by briefly contrasting differences in the biological, technological and statistical aspects of RNA-, DNA-, and methyl-seq, with a brief overview of the resources available for further study.

Instructor 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

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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, semi-competing 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.

ENAR 2016 Round Tables

Registration is Required **$40.00**

Monday March 7 | 12:15 pm - 1:30 pm

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 associations using studies in which the disease has been studied with the anatomic site of origin of the cancer as the organizing framework. In the clinical research arena the advent of powerful technologies for examining tumors at the molecular level are 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.

SOLD OUT

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

Sebatstein Haneuse
Harvard University

Description: Electronic health record (EHR) data present an incredibly appealing opportunity for public health and medical research. Relative to data from dedicated designs, EHR data often contain rich information on a broad range of patients over long timeframes and in real time. 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.

SOLD OUT

R3: Precision Medicine

Michael Kosorok
University of North Carolina at Chapel Hill

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

SOLD OUT

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 data volume, velocity and variety. It has been argued 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 quantitative safety review at FDA's Center for Drug Evaluation and Research (CDER). The following topics will be the bases of the discussion:

SOLD OUT

» 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 our society, coupled with the emergence of contributions from varied quantitative disciplines. In this roundtable, we will discuss leadership opportunities for statisticians. We will examine key elements of being an effective leader, both within one's field and 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.

SOLD OUT

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 one's work ensures that it will be widely disseminated to researchers and practitioners who stand to benefit. In addition, funding agencies and academic institutions place considerable importance on a successful record of publication. Accordingly, understanding the peer review and editorial processes of top journals and mastering the art of writing an effective journal article are keys to success in publishing. How does one determine the best outlet for one's work? What are the essential elements of a successful journal article? How does one maximize the chance of acceptance? What strategies can ensure that a published paper is read and cited? How does one make optimal use of limited space and additional supplementary material in conveying the message? What are the roles of the editor, associate editor, and referees? What considerations do editors use when evaluating a paper? This roundtable will provide a forum for candid discussion of these and other questions.

SOLD OUT

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 are tasked with developing a new one, numerous options exist for delivering the content. Many courses are moving away from traditional classroom lectures. 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?

SOLD OUT

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.

Join Us for the Tuesday Evening Dinner and Social Event

SOLD OUT

Reduced registration fee offered to students to attend (see page 7).

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

Sunday, March 6	**4:00 pm – 6:30 pm**
Monday, March 7	**9:30 am – 4:30 pm**
Tuesday, March 8	**9:30 am – 3:30 pm**

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.

Deadlines

	By Feb.1	After Feb.1
Employer *(3 reps/ 4 job postings)*	$1,550	$1,675
Private Interview Room *(Per 4-hour increments)*	SOLD OUT	
Additional Representatives *(Cost per person includes conference registration)*	$500	$550
Additional Job Postings	$100	$150

Employer

Registration Instructions, Deadlines, and Fees

ALL employers must FULLY complete an online Employer Form located at: **http://www.enar.org/meetings2016/career_center/** for each position listing. Attachments may be included.

Deadlines

	By Feb.1	After Feb.1
Regular Registration	$50	$60
Student Registration	$25	$35

Applicant

Registration Instructions, Deadlines, and Fees

ALL applicants must FULLY complete an online Applicant Form located at: **http://www.enar.org/CareerCenter/** for each job classification.

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.

ENAR 2016 Registration Form

PLEASE PRINT OR TYPE

FIRST NAME _____ MIDDLE INITIAL _____ LAST NAME _____

HIGHEST DEGREE: ❑ BACHELORS ❑ MASTERS ❑ DOCTORATE OR MEDICAL DEGREE ❑ OTHER _____

NAME FOR BADGE IF DIFFERENT _____ SPOUSE/GUEST NAME FOR BADGE _____

ORGANIZATION _____

MAILING ADDRESS _____ CITY _____ STATE _____ ZIP CODE _____ COUNTRY _____

DAYTIME PHONE _____ FAX _____ E-MAIL _____

Membership in Participating Societies (Check all that apply.)

❑ ENAR ❑ WNAR ❑ ASA ❑ IMS ❑ IBS

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

❑ ENAR/WNAR/IBS Member
$400 ($475 after 2/1) $ _____

❑ ASA Member (not a member of ENAR/WNAR/IBS)
$540 ($615 after 2/1) $ _____

❑ IMS Member (not a member of ENAR/WNAR/IBS)
$420 – $20 IMS contribution = **$400** ($475 after 2/1) $ _____

❑ Nonmember (in any participating society)
$590* ($665 after 2/1) $ _____
*Includes membership in ENAR through December 31, 2016

❑ Student (With letter from major professor verifying status.)
$165 ($175 after 2/1) $ _____

❑ Nonmember Student (With letter from major professor verifying status.)
$200 ($210 after 2/1) $ _____

❑ Guest
$85 ($95 after 2/1) $ _____

Short Courses

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

❑ Member (participating society) SC _____ SC _____
Full Day: **$325** ($350 after 2/1) $ _____
Half Day: **$225** ($250 after 2/1) $ _____
Second Half Day: **$190** ($215 after 2/1) $ _____

❑ Nonmember* SC _____ SC _____
Full Day: **$375** ($400 after 2/1) $ _____
Half Day: **$275** ($300 after 2/1) $ _____
Second Half Day: **$240** ($265 after 2/1) $ _____

Tutorials

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

	Member	Nonmember	Student
T1	❑ **$75** ($85 after 2/1)	❑ **$85** ($95 after 2/1)	❑ **$40** ($50 after 2/1)
T2	❑ **$75** ($85 after 2/1)	❑ **$85** ($95 after 2/1)	❑ **$40** ($50 after 2/1)
T3	❑ **$75** ($85 after 2/1)	❑ **$85** ($95 after 2/1)	❑ **$40** ($50 after 2/1)
T4	❑ **$75** ($85 after 2/1)	❑ **$85** ($95 after 2/1)	❑ **$40** ($50 after 2/1)
T5	❑ **$75** ($85 after 2/1)	❑ **$85** ($95 after 2/1)	❑ **$40** ($50 after 2/1)
T6	❑ **$75** ($85 after 2/1)	❑ **$85** ($95 after 2/1)	❑ **$40** ($50 after 2/1)
T7	❑ **$75** ($85 after 2/1)	❑ **$85** ($95 after 2/1)	❑ **$40** ($50 after 2/1)

Roundtables

The roundtables will be held on Monday, March 7. Space is limited. Preregistration is required. Indicate the number of your 1st, 2nd, and 3rd choices:

1st # _____ 2nd # _____ 3rd # _____

Fee: $40 $ _____

Please make lunch vegetarian ❑ YES ❑ NO

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

❑ Regular: $95 $ SOLD OUT
❑ Student: $50 $ SOLD OUT

Membership

❑ YES, I want to renew my 2016 ENAR membership or become an ENAR member.

❑ 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

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

TOTAL PAYMENT $ _____

FORM OF PAYMENT

❑ Check* ❑ Money Order* ❑ MasterCard ❑ Visa ❑ AmEx

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

Credit Card Information

CARD NO. _____ EXP. DATE _____

NAME ON CARD _____ SIGNATURE _____

The International Biometric Society

ENAR

Membership Application

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

Please Check One: ❑ New Member ❑ Renewal

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)
❑ Animal and Veterinary Science (02)
❑ Clinical Trials (03)
❑ Epidemiology (04)
❑ Genetics and Heredity (05)
❑ Molecular Biology and Biotechnology (06)
❑ Toxicology (07)

NATURAL RESOURCES

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

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

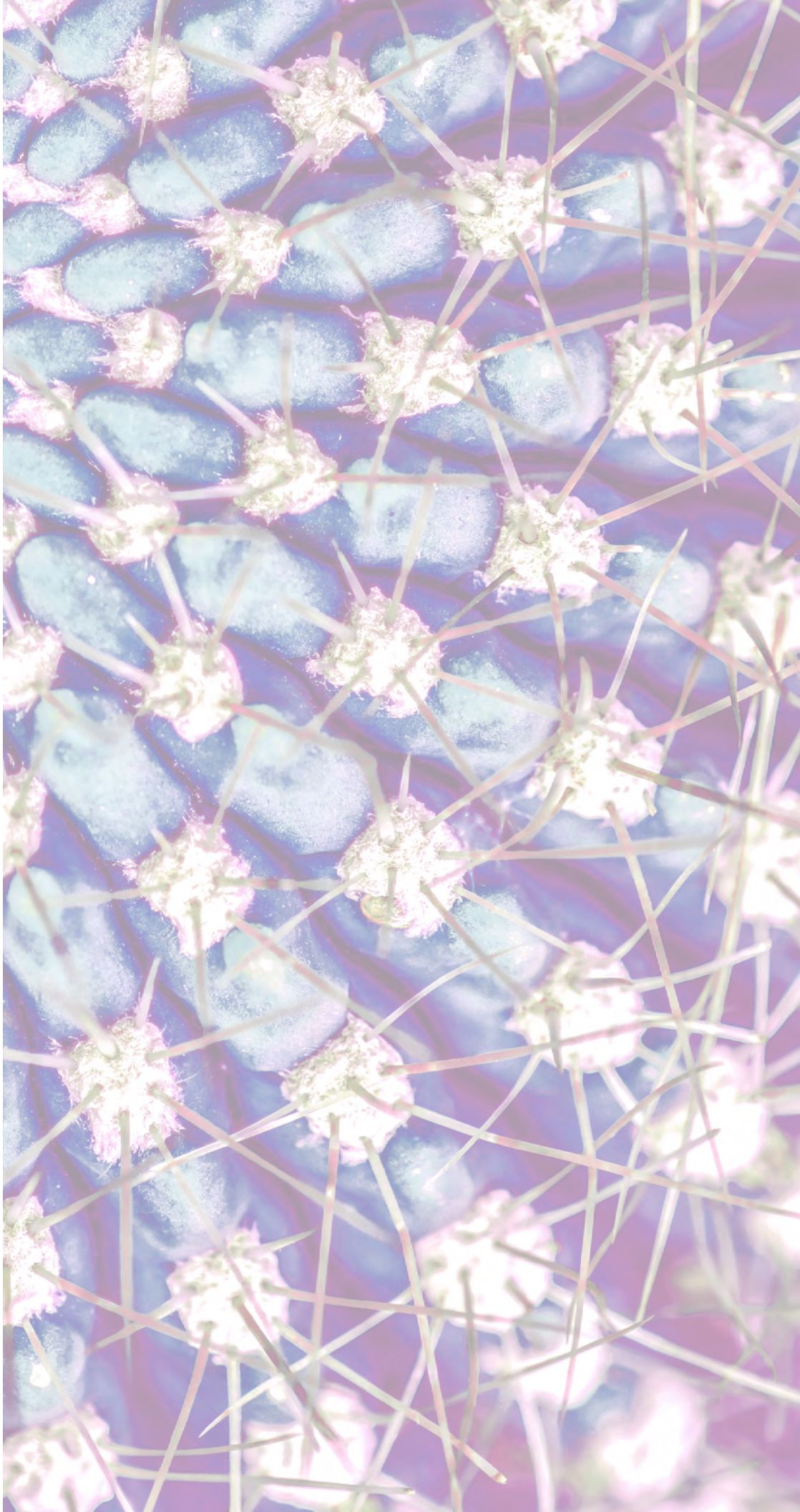
NAME ON CARD | SIGNATURE

MAIL TO:

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

ENAR 2016 Spring Meeting

March 6-9 2016 | JW Marriott Austin | Austin, TX



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