



ENAR 2018

SPRING MEETING
With IMS & Sections of ASA

March 25-28

Hyatt Regency
Atlanta on Peachtree St

Atlanta, GA



PRELIMINARY PROGRAM

Early Bird Deadline: February 1st, 2018



ENAR 2018

SPRING MEETING

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Welcome! I am excited to welcome you to the 2018 ENAR Spring Meeting! For those of you who are attending your first ENAR, I would like to extend to you a special welcome and hope you enjoy the scientifically, professionally, and socially stimulating environment that this meeting affords, and will return for future meetings and get more involved in our organization!

The 2018 ENAR Spring Meeting will be held at the Hyatt Regency Atlanta in Atlanta, Georgia, conveniently located near many of Atlanta's great tourist attractions, including the world-renowned Georgia Aquarium, the World of Coca-Cola, the Center for Civil and Human Rights, and the Children's Museum of Atlanta. Many other locations of interest, as well as great restaurants, are in the area and easily accessible from the venue. As summarized below, we have diverse and exciting scientific and educational programs that we hope offer something for everyone, and for anyone wishing to participate in the contributed program, the October 15th submission deadline is quickly approaching!

The four-day meeting, **March 25-28, 2018**, will host students, researchers, and practitioners from all over our biostatistics profession, from academia to industry and government, brought together to learn from each other and push the discipline of Biostatistics forward! As we well know, our quantitative skills are central to the key ventures of these institutions, and it is through meetings like these that we have the opportunity to share ideas with each other and build connections to equip each of us to take leadership and make an impact in our respective areas of work. Continuing in ENAR's strong tradition, the meeting will offer numerous opportunities through the Scientific and Educational offerings to keep up with the latest developments in the field, become familiar with state-of-the-art statistical methods and software, see creative applications of statistical methods make a practical difference in many areas of application, and see how statistics can inform policy and decision-making. Additionally, the meetings are an outstanding opportunity for networking and meeting others in the discipline, to connect job-seekers and employers, and to reconnect with friends and colleagues. There will also be opportunities to check out the latest textbooks and software from our exhibitors and vendors, who have partnered with ENAR.

The ENAR Spring Meeting can only happen through teamwork from a large number of people volunteering their time and energy, contributing their ideas, coordinating and organizing the program, and managing the meeting logistics. I express my true gratitude to each of you! Your efforts and commitment are essential to the success of these meetings!

Scientific Program

Through the leadership of Program Chair Veera Baladandayuthapani (The University of Texas M.D. Anderson Cancer Center) and Associate

Chair Jeff Goldsmith (Columbia University Mailman School of Public Health), and with contributions from many of you, the Program Committee (consisting of 13 ASA section representatives from and 6 at-large members) has put together a diverse and exciting invited program! The sessions cover a wide range of topics, including statistical learning for precision medicine, neuroimaging data, meta-analysis, integrative genomics modeling, next generation sequencing data, single-cell sequencing data, spatial modeling, microbiome analysis, heterogeneity discovery, causal inference and propensity score analysis, functional data analysis, dynamic treatment regimes, survival data, diagnostic testing and agreement, graphical models, clinical trial design, electronic health records, and methods for complex high dimensional data. The IMS invited program, assembled by Program Chair Fan Li (Duke University), also features an exciting slate of sessions on topics including big data, neuroimaging data, single-cell genomics, geometry in statistical inference, clinical trial design, hierarchical modeling, complex dependency, randomization inference, and statistics and human rights, which complements and enhances the other elements of the invited program.

Poster sessions have been growing in prominence at the ENAR meetings, and continue to be a vital part of the program. In addition to contributed and invited posters, as done each year since 2015, the 2018 ENAR meeting will have contributed oral poster sessions in which presenters will be able to give a two-minute elevator speech on the highlights of their posters. This is an excellent format providing the exposure of an oral presentation with the interactions, feedback, and customization potential of a poster session. Monday, March 26th will feature the thematically grouped, contributed oral poster sessions. These will feature two invited posters from established and well-known researchers, and will run parallel with the rest of the sessions in the scientific program. As in previous years, the regular contributed and invited posters will be featured during the Opening Mixer on Sunday evening. Posters in this session will be eligible to win a poster award as part of the ENAR Regional Advisory Board's poster competition!

Educational Program

Be sure to check out the offerings in our educational program, which provide great opportunities to gain an overview of an area of research, develop new computational skills, or gain exposure to one of the hot new emerging topics within the field. The Educational Advisory Committee has assembled a superb program of short courses, tutorials, and roundtables for the 2018 ENAR Spring Meeting. These offerings are presented by some of the leading experts in their respective fields, who also happen to be renowned instructors, covering a broad variety of topics, so there should be something for everyone.

Short course topics include full-day offerings on adaptive clinical trials, machine learning for biomarker discovery, and joint modeling of longitudinal and survival data, and half-day offerings on causal inference, survival for precision medicine, reproducible research with R/RStudio, and an introduction to neuroimaging analysis within R. Tutorial topics include mobile health, electronic health records, multi-modal imaging data, processing RNAseq data in Bioconductor, integrative genomics, and FDA guidance on multiple endpoints. We also have a number of roundtable lunches in which you will get to interact with distinguished statisticians on such topics as effective interdisciplinary collaboration, clinical trial design, modeling spatial-temporal big data, connectivity, wearable computing, grant funding opportunities, grant proposal writing strategies, and career opportunities at the Center for Disease Control and Prevention right here in Atlanta.

I would like to extend a special thanks to the members of the Educational Advisory Committee – Simone Gray, Ali Shojaie, Lorenzo Trippa, Wenyi Wang, and Zhenke Wu, for their insights and efforts in putting together such an outstanding educational program.

Keynote Lecture

I am excited to announce that the 2018 ENAR Presidential Invited Address will be given by Dr. Roderick J. Little, the Richard D. Remington Distinguished University Professor

of Biostatistics at the University of Michigan. Professor Little is a pioneer and research leader in the fields of data analysis with missing values and model-based survey inference, and his methodological work has been closely tied to his applied work. He has been recognized with many honors and awards, including the American Statistical Association's Wilks Medal, the COPSS Fisher Lecturer, his election to the American Academy of Arts and Sciences and the Institute of Medicine, and is an ISI highly cited researcher, with more than 250 publications having nearly 50,000 citations, including 12 with more than 500 citations (Google Scholar). His lecture will be on "Statistics as Prediction," providing an illuminating general discussion of how prediction can serve as a unified motivation to all of statistical inference, and encompassing both frequentist and Bayesian approaches. If you have ever heard Professor Little speak, you already know how engaging and insightful he is, with a sharp and incisive mind and the ability to express deep ideas in a clear and accessible manner. If you have not yet heard him, you are in for a real treat! To learn more about Dr. Little and his Invited Address, please see page 13.

Additional Meeting Activities

The 2018 ENAR Spring Meeting will feature a number of other activities in addition to the scientific and educational programs. On Sunday, March 25th, there will be the

Fostering Diversity in Biostatistics Workshop, organized by Dr. Emma Benn (Icahn School of Medicine at Mount Sinai) and Portia Parker (SAS, Inc.). Dr. Dionne Price (U.S. Food and Drug Administration) will serve as keynote speaker, and there will also be roundtable discussions for students and professionals, as well as panel discussions on career opportunities and mentoring. This workshop has been very popular and impactful and registration typically fills up very quickly, so please be sure to register early if you are interested in attending!

The Networking Mixer on Monday evening and the Tuesday luncheon event organized by the Council for Emerging and New Statisticians (CENS) will provide plentiful networking opportunities for students, recent graduates, and other young professionals. Attendees seeking employment and prospective employers have the opportunity to connect at the Career Placement Center. Also, be sure to visit our exhibitors' area to check out the latest books and software in the field.

The evenings provide great opportunities to get together with friends, collaborators, and former colleagues to catch up and enjoy some of the engaging sites and activities near the conference center, as well as delectable dining options in the heart of Atlanta. The Local Arrangements Committee, chaired by Howard Chang (Emory University), will provide some specific recommendations in the forthcoming full ENAR program of activities to try with your group as you experience all that Atlanta has to offer.

We hope to see you in Atlanta for the 2018 ENAR Spring Meeting!

Jeffrey S. Morris | ENAR President

Kathy Hoskins | ENAR Executive Director



LOCATION

Hyatt Regency Atlanta

265 Peachtree St NE

Atlanta, GA 30303

TEL: +1.404.577.1234

<https://aws.passkey.com/e/49190027>**Registration Hours:**» **Saturday, March 24:** 3:00 pm to 5:00 pm» **Sunday, March 25:** 7:30 am to 6:00 pm

MEETING REGISTRATION FEES	BY FEB 1 ST	AFTER FEB 1 ST
ENAR/WNAR/IBS Member	\$420	\$495
ASA Member <i>not an ENAR/WNAR/IBS member</i>	\$560	\$635
IMS Member <i>not an ENAR/WNAR/IBS member</i> <i>(\$440-\$20 IMS Contribution: \$420)</i>	\$420	\$495
Student Member	\$165	\$175
Guest Fee	\$95	\$105
Nonmember <i>of any participating society</i>	\$610	\$685
Student Nonmember	\$200	\$210

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, 2018**.

Short Courses: The 2018 ENAR meeting will begin with an excellent set of short courses on **Sunday, March 25**. 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 115 or the electronic registration form available on the ENAR website.

SHORT COURSE REGISTRATION FEES

	BY FEB 1 ST		AFTER FEB 1 ST	
	HALF DAY	FULL DAY	HALF DAY	FULL DAY
Member	\$225	\$325	\$250	\$350
Nonmember	\$275	\$375	\$300	\$400

Register for two half day courses and save! See pages 20-23 for course details and savings.

Tutorials: Tutorials will be offered on **Monday and Tuesday**, and are held concurrent with the scientific program sessions. 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, 2018) and \$85 for non-members (\$95 after February 1, 2018). The student registration fee for the tutorials is \$40 (\$50 after February 1, 2018). Be sure to register in advance, since tutorials will be closed once they are full. For full descriptions of the tutorial sessions, please refer to pages 107-109.

Roundtable Luncheons: This year, the roundtable luncheons will be held on **Monday, March 26**, from 12:15 to 1:30 pm. Space for each roundtable is limited and pre-registration is highly recommended. The fee is \$40 per person and includes lunch. For full descriptions of the roundtable discussion topics, please refer to pages 110-111.

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 25**. All new ENAR members are cordially invited to attend. The Opening Mixer and Poster Session will take place from 8:00 to 11:00 pm on **Sunday, March 25**.

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 2018 Spring Meeting is to improve the networking experience for all attendees. CENS will organize lunches on **Tuesday, March 27, 2018** 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 Networking Mixer: All students and recent graduates are invited to attend the CENS networking mixer on **Monday, March 26**, from 6:30 to 7:30 pm. Registration is not required – so please plan to attend!

Placement Service: ENAR will conduct a job placement service at the 2018 Spring Meeting. Additional information regarding the placement center is located on pages 113-114.

2018 ENAR MOBILE APP

ENAR is going mobile again in 2018 with our Spring Meeting app! The mobile app will make this year's meeting more valuable for our attendees, sponsors, exhibitors, and speakers. The app will provide an efficient 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 2018 Spring Meeting, you will 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** (\$10.00 fee) containing all session and speaker names, session times, and locations (please refer to the registration form on page 33 and select this option when registering).

Note: The larger final program and abstract book is not printed and can only be accessed via the ENAR website.

Hotel & Transportation:

Hyatt Regency Atlanta

265 Peachtree St NE | Atlanta, GA 30303

TEL: +1.404.577.1234

<https://aws.passkey.com/e/49190027>

Room Reservations: ENAR has negotiated a group hotel room rate of \$195.00 for single and double occupancy rooms. **Cut-off date:** All reservations must be made by **March 2, 2018**. To receive this special ENAR meeting rate, you must make your reservations directly with the Hyatt Regency Atlanta at +1.888.421.1442 or online at <https://aws.passkey.com/e/49190027>. Be sure to mention that you are with the ENAR 2018 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 Hyatt Regency Atlanta: Valet parking is available on-site for a fee of \$35 for 24 hours, with in/out privileges. These parking rates are subject to change and are not inclusive of tax. Please note the hotel does not offer self-parking on-site; however, guests may elect to self-park at off-property locations, such as 31 Baker St. (31 Baker St. NE). This covered garage is one block from the hotel, and is available at a discounted rate for Hyatt guests. Charges are \$20 for 24 hours with no in/out privileges, valid Friday-Sunday.

Transportation: The Peachtree Center Transit Station is located two blocks from the hotel, on the corner of Peachtree St. & Fourth St. Exit the station and turn left on Peachtree St., walk two blocks north to Hyatt Regency Atlanta: 265 Peachtree Street NE.

International Airport: The Hartsfield-Jackson International Airport International Terminal is located at 2600 Maynard H. Jackson Jr. Blvd. and handles all international flights into Atlanta separate from the domestic terminal building.

To get there on MARTA, take any southbound train to the Airport MARTA Station, which travels directly into the domestic terminal. Exit the train and go down the escalator/steps to exit the station. Turn right after going through the fare gate to enter the baggage claim area in the South Terminal. Immediately turn right again and exit out of the building (W-2 door), making sure to follow signs to Ground Transportation. A shuttle bus is available just outside the door that is clearly marked as the international shuttle.

If you are arriving at the international airport, again, follow signs to ground transportation/domestic airport shuttle. MARTA is just inside the airport once you arrive at the domestic terminal.

Taxi: \$32.00 for one person, \$2.00 for each additional person

MARTA (Metro Atlanta Rapid Transit Authority): \$2.50 per ride, plus a one-time reloadable card purchase of \$1.00. Rail system runs approximately every 10 minutes. Hyatt Regency Atlanta is connected to Peachtree Center Train Station via Peachtree Center Mall. 20 minutes from Airport. (Airport pickup at baggage claim, TH Terminal). To get to Hyatt, take MARTA to the Peachtree Center Station and exit Northeast toward Peachtree Center Mall. Hyatt is connected to this Mall with access via a skybridge directly into the hotel.

Welcome to Atlanta!

Atlanta is known for its rich history in civil rights, dense tree coverage (nicknamed “city in a forest”), and the world’s busiest airport. It is also home to numerous public health institutions including the U.S. Centers for Disease Control and Prevention, CARE, the American Cancer Society, the Task Force for Global Health, and the Carter Center. Since the 1996 Summer Olympic Games, Atlanta has experienced rapid transformations in demography, infrastructure and culture. In 2015, Money magazine ranked Atlanta 2nd as the best city for millennials based on job growth, cost-of-living, and other amenities. With more than 55 percent of residents from out-of-state or foreign-born, Atlanta also boasts immense diversity in food, music and cultural events, in addition to its Southern charm.

Ocean Voyager Exhibit Tunnel
Georgia Aquarium



Georgia Aquarium: A 10-minute walk from the Hyatt Regency, the Georgia Aquarium is the largest aquarium in the Western Hemisphere with more than 500 species in 60 habitats. Must-sees include beluga whales, manta ray, dolphins, and whale sharks. There are five themed exhibits, plus a 4-D movie theater. The prize exhibit is the six million gallon tank featuring the Western Hemisphere's only two whale sharks in captivity.

The World of Coca-Cola: Less than a 10-minute walk north of the Hyatt Regency Atlanta, the new World of Coca-Cola is better than ever. Featuring the world's smallest bottling plant, a 4-D movie theater and the famous fountain drink tasting room; the facility has drawn record crowds. Learn more about the world's most popular soft drinks through memorabilia, video presentations and displays. Included is a recreation of a 1930's soda fountain and the "Everything Coca-Cola" retail store.

CNN Studio Tour: This tour of the world's largest newsgathering organization is lots of fun, and a uniquely Atlanta experience. The CNN Center, which is headquarters for CNN, CNN International, and Headline News, is located within a 12-minute walk south of the Hyatt Regency Atlanta. During 40-minute guided walking tours, visitors get a behind-the-scenes look at the high-tech world of 24-hour TV network news in action.

Zoo Atlanta: In historic Grant Park, the Zoo features 250 species of animals from all over the world. Some unusual creatures include the Sumatran orangutans, Western Lowland gorillas, and black rhinos. Atlanta's newest visitors, a pair of Giant Pandas from China, arrived in 1999.

History & Art Museums

› The National Center for Civil and Human

Rights: See the history of the Civil Rights Movement in Atlanta and America in this world-class interactive museum. Walk in the footsteps of Civil Rights heroes, both through America's past and present. The Center houses three levels of exhibits, and houses the Morehouse College collection of Dr. Martin Luther King Jr.'s papers, articles and personal effects. Hyatt Regency Atlanta is a proud partner with the Center for Civil and Human Rights.

› **High Museum of Art:** The High Museum of Art displays European and American paintings, African, decorative and 20th century art and traveling exhibits by artists such as Picasso, Matisse, Monet, and Rockwell. The museum also offers weekly film screenings, jazz on select Friday nights, lectures, and tours.

› **Fernbank Museum of Natural History:** This museum includes exhibition galleries and an IMAX theater. Special features include displays of Argentinosaurus, the largest dinosaur ever unearthed and Giganotosaurus, the largest meat eater ever discovered. The complex includes a science center, planetarium, observatory and a forest featuring trails through majestic old trees. Every Friday night Fernbank offers Martinis and IMAX.

› **Jimmy Carter Presidential Library and Museum:** Visitors to this facility dedicated to the work of former U.S. President and Georgia native Jimmy Carter are surrounded by nature yet able to enjoy a view of the Atlanta Skyline. Such is the case in the Japanese Garden featuring two waterfalls cascading over rocks into a pool. Inside is memorabilia from Carter's presidency.

› **William Breman Jewish Heritage Museum:** Through its exhibitions, public programs, publications, and resources, this museum explores Jewish heritage in general and how it relates to other cultures and religions. It contains two permanent galleries and hosts rotating exhibits year-round.

Atlanta Parks



› **Centennial Olympic Park:** This 21-acre site was one of the most popular spots in the city during the 1996 Centennial Olympic Games, and is a 10-minute walk from the Hyatt Regency Atlanta. Today, year-round programming featuring concerts, family activities and artists' markets, which make the park a gathering place for Atlantans and visitors alike. The park features the world's largest Olympic Ring fountain, Quilts Plaza, and Water Gardens that weave together to tell the dramatic story of the 1996 Olympics.

› **Piedmont Park:** This is the largest park within the city of Atlanta, at 185 acres, and is one of the oldest, founded in 1904. Situated between 10th Street and Piedmont Avenue in Midtown, Piedmont Park features woods, sports fields, Lake Clara Meer, tennis courts, picnic spots, asphalt walking and skating paths, and annual events.

› **Stone Mountain Park:** This 3,200-acre complex features the world's largest mass of exposed granite: Stone Mountain at 825 feet high. The park also has an authentic antebellum plantation, a sky lift to the top of the mountain, a steam driven locomotive, riverboat cruises, the Discovering Stone Mountain Museum and a Laser Show on the side of the mountain.

Midtown: Directly north of the Hyatt Regency is the Midtown neighborhood – the art and culture center of Atlanta. Attractions include the Atlanta Botanical Garden, the High Museum of Art, the Center for Puppetry Arts, and venues for theatre and music. A large concentration of nightclubs and restaurants are also located in Midtown.

Peachtree Center Mall: Immediately outside of the Hyatt Regency Atlanta, Peachtree Center Mall offers a variety of fun activities for all ages. Situated in the heart of downtown at Peachtree Street and International Boulevard, Peachtree Center Mall is connected to Hyatt Regency Atlanta by a cov-

ered walkway. Studios, galleries and a variety of shops will keep you entertained for hours at Peachtree Mall.

Restaurants: In 2016, the New York Times described the Atlanta restaurant scene as “originality and technique have joined a reverence for simplicity and Southern ingredients.” Local favorites and foodie destinations cluster in neighborhoods such as West Midtown, Inman Park, and Decatur. Popular Authentic ethnic cuisines (e.g. Mexican, Chinese, Korean, Vietnamese) can be found along Buford Highway, about 30 minutes from downtown Atlanta. Don't forget southern classics like shrimp and grits, barbecue, and fried chicken!

SPECIAL THANKS TO THE 2018 PROGRAM COMMITTEE

Program Chair

Veera Baladandayuthapani, The University of Texas M.D. Anderson Cancer Center

Associate Program Chair

Jeff Goldsmith, Columbia University Mailman School of Public Health

IMS Program Chair

Fan Li, Duke University

Local Arrangements Chair

Howard Chang, Emory University Rollins School of Public Health

ASA Section Representatives

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Hongyuan Cao, University of Missouri, ASA Mental Health Section

Kassie Fronczyk, Lawrence Livermore National Laboratory, ASA Statistics in Defense & National Security Section

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Ying Guo, Emory University Rollins School of Public Health, ASA Statistics in Imaging Section

Charles Hall, Albert Einstein College of Medicine, ASA Statistics in Epidemiology Section

Nicholas Horton, Amherst College, ASA Statistical Education Section

Rebecca Hubbard, University of Pennsylvania Perelman School of Medicine, ASA Health Policy Statistics Section

Qi Jiang, Amgen, Inc. ASA Biopharmaceutical Section

Eric Laber, North Carolina State University, ASA Statistical Learning & Data Mining Section

Elizabeth Mannhardt, North Carolina State University, ASA Statistics & the Environment Section

Debajyoti Sinha, Florida State University ASA Section on Bayesian Statistical Science

Jung-Ying Tzeng, North Carolina State University, ASA Statistics in Genomics & Genetics Section

ENAR At-Large Members

Ani Eloyan, Brown University School of Public Health

Brian Hobbs, The University of Texas M.D. Anderson Cancer Center

Christina Kendziorski, University of Wisconsin

Eric Lock, University of Minnesota School of Public Health

Dionne Price, U.S. Food and Drug Administration

Yu Shen, The University of Texas M.D. Anderson Cancer Center

Educational Advisory Committee

Simone Gray, Centers for Disease Control

Ali Shojaie, University of Washington

Lorenzo Trippa, Harvard T.H. Chan School of Public Health

Wenyi Wang, The University of Texas M.D. Anderson Cancer Center

Zhenke Wu, University of Michigan School of Public Health

2018 ENAR Student Awards

Jianwen Cai, University of North Carolina Gillings School of Global Public Health

ENAR Fostering Diversity in Biostatistics Workshop

Emma Benn, Icahn School of Medicine at Mount Sinai

Portia Parker, SAS Institute, Inc.

ENAR Executive Team

Kathy Hoskins, Executive Director

Katie Earley, Program Manager

Cathy Marros, Administrator

Laura Stapleton, Administrative Assistant

Challee Blackwelder, Graphic Designer





Roderick J. Little

University of Michigan

Professor of Biostatistics, Richard D. Remington Distinguished University Professor, Department of Statistics
 Research Professor, Institute for Social Research
 Senior Fellow, Michigan Society of Fellows

Statistics as Prediction: I have always thought that a simple and unified approach to problems in statistics is from the prediction perspective – the objective is to predict the things you don't know, with appropriate measures of uncertainty. My inferential philosophy is “calibrated Bayes” – Bayesian predictive inference for a statistical model that is developed to have good frequentist properties. I discuss this viewpoint for a number of problems in missing data and causal inference, contrasting it with other approaches.

Biography: Roderick J. Little received his BA in Mathematics from Cambridge University, and MS and PhD degrees in Statistics from Imperial College, London. He has held faculty appointments from the University of California at Los Angeles and the University of Chicago, in addition to non-academic positions as ASA/Census/NSF Research Fellow at the US Bureau of the Census, before moving to the University of Michigan in 1993 where he served as Department Chair in the Department of Biostatistics for 11 years. In 2014, he was appointed the Richard D. Remington Distinguished University Professor of Biostatistics at the University of Michigan, where he also holds appointments in the Department of Statistics and the Institute for Social Research.

He has more than 250 publications, notably on methods for the analysis of data with missing values and model-based survey inference, and

the application of statistics to diverse scientific areas, including medicine, demography, economics, psychiatry, aging and the environment. He literally “wrote the book” on missing data analysis with his seminal book “Statistical Analysis with Missing Data” with Dr. Donald B. Rubin that has been cited more than 22,000 times since its first publishing in 1987. He is an ISI highly cited researcher, with more than 49,000 total citations of his works including 11 papers with more than 500 citations and 4 papers with more than 1,000 citations (Google Scholar). His work has made fundamental theoretical and applied impact, and serves as a model for how effective application-driven methodological research can effectively be done.

Little is an elected member of the International Statistical Institute, a Fellow of the American Statistical Association and the American Academy of Arts and Sciences, and a member of the National Academy of Medicine. In 2005, Little was awarded the American Statistical Association's Wilks Medal for research contributions, and he gave the President's Invited Address at the Joint Statistical Meetings. He was the COPSS Fisher Lecturer at the 2012 Joint Statistics Meetings. He has served as the coordinating and applications editor for the Journal of the American Statistical Association from 1992-1994, and Vice-President of the American Statistical Association from 2010-2012.

SUNDAY MARCH 257:30 am - 6:30 pm **CONFERENCE REGISTRATION****8:00 am - 12:00 pm SHORT COURSES****SC4.** Neuroimaging Analysis with R**SC5.** Causal Inference Structural Nested Mean Models**8:00 am - 5:00 pm SHORT COURSES****SC1.** Bayesian Adaptive Clinical Trials**SC2.** Machine Learning for Biomarker Discovery**SC3.** An Introduction to the Joint Modeling of Longitudinal & Survival Data, with Applications in R12:30 pm - 5:30 pm **DIVERSITY WORKSHOP****1:00 pm - 5:00 pm SHORT COURSES****SC6.** Reproducible Research with R & RStudio**SC7.** Survival for Precision Medicine3:00 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 & POSTER SESSION**

1. POSTERS: Biomarkers
2. POSTERS: Longitudinal Data Analysis
3. POSTERS: Statistical Genetics and Genomics
4. POSTERS: Missing Data and Measurement Error
5. POSTERS: Genome-Wide Association Studies
6. POSTERS: Survival Methods
7. POSTERS: Epidemiological Methods and Causal Inference
8. POSTERS: Cancer Applications
9. POSTERS: Bayesian Methods
10. POSTERS: Functional Data Analysis
11. POSTERS: High Dimensional Data and Computational Methods
12. POSTERS: Prediction, Diagnostics, and Risk Factor Identification

- 13. POSTERS: Clinical Trials and Biopharmaceutical Research Methods
- 14. POSTERS: Imaging and Neuroscience
- 15. POSTERS: Methods for Categorical and Ordinal Data
- 16. POSTERS: Spatial and Temporal Modeling

MONDAY MARCH 26

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 **SCIENTIFIC PROGRAM**

- 17. Human Microbiome Analysis: New Study Designs, Novel Methods, and Practical Considerations
- 18. Recent Innovation in Network Meta-Analysis
- 19. Statistical Analysis of Tracking Data from Personal Wearable Devices
- 20. Teaching Data Science at all Levels
- 21. Rich Data Visualizations for Informative Health Care Decisions
- 22. Modern Randomized Trial Designs
- 23. CONTRIBUTED PAPERS: Clinical Trial Methods
- 24. CONTRIBUTED PAPERS: Environmental and Ecological Applications
- 25. CONTRIBUTED PAPERS: Generalized Linear Models
- 26. CONTRIBUTED PAPERS: Measurement Error
- 27. CONTRIBUTED PAPERS: Methods for Next Generation Sequencing Data
- 28. CONTRIBUTED PAPERS: Statistics in Imaging

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**

T1. MICRO-RANDOMIZED TRIALS FOR CONSTRUCTING MOBILE HEALTH INTERVENTIONS

SCIENTIFIC PROGRAM

- 29. ORAL POSTERS: Network Science
- 30. Modern Methods for Using Historical and other Auxiliary Data in Adaptive Clinical Trials

31. Statistical Advances in Health Policy Research
32. Integrative Analysis of Multi-Omics Data with Applications to Precision Medicine
33. Functional Data Analysis in Biosciences
34. New Advances in Analysis of Survival Data from Biased Sampling
35. Estimation and Optimization for the Effects of Screening Schedules and Treatment Timing
36. CONTRIBUTED PAPERS: Clustered Data Methods
37. CONTRIBUTED PAPERS: Advances in Causal Inference
38. CONTRIBUTED PAPERS: Imputation Approaches with Missing Data
39. CONTRIBUTED PAPERS: Methods for Longitudinal Data Analysis
40. CONTRIBUTED PAPERS: Microbiome Research Methods
41. CONTRIBUTED PAPERS: Personalized / Precision Medicine

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

T2. DESIGN & ANALYSIS OF MEDICAL STUDIES USING ELECTRONIC HEALTH RECORDS DATA

SCIENTIFIC PROGRAM

42. ORAL POSTERS: Health Services and Health Policy
43. Recent Innovations in Practical Clinical Trial Design
44. Machine Learning Methods for Imaging Data Analysis
45. Making Sense of Whole Genome Sequencing Data in Population Science: Statistical Challenges and Solutions
46. Machine Learning Methods for Precision Medicine
47. Multi-Omics and Graphical Models for Precision Medicine
48. Recent Advances in Propensity Score Analysis
49. CONTRIBUTED PAPERS: Causal Inference and Epidemiological Methods
50. CONTRIBUTED PAPERS: Epidemiological Methods
51. CONTRIBUTED PAPERS: Infectious Disease Models
52. CONTRIBUTED PAPERS: Multivariate Survival Analysis
53. CONTRIBUTED PAPERS: Nonparametric Methods
54. CONTRIBUTED PAPERS: Pharmacokinetic / Pharmacodynamics and Biopharmaceutical Research

3:30 pm - 3:45 pm **REFRESHMENT BREAK WITH OUR EXHIBITORS**

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

T3. OVERVIEW OF THE FDA DRAFT GUIDANCE ON MULTIPLE ENDPOINTS

SCIENTIFIC PROGRAM

- 55. ORAL POSTERS: Medical Imaging
- 56. Quantifying Complex Dependency
- 57. Preparing for the Job Market
- 58. Novel Clinical Trial Designs
- 59. New Methods in Brain Connectivity
- 60. Statistical Methods for Emerging Spatial and Spatiotemporal Data
- 61. Novel Statistical Learning Methodologies for Precision Medicine
- 62. CONTRIBUTED PAPERS: Comparative Effectiveness Research
- 63. CONTRIBUTED PAPERS: Competing Risks
- 64. CONTRIBUTED PAPERS: Genome-Wide Association Studies
- 65. CONTRIBUTED PAPERS: Meta-Analysis
- 66. CONTRIBUTED PAPERS: Missing Data Methods
- 67. CONTRIBUTED PAPERS: Wearable and Portable Devices

5:30 pm - 6:30 pm **CENS NETWORKING MIXER**

6:30 pm - 7:30 pm **PRESIDENT'S RECEPTION (BY INVITATION ONLY)**

TUESDAY MARCH 27

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**

T4. FAST & EASY RNA-SEQ COMPUTATIONAL WORKFLOW USING BIOCONDUCTOR

SCIENTIFIC PROGRAM

- 68. Challenges, Opportunities, and Methods for Learning from Large-Scale Electronic Health Records Databases
- 69. Geometry and Topology in Statistical Inference

- 70. Predictive Modeling of Accelerometry, Electronic Diaries, and Passively Recorded Voice Data
- 71. Integrative Analysis for Brain Imaging Studies
- 72. Novel Extensions and Applications of Causal Inference Models
- 73. Statistical Methods in Single-Cell Genomics
- 74. CONTRIBUTED PAPERS: Functional Data Analysis
- 75. CONTRIBUTED PAPERS: High Dimensional Data Analysis
- 76. CONTRIBUTED PAPERS: Methods for Categorical and Ordinal Data
- 77. CONTRIBUTED PAPERS: Multivariate Methods
- 78. CONTRIBUTED PAPERS: SMART Designs and Dynamic Treatment Regimens
- 79. CONTRIBUTED PAPERS: Survival Analysis and Semi- and Non-Parametric Models
- 80. CONTRIBUTED PAPERS: Cancer Applications

10:15 am - 10:30 am **REFRESHMENT BREAK WITH OUR EXHIBITORS**

10:30 am - 12:15 pm

81. PRESIDENTIAL INVITED ADDRESS

12:30 pm - 4:30 pm **REGIONAL COMMITTEE LUNCHEON MEETING (BY INVITATION ONLY)**

1:45 pm - 3:30 pm TUTORIAL

T5. MULTI-MODAL IMAGING: PROMISES AND PITFALLS

SCIENTIFIC PROGRAM

- 82. Statistical Frontiers in Dynamic Treatment Regimes Leading Toward Personalized Health Care
- 83. Advanced Weighting Methods for Observational Studies
- 84. Spatial Modeling of Environmental and Epidemiological Data
- 85. Latest Development of Statistical Methods for Tumor Heterogeneity and Deconvolution
- 86. Statistical Analysis of Microbiome Data
- 87. Recent Advances in Statistical Methods for Imaging Genetics
- 88. CONTRIBUTED PAPERS: Clinical Trials and Biopharmaceutical Research
- 89. CONTRIBUTED PAPERS: Clustered and Hierarchical Data
- 90. CONTRIBUTED PAPERS: Experiment Design
- 91. CONTRIBUTED PAPERS: Nonlinear and Semi-Parametric Models
- 92. CONTRIBUTED PAPERS: Prediction and Prognostic Modeling

93. CONTRIBUTED PAPERS: Statistical Genetics and Genomics

94. CONTRIBUTED PAPERS: Survival Analysis in Epidemiology

3:30 pm - 3:45 pm **REFRESHMENT BREAK WITH OUR EXHIBITORS**

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

T6. INTEGRATIVE ANALYSES OF HIGH-THROUGH-PUT MULTI-PLATFORM GENOMICS DATA

SCIENTIFIC PROGRAM

95. Novel Statistical Approaches for Estimating Health Effects of Complex Environmental Exposures

96. Statistical Approaches for Handling Important Challenges Facing Current Aging Research

97. Recent Advances in the Estimation of Graphical and Covariance Models

98. Statistical Methods for Cancer Radiomics

99. Advancing the Analysis of Multiway (Tensor) Data

100. Modern Statistical Methods for the EHR Era

101. CONTRIBUTED PAPERS: Adaptive Design/Adaptive Randomization in Clinical Trials

102. CONTRIBUTED PAPERS: Functional Regression Models

103. CONTRIBUTED PAPERS: Analysis of ROC Curves

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

105. CONTRIBUTED PAPERS: Biomarkers

106. CONTRIBUTED PAPERS: Bayesian Methods for Genetics and Genomics

5:30 pm - 6:30 pm **ENAR BUSINESS MEETING (OPEN TO ALL ENAR MEMBERS)**

WEDNESDAY MARCH 28

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. Uncovering Heterogeneity in Longitudinal Data: Clustering and Mixture Modeling

108. Statistical Methods for Cancer-Omic Data

109. Geometric Approaches to Functional Data Analysis for Biomedical Applications

- 110. Randomization Inference: A Back to the Future Perspective
- 111. Frontiers in High-Dimensional Data & Big Data Analysis
- 112. CONTRIBUTED PAPERS: Functional Connectivity and Networks
- 113. CONTRIBUTED PAPERS: Individualized Treatment Rules
- 114. CONTRIBUTED PAPERS: Metabolomics and Proteomics
- 115. CONTRIBUTED PAPERS: Bayesian High Dimensional Data and Variable Selection
- 116. CONTRIBUTED PAPERS: Methods for Survival Analysis
- 117. CONTRIBUTED PAPERS: Variable Subset and Model Selection
- 118. CONTRIBUTED PAPERS: Methods for Single-Cell Analysis

10:15 am - 10:30 am **REFRESHMENT BREAK WITH OUR EXHIBITORS**

10:30 am - 12:15 pm SCIENTIFIC PROGRAM

- 119. Modern Hierarchical Approaches to Statistical Modeling
- 120. Advances and Innovative Applications of Joint Modeling to Public Health Research
- 121. STATISTICS AND INFORMATICS: Stronger Together
- 122. Recent Developments in Statistical Analysis of Brain Data
- 123. Statistical Modeling to Address Human Rights Issues
- 124. CONTRIBUTED PAPERS: Latent Variables
- 125. CONTRIBUTED PAPERS: Causal Inference in Survival Analysis
- 126. CONTRIBUTED PAPERS: Electronic Health Records
- 127. CONTRIBUTED PAPERS: Methods for RNA-seq Data
- 128. CONTRIBUTED PAPERS: Multiple Testing
- 129. CONTRIBUTED PAPERS: Cancer Genomics

SUNDAY MARCH 25**8:00 pm - 11:00 pm POSTER PRESENTATIONS****I. POSTERS: BIOMAKERS****Sponsor** ENAR**1a P-value Evaluation, Variability Index and Biomarker Categorization for Adaptively Weighted Fisher's Meta-Analysis Method in Omics Applications**

Zhiguang Huo Huo*, University of Florida; Shaowu Tang, Roche Molecular Systems, Inc.; Yongseok Park, University of Florida; George Tseng, University of Pittsburgh

1b Evaluating Alternative Approaches to Bootstrap Estimation Procedures in Two-Stage Group Sequential Designs

Sara Biesiadny*, Rice University; Nabihah Tayob, University of Texas MD Anderson Cancer Center

1c Novel Quantile Approach for the Identification of Biomarkers Associated with Type II Diabetes Using NHANES Database

Hanying Yan*, Columbia University; Ying Li, IBM T. J. Watson Research Center; Xiaoyu Song, Icahn School of Medicine at Mount Sinai

1d Learning Subject-Specific Directed Acyclic Graphs (DAGs) from High-Dimensional Biomarker Data

Shanghong Xie*, Columbia University; Xiang Li, Janssen Research & Development, LLC; Peter McColgan, UCL Institute of Neurology, London; Sarah J. Tabrizi, UCL Institute of Neurology, London and National Hospital for Neurology and Neurosurgery, London; Rachael I. Scahill, UCL Institute of Neurology, London; Donglin Zeng, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University

1e A Regression-Based Approach Incorporating Patients' Characteristics to Optimize Continuous Diagnostic Marker Cutoff

Yan Li* and Chap T. Le, University of Minnesota

1f gClinBiomarker: An R Package for Clinical Biomarker Analyses, along with "One-Click" Report Generating Templates

Ning Leng*, Alexey Pronin, Christina Rabe, Doug Kelkhoff, Kwame Okrah, Jane Fridlyand, Zhuoye Xu and Imola Fodor, Genentech

2. POSTERS: LONGITUDINAL DATA ANALYSIS**Sponsor** ENAR**2a Penalized Smoothing Splines in Adolescent Growth Studies**

Justin M. Leach* and Inmaculada Aban, University of Alabama at Birmingham

2b Inference on Mean Quality Adjusted Lifetime Using Joint Models for Continuous Quality of Life Process and Time to Event

Xiaotian Gao*, University of Pittsburgh; Xinxin Dong, Takeda Development Center Americas, Inc.; Chaeryon Kang and Abdus S. Wahed, University of Pittsburgh

2c A Bayesian Joint Frailty-Copula Model for Recurrent Events and a Terminal Event

Zheng Li*, Vernon M. Chinchilli and Ming Wang, The Pennsylvania State Health Milton S. Hershey Medical Center

2d Sample Size Calculation for a Two-Group Comparison of Repeated Count Outcomes Using GEE with Negative Binomial Distribution

Dateng Li* and Jing Cao, Southern Methodist University; Song Zhang, University of Texas Southwestern

2e Bayesian Longitudinal Multiple Outcomes Models for Exposure Effects

Omar Mbowe*, Edwin van Wijngaarden, Daniel W. Mruzek and Sally W. Thurston, University of Rochester

3. POSTERS: STATISTICAL GENETICS AND GENOMICS

Sponsor ENAR

3a SAME-Clustering: Single-Cell Aggregated Clustering via Mixture Model Ensemble

Ruth Huh*, Yuchen Yang, Jin Szatkiewicz and Yun Li, University of North Carolina, Chapel Hill

3b Integrating eQTL Data with GWAS Summary Statistics in Pathway-Based Analysis

Chong Wu* and Wei Pan, University of Minnesota

3c MethylSeqDesign: A Framework for Methyl-Seq Genome-Wide Power Calculation and Study Design Issues

Peng Liu* and George C. Tseng, University of Pittsburgh

3d Single Cell RNA Sequencing Count Modelling and Differential Expression Analysis Using Unique Molecular Identifier

Wenan Chen*, Peer Karmaus and Celeste Rosencrance, St. Jude Children's Research Hospital; Yan Li, University of Minnesota; John Easton, Hongbo Chi, Gang Wu and Xiang Chen, St. Jude Children's Research Hospital

3e Statistical Method of Gene Set Analysis for Single-Cell RNA-seq Data

Di Ran*, Shanshan Zhang and Lingling An, University of Arizona

3f TWO-SIGMA: A Two-Component Generalized Linear Mixed Model for scRNA-Seq Association Analysis

Eric Van Buren* and Yun Li, University of North Carolina, Chapel Hill; Ming Hu, Cleveland Clinic Foundation; Di Wu, University of North Carolina, Chapel Hill

3g Differentially Methylated Genes Associated with Drug Response

Hongyan Xu*, Augusta University; Fengjiao Hu, National Institute of Environmental Health Sciences, National Institutes of Health; Santu Ghosh, Augusta University; Sunil Mathur, Texas A&M University, Corpus Christi; Varghese George, Augusta University

3h Integrated Modeling of Massive Multiple-Domain Data

Dongyan Yan*, University of Missouri; Veerabhadran Baladandayuthapani, University of Texas MD Anderson Cancer Center; Subharup Guha, University of Missouri

3i Integrative Gene-Environment Interactions from Multi-Dimensional Omics Data in Cancer Prognosis

Yinhao Du*, Guotao Chu, Fei Zhou and Cen Wu, Kansas State University

3j eQTL Analysis Using Human RNA-seq Data with TrecASE and RASQUAL

Vasyl Zhabotynsky*, University of North Carolina, Chapel Hill; Yi-Juan Hu, Emory University; Fei Zou, University of North Carolina, Chapel Hill; Wei Sun, Fred Hutchinson Cancer Research Center

4. POSTERS: MISSING DATA AND MEASUREMENT ERROR

Sponsor ENAR

4a An Estimating Equation Approach to Accounting for Case Contamination in EHR-Based Case-Control Studies

Lu Wang*, University of Pennsylvania; Aeron Small, Yale University; Rebecca A. Hubbard, Scott M. Damrauer and Jinbo Chen, University of Pennsylvania

4b Bayesian Nonparametric Analysis of Longitudinal Data with Non-Ignorable Non-Monotone Missingness

Yu Cao* and Nitai Mukhopadhyay, Virginia Commonwealth University

4c Informative Dropout with Nested Repeated Measures Data

Enas Mustfa Ghulam* and Rhonda D. Szczesniak, Cincinnati Children's Hospital Medical Center

4d Multiple Imputation Strategies for Missing Continuous Outcomes in Non-Inferiority Randomized Trials

Lin Taft*, Douglas Thompson, Juan Abellan and Andre Acosta, GlaxoSmithKline

4e Measurement Error Models with High-Dimensional Longitudinal Predictors

Hyung Gyu Park* and Seonjoo Lee, Columbia University

4f Combining Inverse Probability Weighting and Multiple Imputation to Adjust for Selection Bias in Electronic Health Records-Based Research

Tanayott Thaweethai*, Harvard University; David Arterburn, Kaiser Permanente Washington Health Research Institute; Sebastien Haneuse, Harvard University

5. POSTERS: GENOME-WIDE ASSOCIATION STUDIES

Sponsor ENAR

5a **Approximate Conditional Trait Analysis Based on Marginal GWAS Summary Statistics**

Peitao Wu* and Biqi Wang, Boston University School of Public Health; James B. Meigs, Massachusetts General Hospital, Harvard Medical School and Broad Institute; Josée Dupuis, Boston University School of Public Health

5b **A New Approach for Evaluating the Global Impact of Mutations on Genetic Networks**

Mengqi Zhang* and Andrew S. Allen, Duke University

5c **Estimation of Complex Effect-Size Distributions Using Summary-Level Statistics from Genome-Wide Association Studies**

Yan Zhang* and Guanghao Qi, Johns Hopkins University; Juhyun Park, Dongguk University; Nilanjan Chatterjee, Johns Hopkins University

5d **Integrating Genetic, Transcriptional and Biological Information Provides Insights into Obesity: The Framingham Heart Study**

Jeremiah Perez*, Lan Wang and Nancy Heard-Costa, Boston University; Audrey Y. Chu, National Heart, Lung, and Blood Institute, National Institutes of Health; Roby Joehanes, Harvard Medical School; Daniel Levy, National Heart, Lung, and Blood Institute, National Institutes of Health

5e **PCA Based Adaptive Multi-Trait SNP-Set Association Test Using the GWAS Summary Statistics**

Bin Guo* and Baolin Wu, University of Minnesota

6. POSTERS: SURVIVAL METHODS

Sponsor ENAR

6a **Semi-Parametric Multistate Markov Model with Transition-Specific Frailty for Interval Censored Life History Data**

Daewoo Pak*, Chenxi Li and David Todem, Michigan State University

6b **Survival Analysis Under Dependent Truncation**

Lior Rennert* and Sharon X. Xie, University of Pennsylvania

6c **Diagnostic Accuracy Analysis for Ordinal Competing Risk Outcomes Using ROC Surface**

Song Zhang*, University of Pittsburgh

6d **Empirical Likelihood Inference for Semiparametric Transformation Models with Length-Biased Sampling**

Xue Yu* and Yichuan Zhao, Georgia State University

6e Random Forests based Approach for Prediction of Competing Risks under Missing Cause of Failure

Jun Park*, Giorgos Bakoyannis, Ying Zhang and Constantin T. Yiannoutsos, Indiana University School of Public Health and School of Medicine

6f Impact of Non-Terminal Event Status on Hazard of Terminal Event in Semi-Competing Risks Data

Jing Li*, Ying Zhang and Giorgos Bakoyannis, Indiana University School of Public Health

6g Bayesian Analysis of Survival Data with Missing Censoring Indicators

Veronica J. Bunn*, Debajyoti Sinha and Naomi Brownstein, Florida State University

6h Statistical Inference on the Cure Time via Conditional Survival

Yueh Wang* and Hung Hung, National Taiwan University

6i Challenges and Pitfalls in Time-Dependent Survival Analysis

Abigail R. Smith*, Qian Liu, Margaret E. Helmuth, Alan B. Leichtman and Jarcy Zee, Arbor Research Collaborative for Health

6j Method for Evaluating Longitudinal Follow-Up Frequency: Application to Dementia Research

Leah H. Suttner* and Sharon X. Xie, University of Pennsylvania

6k Optimal Bayesian Estimates of Inverse Weibull Progressive Type-II Censored Data

Sarbesh R. Pandeya*, Hani Samawi and Xinyan Zhang, Georgia Southern University

7. POSTERS: EPIDEMIOLOGICAL METHODS AND CAUSAL INFERENCE

Sponsor ENAR

7a Impacts of Gestational Age Uncertainty in Estimating Associations between Preterm Birth and Ambient Air Pollution

Benjamin E. Nealy* and Howard H. Chang, Emory University; Joshua L. Warren, Yale University; Lyndsey A. Darrow and Matthew J. Strickland, University of Nevada, Reno

7b A Spatial Factor Model Approach for Assessing the Opioid Epidemic in Ohio

David M. Kline*, The Ohio State University; Staci A. Hepler, Wake Forest University; Andrea E. Bonny and Erin R. McKnight, Nationwide Children's Hospital

7c A Biometrical Genetic Model for Heritability under Environmental Exposure over Multiple Generations

Jiali Zhu* and Wei-Wen Hsu, Kansas State University; David Todem, Michigan State University; Wilfried Karmaus, University of Memphis

7d Propensity Score Matching with Multilevel Data

Qixing Liang* and Min Zhang, University of Michigan

7e Assessment of Residential History as a Surrogate for Environmental Exposure

Anny-Claude Joseph* and David C. Wheeler, Virginia Commonwealth University

7f Evaluating Sample Sizes in Comparing Over-Dispersed Count Data Under Incorrect Variance Structure

Masataka Igeta*, Hyogo College of Medicine; Kunihiro Takahashi and Shigeyuki Matsui, Nagoya University

8. POSTERS: CANCER APPLICATIONS**Sponsor** ENAR**8a Estimating Lead-Time Bias in Lung Cancer Diagnosis of Cancer Survivors**

Zhiyun Ge* and Daniel Heitjan, University of Texas Southwestern Medical Center and Southern Methodist University; David Gerber, Lei Xuan and Sandi Pruitt, University of Texas Southwestern Medical Center

8b Cancer Mortality in USA 1999-2014: A Review and Inter-State Comparisons

Desale Habtezgi*, DePaul University; Dimitre Stefanov and Midha Chand, University of Akron; Ashish Das, Indian Institute of Technology, Bombay

8c Propensity Score Estimation with Missing Covariate Data

Joanna G. Harton*, Weiwei Feng and Nandita Mitra, University of Pennsylvania

8d Statistical Considerations in Tumor-Only Variant Calling

Paul L. Little*, University of North Carolina Lineberger Comprehensive Cancer Center; David N. Hayes, University of North Carolina Lineberger Comprehensive Cancer Center, West Cancer Center and University of Tennessee Health Science Center; Joel Parker and Alan Hoyle, University of North Carolina Lineberger Comprehensive Cancer Center; Jose Zevallos, Washington University School of Medicine, St. Louis; Heejoon Jo and Angela Mazul, University of North Carolina Lineberger Comprehensive Cancer Center

8e Intensity Normalization of MRI Images Specific to Patients with Glioblastomas to Improve Prediction of Treatment Outcomes using Radiomics

Abdhi Sarkar* and Russel T. Shinohara, University of Pennsylvania

8f Assessing Time-Dependent Treatment Effect with Joint Model of Intermediate and Terminal Events

Wenjia Wang* and Alexander Tsodikov, University of Michigan

8g A Matrix-Based Approach for Two-Group Comparison with Correlated Observations and Heterogeneous Variance Structure

Yun Zhang* and Xing Qiu, University of Rochester

8h Predicting Survival Time in Cancer Patients using Genetic Data and Immune Cell Composition

Licai Huang*, Fred Hutchinson Cancer Research Center; Paul Little, University of North Carolina, Chapel Hill; Wei Sun, Fred Hutchinson Cancer Research Center; Qian Shi, Mayo Clinic; Tabitha Harrison and Riki Peters, Fred Hutchinson Cancer Research Center; Andy Chan, Massachusetts General Hospital and Harvard Medical School; Polly Newcomb, Fred Hutchinson Cancer Research Center

9. POSTERS: BAYESIAN METHODS**Sponsor** ENAR**9a Bayesian Parametric Covariance Regression Analysis**

Guanyu Hu*, Fred Huffer and Jonathan Bradley, Florida State University

9b A Sequential Approach to Bayesian Joint Modeling of Longitudinal and Survival Data

Danilo Alvares*, Harvard School of Public Health; Carmen Armero and Anabel Forte, University of Valencia; Nicolas Chopin, CREST-ENSAE and HEC Paris

9c Comparison of Confidence Interval Estimation in Linear Excess Relative Risk Models Between Bayesian Model Averaging and Expanded Interval Estimation when Exposure Uncertainty is Complex

Deukwo Kwon*, University of Miami; Steven L. Simon, National Cancer Institute, National Institutes of Health; F. Owen Hoffman, Oak Ridge Center for Risk Analysis

9d Application of Bayesian Hierarchical Models for Estimating Annual Global Burden of Influenza-Associated Hospitalization

Guandong Yang*, Howard H. Chang and Mingrui Liang, Emory University; Katherine M. Roguski and Jeremy Reich, Centers for Disease Control and Prevention; Neha Patel, Emory University; Vanessa Cozza and Julia Fitzner, World Health Organization, Switzerland; Danielle A. Iuliano, Centers for Disease Control and Prevention

9e A Spatially Varying Change Point Model for Determining Glaucoma Progression Using Visual Field Data

Samuel I. Berchuck*, University of North Carolina, Chapel Hill; Joshua L. Warren, Yale University; Jean-Claude Mwanza, University of North Carolina, Chapel Hill

9f Bayesian Biclustering Analysis via Adaptive Structured Shrinkage

Ziyi Li*, Emory University; Changgee Chang, University of Pennsylvania; Suprateek Kundu, Emory University; Qi Long, University of Pennsylvania

9g Bayesian Nonparametric Functional Models in Matched Case-Crossover Studies

Wenyu Gao* and Inyoung Kim, Virginia Tech

9h Bayesian Single Index Model with Covariates Missing at Random

Kumaresh Dhara*, Florida State University; Debdeep Pati, Texas A&M University; Debajoyti Sinha, Florida State University; Stuart Lipsitz, Harvard Medical School

9i A Latent Bayesian Classification Model to Predict Kidney Obstruction based on Renography and Expert Ratings

Changgee Chang*, University of Pennsylvania; Jeong Hoon Jang and Amita Manatunga, Emory University; Qi Long, University of Pennsylvania

9j Bayesian Network Meta-Regression Models Using Heavy-Tailed Multivariate Random Effects with Covariates-Dependent Variances

Hao Li* and Ming-Hui Chen, University of Connecticut; Joseph G. Ibrahim, University of North Carolina, Chapel Hill; Sungduk Kim, National Cancer Institute, National Institutes of Health; Arvind K. Shah and Jianxin Lin, Merck & Co., Inc.

9k Bayesian Design Optimization of an Olfactory Sensor System and a New Measure of Analytical Selectivity

David Han*, University of Texas, San Antonio

10. POSTERS: FUNCTIONAL DATA ANALYSIS

Sponsor ENAR

10a Shape Constrained Univariate Density Estimation

Sutanoy Dasgupta*, Florida State University; Debdeep Pati, Texas A&M University; Ian Jermyn, Durham University; Anuj Srivastava, Florida State University

10b Hybrid Principal Components Analysis for Region-Referenced Longitudinal Functional EEG Data

Aaron W. Scheffler*, Donatello Telesca, Qian Li, Catherine Sugar, Charlotte DiStefano, Shafali Jeste and Damla Senturk, University of California, Los Angeles

10c Testing for Interaction in Functional Varying-Coefficient Models

Merve Yasemin Tekbudak* and Arnab Maity, North Carolina State University

10d Comparison of Statistical Methods to Calculate a Temporal Binding Window

John Bassler*, West Virginia University and University of Alabama at Birmingham; Sijin Wen, Paula Webster and James Lewis, West Virginia University

10e Rank Based Group Variable Selection for Functional Regression Model

Jieun Park*, Ash Abebe and Nedret Billor, Auburn University

10f Functional Data Analyses of Gait Data Measured Using In-Shoe Sensors

Jihui Lee* and Gen Li, Columbia University; William F. Christensen, Gavin Collins and Matthew Seeley, Brigham Young University; Jeff Goldsmith, Columbia University

10g Using Data from Multiple Studies to Develop a Child Growth Correlation Matrix

Luo Xiao*, North Carolina State University; Craig Anderson, University of Glasgow; William Checkley, Johns Hopkins University

II. POSTERS: HIGH DIMENSIONAL DATA AND COMPUTATIONAL METHODS

Sponsor ENAR

11a SurvBoost: An R Package for High-Dimensional Variable Selection in the Stratified Proportional Hazards Model via Gradient Boosting

Emily L. Morris*, Zhi He, Yanming Li, Yi Li and Jian Kang, University of Michigan

11b Renewable Estimation and Inference in Generalized Linear Model with Streaming Datasets

Lan Luo* and Peter X.K. Song, University of Michigan

11c Confidence Interval for the Ratio of Two Standard Deviations of Normal Distributions with Known Coefficients of Variation

Wararit Panichkitkosolkul*, Thammasat University, Thailand

11d Clustering Matrix Variate Data Using Finite Mixture Models with Component-Wise Regularization

Peter A. Tait* and Paul D. McNicholas, McMaster University

11e Jackknife Empirical Likelihood Inference for the Mean Difference of Two Zero Inflated Skewed Populations

Faysal I. Satter* and Yichuan Zhao, Georgia State University

11f Application of Novel Statistical Method for Body Posture Recognition Using Wrist-Worn Accelerometer to Assess Daily Standing Patterns in HIV-Infected Patients

Marcin Straczekiewicz*, Indiana University; Christopher Sorensen and Beau Ances, Washington University School of Medicine, St. Louis; Jaroslaw Harezlak, Indiana University

11g SAFE-Clustering: Single-Cell Aggregated (From Ensemble) Clustering for Single-Cell RNA-seq Data

Yuchen Yang*, Ruth Huh, Houston Culpepper and Yun Li, University of North Carolina, Chapel Hill

11h The N-leap Method for Stochastic Simulation of Coupled Chemical Reactions

Yuting Xu*, Merck & Co.; Yueheng Lan, Beijing University of Posts and Telecommunications

11i The Efficiency of Ranking Count Data with Excess Zeros

Deborah A. Kanda* and Jingjing Yin, Georgia Southern University

11j Neighborhood Selection with Application to Social Networks

Nana Wang* and Wolfgang Polonik, University of California, Davis

11k Simulation Study and Applications of the Burr XII Weibull Distribution

Sarah Ayoku* and Broderick Oluyede, Georgia Southern University

12. POSTERS: PREDICTION, DIAGNOSTICS, AND RISK FACTOR IDENTIFICATION**Sponsor** ENAR**12a Infectious Disease Detection Using Specimen Pooling with Multiplex Assays when Risk-Factor Information is Present**

Christopher R. Bilder*, University of Nebraska-Lincoln; Joshua M. Tebbs, University of South Carolina; Christopher S. McMahan, Clemson University

12b A Group Testing Design that can Achieve More by Doing Less

Dewei Wang*, University of South Carolina

12c Statistical Models for Predicting Knee Osteoarthritis Endpoints: data from the Osteoarthritis Initiative

Robin M. Dunn* and Joel Greenhouse, Carnegie Mellon University; Peter Mesenbrink, David James and David Ohlssen, Novartis Pharmaceuticals Corporation

12d Open Source Machine Learning Algorithms for Prediction of Optimal Cancer Drug Therapy

Cai Huang*, Georgia Institute of Technology

12e Copas-Like Selection Model to Correct Publication Bias in Systematic Review of Diagnostic Test Studies

Jin Piao*, University of Southern California; Yulun Liu and Yong Chen, University of Pennsylvania; Jing Ning, University of Texas MD Anderson Cancer Center

12f Using Biostatistics to Improve Health Outcomes on the Last Mile of a Learning Healthcare System

Daniel W. Byrne*, Henry J. Domenico and Li Wang, Vanderbilt University

12g Using Frailty Models to Improve Breast Cancer Risk Prediction

Theodore J. Huang* and Danielle Braun, Harvard School of Public Health and Dana-Farber Cancer Institute; Malka Gorfine, Tel Aviv University; Li Hsu, Fred Hutchinson Cancer Research Center; Giovanni Parmigiani, Harvard School of Public Health and Dana-Farber Cancer Institute

12h An Ensemble Modeling Approach for Estimating Global Burden of Influenza-Associated Hospitalizations

Mingrui Liang*, Howard Chang and Guandong Yang, Emory University; Katherine Roguski, Jeremy Reich and Danielle Iuliano, Centers for Disease Control and Prevention; Neha Patel, Emory University; Vanessa Cozza and Julia Fitzner, World Health Organization

12i Net Benefit Curves: A Model Performance Measure for Examining Clinical Usefulness

Anwasha Mukherjee* and Daniel L. McGee, Florida State University

13. POSTERS: CLINICAL TRIALS AND BIOPHARMACEUTICAL RESEARCH METHODS**Sponsor** ENAR**13a Adaptive Bayesian Phase I Clinical Trial Design for Estimation of Maximum Tolerated Doses of Two Drugs while Fully Utilizing all Toxicity Information**

Yuzi Zhang*, Michael Kutner, Jeanne Kowalski and Zhengjia Chen, Emory University

13b Analyses of Longitudinal Clinical Data with Time-Varying Covariates in Large and Long-Term Trials

Qianyi Zhang* and Rong Liu, Eli Lilly and Company

13c Two-Stage Design Considering Superiority and Non-Inferiority Tests in Three-Arm Clinical Trials

Yoshikazu Ajisawa*, Tokyo University of Science; Shogo Nomura, National Cancer Center, Japan; Takashi Sozu, Tokyo University of Science

13d Optimal Sample Size for Cluster Randomized Trials Based on Simulation and Randomization Distribution

Ruoshui Zhai* and Roe Gutman, Brown University

13e Quantal Response Data Analysis with Covariates

Lili Tong* and Edsel Pena, University of South Carolina

13f Modified Wald Tests for Reference Scaled Equivalence Assessment of Analytical Biosimilarity

Yu-Ting Weng*, Yi Tsong, Meiyu Shen and Chao Wang, U.S. Food and Drug Administration

13g Power and Type I Error Rate Estimation via Simulation for Multistate Endpoints

Ryan A. Peterson*, University of Iowa; Jennifer G. Rademacher, Sumithra J. Mandrekar and Terry M. Therneau, Mayo Clinic

13h An Application of Augmented Beta Regression Techniques in Pharmacokinetic-Pharmacodynamic Modeling of a Bounded Outcome in Psoriasis

James A. Rogers* and Jonathan French, Metrum Research Group; Bojan Lalovic, Eisai Co. Ltd.

13i Breast Cancer Multi-Arm Clinical Trials with Multiple Objectives: A Literature Review of Major Journals

Yu Miyauchi*, Tokyo University of Science; Shogo Nomura, National Cancer Center, Japan; Yoshikazu Ajisawa and Takashi Sozu, Tokyo University of Science

14. POSTERS: IMAGING AND NEUROSCIENCE

Sponsor ENAR

14a Image-on-Image Regression: A Spatial Bayesian Latent Factor Model for Predicting Task-Evoked Brain Activity Using Task-Free MRI

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

14b Features Extraction in Brain Video via Deep Convolutional Autoencoder

Jiahui Guan*, University of California, Davis

14c Powerful Permutation Tests for Neuroimaging using Voxel-Wise Transformations

Simon N. Vandekar*, Theodore D. Satterthwaite, Adon Rosen, Rastko Ciric, David R. Roalf, Kosha Ruparel, Ruben C. Gur, Raquel E. Gur and Russell T. Shinohara, University of Pennsylvania

14d Multiple Testing Based on Semi-Parametric Hierarchical Mixture Models under Dependency in Disease-Association Studies with Neuroimaging Data

Ryo Emoto*, Nagoya University; Atsushi Kawaguchi and Hisako Yoshida, Saga University; Shigeyuki Matsui, Nagoya University

14e Statistical Inference for the First Passage Time of a Diffusion Process of Neural Activity

Bowen Yi* and Satish Iyengar, University of Pittsburgh

14f Global PCA of Local Moments with Applications to MRI Segmentation

Jacob M. Maronge*, University of Wisconsin, Madison; John Muschelli and Ciprian M. Crainiceanu, Johns Hopkins Bloomberg School of Public Health

14g A Non-Parametric, Network-Based Test for Group Differences in Multivariate Subject-Level Histograms

Jordan D. Dworkin* and Russell T. Shinohara, University of Pennsylvania

15. POSTERS: METHODS FOR CATEGORICAL AND ORDINAL DATA

Sponsor ENAR

15a A Smooth Nonparametric Approach to Determining Cut-Points of a Continuous Scale

Zhiping Qiu*, Limin Peng, Amita Manatunga and Ying Guo, Emory University

15b Testing Homogeneity of Difference of Two Proportions for Stratified Correlated Paired Binary Data

Xi Shen* and Changxing Ma, State University of New York at Buffalo

15c Assess Treatment Effects for Multiple Groups for Ordinal Outcome when Confounding Exists

Soutik Ghosal* and Maiying Kong, University of Louisville

15d Comparing Multistate Modeling Methods with Application to Alzheimer's Disease

Jacquelyn E. Neal* and Dandan Liu, Vanderbilt University

15e Asymptotic Confidence Interval Construction for Proportion Ratio Based on Correlated Paired Data

Xuan Peng* and Changxing Ma, State University of New York at Buffalo; Song Liu, Roswell Park Cancer Institute

16. POSTERS: SPATIAL AND TEMPORAL MODELING

Sponsor ENAR

16a Analyzing Spatial Longitudinal Incidence Patterns using Dynamic Multivariate Poisson Models

Yihan Sui*, Chi Song and Grzegorz Rempala, The Ohio State University

16b Online Sequential Monitoring of Disease Incidence Rates with an Application to the Florida Influenza-Like Illness Data

Kai Yang* and Peihua Qiu, University of Florida

16c Pointwise Tolerance Intervals for Autoregressive Models, with an Application to Hospital Waiting Lists

Kedai Cheng* and Derek S. Young, University of Kentucky

16d Characterizing Spatial Dependence on Stream Networks: Bayesian Hierarchical Model Approximation

Yingying Liu*, University of Iowa

16e Multivariate Air Pollutant Exposure Prediction in South Carolina

Ray Boaz*, Andrew Lawson and John Pearce, Medical University of South Carolina

16f A Bayesian GLMM for Modeling Spatially Varying Trends in Disease Prevalence with an Application to Lyme Disease

Stella C. Watson*, Christopher S. McMahan, Andrew Brown and Robert Lund, Clemson University

16g Modeling High Dimensional Multichannel Brain Signals

Lechuan Hu* and Norbert J. Fortin, University of California, Irvine; Hernando Ombao, King Abdullah University of Science and Technology

16h Identifying Non-Stationarity in PM2.5 Data via an M-RA and Mixture Priors

Marco Henry Benedetti* and Veronica Berrocal, University of Michigan; Naveen Narisetty, University of Illinois at Urbana-Champaign

16i Temporally Dependent Accelerated Failure Time Model for Capturing the Impact of Events that Alter Survival in Disease Mapping

Rachel M. Carroll* and Shanshan Zhao, National Institute of Environmental Health Sciences, National Institutes of Health; Andrew B. Lawson, Medical University of South Carolina

MONDAY MARCH 26**8:30 am - 10:15 am****17. HUMAN MICROBIOME ANALYSIS: NEW STUDY DESIGNS, NOVEL METHODS, AND PRACTICAL CONSIDERATIONS****Sponsors** ENAR, ASA Statistics in Genomics and Genetics Section**Organizer** Ni Zhao, Johns Hopkins University**Chair** Min Jin Ha, University of Texas MD Anderson Cancer Center**8:30 Methods for Inferring Growth Dynamics of Gut Microbiota from Metagenomics Samples**

Hongzhe Li*, University of Pennsylvania

8:55 Identifying Host Genetic Variants Associated with Microbiome Composition in Genome-Wide Association Studies

Jianxin Shi* and Xing Hua, National Cancer Institute, National Institutes of Health

9:20 Practical Issues in Analyzing Longitudinal Human Microbiome Data

Snehalata Huzurbazar* and Eugenie Jackson, West Virginia University

9:45 Kernel Machine Regression Methods for Correlated Microbiome Community Data

Ni Zhao*, Johns Hopkins University; Haotian Zheng, Tsinghua University; Xiang Zhan, The Pennsylvania State University

10:10 Floor Discussion**18. RECENT INNOVATION IN NETWORK META-ANALYSIS****Sponsors** ENAR, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Biopharmaceutical Section, IMS**Organizer** Ming-Hui Chen, University of Connecticut**Chair** Dipak Dey, University of Connecticut**8:30 Bayesian Inference for Network Meta-Regression Using Multivariate Random Effects with Applications to Cholesterol Lowering Drugs**

Joseph G. Ibrahim*, University of North Carolina, Chapel Hill; Ming-Hui Chen, University of Connecticut; Arvind Shah, Merck & Co., Inc.; Hao Li, University of Connecticut; Sunduk Kim, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health; Jianxin Lin and Andrew Tershakovec, Merck & Co., Inc.

8:55 A Bayesian Hierarchical Model for Network Meta-Analysis of Diagnostic Tests

Haitao Chu*, Xiaoye Ma and Qinshu Lian, University of Minnesota; Joseph G. Ibrahim, University of North Carolina, Chapel Hill; Yong Chen, University of Pennsylvania

9:20 N-of-1 Trials for Making Personalized Treatment Decisions

Christopher H. Schmid*, Brown University

9:45 Network Meta-Regression for Ordinal Outcomes: Applications in Comparing Crohn's Disease Treatments

Ming-Hui Chen* and Yeongjin Gwon, University of Connecticut; May Mo, Amgen Inc.; Juan Li, Eli Lilly and Company; H. Amy Xia, Amgen Inc.; Joseph G. Ibrahim, University of North Carolina, Chapel Hill

10:10 Floor Discussion**19. STATISTICAL ANALYSIS OF TRACKING DATA FROM PERSONAL WEARABLE DEVICES**

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

Organizer Peter Song, University of Michigan

Chair Peter Song, University of Michigan

8:30 Emerging Biostatistical Problems in Wearable and Implantable Technology (WIT)

Ciprian M. Crainiceanu*, Johns Hopkins University

8:55 Use of Accelerometers in Clinical Trials

John W. Staudenmayer*, University of Massachusetts, Amherst

9:20 Statistical Analysis of Social and Behavioral Markers from Smartphone Data

Jukka-Pekka Onnela*, Harvard University

9:45 Quantifying Heritability of Physical Activity Patterns Based using Functional ACE Models

Haochang Shou*, University of Pennsylvania; Joanne Carpenter, University of Sydney; Kathleen Merikangas, National Institute of Mental Health, National Institutes of Health; Ian Hickie, University of Sydney

10:10 Floor Discussion

20. TEACHING DATA SCIENCE AT ALL LEVELS

Sponsors ENAR, ASA Statistical Education Section

Organizer Mine Cetinkaya-Rundel, Duke University and RStudio

Chair Lance Waller, Emory University

8:30 Data Science as a Gateway to Statistics

Mine Cetinkaya-Rundel*, Duke University and RStudio

8:55 Teaching Data Science for Life Sciences

Michael I. Love*, University of North Carolina, Chapel Hill

9:20 Make Interactive Web Tutorials with learnr and R

Garrett Grolemond*, RStudio, Inc.

9:45 Teaching Survey and Data Science Outside Regular Classroom Settings

Frauke Kreuter*, University of Maryland and University of Mannheim

10:10 Floor Discussion

21. RICH DATA VISUALIZATIONS FOR INFORMATIVE HEALTH CARE DECISIONS

Sponsors ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology, ASA Section on Statistics in Imaging

Organizer Tanya Garcia, Texas A&M University

Chair Tanya Garcia, Texas A&M University

8:30 Flexible and Interpretable Regression in High Dimensions

Ashley Petersen*, University of Minnesota; Daniela Witten, University of Washington

8:55 Visualising Model Stability Information for Better Prognosis Based Network-Type Feature Extraction

Samuel Mueller*, Connor Smith and Boris Guennewig, University of Sydney

9:20 Vizualizations for Joint Modeling of Survival and Multivariate Longitudinal Data in Huntington's Disease

Jeffrey D. Long*, University of Iowa

9:45 Discordancy Partitioning for Validating Potentially Inconsistent Pharmacogenomic Studies

J. Sunil Rao* and Hongmei Liu, University of Miami

10:10 Floor Discussion

22. MODERN RANDOMIZED TRIAL DESIGNS

Sponsors ENAR, IMS

Organizer Benjamin Goldstein, Duke University

Chair Benjamin Goldstein, Duke University and Hwanhee Hong, Johns Hopkins University

8:30 The IMP: Interference Manipulating Permutation

Michael Baiocchi*, Stanford University

8:55 Translating Clinical Trial Results to a Target EHR Population Using Machine Learning and Causal Inference

Benjamin A. Goldstein*, Duke University; Matt Phelan, Duke Clinical Research Institute; Neha Pagidipati, Duke University

9:20 Evaluating Effectiveness and Safety of Low and High Dose Aspirin: A Pragmatic Trial Approach

Zhen Huang*, Jennifer White and Frank Rockhold, Duke Clinical Research Institute

9:45 Causal Analysis of Self-Trackd Time Series Data using a Counterfactual Framework for N-of-1 Trials

Eric J. Daza*, Stanford Prevention Research Center

10:10 Floor Discussion

23. CONTRIBUTED PAPERS: CLINICAL TRIAL METHODS

Sponsor ENAR

Chair Bin Dong, Janssen Research & Development

8:30 Bayesian Continuous Monitoring for Phase I Cohort Expansion and Phase II Cancer Clinical Trials

Youjiao Yu*, Baylor University

8:45 Using Multi-State Models in Cancer Clinical Trials

Jennifer G. Le-Rademacher*, Mayo Clinic; Ryan A. Peterson, University of Iowa; Terry M. Therneau and Sumithra J. Mandrekar, Mayo Clinic

9:00 Clarifying Common Misconceptions about Covariate Adjustment in Randomized Trials

Bingkai Wang* and Michael Rosenblum, Johns Hopkins Bloomberg School of Public Health

9:15 MMRM Estimates Consideration for Longitudinal Data in Clinical Trials

Zheng (Jason) Yuan*, Chenkun Wang and Bingming Yi, Vertex Pharmaceuticals

9:30 Surrogate Endpoint Evaluation: Meta-Analysis, Information Theory, and Causal Inference

Geert Molenberghs*, I-BioStat, Hasselt University and Katholieke Universiteit Leuven

9:45 Milestone Prediction for Time-to-Event Endpoint Monitoring in Clinical Trials

Fang-Shu Ou*, Mayo Clinic; Martin A. Heller, Alpha Statistical Consulting; Qian Shi, Mayo Clinic

10:00 Floor Discussion

24. CONTRIBUTED PAPERS: ENVIRONMENTAL AND ECOLOGICAL APPLICATIONS

Sponsor ENAR

Chair Jan Gertheiss, Clausthal University of Technology

8:30 Modeling Hourly Soil Temperature Measurements

Nels G. Johnson*, David R. Weise, Stephen S. Sackett and Sally M. Haase, U.S. Forest Service, Pacific Southwest Research Station

8:45 Efficient Estimation for Non-Stationary Spatial Covariance Functions with Application to Climate Model Downscaling

Yuxiao Li*• and Ying Sun, King Abdullah University of Science and Technology

9:00 Modeling Exposures to Pollutants and Infertility in Couples: A Kernel Machine Regression Approach

Zhen Chen*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

9:15 Causal Kernel Machine Mediation Analysis for Estimating Direct and Indirect Effects of an Environmental Mixture

Katrina L. Devick*, Harvard School of Public Health; Jennifer F. Bobb, Group Health Research Institute; Maitreyi Mazumdar, Boston Children's Hospital; Birgit Claus Henn, Boston University School of Public Health; David C. Bellinger, Boston Children's Hospital; David C. Christiani, Harvard School of Public Health; Robert O. Wright, Icahn School of Medicine at Mount Sinai; Brent A. Coull, Harvard School of Public Health; Linda Valeri, McLean Hospital

9:30 Using Deep Q-Learning to Manage Foot and Mouth Disease Outbreaks

Sandya Lakur* and Christopher Fonnesebeck, Vanderbilt University

9:45 Identifying Epigenetic Regions Exhibiting Critical Windows of Susceptibility to Air Pollution

Michele S. Zemplenyi*, Harvard University; Mark J. Meyer, Georgetown University; Brent A. Coull, Harvard University

10:00 Combining Satellite Imagery and Numerical Model Simulation to Estimate Ambient Air Pollution: An Ensemble Averaging Approach

Nancy Murray*, Howard H. Chang and Yang Liu, Emory University; Heather Holmes, University of Nevada, Reno

25. CONTRIBUTED PAPERS: GENERALIZED LINEAR MODELS

Sponsor ENAR

Chair Harrison Quick, Drexel University

8:30 Convergence Properties of Gibbs Samplers for Bayesian Probit Regression with Proper Priors

Saptarshi Chakraborty* and Kshitij Khare, University of Florida

8:45 Identifiability and Bias Reduction in the Skew-Probit Model for a Binary Response

DongHyuk Lee* and Samiran Sinha, Texas A&M University

9:00 A Flexible Zero-Inflated Count Model to Address Data Dispersion

Kimberly F. Sellers*, Georgetown University; Andrew Raim, U.S. Census Bureau

9:15 A Robust Wald Test of Homogeneity for Correlated Count Data with Excess Zeros

Nadeesha R. Mawella* and Wei-Wen Hsu, Kansas State University; David Todem, Michigan State University; KyungMann Kim, University of Wisconsin, Madison

9:30 Generalized Linear Models with Linear Constraints for Microbiome Compositional Data

Jiarui Lu*•, Pixu Shi and Hongzhe Li, University of Pennsylvania

9:45 A GLM-Based Latent Variable Ordination Method for Microbiome Samples

Michael B. Sohn* and Hongzhe Li, University of Pennsylvania

10:00 Floor Discussion

26. CONTRIBUTED PAPERS: MEASUREMENT ERROR

Sponsor ENAR

Chair Xichen Mou, University of South Carolina

8:30 Causal Inference in the Context of an Error Prone Exposure: Air Pollution and Mortality

Xiao Wu* and Danielle Braun, Harvard School of Public Health; Marianthi-Anna Kioumourtzoglou, Columbia University School of Public Health; Christine Choirat, Qian Di and Francesca Dominici, Harvard School of Public Health

8:45 Measurement Error Models for Group Testing Data

Md S. Warasi*, Radford University; Joshua M. Tebbs, University of South Carolina

9:00 Statistical Strategies for the Analysis of Diet-Disease Models that Correct for Error-Prone Exposures within a Complex Survey Design

Pedro L. Baldoni and Daniela T. Sotres-Alvarez*, University of North Carolina, Chapel Hill; Pamela A. Shaw, University of Pennsylvania School of Medicine

9:15 Correction of Misclassification Error in Presence of Non-Ignorable Missing Data

Haresh Dharmu Rochani*, Lili Yu and Hani Samawi, Georgia Southern University

9:30 Misclassification Simulation Extrapolation Procedure for Log-Logistic Survival Data

Varadan Sevilimedu, Lili Yu*, Hani Samawi and Haresh Rochani, Georgia Southern University

9:45 Floor Discussion

27. CONTRIBUTED PAPERS: METHODS FOR NEXT GENERATION SEQUENCING DATA

Sponsor ENAR

Chair Davide Risso, Weill Cornell Medicine

8:30 A Statistical Method for the Analysis of Multiple ChIP-Seq Datasets

Pedro Baldoni*, Naim Rashid and Joseph Ibrahim, University of North Carolina, Chapel Hill

8:45 Trendy: Segmented Regression Analysis of Expression Dynamics for High-Throughput Ordered Profiling Experiments

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

9:00 DNA Copy Number Variants Detection Using a Modified Information Criterion in the DNA-seq Data

Jaeun Lee* and Jie Chen, Augusta University

9:15 An Effective Normalization Method for Metagenomic Compositional Data

Ruofei Du*, University of New Mexico Comprehensive Cancer Center; Michael Sohn, University of Pennsylvania; Zhide Fang, Louisiana State University Health Sciences Center, New Orleans; Lingling An, University of Arizona

9:30 FunSPU: A Versatile and Adaptive Multiple Functional Annotations-Based Association Test of Whole Genome Sequencing Data

Yiding Ma*, University of Texas Health Science Center at Houston; Peng Wei, University of Texas MD Anderson Cancer Center

9:45 A Powerful and Data-Adaptive Test for Rare-Variant-Based GxE Analysis

Tianzhong Yang*, University of Texas Health Science Center at Houston; Peng Weo and Peng Wei, University of Texas MD Anderson Cancer Center

10:00 Floor Discussion**28. CONTRIBUTED PAPERS:
STATISTICS IN IMAGING**

Sponsor ENAR

Chair Amanda Mejia, Indiana University

8:30 Matrix Decomposition for Modeling Multiple Sclerosis Lesion Development Processes

Menghan Hu*, Brown University; Russell Takeshi Shinohara, University of Pennsylvania; Ciprian Crainiceanu, John Hopkins University; Ani Eloyan, Brown University

8:45 Sparse Dynamic Structural Equation Model with Integer Programming and its Application to Longitudinal Genetic-Imaging Data Analysis

Nan Lin*, Rong Jiao and Momiao Xiong, University of Texas Health Science Center at Houston

9:00 Incorporating Prior Information with Fused Sparse Group Lasso: Application to Prediction of Clinical Measures from Neuroimages

Joanne C. Beer*, Howard J. Aizenstein, Stewart J. Anderson and Robert T. Krafty, University of Pittsburgh

9:15 Statistical Approaches for Longitudinal Brain Lesion Segmentation

Shiyu Wang*, University of Pennsylvania

9:30 Estimating Dynamic Connectivity States in Multi-Subject fMRI Data

Chee-Ming Ting* and Hernando Ombao, King Abdullah University of Science and Technology; Steven L. Small, University of California, Irvine; Jeremy I. Skipper, University College London

9:45 Averaging Symmetric Positive-Definite Matrices in the Space of Eigen-Decompositions

Brian Thomas Rooks* and Sungkyu Jung, University of Pittsburgh

10:00 Floor Discussion

MONDAY MARCH 26**10:15 am - 10:30 am REFRESHMENT BREAK WITH OUR EXHIBITORS****MONDAY MARCH 26****10:30 am - 12:15 pm****29. ORAL POSTERS: NETWORK SCIENCE****Sponsor** ENAR**Chair** Pei Wang, Icahn School of Medicine at Mount Sinai**29a INVITED ORAL POSTER: The Reduced PC-Algorithm: Improved Causal Structure Learning in Large Random Networks**

Ali Shojaie* and Arjun Sondhi, University of Washington

29b INVITED ORAL POSTER: An Integrative Graphical Modeling Approach for Multiple Heterogeneous Omics Data

George Michailidis*, University of Florida

29c Selection for Semiparametric Odds Ratio Model via Adaptive Screening

Jinsong Chen* and Hua Yun Chen, University of Illinois, Chicago

29d BayesNetBP: An R Package for Probabilistic Reasoning in Bayesian Networks

Han Yu*, Janhavi Moharil and Rachael Hageman Blair, State University of New York at Buffalo

29e Dynamic Network Community Discovery

Shiwen Shen*, University of South Carolina

29f Assessing the Effective Degree of SNPs in eQTL Networks

Sheila Gaynor*, Harvard University; Maud Fagny and John Platig, Dana-Farber Cancer Institute; Xihong Lin, Harvard University; John Quackenbush, Dana-Farber Cancer Institute

29g Bayesian Inference in Nonparanormal Graphical Models

Jami J. Mulgrave* and Subhashis Ghosal, North Carolina State University

29h Integrative Analysis of Brain Functional Networks Based on Anatomical Knowledge

Ixavier A. Higgins*, Emory University

30. MODERN METHODS FOR USING HISTORICAL AND OTHER AUXILIARY DATA IN ADAPTIVE CLINICAL TRIALS

Sponsors ENAR, ASA Bayesian Statistical Science Section, ASA Biopharmaceutical Section, ASA Health Policy Statistics Section

Organizer Bradley Carlin, University of Minnesota

Chair Laura Hatfield, Harvard Medical School

10:30 Design and Cost-Benefit Issues in Historical Data-Incorporating Oncology Platform Trials

James P. Normington*, University of Minnesota; Somnath Sarkar and Jiawen Zhu, Roche-Genentech

11:00 Mean Benefit for Biomarker-Guided Treatment Strategies

Meilin Huang* and Brian Hobbs, University of Texas MD Anderson Cancer Center

11:30 A Multi-Source Adaptive Platform Design for Emerging Infectious Diseases

Alexander M. Kaizer*, Colorado School of Public Health; Brian P. Hobbs, University of Texas MD Anderson Cancer Center; Joseph S. Koopmeiners, University of Minnesota

12:00 Discussant:

Meg Gamalo-Siebers, Eli Lilly and Company

31. STATISTICAL ADVANCES IN HEALTH POLICY RESEARCH

Sponsors ENAR, ASA Section on Statistics in Epidemiology, ASA Health Policy Statistics Section

Organizer Nandita Mitra, University of Pennsylvania

Chair Jason Roy, University of Pennsylvania

10:30 Robust Estimation for Multiple Unordered Treatments

Sherri Rose*, Harvard Medical School; Sharon-Lise Normand, Harvard Medical School and Harvard School of Public Health

11:00 Causal Approaches to Cost and Cost-Effectiveness Analysis with Time-Dependent Treatment Regimes

Andrew J. Spieker*, Jason A. Roy and Nandita Mitra, University of Pennsylvania

11:30 Optimal Matching Approaches in Health Policy Evaluations Under Rolling Enrollment

Lauren Vollmer*, Jiaqi Li and Jonathan Gellar, Mathematica Policy Research; Bonnie Harvey, ComScore; Sam Pimentel, University of California, Berkeley

12:00 Discussant:

Sharon-Lise Normand, Harvard University

32. INTEGRATIVE ANALYSIS OF MULTI-OMICS DATA WITH APPLICATIONS TO PRECISION MEDICINE

Sponsors ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section, ASA Statistical Learning and Data Mining Section

Organizer Gen Li, Columbia University

Chair Gen Li, Columbia University

10:30 Statistical and Informatic Issues in Integrating Genomic and Imaging Data

Debashis Ghosh*, Colorado School of Public Health

10:55 Bayesian Variable Selection for Multi-Layer Overlapping Group Structure in Linear Regression and Clustering Settings with Applications to Multi-Level Omics Data Integration

George Tseng* and Li Zhu, University of Pittsburgh

11:20 Pathway-and Network-Based Integrative Bayesian Modeling of Multiplatform Genomics Data

Veera Baladandayuthapani*, Jeffrey S. Morris and Min Jin Ha, University of Texas MD Anderson Cancer Center; Raymond J. Carroll, Texas A&M University; Elizabeth J. McGuffey, United States Naval Academy

11:45 Integrating Large-Scale Sequencing Data for Cancer Classification

Ronglai Shen*, Memorial Sloan-Kettering Cancer Center

12:10 Floor Discussion

33. FUNCTIONAL DATA ANALYSIS IN BIOSCIENCES

Sponsors ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology

Organizer Andrada Ivanescu, Montclair State University

Chair Ciprian Crainiceanu, Johns Hopkins University

10:30 Scalar-on-Image Regression via the Soft-Thresholded Gaussian Process

Ana-Maria Staicu*, North Carolina State University; Jian Kang, University of Michigan; Brian J. Reich, North Carolina State University

10:55 Functional Data Analysis with Highly Irregular Designs with Applications to Head Circumference Growth

Matthew Reimherr* and Justin Petrovich, The Pennsylvania State University; Carrie Daymont, The Pennsylvania State Health Milton S. Hershey Medical Center

11:20 Outlier Detection in Dynamic Functional Models

Andrada E. Ivanescu*, Montclair State University; Ciprian M. Crainiceanu and William Checkley, Johns Hopkins University

11:45 Matrix Factorization Approaches to Analysis of Functional Count Data

Jeff Goldsmith* and Daniel Backenroth, Columbia University; Jennifer Schrack, Johns Hopkins University; Taki Shinohara, University of Pennsylvania

12:10 Floor Discussion**34. NEW ADVANCES IN ANALYSIS OF SURVIVAL DATA FROM BIASED SAMPLING**

Sponsors ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section, ASA Section on Statistics in Epidemiology

Organizer Jianwen Cai, University of North Carolina, Chapel Hill

Chair Jianwen Cai, University of North Carolina, Chapel Hill

10:30 Semiparametric Model and Inference for Bivariate Survival Data Subject to Biased Sampling

Jing Ning*, University of Texas MD Anderson Cancer Center; Jin Piao, University of Southern California; Yu Shen, University of Texas MD Anderson Cancer Center

10:55 Efficient Secondary Analysis in Two Phase Studies

Haibo Zhou*, University of North Carolina, Chapel Hill; Yinghao Pan, Fred Hutchinson Cancer Research Center

11:20 Estimation of Generalized Semiparametric Regression Models for the Cumulative Incidence Functions with Missing Covariates

Yanqing Sun*, University of North Carolina, Charlotte; Unkyung Lee, Texas A&M University; Thomas H. Scheike, University of Copenhagen; Peter B. Gilbert, University of Washington and Fred Hutchinson Cancer Research Center

11:45 Fitting Accelerated Failure Time Model using Calibrated Weights for Case-Cohort Studies

Sangwook Kang* and Dahhay Lee, Yonsei University

12:00 Floor Discussion**35. ESTIMATION AND OPTIMIZATION FOR THE EFFECTS OF SCREENING SCHEDULES AND TREATMENT TIMING**

Sponsors ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section

Organizer Xuelin Huang, University of Texas MD Anderson Cancer Center

Chair Yayuan Zhu, University of Texas MD Anderson Cancer Center

10:30 Designing Screening Tests that Minimize the Time Between Infection and Positive Diagnosis in HIV/AIDS

Robert Strawderman*, University of Rochester; John Rice, University of Colorado, Denver; Brent Johnson, University of Rochester

10:55 Modeling the Effect of Cancer Screening on Mortality

Alex Tsodikov*, University of Michigan

11:20 Causality in the Joint Analysis of Longitudinal and Survival Data

Lei Liu*, Washington University in St. Louis; Cheng Zheng, University of Wisconsin, Milwaukee; Joseph Kang, Centers for Disease Control and Prevention

11:45 Optimal Timing of Stem Cell Transplant for Leukemia Patients

Xuelin Huang*, Xiao Lin and Jorge Cortes, University of Texas MD Anderson Cancer Center

12:10 Floor Discussion

36. CONTRIBUTED PAPERS: CLUSTERED DATA METHODS

Sponsor ENAR

Chair Tom Chen, Harvard School of Public Health

10:30 Robust Clustering with Subpopulation-Specific Deviations

Briana Joy K. Stephenson*•, University of North Carolina, Chapel Hill; Amy H. Herring, Duke University; Andrew Olshan, University of North Carolina, Chapel Hill

10:45 An Improved Dissimilarity Measure for Clustering Data with Mixed Data Types

Shu Wang*, Jonathan G. Yabes and Chung-Chou H. Chang, University of Pittsburgh

11:00 Cluster-Stratified Outcome-Dependent Sampling in Resource-Limited Settings: Inference and Design Considerations

Sara Sauer* and Sebastien Haneuse, Harvard School of Public Health; Bethany Hedt-Gauthier, Harvard Medical School; Catherine Kirk and Alphonse Nshimiyiryo, Partners in Health Rwanda

11:15 Pairwise Covariates-Adjusted Block Model for Community Detection

Sihan Huang* and Yang Feng, Columbia University

11:30 A Weibull-Count Approach for Handling Under- and/or Over-Dispersed Clustered Data Structures

Martial Luyts*, I-Biostat and Katholieke Universiteit Leuven; Geert Molenberghs*, I-BioStat, Hasselt University and Katholieke Universiteit Leuven; Geert Verbeke, I-Biostat and Katholieke Universiteit Leuven; Koen Matthijs, Katholieke Universiteit Leuven; Clarice Demétrio, University of São Paulo, Brazil; John Hinde, NUI Galway, Ireland

11:45 Homogeneity Test of Risk Ratios for Stratified Correlated Binary Data

Yuqing Xue* and Chang-Xing Ma, State University of New York at Buffalo

12:00 Sample Size Determination for GEE Analyses of Stepped Wedge Cluster Randomized Trials

Fan Li*• and Elizabeth L. Turner, Duke University; John S. Preisser, University of North Carolina, Chapel Hill

37. CONTRIBUTED PAPERS: ADVANCES IN CAUSAL INFERENCE

Sponsor ENAR

Chair Samuel Pimentel, University of California, Berkeley

10:30 Assessing Sensitivity to Unmeasured Confounding with Multiple Treatments and Binary Outcomes: A Bayesian Approach

Liangyuan Hu*, Icahn School of Medicine at Mount Sinai; Chenyang Gu, Harvard University; Michael Lopez, Skidmore College

10:45 Causal Inference for Interfering Units for Cluster and Population Level Intervention Programs

Georgia Papadogeogrou*, Harvard University; Fabrizia Mealli, University of Florence; Corwin Zigler, Harvard School of Public Health

11:00 A Bayesian Regularized Mediation Analysis with Multiple Exposures

Yu-Bo Wang* and Zhen Chen, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health; Jill M. Goldstein, Harvard Medical School, Brigham and Women's Hospital and Massachusetts General Hospital; Germaine M. Buck Louis and Stephen E. Gilman, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

11:15 An Alternative Robust Estimator of Average Treatment Effect in Causal Inference

Jianxuan Liu*, Bowling Green State University; Yanyuan Ma, The Pennsylvania State University; Lan Wang, University of Minnesota

11:30 The Generalized Front-Door Formula for Estimation of Indirect Causal Effects of a Confounded Treatment

Isabel R. Fulcher*, Harvard University; Ilya Shpitser, Johns Hopkins University; Eric Tchetgen Tchetgen, Harvard University

11:45 Longitudinal Variable Selection in Causal Inference with Collaborative Targeted Minimum Loss-Based Estimation

Mireille E. Schnitzer*, Université de Montréal; Joel Sango, Statistics Canada; Steve Ferreira-Guerra, Université de Montréal; Mark J. van der Laan, University of California, Berkeley

12:00 Floor Discussion

38. CONTRIBUTED PAPERS: IMPUTATION APPROACHES WITH MISSING DATA

Sponsor ENAR

Chair Lin Taft, GSK

10:30 Bayesian Regression Analysis for Handling Covariates with Missing Values Below the Limit of Detection

Xiaoyan Lin*, University of South Carolina; Haiying Chen, Wake Forest School of Medicine

10:45 Analysis of Binary Response Endpoint with Missing Data in Small Study Population

JD Lu*, Bioverativ, Inc.

11:00 Maximum Likelihood Estimation in Regression Models with Censored Covariates

Jingyao Hou* and Jing Qian, University of Massachusetts, Amherst

11:15 Multiple Imputation Using Bootstrap

Hejian Sang* and JaeKwang Kim, Iowa State University

11:30 Sequential Regression Imputation in Multilevel Data

Gang Liu* and Recai Yucel, State University of New York at Albany

11:45 Imputation for Investigation of Social Support and Disability Progression in Multiple Sclerosis

Anastasia M. Hartzes* and Stacey S. Cofield, University of Alabama at Birmingham

12:00 Floor Discussion**39. CONTRIBUTED PAPERS:
METHODS FOR LONGITUDINAL DATA ANALYSIS****Sponsor** ENAR**Chair** Brianna C. Heggeseth, Williams College**10:30 Analysis of Longitudinal Data with Omitted Asynchronous Longitudinal Covariates**

Li Chen* and Hongyuan Cao, University of Missouri

10:45 Analysis of the High School Longitudinal Study Data to Assess the Roles of Mentorship on Mathematics Achievement and Students' Intentions to Enroll in STEM Programs

Anarina L. Murillo*, Olivia Affuso and Hemant K. Tiwari, University of Alabama at Birmingham

11:00 A Comparison Study of Methods for Longitudinal Biomarker Combination: How Random Observation Time Plays a Role

Yongli Justin Han* and Danping Liu, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

11:15 Regression Modeling of Logic Rules for Longitudinal Data

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

11:30 Non-Gaussian Longitudinal Data Analysis

Ozgur Asar*, Acibadem University; David Bolin, Chalmers University of Technology; Peter Diggle, Lancaster University; Jonas Wallin, Lund University

11:45 An R2 Statistic for Covariance Model Selection in the Linear Mixed Model

Byron Casey Jaeger*• and Lloyd J. Edwards, University of Alabama at Birmingham

12:00 Floor Discussion

40. CONTRIBUTED PAPERS: MICROBIOME RESEARCH METHODS

Sponsor ENAR

Chair Lingling An, University of Arizona

10:30 A Sparse Regression Framework for Integrating Phylogenetic Tree in Predictive Modeling of Microbiome Data

Li Chen*, Auburn University; Jun Chen, Mayo Clinic

10:50 A Permutation Framework for Differential Abundance Analysis of Microbiome Sequencing Data

Jun Chen*, Mayo Clinic

11:10 Sparse High-Dimensional Precision Matrix Estimation for Compositional Data

Rong Ma*, Yuanpei Gao and Hongzhe Li, University of Pennsylvania

11:30 PERfect: Permutation Filtration of Microbiome Data

Ekaterina Smirnova*, University of Montana; Snehalata Huzurbazar, West Virginia University; Farhad Jafari, University of Wyoming

11:50 Floor Discussion

41. CONTRIBUTED PAPERS: PERSONALIZED / PRECISION MEDICINE

Sponsor ENAR

Chair Parichoy Pal Choudhury, Johns Hopkins University

10:30 Relative Efficiency of Precision Medicine Designs for Clinical Trials with Predictive Biomarkers

Weichung Joe Shih* and Yong Lin, Rutgers University

10:45 PartialCOXEN: In Vitro Gene Expression-Based Prediction of Response to Anticancer Drug in Cancer Patients

Youngchul Kim*, Moffitt Cancer Center and Research Institute

11:00 Prediction and Prevention of Hospital Adverse Events Using Routinely Collected Patient Data with a Mechanism for Evaluating Effectiveness

Henry J. Domenico* and Daniel W. Byrne, Vanderbilt University Medical Center

11:15 A Stochastic Search Approach to Study Heterogeneity of Treatment Effect

Yang Hu* and Changyu Shen, Beth Israel Deaconess Medical Center, Harvard Medical School

11:30 Assessing SNP Effects on Treatment Efficacy in Tailored Drug Development: Issues and Remedies

Yue Wei* and Ying Ding, University of Pittsburgh

11:45 Sparse Concordance-Assisted Learning for Optimal Treatment Decision

Shuhan Liang*, Wenbin Lu, Rui Song and Lan Wang, North Carolina State University

12:00 Floor Discussion**MONDAY MARCH 26****12:15 pm - 1:30 pm ROUNDTABLE LUNCHEONS****MONDAY MARCH 26****1:45 pm - 3:30 pm****42. ORAL POSTERS: HEALTH SERVICES AND HEALTH POLICY****Sponsor** ENAR**Chair** Young-Geun Choi, Fred Hutchinson Cancer Research Center**42a INVITED ORAL POSTER: Profiling Medical Providers using Methods based on the Empirical Null**

John D. Kalbfleisch*, Lu Xia, Zhi Keving He and Yanming Li, University of Michigan

42b INVITED ORAL POSTER: Pointwise Mutual Information and Similarity Indices to Identify Treatments and Diagnoses in SEER-Medicare

Brian L. Egleston*, Fox Chase Cancer Center; Tian Bai and Ashis Chanda, Temple University; Richard J. Bleicher, Fox Chase Cancer Center; Slobodan Vucetic, Temple University

42c INVITED ORAL POSTER: Introduction to Tools for Learning and Implementing Bayesian Adaptive Designs

J. Jack Lee*, University of Texas MD Anderson Cancer Center

42d Bayesian Hierarchical Multivariate Poisson Regression Models for Characterizing the Diffusion of New Antipsychotic Drugs

Chenyang Gu* and Haiden Huskamp, Harvard Medical School; Julie Donohue, University of Pittsburgh; Sharon-Lise Normand, Harvard Medical School and Harvard School of Public Health

42e Challenges of Using Electronic Health Records for Risk Prediction in Adults with Type 2 Diabetes

Douglas David Gunzler*, Case Western Reserve University

42f Robust Interrupted Time Series Model for Assessing an Intervention in Multiple Healthcare Units

Maricela F. Cruz*, Miriam Bender and Daniel L. Gillen, University of California, Irvine; Hernando Ombao, King Abdullah University of Science and Technology

42g Propensity Score Matching for Multilevel Spatial Data: Accounting for Geographic Confounding in Health Disparity Studies

Melanie L. Davis*, Brian Neelon, Paul J. Nietert and Kelly J. Hunt, Medical University of South Carolina; Lane F. Burgette, RAND Corporation; Andrew B. Lawson, Medical University of South Carolina; Leonard E. Egede, Medical College of Wisconsin

42h Shortening Patient Reported Outcome Measures with Optimal Test Assembly

Daphna Harel*, New York University

42i Trends in Tract-Level Obesity Rates in Philadelphia by Race, Space, and Time

Yaxin Wu*, Dina Terloyeva and Harrison Quick, Drexel University

42j Biostatisticians in the Industry have Real World Impact on the Opioid Crisis

Meridith Blevins Peratikos*, Axial Healthcare, Inc.

43. RECENT INNOVATIONS IN PRACTICAL CLINICAL TRIAL DESIGN

Sponsors ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section

Organizer Peter F. Thall, University of Texas MD Anderson Cancer Center

Chair Jing Ning, University of Texas MD Anderson Cancer Center

1:45 Utility-Based Designs for Clinical Trials with Multiple Outcomes

Thomas A. Murray*, University of Minnesota; Ying Yuan and Peter F. Thall, University of Texas MD Anderson Cancer Center

2:10 Sample Size Considerations for the Analysis of Time-Varying Causal Effects in Stratified Micro-Randomized Trials

Walter Dempsey*, Harvard University; Peng Liao, University of Michigan; Santosh Kumar, University of Memphis; Susan A. Murphy, Harvard University

2:35 Bayesian Phase I/II Biomarker-Based Dose Finding for Precision Medicine with Molecularly Targeted Agents

Ying Yuan*, University of Texas MD Anderson Cancer Center; Beibei Guo, Louisiana State University

3:00 Robust Treatment Comparison Based on Utilities of Semi-Competing Risks in Non-Small-Cell Lung Cancer

Peter F. Thall*, University of Texas MD Anderson Cancer Center; Thomas A. Murray, University of Minnesota; Ying Yuan, University of Texas MD Anderson Cancer Center

3:25 Floor Discussion

44. MACHINE LEARNING METHODS FOR IMAGING DATA ANALYSIS**Sponsors** ENAR, ASA Section on Statistics in Imaging, ASA Statistical Learning and Data Mining Section**Organizer** Ruoqing Zhu, University of Illinois, Urbana-Champaign**Chair** Ruoqing Zhu, University of Illinois, Urbana-Champaign**1:45 Improving Prediction Accuracy Through Training Sample Enrichment for Heavily Unbalanced Data**

Peng Huang*, Johns Hopkins University

2:10 Computational Discovery of Tissue Morphology Biomarker for Pancreatic Ductal Adenocarcinoma

Pei-Hsun Wu*, Johns Hopkins University; Laura D. Wood, Johns Hopkins University School of Medicine; Jacob Sarnecki, Johns Hopkins University; Ralph H. Hruban, Johns Hopkins University School of Medicine; Anirban Maitra, University of Texas MD Anderson Cancer Center; Denis Wirtz, Johns Hopkins University

2:35 Residual-Based Alternative Partial Least Squares for Functional Linear Models

Yue Wang* and Joseph Ibrahim, University of North Carolina, Chapel Hill; Hongtu Zhu, University of Texas MD Anderson Cancer Center

3:00 Individualized Multilayer Tensor Learning with an Application in Imaging Analysis

Xiwei Tang*, University of Virginia; Xuan Bi, Yale University; Annie Qu, University of Illinois, Urbana-Champaign

3:25 Floor Discussion**45. MAKING SENSE OF WHOLE GENOME SEQUENCING DATA IN POPULATION SCIENCE: STATISTICAL CHALLENGES AND SOLUTIONS****Sponsor** ASA Statistics in Genomics and Genetics Section**Organizer** Han Chen, University of Texas Health Science Center at Houston**Chair** Han Chen, University of Texas Health Science Center at Houston**1:45 Analysis of Whole Genome Sequencing Association Studies: Challenges and Opportunities**

Xihong Lin*, Harvard University

2:10 We did not See this in GWAS: Understanding and Fixing Unfamiliar Problems in Association Analyses, when Pooling Whole Genome Sequence Data from Multiple Studies

Kenneth M. Rice*, Xiuwen Zheng, Stephanie Gogarten, Tamar Sofer, Cecelia Laurie, Cathy Laurie, Bruce Weir, Tim Thornton, Adam Szpiro and Jen Brody, University of Washington

2:35 Statistical Methods and Tools for Whole-Genome Sequencing Data Analysis of 100,000 Samples

Seunggeun Lee*, University of Michigan

3:00 A Semi-Supervised Approach for Predicting Tissue Specific Functional Effects of Noncoding Variation

Iuliana Ionita-Laza* and Zihuai He, Columbia University

3:25 Floor Discussion**46. MACHINE LEARNING METHODS FOR PRECISION MEDICINE****Sponsors** ENAR, ASA Biometrics Section, ASA Statistical Learning and Data Mining Section, IMS**Organizer** Yingqi Zhao, Fred Hutchinson Cancer Research Center and Eric Laber, North Carolina State University**Chair** Eric Laber, North Carolina State University**1:45 Recent Developments in Reinforcement Learning for Decision Science**

Michael R. Kosorok*, University of North Carolina, Chapel Hill

2:10 Targeted Machine Learning for Precision Medicine

Mark J. van der Laan*, University of California, Berkeley; Alex Luedtke, Fred Hutchinson Cancer Research Center

2:35 Generalized Random Forests

Stefan Wager*, Stanford University; Julie Tibshirani, Palantir Technologies; Susan Athey, Stanford University

3:00 Optimal Individualized Treatments when Measuring Covariates is Expensive

Alex Luedtke*, Fred Hutchinson Cancer Research Center

3:25 Floor Discussion**47. MULTI-OMICS AND GRAPHICAL MODELS FOR PRECISION MEDICINE****Sponsors** ENAR, ASA Biometrics Section**Organizer** Min Jin Ha, University of Texas MD Anderson Center**Chair** Christine B. Peterson, University of Texas MD Anderson Cancer Center**1:45 Heterogeneous Reciprocal Graphical Models**

Yuan Ji*, NorthShore University HealthSystem and University of Chicago

2:10 Constructing Tumor-Specific Gene Regulatory Networks Based on Samples with Tumor Purity Heterogeneity

Pei Wang*, Francesca Petralia and Li Wang, Icahn School of Medicine at Mount Sinai; Jie Peng, University of California, Davis

2:35 Joint Skeleton Estimation of Multiple Directed Acyclic Graphs for Heterogeneous Population

Jianyu Liu*, University of North Carolina, Chapel Hill; Wei Sun, Fred Hutchinson Cancer Research Center; Yufeng Liu, University of North Carolina, Chapel Hill

3:00 Bayesian Multi-Layered Gaussian Graphical Models

Min Jin Ha*, University of Texas MD Anderson Cancer Center; Francesco Stingo, University of Florence; Veerabhadran Baladandayuthapani, University of Texas MD Anderson Cancer Center

3:25 Floor Discussion**48. RECENT ADVANCES IN PROPENSITY SCORE ANALYSIS**

Sponsors ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section, ASA Section on Statistics in Epidemiology

Organizer Liang Li, University of Texas MD Anderson Cancer Center

Chair Liang Li, University of Texas MD Anderson Cancer Center

1:45 Utilizing Propensity Score Methodology in the Observational Studies with “Big Data” in the Regulatory Settings

Lilly Q. Yue*, U.S. Food and Drug Administration

2:15 Subgroup Balancing Propensity Score

Fan Li*, Duke University; Jing Dong, Industrial and Commercial Bank of China; Junni Zhang, Peking University

2:45 Propensity Score Analysis with Complex Survey Data: When Treatment Assignment and Treatment Effects Vary Across Strata and Clusters

Trang Q. Nguyen* and Elizabeth A. Stuart, Johns Hopkins Bloomberg School of Public Health

3:15 Discussant:

Donald B. Rubin, Harvard University

49. CONTRIBUTED PAPERS: CAUSAL INFERENCE AND EPIDEMIOLOGICAL METHODS

Sponsor ENAR

Chair Amelia M. Haviland, Carnegie Mellon University

1:45 A Novel Non-Parametric Method for Ordinal Propensity Score Matching and Stratification

Thomas James Greene*, Stacia M. DeSantis and Michael D. Swartz, University of Texas Health Science Center at Houston

2:00 Optimal Tradeoffs in Matched Designs for Observational Studies

Samuel D. Pimentel*, University of California, Berkeley; Rachel R. Kelz, University of Pennsylvania

2:15 Evaluating the Performance of Balancing Scores Using the ANCOVA Approach for Estimating Average Treatment Effects in Observational Studies: A Simulation Study

Woon Yuen Koh* and Chunhao Tu, University of New England

2:30 Principal Stratification for Longitudinal Data in Environmental Trials

Joshua P. Keller*, Roger D. Peng and Elizabeth C. Matsui, Johns Hopkins University

2:45 Efficient Computation of the Joint Probability of Multiple Germline Mutations from Pedigree Data

Thomas Madsen*, Harvard School of Public Health; Danielle Braun, Lorenzo Trippa and Giovanni Parmigiani, Dana-Farber Cancer Institute

3:00 A Dynamic Model for Evaluation of Bias of Estimates of Influenza Vaccine Effectiveness from Observational Studies

Kylie E. C. Ainslie* and Michael Haber, Emory University

3:15 Floor Discussion**50. CONTRIBUTED PAPERS:
EPIDEMIOLOGICAL METHODS****Sponsor** ENAR**Chair** Shelley Liu, Icahn School of Medicine at Mount Sinai**1:45 Application of Regression Analysis on Text-Mining Data Associated with Autism Spectrum Disorder from Twitter: A Pilot Study**

Chen Mo*, Jingjing Yin and Isaac Chun-Hai Fung, Georgia Southern University; Zion Tse, University of Georgia

2:00 A Pseudolikelihood Method for Estimating Misclassification Probabilities when True Outcomes are Partially Observed

Philani Brian Mpofu*, Giorgos Bakoyannis and Constantin Yiannoutsos, Indiana University Purdue University, Indianapolis

2:15 Correcting for Risk Factor Misclassification in the Partial Population Attributable Risk

Benedict Wong*, Harvard School of Public Health

2:30 Regression Analysis of Temporal Biomarker Effects Under Nested Case-Control Studies

Yiding Zhang*, Jing Qian and Susan E. Hankinson, University of Massachusetts, Amherst

2:45 A Novel Goodness-of-Fit Based Two-Phase Sampling Design for Studying Binary Outcomes

Le Wang*, Xinglei Chai, Yong Chen and Jinbo Chen, University of Pennsylvania

3:00 On Optimal Two-Phase Designs

Ran Tao*, Vanderbilt University Medical Center; Donglin Zeng and Danyu Lin, University of North Carolina, Chapel Hill

3:15 Floor Discussion

51. CONTRIBUTED PAPERS: INFECTIOUS DISEASE MODELS

Sponsor ENAR

Chair Dewei Wang, University of South Carolina

1:45 A Bayesian Generalized Additive Model for Group Testing Data

Christopher S. McMahan*, Clemson University; Yan Liu, University of Nevada, Reno; Joshua M. Tebbs, University of South Carolina; Christopher R. Bilder, University of Nebraska-Lincoln; Colin M. Gallagher, Clemson University

2:00 A General Multivariate Bayesian Regression Model for Group Testing Data

Paul J. Cubre*, Christopher S. McMahan and Yingbo Li, Clemson University

2:15 Bayesian Regression Analysis of Multiple-Infection Group Testing Data with a Consideration of Dilution Effects

Juexin Lin* and Dewei Wang, University of South Carolina

2:30 Studying the Pattern of Temporal Associations between Rare Disease Incidence and Meteorological Factors Using a Bayesian Conditional Poisson Model with a Gaussian Process Prior over the Distributed Lag Coefficients

James L. Crooks*, National Jewish Health

2:45 Pairwise Accelerated Failure Time Models for Infectious Disease Transmission within and between Households

Yushuf Sharker*, Yale School of Public Health; Eben Kenah, The Ohio State University

3:00 Floor Discussion

52. CONTRIBUTED PAPERS: MULTIVARIATE SURVIVAL ANALYSIS

Sponsor ENAR

Chair Ina Jazic, Harvard School of Public Health

1:45 Spearman's Rank Correlation Adjusting for Covariates in Bivariate Survival Data

Svetlana K. Eden*, Vanderbilt University; Chun Li, Case Western Reserve University; Bryan E. Shepherd, Vanderbilt University

2:00 Copula-Based Semiparametric Sieve Model for Bivariate Interval-Censored Data, with an Application to Study AMD Progression

Tao Sun*, Wei Chen and Ying Ding, University of Pittsburgh

2:15 EM Algorithms for Fitting Multistate Cure Models

Lauren J. Beesley* and Jeremy M. G. Taylor, University of Michigan

2:30 Prioritized Concordance Index for Composite Survival Outcomes

Li C. Cheung*, National Cancer Institute, National Institutes of Health; Qing Pan, George Washington University; Noorie Hyun and Hormuzd A. Katki, National Cancer Institute, National Institutes of Health

2:45 Multi-Level Variable Selection for Marginal Proportional Hazards Model

Natasha A. Sahr*, Soyoung Kim and Kwang Woo Ahn, Medical College of Wisconsin

3:00 Floor Discussion

53. CONTRIBUTED PAPERS: NONPARAMETRIC METHODS

Sponsor ENAR

Chair Shi Zhao, Indiana University School of Medicine

1:45 L-statistics for Quantifying the Agreement Between Two Variables

Elahe Tashakor* and Vernon M. Chinchilli, The Pennsylvania State Health Milton S. Hershey Medical Center

2:00 Assessing Alignment Between Functional Markers and Ordinal Outcomes Based on Broad Sense Agreement

Jeong Hoon Jang*, Limin Peng and Amita K. Manatunga, Emory University

2:15 On Quantiles Estimation Based on Different Stratified Sampling with Optimal Allocation

Hani M. Samawi*, Jingjing Yin, Arpita Chatterjee and Haresh Rochani, Georgia Southern University

2:30 Adjusted Empirical Likelihood Based Confidence Interval of ROC Curves

Haiyan Su*, Montclair State University

2:45 Exact Nonparametric Confidence Intervals for Quantiles

Xin Yang*, State University of New York at Buffalo; Alan D. Hutson, Roswell Park Cancer Institute and State University of New York at Buffalo; Dongliang Wang, State University of New York Upstate Medical University

3:00 Nonidentifiability in the Presence of Factorization for Truncated Data

Jing Qian*, University of Massachusetts, Amherst; Bella Vakulenko-Lagun, Harvard School of Public Health; Sy Han Chiou, University of Texas, Dallas; Rebecca A. Betensky, Harvard School of Public Health

3:15 Floor Discussion

54. CONTRIBUTED PAPERS: PHARMACOKINETIC/ PHARMACODYNAMICS AND BIOPHARMACEUTICAL RESEARCH

Sponsor ENAR

Chair Ming Sun, Columbia University

1:45 Bayesian Inference from a Nested Case-Cohort Design Linked with a Pharmacokinetic Model Using Bayesian Additive Regression Trees to Infer the Protective Effect of Tenofovir Against HIV Infection

Claire F. Ruberman* and Michael A. Rosenblum, Johns Hopkins Bloomberg School of Public Health; Gary L. Rosner and Craig W. Hendrix, Johns Hopkins School of Medicine; Katarina Vucicevic and Rada Savic, University of California, San Francisco

2:00 Bayesian Personalized Multi-Criteria Benefit-Risk Assessment of Medical Products

Kan Li*, University of Texas Health Science Center at Houston; Sheng Luo, Duke University Medical Center

2:15 Two/Three-Stage Designs for Phase 1 Dose-Finding

Wenchuan Guo*, University of California, Riverside; Bob Zhong, Johnson & Johnson

2:30 Non-Inferiority Testing for Three-Arm Trials with Binary Outcome: Novel Frequentist and Bayesian Proposals

Shrabanti Chowdhury*, Wayne State University School of Medicine; Ram C. Tiwari, U.S. Food and Drug Administration; Samiran Ghosh, Wayne State University School of Medicine

2:45 Bayesian Interval-Based Dose Finding Design with Quasi-Continuous Toxicity Model

Dan Zhao*, University of Illinois, Chicago; Jian Zhu, Takeda Pharmaceuticals; Eric Westin, ImmunoGen; Ling Wang, Takeda Pharmaceuticals

3:00 A Bayesian Framework for Individualizing Treatment with Therapeutic Drug Monitoring

Hannah L. Weeks*, Ryan T. Jarrett, William H. Fissell and Matthew S. Shotwell, Vanderbilt University

3:15 Floor Discussion

MONDAY MARCH 26

3:30 pm - 3:45 pm REFRESHMENT BREAK WITH OUR EXHIBITORS

MONDAY MARCH 26

3:45 pm - 5:30 pm

55. ORAL POSTERS: MEDICAL IMAGING**Sponsor** ENAR**Chair** Jeff Goldsmith, Columbia University**55a INVITED ORAL POSTER: Exploratory Tools for Dynamic Connectivity and Low Dimensional Representations of Brain Signals**

Hernando Ombao*, King Abdullah University of Science and Technology; Hector Flores, University of California, Irvine; Abdulrahman Althobaiti, Rutgers University; Altyn Zhelambayeva, Nazarbayev University

55b INVITED ORAL POSTER: Regression Models for Complex Biomedical Imaging Data

Jeff Morris*, University of Texas MD Anderson Cancer Center; Hongxiao Zhu, Virginia Tech; Veera Baladandayuthapani, University of Texas MD Anderson Cancer Center; Hojin Yang, University of North Carolina, Chapel Hill

55c INVITED ORAL POSTER: Penalized Models to Detect Subtle Multiple Sclerosis Abnormalities in White and Grey Matter Using Functional Data Analysis of Multiple Non-Conventional MRI Contrasts

Lynn E. Eberly*, University of Minnesota; Kristine Kubisiak, Chronic Disease Research Group; Mark Fiecas, University of Minnesota

55d MIMoSA: A Method for Inter-Modal Segmentation Analysis of T2 Hyperintensities and T1 Black Holes in Multiple Sclerosis

Alessandra M. Valcarcel* and Kristin A. Linn, University of Pennsylvania; Fariha Khalid, Brigham and Women's Hospital; Simon N. Vandekar and Theodore D. Satterthwaite, University of Pennsylvania; Rohit Bakshi, Brigham and Women's Hospital; Russell T. Shinohara, University of Pennsylvania

55e Spatially Adaptive Colocalization Analysis in Dual-Color Fluorescence Microscopy

Shulei Wang*, University of Wisconsin, Madison and Columbia University; Ellen T. Arena, Jordan T. Becker, William M. Bement, Nathan M. Sherer and Kevin W. Eliceiri, University of Wisconsin, Madison; Ming Yuan, Columbia University and University of Wisconsin, Madison

55f A Longitudinal Model for Functional Connectivity Networks Using Resting-State fMRI

Brian B. Hart*, University of Minnesota; Ivor Cribben, University of Alberta; Mark Fiecas, University of Minnesota

55g Low-Rank Structure Based Brain Connectivity GWAS Study

Ziliang Zhu*, Fan Zhou, Liuqing Yang, Yue Shan, Jingwen Zhang and Joseph G. Ibrahim, University of North Carolina, Chapel Hill; Hongtu Zhu, University of Texas MD Anderson Cancer Center

55h Bayesian Integrative Analysis of Radiogenomics

Yuyi Zhang* and Jeffrey S. Morris, University of Texas MD Anderson Cancer Center; Shivali Narang Aerry, Johns Hopkins University; Arvind U.K. Rao and Veerabhadran Baladandayuthapani, University of Texas MD Anderson Cancer Center

55i How to Exploit the Brain Connectivity Information and Increase the Estimation Accuracy Under Repeated Measures Design?

Damian Brzyski*, Indiana University, Bloomington; Marta Karas, Johns Hopkins University; Beau Ances, Washington University School of Medicine; Joaquin Goni, Purdue University; Timothy W. Randolph, Fred Hutchinson Cancer Research Center; Jaroslaw Harezlak, Indiana University, Bloomington

55j Assessing the Relationship Between Cortical Thinning and Myelin Measurements in Multiple Sclerosis Disease Subtypes: A Whole Brain Approach

Sandra Hurtado Rua*, Cleveland State University; Michael Dayan, Susan A. Gauthier, Elizabeth Monohan, Kyoko Fujimoto, Sneha Pandya, Eve LoCastro, Tim Vartanian and Thanh D. Nguyen, Weill Cornell Medicine

55k Bayesian Joint Modeling of Multiple Brain Functional Networks

Joshua Lukemire* and Suprateek Kundu, Emory University; Giuseppe Pagnoni, University of Modena and Reggio Emilia; Ying Guo, Emory University

56. QUANTIFYING COMPLEX DEPENDENCY

Sponsors ENAR, IMS

Organizer Ma Li, Duke University

Chair Haiyan Huang, University of California, Berkeley

3:45 Dependence Measures: Something Old and Something New, Something Borrowed, and Something Blue

Gabor J. Szekely*, National Science Foundation

4:10 BET on Independence

Kai Zhang*, University of North Carolina, Chapel Hill

4:35 Fisher Exact Scanning for Dependency

Li Ma* and Jialiang Mao, Duke University

5:00 Generalized R-squared for Measuring Dependence

Jun Liu*, Harvard University; Xufei Wang and Bo Jiang, Two Sigma Inc.

5:25 Floor Discussion

57. PREPARING FOR THE JOB MARKET**Sponsor** ENAR**Organizer** Kylie Ainslie, Emory University**Chair** Jacqueline Milton, Boston University**3:45 Panel Discussion:**

Pallavi Mishra-Kalyani, U.S. Food and Drug Administration

Brooke Alhanti, North Carolina State University

Barbara Wendelberger, Berry Consultants

Ning Leng, Genentech

5:15 Floor Discussion**58. NOVEL CLINICAL TRIAL DESIGNS****Sponsors** ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section**Organizer** Judith Lok, Harvard University**Chair** Donna Spiegelman, Harvard University**3:45 Novel Response Adaptive Allocations in Factorial Designs: A Case Study**

John A. Kairalla*, Rachel S. Zahigian and Samuel S. Wu, University of Florida

4:15 Methods and Software for Optimizing Adaptive Enrichment Designs

Michael Rosenblum*, Johns Hopkins Bloomberg School of Public Health; Jon Arni Steingrimsson, Brown School of Public Health; Josh Betz, Johns Hopkins Bloomberg School of Public Health; Aaron Joel Fisher, Harvard School of Public Health; Tianchen Qian, Harvard University; Adi Gherman and Yu Du, Johns Hopkins Bloomberg School of Public Health

4:45 The Adaptive Learn-As-You-Go Design for Multi-Stage Intervention Studies

Judith J. Lok*, Daniel Nevo and Donna Spiegelman, Harvard School of Public Health

5:15 Discussant:

Susan Murphy, Harvard University

59. NEW METHODS IN BRAIN CONNECTIVITY**Sponsor** ASA Section on Statistics in Imaging**Organizer** Martin Lindquist, Johns Hopkins University**Chair** Martin Lindquist, Johns Hopkins University**3:45 Bayesian Low-Rank Graph Regression Models for Mapping Human Connectome Data**

Eunjee Lee*, University of Michigan; Joseph Ibrahim, University of North Carolina, Chapel Hill; Yong Fan, University of Pennsylvania; Hongtu Zhu, University of North Carolina, Chapel Hill and University of Texas MD Anderson Cancer Center

4:10 Methods for Longitudinal Complex Network Analysis in Neuroscience

Heather Shappell*, Johns Hopkins Bloomberg School of Public Health; Yorghos Tripodis, Ronald J. Killiany and Eric D. Kolaczyk, Boston University

4:35 Causal Mediation Analysis in Neuroimaging

Yi Zhao*, Johns Hopkins University; Xi Luo, Brown University; Martin Lindquist and Brian Caffo, Johns Hopkins University

5:00 Template ICA: Estimating Resting-State Networks from fMRI in Individual Subjects using Empirical Population Priors

Amanda F. Mejia*, Indiana University; Yikai Wang[•], Emory University; Brian Caffo, Johns Hopkins University; Ying Guo, Emory University

5:25 Floor Discussion**60. STATISTICAL METHODS FOR EMERGING SPATIAL AND SPATIOTEMPORAL DATA**

Sponsors ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Section on Statistics in Epidemiology, ASA Section on Statistics and the Environment

Organizer Howard Chang, Emory University

Chair Howard Chang, Emory University

3:45 A Causal Inference Analysis of the Effect of Wildland Fire Smoke on Ambient Air Pollution Levels

Brian J. Reich* and Alexandra Larsen, North Carolina State University; Ana Rappold, U.S. Environmental Protection Agency

4:10 Adolescent Activity Patterns and Ecological Networks

Catherine Calder*, Christopher Browning, Beth Boettner and Wenna Xi, The Ohio State University

4:35 Diagnosing Glaucoma Progression with Visual Field Data Using a Spatiotemporal Boundary Detection Method

Joshua L. Warren*, Yale School of Public Health; Samuel I. Berchuck and Jean-Claude Mwanza, University of North Carolina, Chapel Hill

5:00 On New Classes of Spatial Disease Mapping Models Based Upon Directed Acyclic Graphs

Sudipto Banerjee*, University of California, Los Angeles; Abhirup Datta, Johns Hopkins University; James S. Hodges, University of Minnesota

5:25 Floor Discussion

61. NOVEL STATISTICAL LEARNING METHODOLOGIES FOR PRECISION MEDICINE**Sponsors** ENAR, ASA Biometrics Section, ASA Statistical Learning and Data Mining Section**Organizer** Min Qian, Columbia University**Chair** Min Qian, Columbia University**3:45 Computationally Efficient Learning for Optimal Individualized Treatment Rules with Multiple Treatments**

Donglin Zeng* and Xuan Zhou, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University

4:10 Tree-Based Reinforcement Learning for Estimating Optimal Dynamic Treatment Regimes

Lu Wang*, Yebin Tao and Danny Almirall, University of Michigan

4:35 Effect Heterogeneity and Subgroup Identification for Long-Term Interventions

Menggang Yu*, University of Wisconsin, Madison

5:00 Shared-Parameter G-estimation of Optimal Treatments for Rheumatoid Arthritis

Erica E. M. Moodie*, McGill University

5:25 Floor Discussion**62. CONTRIBUTED PAPERS:
COMPARATIVE EFFECTIVENESS RESEARCH****Sponsor** ENAR**Chair** Andrew J. Spieker, University of Pennsylvania**3:45 Optimal Weights for Propensity Score Stratification**

Roland A. Matsouaka*, Duke University

4:00 Variance Estimation for the Matched Win Ratio

Adrian Coles* and Roland A. Matsouaka, Duke Clinical Research Institute

4:15 Clinical Trial Simulation Using Electronic Medical Records

Xiaochen Wang*, Yale University; Lauren Cain, Ray Liu, Dorothy Romanus and Greg Hather, Takeda Pharmaceuticals

4:30 Estimating Population Treatment Effects Using Meta-Analysis

Hwanhee Hong* and Elizabeth A. Stuart, Johns Hopkins Bloomberg School of Public Health

4:45 Efficient and Robust Semi-Supervised Estimation of Average Treatment Effects in Electronic Medical Records Data

David Cheng*•, Harvard School of Public Health; Ashwin Ananthakrishnan, Massachusetts General Hospital; Tianxi Cai, Harvard School of Public Health

5:00 Applications of Multiple Imputation in the Context of Propensity Score Matching

Albee Ling*, Maya Mathur, Kris Kapphahn, Maria Montez-Rath and Manisha Desai, Stanford University

5:15 Floor Discussion**63. CONTRIBUTED PAPERS:
COMPETING RISKS****Sponsor** ENAR**Chair** Jing Li, Indiana University Fairbanks School of Public Health**3:45 Modeling of Exposure-Time-Response Association in the Presence of Competing Risks**

Xingyuan Li* and Chung-Chou H. Chang, University of Pittsburgh

4:00 Analysis of the Time-Varying Cox Model for Cause-Specific Hazard Functions with Missing Causes

Fei Heng*, University of North Carolina, Charlotte; Seunggeun Hyun, University of South Carolina Upstate; Yanqing Sun, University of North Carolina, Charlotte; Peter B. Gilbert, Fred Hutchinson Cancer Research Center

4:15 Joint Risk Prediction in the Semi-Competing Risks Setting

Catherine Lee*, Kaiser Permanente Division of Research; Sebastien Haneuse, Harvard School of Public Health

4:30 Inference on the Win Ratio for Clustered Semi-Competing Risk Data

Di Zhang* and Jong-Hyeon Jeong, University of Pittsburgh

4:45 Competing Risks Regression for Case-Cohort Design

Soyoung Kim*, Yayun Xu, Mei-Jie Zhang and Kwang Woo Ahn, Medical College of Wisconsin

5:00 Adjusting for Covariate Measurement Error in Failure Time Analysis under Competing Risks

Carrie Caswell* and Sharon X. Xie, University of Pennsylvania

5:15 Joint Modeling of Competing Risks and Current Status Data: An Application to Spontaneous Labor Study

Youjin Lee* and Mei-Cheng Wang, Johns Hopkins School of Public Health; Rajeshwari Sundaram, Eunice Kennedy Shriver National Institute of Child Health & Human Development, National Institutes of Health

**64. CONTRIBUTED PAPERS:
GENOME-WIDE ASSOCIATION STUDIES****Sponsor** ENAR**Chair** Bin Guo, University of Minnesota**3:45 Genetic Association Analysis of a Missing Target Phenotype using Multiple Surrogate Phenotypes**

Zachary R. McCaw* and Xihong Lin, Harvard School of Public Health

4:00 Adaptive SNP-Set Association Testing in Generalized Linear Mixed Models with Application to Family Studies

Jun Young Park*, Chong Wu, Saonli Basu, Matt McGue and Wei Pan, University of Minnesota

4:15 Incorporating Genetic Networks into Case-Control Association Studies with High-Dimensional DNA Methylation Data

Hokeun Sun* and Kipoong Kim, Pusan National University

4:30 Cauchy Combination Test: A Powerful Test with Analytic P-value Calculation under Arbitrary Dependency Structures

Yaowu Liu*, Harvard University; Jun Xie, Purdue University; Xihong Lin, Harvard University

4:45 Simultaneous Selection of Multiple Important Single Nucleotide Polymorphisms in Familial Genome Wide Association Studies Data

Subho Majumdar*, University of Florida; Saonli Basu and Snigdhasu Chatterjee, University of Minnesota

5:00 A Unified Framework to Perform Inference for Pleiotropy, Mediation, and Replication in Genetic Association Studies

Ryan Sun* and Xihong Lin, Harvard School of Public Health

5:15 Penalized Inference with Mantel's Test for Multi-Modal Associations

Dustin S. Pluta*• and Tong Shen, University of California, Irvine; Hernando Ombao, King Abdullah University of Science and Technology; Zhaoxia Yu, University of California, Irvine

**65. CONTRIBUTED PAPERS:
META-ANALYSIS****Sponsor** ENAR**Chair** Jin Piao, University of Southern California**3:45 Causal Effects in Meta-Analysis of Randomized Clinical Trials with Noncompliance: A Bayesian Hierarchical Model**

Jincheng Zhou*, M. Fareed Khan Suri and Haitao Chu, University of Minnesota

4:00 Quantifying and Presenting Overall Evidence in Network Meta-Analysis

Lifeng Lin*, Florida State University

4:15 Correcting for Exposure Misclassification in Meta-Analysis: A Bayesian Approach

Qinshu Lian*•, James S. Hodges, Richard Maclehorse and Haitao Chu, University of Minnesota

4:30 EAMA: Empirically Adjusted Meta-Analysis for Large-Scale Simultaneous Hypothesis Testing in Genomic Experiments

Sinjini Sikdar*, National Institute of Environmental Health Sciences, National Institutes of Health; Somnath Datta and Susmita Datta, University of Florida

4:45 Meta-Analysis of Incidence of Rare Events Using Individual Patient-Level Data

Yan Ma* and Chen Chen, The George Washington University; Yong Ma, U.S. Food and Drug Administration

5:00 Multilevel Mixed-Effect Statistical Models for Individual Participant Data Meta-Analysis

Ying Zhang* and Vernon M. Chinchilli, The Pennsylvania State Health Milton S. Hershey Medical Center

5:15 Testing Equality of Means in Partially Paired Data with Incompleteness in Single Response

Qianya Qi*, State University of New York at Buffalo; Li Yan, Roswell Park Cancer Institute; Lili Tian, State University of New York at Buffalo

**66. CONTRIBUTED PAPERS:
MISSING DATA METHODS****Sponsor** ENAR**Chair** Anastasia Hartzes, University of Alabama at Birmingham**3:45 Coarsened Propensity Scores and Hybrid Estimators for Missing Data and Causal Inference**

Jie Zhou*, U.S. Food and Drug Administration; Zhiwei Zhang, University of California, Riverside; Zhaohai Li, The George Washington University; Jun Zhang, Shanghai Jiaotong University School of Medicine

4:00 Empirical-Likelihood-Based Criteria for Joint Model Selection on Weighted Generalized Estimating Equation Analysis of Longitudinal Data with Dropout Missingness

Chixiang Chen* and Ming Wang, The Pennsylvania State University

4:15 Multiply Robust Estimation in Nonparametric Regression with Missing Data

Yilun Sun*• and Lu Wang, University of Michigan; Peisong Han, University of Waterloo

4:30 Correcting Bias from Estimating Risk of Alzheimer's Disease from Informative Censoring using Auxiliary Information

Cuiling Wang*, Charles Hall, Richard Lipton, Joe Verghese, Mindy Katz and Qi Gao, Albert Einstein College of Medicine

4:45 Variable Selection for Non-Normally Distributed Data under an Arbitrary Missingness

Yang Yang* and Jiwei Zhao, State University of New York at Buffalo

5:00 Regression of Observations below the Limit of Detection: A Pseudo-Value Approach

Sandipan Dutta* and Susan Halabi, Duke University

5:15 Floor Discussion

67. CONTRIBUTED PAPERS: WEARABLE AND PORTABLE DEVICES

Sponsor ENAR

Chair Haochang Shou, University of Pennsylvania

3:45 Analysis of Tensor Cumulants and its Application to NHANES

Junrui Di* and Vadim Zipunnikov, Johns Hopkins Bloomberg School of Public Health

4:00 Unsupervised Clustering of Physical Activities and its Application in Health Studies

Jiawei Bai* and Ciprian M. Crainiceanu, Johns Hopkins University

4:15 Penalized Augmented Estimating Equations for Modeling Wearable Sensor Data with Informative Observation Times and Censoring Time

Jaejoon Song*, University of Texas MD Anderson Cancer Center; Michael D. Swartz, José-Miguel Yamal and Kelley Pettee Gabriel, University of Texas Health Science Center at Houston; Karen Basen-Engquist, University of Texas MD Anderson Cancer Center

4:30 Change Point Detection for Multivariate Digital Phenotypes

Ian J. Barnett*, University of Pennsylvania

4:45 Automated Longitudinal Latent Interval Estimation with Applications to Sleep

Patrick Staples*, Harvard School of Public Health

5:00 Floor Discussion

TUESDAY MARCH 27

8:30 am - 10:15 am

68. CHALLENGES, OPPORTUNITIES, AND METHODS FOR LEARNING FROM LARGE-SCALE ELECTRONIC HEALTH RECORDS DATABASES

Sponsors ENAR, ASA Biometrics Section, ASA Mental Health Statistics Section, ASA Section on Statistics in Epidemiology

Organizer Yuanjia Wang, Columbia University

Chair Donglin Zhen, University of North Carolina, Chapel Hill

8:30 Adjusting for Selection Bias in Electronic Health Records-Based Research

Sebastien Haneuse*, Harvard School of Public Health; Sarah Peskoe, Duke University; David Arterburn, Kaiser Permanente Washington Health Research Institute; Michael Daniels, University of Florida

8:55 Accounting for Informative Presence Bias and Lack of Portability in EHR-Derived Phenotypes

Rebecca A. Hubbard*, Joanna Horton, Jing Huang and Yong Chen, University of Pennsylvania

9:20 Learning Individualized Treatment Rules from Electronic Health Records

Yuanjia Wang*, Columbia University

9:45 Using Electronic Health Records Data to Target Suicide Prevention Care

Susan M. Shortreed*, Gregory E. Simon and Eric Johnson, Kaiser Permanente Washington Health Research Institute; Jean M. Lawrence, Kaiser Permanente Southern California; Rebecca C. Rossum, HealthPartners Institute; Brian Ahmedani, Henry Ford Health System; Frances M. Lynch, Kaiser Permanente Northwest Center for Health Research; Arne Beck, Kaiser Permanente Colorado Institute for Health Research; Rebecca Ziebell and Robert B. Penfold, Kaiser Permanente Washington Health Research Institute

10:10 Floor Discussion**69. GEOMETRY AND TOPOLOGY IN STATISTICAL INFERENCE**

Sponsors ENAR, IMS
Organizer Mukherjee Sayan, Duke University
Chair Mukherjee Sayan, Duke University

8:30 Manifold Learning on Fibre Bundles

Tingran Gao*, University of Chicago; Jacek Brodzki, University of Southampton; Sayan Mukherjee, Duke University

8:55 Hypothesis Testing for Spatially Complex Data using Persistent Homology Summaries

Jessi Cisewski-Kehe*, Yale University

9:20 Functional Data Analysis using a Topological Summary Statistic: The Smooth Euler Characteristic Transform

Lorin Crawford*, Brown University School of Public Health; Anthea Monod and Andrew X. Chen, Columbia University; Sayan Mukherjee, Duke University; Raúl Rabadán, Columbia University

9:45 Geometric Methods for Modeling Time Evolution in Human Microbiota

Justin D. Silverman*, Sayan Mukherjee and Lawrence A. David, Duke University

10:10 Floor Discussion**70. PREDICTIVE MODELING OF ACCELEROMETRY, ELECTRONIC DIARIES, AND PASSIVELY RECORDED VOICE DATA**

Sponsors ENAR, ASA Biometrics Section, ASA Mental Health Statistics Section
Organizer Vadim Zipunnikov, Johns Hopkins Bloomberg School of Public Health
Chair Jacek Urbanek, Johns Hopkins Bloomberg School of Public Health

8:30 How Rich is the Raw Accelerometry Data? Walking vs. Stair Climbing

Jaroslav Harezlak* and William Fadel, Indiana University Fairbanks School of Public Health; Jacek Urbanek, Johns Hopkins University School of Medicine; Xiaochun Li, Indiana University School of Medicine; Steven Albertson, Indiana University Purdue University, Indianapolis

8:55 Week-to-Week Actigraphy Tracking of Clinical Populations using Multi-Domain Decomposition

Vadim Zipunnikov*, Johns Hopkins Bloomberg School of Public Health

9:20 Predicting Mood States in Bipolar Disorder from Analyses of Acoustic Patterns Recorded from Mobile Telephone Calls

Melvin Mcinnis*, Soheil Khorram, John Gideon and Emily Mower Provost, University of Michigan

9:45 Improved Modeling of Smartphone-Based Ecological Momentary Assessment Data for Dietary Lapse Prediction

Fengqing Zhang*, Tinashe M. Tapera, Stephanie P. Goldstein and Evan M. Forman, Drexel University

10:10 Floor Discussion**71. INTEGRATIVE ANALYSIS FOR BRAIN IMAGING STUDIES****Sponsors** ENAR, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Mental Health Statistics Section, ASA Section on Statistics in Imaging**Organizer** Suprateek Kundu, Emory University**Chair** Suprateek Kundu, Emory University**8:30 Intermodal Coupling Analytics for Multimodal Neuroimaging Studies**

Russell T. Shinohara*, University of Pennsylvania

8:55 Joint Analysis of Multimodal Imaging Data via Nested Copulas

Jian Kang* and Peter X.K. Song, University of Michigan

9:20 A Bayesian Predictive Model for Imaging Genetics with Application to Schizophrenia

Francesco C. Stingo*, University of Florence; Thierry Chekouo, University of Minnesota; Michele Guindani, University of California, Irvine; Kim-Anh Do, University of Texas MD Anderson Cancer Center

9:45 Integrative Methods for Functional and Structural Connectivity

DuBois Bowman*, Columbia University

10:10 Floor Discussion**72. NOVEL EXTENSIONS AND APPLICATIONS OF CAUSAL INFERENCE MODELS****Sponsors** ENAR, ASA Section on Statistics in Epidemiology**Organizer** Ashley Buchanan, University of Rhode Island**Chair** Donna Spiegelman, Harvard School of Public Health**8:30 Model-Based Standardization Using an Outcome Model with Random Effects**

Babette Anne Brumback*, Zhongkai Wang, Adel Alrwisan and Almut Winterstein, University of Florida

9:00 Assessing Individual and Disseminated Causal Package Effects in Network HIV Treatment and Prevention Trials

Ashley Buchanan*, University of Rhode Island; Donna Spiegelman, Harvard School of Public Health; Sten Vermund, Yale School of Public Health; Samuel Friedman, National Development and Research Institutes, Inc.; Judith Lok, Harvard School of Public Health

9:30 A “Potential Outcomes” Approach to Account for Measurement Error in Marginal Structural Models

Jessie K. Edwards*, University of North Carolina, Chapel Hill

10:00 Discussant:

James Robins, Harvard School of Public Health

73. STATISTICAL METHODS IN SINGLE-CELL GENOMICS**Sponsors** ENAR, IMS**Organizer** Jiang Yuchao, University of North Carolina, Chapel Hill**Chair** Nancy R. Zhang, University of Pennsylvania**8:30 Removing Unwanted Variation using both Control and Target Genes in Single Cell RNA Sequencing Studies**

Mengjie Chen*, University of Chicago; Xiang Zhou, University of Michigan

8:55 Cell Similarity Measures for Identifying Cell Subpopulations from Single-Cell RNA-Seq Data

Haiyan Huang*, University of California, Berkeley

9:20 Single-Cell ATAC-seq Signal Extraction and Enhancement

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

9:45 Normalization and Reproducibility in Single Cell RNA-seq

Zhijin Wu*, Brown University

10:10 Floor Discussion**74. CONTRIBUTED PAPERS:
FUNCTIONAL DATA ANALYSIS****Sponsor** ENAR**Chair** Ana-Maria Staicu, North Carolina State University**8:30 Statistical Models in Sensory Quality Control: The Case of Boar Taint**

Jan Gertheiss*, Clausthal University of Technology; Johanna Mörlein, Lisa Meier-Dinkel and Daniel Mörlein, Georg August University Göttingen

8:45 Principal Component Analysis for Spatially Dependent Functional Data

Haozhe Zhang* and Yehua Li, Iowa State University

9:00 Non-Parametric Functional Association Test

Sneha Jadhav* and Shuangge Ma, Yale University

9:15 Registration for Exponential Family Functional Data

Julia Wrobel*• and Jeff Goldsmith, Columbia University

9:30 Optimal Design for Classification of Functional Data

Cai Li* and Luo Xiao, North Carolina State University

9:45 Floor Discussion**75. CONTRIBUTED PAPERS:
HIGH DIMENSIONAL DATA ANALYSIS****Sponsor** ENAR**Chair** Wenyu Gao, Virginia Tech**8:30 Robust Analysis of High Dimensional Data**

Quefeng Li*, University of North Carolina, Chapel Hill; Marco Avella-Medina, Massachusetts Institute of Technology; Jianqing Fan, Princeton University; Heather Batty, Imperial College London

8:45 A Distributed and Integrated Method of Moments for High-Dimensional Correlated Data Analysis

Emily C. Hector*• and Peter X. K. Song, University of Michigan

9:00 Tropical Principal Component Analysis and its Application to Phylogenetics

Xu Zhang*, University of Kentucky; Ruriko Yoshida, Naval Postgraduate School; Leon Zhang, University of California, Berkeley

9:15 Using Sufficient Direction Factor Model to Analyze Breast Cancer Pathway Effects

Seungchul Baek* and Yen-Yi Ho, University of South Carolina; Yanyuan Ma, The Pennsylvania State University

9:30 Inference for High-Dimensional Linear Mediation Analysis Models in Genomics

Ruixuan Zhou*, University of Illinois at Urbana-Champaign; Liewei Wang, Mayo Clinic; Sihai Dave Zhao, University of Illinois at Urbana-Champaign

9:45 Multivariate Density Estimation via Minimal Spanning Tree and Discrete Convolution

Zhipeng Wang* and David Scott, Rice University

10:00 Imputation Using Linked Matrix Factorization

Michael J. O'Connell* and Eric F. Lock, University of Minnesota

76. CONTRIBUTED PAPERS: METHODS FOR CATEGORICAL AND ORDINAL DATA

Sponsor ENAR

Chair Julia Crook, Mayo Clinic

8:30 Bayesian Testing for Independence of Two Categorical Variables with Covariates under Cluster Sampling

Dilli Bhatta*, University of South Carolina Upstate

8:45 A Review and Critique of Statistical Methods for the Analysis of Ventilator-Free Days

Charity J. Morgan* and Yuliang Liu, University of Alabama at Birmingham

9:00 Online Robust Fisher Discriminant Analysis

Hsin-Hsiung Huang* and Teng Zhang, University of Central Florida

9:15 Bayesian Ordinal Response Models for Identifying Molecular Mechanisms in the Progression to Cervical Cancer

Kellie J. Archer* and Yiran Zhang, The Ohio State University; Qing Zhou, U.S. Food and Drug Administration

9:30 Sample Size Estimation for Marginalized Zero-Inflated Count Regression Models

Leann Long* and Dustin Long, University of Alabama at Birmingham; John S. Preisser, University of North Carolina, Chapel Hill

9:45 Floor Discussion

77. CONTRIBUTED PAPERS: MULTIVARIATE METHODS

Sponsor ENAR

Chair Sabrina Vettori, King Abdullah University of Science and Technology

8:30 Regression Trees and Ensemble Methods for Multivariate Outcomes

Evan L. Reynolds* and Mousumi Banerjee, University of Michigan

8:45 SimMultiCorrData: An R Package for Simulation of Correlated Variables of Multiple Data Types

Allison C. Fialkowski* and Hemant K. Tiwari, University of Alabama at Birmingham

9:00 Sparse Multiple Co-Inertia Analysis with Applications to 'Omics Data

Eun Jeong Min* and Qi Long, University of Pennsylvania

9:15 Small Sphere Distributions for Directional Data with Application to Medical Imaging

Byungwon Kim*, University of Pittsburgh; Stephan Huckemann, University of Göttingen; Jorn Schulz, University of Stavanger; Sungkyu Jung, University of Pittsburgh

9:30 Super-Delta: A New Approach that Combines Gene Expression Data Normalization and Differential Expression Analysis

Yuhang Liu* and Jinfeng Zhang, Florida State University; Xing Qiu, University of Rochester

9:45 Exceedance Probabilities for Exchangeable Random Variables

Satish Iyengar*, University of Pittsburgh; Burcin Simsek, Bristol-Myers Squibb

10:00 Floor Discussion**78. CONTRIBUTED PAPERS:
SMART DESIGNS AND DYNAMIC TREATMENT REGIMENS****Sponsor** ENAR**Chair** Thomas A. Murray, University of Minnesota**8:30 A Bayesian Analysis of Small n Sequential Multiple Assignment Randomized Trials (snSMARTs)**

Boxian Wei* and Thomas M. Braun, University of Michigan; Roy N. Tamura, University of South Florida; Kelley M. Kidwell, University of Michigan

8:45 Evaluating the Effects of Misclassification in Sequential Multiple Assignment Randomized Trials (SMART)

Jun He*, Donna McClish and Roy Sabo, Virginia Commonwealth University

9:00 Power Analysis in a SMART Design: Sample Size Estimation for Determining the Best Dynamic Treatment Regime

William J. Artman*, University of Rochester; Tianshuang Wu, AbbVie; Ashkan Ertefaie, University of Rochester

9:15 Dynamic Treatment Regimes with Survival Outcomes

Gabrielle Simoneau*, Robert W. Platt and Erica E.M. Moodie, McGill University

9:30 Floor Discussion**79. CONTRIBUTED PAPERS:
SURVIVAL ANALYSIS AND SEMI- AND NON-PARAMETRIC MODELS****Sponsor** ENAR**Chair** Samuel Tracy, Harvard School of Public Health**8:30 Martingale-Based Omnibus Tests for Semiparametric Transformation Model with Censored Data**

Soutrik Mandal*, Suojin Wang and Samiran Sinha, Texas A&M University

8:45 Penalized Estimation of Generalized Additive Cox Model for Interval-Censored Data

Yan Liu* and Minggen Lu, University of Nevada, Reno; Christopher McMahan, Clemson University

9:00 Restricted Mean Survival Time for Right-Censored Data with Biased Sampling

Chi Hyun Lee*, Jing Ning and Yu Shen, University of Texas MD Anderson Cancer Center

9:15 On the Survivor Cumulative Incidence Function of Recurrent Events

Lu Mao*, University of Wisconsin, Madison

9:30 Some Asymptotic Results for Survival Trees and Forests

Yifan Cui*, University of North Carolina, Chapel Hill; Ruoqing Zhu, University of Illinois at Urbana-Champaign; Mai Zhou, University of Kentucky; Michael Kosorok, University of North Carolina, Chapel Hill

9:45 Additive Rates Model for Recurrent Event Data with Infrequently Observed Time-Dependent Covariates

Tianmeng Lyu*, University of Minnesota; Yifei Sun, Columbia University; Chiung-Yu Huang, University of California, San Francisco; Xianghua Luo, University of Minnesota

10:00 Floor Discussion**80. CONTRIBUTED PAPERS:
CANCER APPLICATIONS****Sponsor** ENAR**Chair** Brian L. Egleston, Fox Chase Cancer Center, Temple University Health System**8:30 Methods for Integrating Methylation and Expression Data for Probing Smoking Exposure Effects in Muscle-Invasive Urothelial Carcinoma Patients**

Miranda L. Lynch*, Roswell Park Cancer Institute; Jessica M. Clement, UConn Health

8:45 Statistical Properties of the D-Metric for Measuring Etiologic Heterogeneity in Case-Control Studies

Emily C. Zabor* and Venkatraman E. Seshan, Memorial Sloan Kettering Cancer Center; Shuang Wang, Columbia University; Colin B. Begg, Memorial Sloan Kettering Cancer Center

9:00 Pathway-Guided Integrative Analysis of High Throughput Genomic Datasets to Improve Cancer Subtype Identification

Dongjun Chung*, Zequn Sun, Andrew Lawson, Brian Neelon and Linda Kelemen, Medical University of South Carolina

9:15 A Fast Score Test for Generalized Mixture Models

Rui Duan*•, University of Pennsylvania; Yang Ning, Cornell University; Shuang Wang, Columbia University; Bruce G. Lindsay, The Pennsylvania State University; Raymond J. Carroll, Texas A&M University; Yong Chen, University of Pennsylvania

9:30 Statistical Approaches for Meta-Analysis of Genetic Mutation Prevalence

Margaux L. Hujoel*, Giovanni Parmigiani and Danielle Braun, Harvard School of Public Health/Dana-Farber Cancer Institute

9:45 Mathematical Modeling Identifies Optimum Lapatinib Dosing Schedules for the Treatment of Glioblastoma Patients

Shayna R. Stein*, Harvard School of Public Health and Dana-Farber Cancer Institute; Franziska Michor, Harvard School of Public Health, Dana-Farber Cancer Institute and Harvard University; Hiroshi Haeno, Kyushu University, Japan; Igor Vivanco, The Institute of Cancer Research, London;

10:00 Floor Discussion**TUESDAY MARCH 27****10:15 am - 10:30 am REFRESHMENT BREAK WITH OUR EXHIBITORS****TUESDAY MARCH 27****10:30 am - 12:15 pm****8I. PRESIDENTIAL INVITED ADDRESS****Sponsor** ENAR**Organizer** Jeffrey S. Morris, UT MD Anderson Cancer Center**Chair** Jeffrey S. Morris, UT MD Anderson Cancer Center**10:30 Introduction****10:35 Distinguished Student Paper Awards****10:45 Statistics as Prediction**

Roderick J. Little, Professor of Biostatistics, Richard D. Remington Distinguished University Professor, Department of Statistics Research Professor, Institute for Social Research Senior Fellow, Michigan Society of Fellows, University of Michigan

TUESDAY MARCH 27

1:45 pm - 3:30 pm

82. STATISTICAL FRONTIERS IN DYNAMIC TREATMENT REGIMES LEADING TOWARD PERSONALIZED HEALTH CARE

Sponsors ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section, ASA Statistical Learning and Data Mining Section, IMS

Organizer Lu Wang, University of Michigan

Chair Lu Wang, University of Michigan

1:45 Challenges in Developing Learning Algorithms to Personalize Treatment in Real Time

Susan A. Murphy*, Harvard University

2:10 Decision Making to Optimize Composite Outcomes

Daniel J. Lockett*, University of North Carolina, Chapel Hill; Eric B. Laber, North Carolina State University; Michael R. Kosorok, University of North Carolina, Chapel Hill

2:35 A Sequential Conditional Test for Medical Decision Making

Min Qian*, Columbia University

3:00 Modeling Survival Distribution as a Function of Time to Treatment Discontinuation: A Dynamic Treatment Regime Approach

Shu Yang* and Anastasios Tsiatis, North Carolina State University; Michael Blazing, Duke University Medical Center

3:25 Floor Discussion**83. ADVANCED WEIGHTING METHODS FOR OBSERVATIONAL STUDIES**

Sponsors ENAR, ASA Biopharmaceutical Section, ASA Section on Statistics in Epidemiology

Organizer Robert Greevy, Vanderbilt University Medical Center

Chair Robert Greevy, Vanderbilt University Medical Center

1:45 The Average Treatment Effect on the Evenly Matchable Units (ATE): A Valuable Estimand in Causal Inference

Lauren R. Samuels* and Robert A. Greevy, Vanderbilt University School of Medicine

2:10 Matching Weights to Simultaneously Compare Three Treatment Groups: Comparison to Three-Way Matching

Kazuki Yoshida* and Sonia Hernandez-Diaz, Harvard School of Public Health; Daniel H. Solomon, Brigham and Women's Hospital; John W. Jackson, Johns Hopkins Bloomberg School of Public Health; Joshua J. Gagne, Robert J. Glynn and Jessica M. Franklin, Brigham and Women's Hospital

2:35 A Tale of Two Tails: Addressing Extreme Propensity Scores via the Overlap Weights

Laine E. Thomas*, Fan Li and Fan Li, Duke University

3:00 Exploring Finite-Sample Bias in Propensity Score Weights

Lucy D'Agostino McGowan* and Robert Greevy, Vanderbilt University

3:25 Floor Discussion**84. SPATIAL MODELING OF ENVIRONMENTAL AND EPIDEMIOLOGICAL DATA****Sponsors** ENAR, ASA Bayesian Statistical Science Section, ASA Section on Statistics and the Environment**Organizer** Elizabeth Mannshardt, U.S. Environmental Protection Agency**Chair** Brian Reich, North Carolina State University**1:45 Bayesian Modeling of Non-Stationary Spatial Processes via Domain Segmentation**

Veronica J. Berrocal*, University of Michigan

2:10 Bayesian Models for High-Dimensional Non-Gaussian Dependent Data

Jonathan R. Bradley*, Florida State University

2:35 Using Point Patterns to Identify Principal Drivers of Heat-Related Morbidity

Matthew J. Heaton*, Brigham Young University; Jacob W. Mortensen, Simon Fraser University; Olga V. Wilhelmi and Cassandra Olenick, National Center for Atmospheric Research

3:00 Multivariate Spatio-Temporal (MVST) Mixture Modeling of Health Risk with Environmental Stressors

Andrew B. Lawson*, Medical University of South Carolina; Rachel Carroll, National Institute of Environmental Health Sciences, National Institutes of Health

3:25 Floor Discussion**85. LATEST DEVELOPMENT OF STATISTICAL METHODS FOR TUMOR HETEROGENEITY AND DECONVOLUTION****Sponsors** ENAR, ASA Statistics in Genomics and Genetics Section**Organizer** Wenyi Wang, University of Texas MD Anderson Cancer Center**Chair** Karthik Bharath, University of Nottingham**1:45 Robust Subclonal Architecture Reconstruction from ~2,700 Cancer Genomes**

Wenyi Wang*, Kaixian Yu and Hongtu Zhu, University of Texas MD Anderson Cancer Center

2:10 Estimation of Intra-Tumor Heterogeneity and Assessing its Impact on Survival Time

Wei Sun*, Fred Hutchinson Cancer Research Center; Chong Jin, Paul Little and Dan-Yu Lin, University of North Carolina, Chapel Hill; Mengjie Chen, University of Chicago

2:35 Cancer Genomics with Bulk and Single Cell Sequencing

Nancy R. Zhang*, University of Pennsylvania; Yuchao Jiang, University of North Carolina, Chapel Hill; Zilu Zhou, University of Pennsylvania

3:00 Understanding Cancer Progression via Tumor Evolution Models

Russell Schwartz*, Carnegie Mellon University

3:25 Floor Discussion**86. STATISTICAL ANALYSIS OF MICROBIOME DATA****Sponsors** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology, ASA Statistics in Genomics and Genetics Section**Organizer** Lei Liu, Northwestern University**Chair** Xuelin Huang, University of Texas MD Anderson Cancer Center**1:45 Variable Selection for High Dimensional Compositional Data with Application in Metagenomics**

Hongmei Jiang*, Northwestern University

2:10 Joint Modeling and Analysis of Microbiome with Other Omics Data

Michael C. Wu*, Fred Hutchinson Cancer Research Center

2:35 A Two-Stage Microbial Association Mapping Framework with Advanced FDR Controlling Procedures

Huilin Li*, Jiyuan Hu, Hyunwook Koh, Linchen He, Menghan Liu and Martin J. Blaser, New York University

3:00 A Novel Approach on Differential Abundance Analysis for Matched Metagenomic Samples

Lingling An*, Wenchi Lu, Di Ran, Dan Luo and Qianwen Luo, University of Arizona; Dailu Chen, University of Texas Southwestern Medical Center

3:25 Floor Discussion**87. RECENT ADVANCES IN STATISTICAL METHODS FOR IMAGING GENETICS****Sponsors** ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section, ASA Section on Statistics in Imaging**Organizer** Yize Zhao, Weill Cornell Medicine, Cornell University**Chair** Yize Zhao, Weill Cornell Medicine, Cornell University**1:45 Moment-Matching Methods for High-Dimensional Heritability and Genetic Correlation Analysis**

Tian Ge* and Chia-Yen Chen, Harvard Medical School; Mert R. Sabuncu, Cornell University; Jordan W. Smoller, Harvard Medical School

2:10 From Association to Causation: Casual Inference in Imaging-Genetic Data Analysis

Momiao Xiong* and Nan Lin, University of Texas Health Science Center at Houston; Zixin Hu, Fudan University; Rong Jiao, University of Texas Health Science Center at Houston; Vince D. Calhoun, The Mind Research Network

2:35 Imaging-Wide Association Study: Integrating Imaging Endophenotypes in GWAS

Wei Pan*, Zhiyuan Xu and Chong Wu, University of Minnesota

3:00 Functional Genome-Wide Association Analysis of Imaging and Genetic Data

Hongtu Zhu*, University of Texas MD Anderson Cancer Center

3:25 Floor Discussion**88. CONTRIBUTED PAPERS:
CLINICAL TRIALS AND BIOPHARMACEUTIAL RESEARCH****Sponsor** ENAR**Chair** Jennifer G. Le-Rademacher, Mayo Clinic**1:45 Formulation of Confidence Intervals for Difference Between Two Binomial Proportions from Logistic Regression**

Ryuji Uozumi*, Kyoto University School of Medicine; Shinjo Yada, A2 Healthcare Corporation; Kazushi Maruo, University of Tsukuba; Atsushi Kawaguchi, Saga University

2:00 Big Data vs Data Re-Use: Example of Patients' Recruitment Modeling

Nicolas J. Savy*, Toulouse Mathematics Institute; Nathan Minois, INSERM Unit 1027; Valerie Lauwers-Cances, CHU Toulouse; Stephanie M. Savy, INSERM Unit 1027; Michel Attal, CHU Toulouse; Sandrine Andrieu, INSERM Unit 1027; Philippe Saint-Pierre, Toulouse Mathematics Institute; Vladimir V. Anisimov, University of Glasgow

2:15 Toward More Flexible and Effective Control of False Positives in Phase III Randomized Clinical Trials

Changyu Shen*, Beth Israel Deaconess Medical Center, Harvard Medical School

2:30 Targeted Maximum Likelihood Estimation to Improve Precision and Reduce Bias in Alzheimer's Disease Clinical Trials

Elizabeth Colantuoni* and Aidan McDermott, Johns Hopkins Bloomberg School of Public Health; Jon Steingrimsson, Brown University School of Public Health; Arnold Baker and Michela Gallagher, Johns Hopkins University School of Medicine; Michael Rosenblum, Johns Hopkins Bloomberg School of Public Health

2:45 Clinical Trial Simulation and Virtual Patients' Generation

Philippe Saint Pierre* and Nicolas J. Savy, Toulouse Mathematics Institute

3:00 Floor Discussion**89. CONTRIBUTED PAPERS:
CLUSTERED AND HIERARCHICAL DATA****Sponsor** ENAR**Chair** Fan Li, Duke University**1:45 The Mixture Approach to Estimating a Population-Averaged Value**

Haoyu Zhang* and Thomas A. Louis, Johns Hopkins Bloomberg School of Public Health

2:00 A Class of Prior Distributions for Adjacency Matrices in Conditional Autoregressive Models

Heli Gao* and Jonathan Bradley, Florida State University

2:15 A Theoretical Exploration of Clusterability Tests

Naomi C. Brownstein*, Florida State University

2:30 A Stochastic Second-Order Generalized Estimating Equations Approach for Estimating Intraclass Correlation in the Presence of Informative Missing Data

Tom Chen*, Eric Tchetgen Tchetgen and Rui Wang, Harvard School of Public Health

2:45 Bayesian Hierarchical Model in Phase I Dose Escalation Study with Different Ethnic Groups

Serena Liao*, Novartis Oncology Pharmaceuticals

3:00 Bayesian Hierarchical Modelling of Air Pollution Extremes Using Multivariate Max-Stable Processes

Sabrina Vettori*•, Raphael Huser and Marc Genton, King Abdullah University of Science and Technology

3:15 Floor Discussion**90. CONTRIBUTED PAPERS:
EXPERIMENT DESIGN****Sponsor** ENAR**Chair** Ran Tao, Vanderbilt University School of Medicine**1:45 Design Analyses of Randomized Clinical Trials Supporting FDA Cancer Drug Approvals**

Emily Lord, Isabelle R. Weir and Ludovic Trinquart*, Boston University School of Public Health

2:00 Sample Size Considerations for Comparing Dynamic Treatment Regimens in a Sequential Multiple-Assignment Randomized Trial with a Continuous Longitudinal Outcome

Nicholas J. Seewald* and Kelley M. Kidwell, University of Michigan; James R. McKay, University of Pennsylvania; Inbal Nahum-Shani and Daniel Almirall, University of Michigan

2:15 Optimal Design of Replication Experiments

Ryan T. Jarrett* and Matthew S. Shotwell, Vanderbilt University

2:30 Design of Noninferiority Randomized Trials using the Difference in Restricted Mean Survival Times

Isabelle R. Weir* and Ludovic Trinquart, Boston University School of Public Health

2:45 Floor Discussion

91. CONTRIBUTED PAPERS: NONLINEAR AND SEMI-PARAMETRIC MODELS

Sponsor ENAR

Chair Julia Wrobel, Columbia University

1:45 Improved Bayesian Scheme for Resolving Intravoxel Neuroanatomy

Sharang Chaudhry* and Kaushik Ghosh, University of Nevada, Las Vegas

2:00 Improving Estimation of Generalized Semi-Parametric Varying-Coefficient Models using Covariance Function

Fang Fang* and Yanqing Sun, University of North Carolina, Charlotte

2:15 Semiparametric Comparison of Nonlinear Curves and Surfaces

Shi Zhao*, Spencer George Lourens, Giorgos Bakoyannis and Wanzhu Tu, Indiana University School of Medicine

2:30 Testing Nonlinear Gene-Environment Interaction Through Varying Coefficient and Linear Mixed Models

Zhengyang Zhou*, Southern Methodist University and University of Texas Southwestern Medical Center; Hung-Chih Ku, DePaul University; Chao Xing, University of Texas Southwestern Medical Center

2:45 Change Point Inference in Presence of Missing Covariate

Tao Yang* and Ying Huang, Fred Hutchinson Cancer Research Center

3:00 Constructing Concurrent Network of Biomarker Processes using Dynamical Systems

Ming Sun*, Columbia University; Donglin Zeng, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University

3:15 Multivariate Skewed Responses: New Semiparametric Regression Model and a Bayesian Recourse

Apurva Chandrashekar Bhingare*• and Debajyoti Sinha, Florida State University; Debdeep Pati, Texas A&M University; Stuart R. Lipsitz, Harvard Medical School; Dipankar Bandyopadhyay, Virginia Commonwealth University

92. CONTRIBUTED PAPERS: PREDICTION AND PROGNOSTIC MODELING

Sponsor ENAR

Chair Young-Geun Choi, Fred Hutchinson Cancer Research Center

1:45 Tuning Parameter Selection for Prediction in High-Dimensional Ridge Regression

Zilin Li*, Harvard School of Public Health; Lee Dicker, Rutgers University; Xihong Lin, Harvard School of Public Health

2:00 A Bayesian Method for Updating Weibull Prediction Models Using Published Summary Data

Wen Ye* and Pin Li, University of Michigan

2:15 Discrimination Index for Multi-Category Outcome

Aya Kuchiba*, National Cancer Center, Japan; Kentaro Sakamaki, University of Tokyo

2:30 Evaluating Discriminatory Accuracy of Models using Partial Risk-Scores in Two-Phase Studies

Parichoy Pal Choudhury*, Johns Hopkins University; Anil K. Chaturvedi, National Cancer Institute, National Institutes of Health; Nilanjan Chatterjee, Johns Hopkins University

2:45 Machine Learning Algorithms for Survival, Longitudinal, and Multivariate (SLAM) Data with Applications to Sudden Cardiac Arrest (SCA)

Shannon Wongvibulsin* and Katherine Wu, Johns Hopkins University School of Medicine; Scott Zeger, Johns Hopkins Bloomberg School of Public Health

3:00 Zero-Inflated Quantile Regression with its Application in NOMAS

Wodan Ling*, Bin Cheng, Ying Wei and Ying Kuen Cheung, Columbia University

3:15 Incorporating Inter-Study Heterogeneity into the Training of Predictors

Prasad Patil* and Giovanni Parmigiani, Harvard School of Public Health/Dana-Farber Cancer Institute

93. CONTRIBUTED PAPERS: STATISTICAL GENETICS AND GENOMICS

Sponsor ENAR

Chair Rongjie Liu, Rice University

1:45 Statistical Approaches to Decreasing the Discrepancy of Non-Detects in qPCR Data

Valeriia Sherina*[•], Helene McMurray, Tanzy M. Love and Matthew N. McCall, University of Rochester Medical Center

2:00 Differential Splicing Analysis Using a Compositional Regression Method

Scott Van Buren* and Naim Rashid, University of North Carolina, Chapel Hill

2:15 Statistical Methods for Profiling 3-Dimensional Chromatin Interactions from Repetitive Regions of Genomes

Ye Zheng*, University of Wisconsin, Madison; Ferhat Ay, La Jolla Institute for Allergy and Immunology; Sunduz Keles, University of Wisconsin, Madison

2:30 Comparison of Weighting Approaches for Genetic Risk Scores in Gene-Environment Interaction Studies

Anke Huels*, Ursula Kraemer and Tamara Schikowski, IUF-Leibniz Research Institute for Environmental Medicine; Katja Ickstadt, TU Dortmund University; Holger Schwender, Heinrich Heine University

2:45 Identification of Conditionally Essential Genes in Transposon Sequencing Studies

Lili Zhao*, University of Michigan

3:00 Floor Discussion

94. CONTRIBUTED PAPERS: SURVIVAL ANALYSIS IN EPIDEMIOLOGY

Sponsor ENAR

Chair Chi Hyun Lee, University of Texas MD Anderson Cancer Center

1:45 Joint Modeling of Recurrent and Terminal Events in Nested Case-Control Studies

Ina Jazic* and Sebastien Haneuse, Harvard School of Public Health; Virginie Rondeau, Université de Bordeaux

2:00 Multiplicative Rates Model for Recurrent Events with Case-Cohort Data

Poulami Maitra* and Jianwen Cai, University of North Carolina, Chapel Hill; Leila D. Amorim, Federal University of Bahia

2:15 Semiparametric Inference for a Two-Stage Outcome-Dependent Sampling Design with Interval-Censored Failure Time Data

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

2:30 Efficient Secondary Analysis of Data from Two-Phase Studies

Yinghao Pan* and Jianwen Cai, University of North Carolina, Chapel Hill; Elizabeth Jensen, Wake Forest University; Haibo Zhou, University of North Carolina, Chapel Hill

2:45 Two-Stage Pseudo Likelihood Approach to Estimation and Inference for Recurrent Events Data: Application to Readmission Time Analysis

Qing Li* and Gideon Zamba, University of Iowa

3:00 Floor Discussion

TUESDAY MARCH 27

3:30 pm - 3:45 pm REFRESHMENT BREAK WITH OUR EXHIBITORS

TUESDAY MARCH 27

3:45 pm - 5:30 pm

95. NOVEL STATISTICAL APPROACHES FOR ESTIMATING HEALTH EFFECTS OF COMPLEX ENVIRONMENTAL EXPOSURES

Sponsors ENAR, ASA Section on Statistics in Epidemiology, ASA Section on Statistics and the Environment

Organizer Jenna Krall, George Mason University

Chair Howard Chang, Emory University

3:45 Discovering Structure in Multiple Outcomes Models for Multiple Environmental Exposure Effects

Tanzyl Love*, University of Rochester; Amy LaLonde, Eli Lilly and Company; Sally W. Thurston and Phil W. Davidson, University of Rochester

4:10 Novel Tests of Measurement Invariance in Factor Models with Applications to Environmental Epidemiology

Brisa N. Sanchez*, University of Michigan; Zhenzhen Zhang, AbbVie Inc.

4:35 Hierarchical Models for Estimating Associations Between Air Pollution and Health in Multicity Studies

Jenna R. Krall*, George Mason University; Howard H. Chang and Stefanie Ebel Sarnat, Emory University

5:00 Bayesian Varying Coefficient Kernel Machine Regression to Assess Cognitive Trajectories Associated with Exposure to Complex Mixtures

Shelley H. Liu*, Icahn School of Medicine at Mount Sinai; Jennifer F. Bobb, Kaiser Permanente Washington Health Research Institute; Birgit Claus Henn, Boston University School of Public Health; Lourdes Schnaas, National Institute of Perinatology, Mexico; Martha M. Tellez-Rojo, National Institute of Public Health, Mexico; David Bellinger, Harvard School of Public Health; Manish Arora and Robert O. Wright, Icahn School of Medicine at Mount Sinai; Brent A. Coull, Harvard School of Public Health

5:25 Floor Discussion**96. STATISTICAL APPROACHES FOR HANDLING IMPORTANT CHALLENGES FACING CURRENT AGING RESEARCH****Sponsors** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology**Organizer** Cuiling Wang, Albert Einstein College of Medicine**Chair** Cuiling Wang, Albert Einstein College of Medicine**3:45 What Exactly are we Measuring? Harmonization of Assessments of Older Adults**

Karen J. Bandeen-Roche*, Johns Hopkins Bloomberg School of Public Health

4:10 Design and Data Features that may Affect the Estimation of the Onset of Accelerated Cognitive Decline

Graciela Muniz Terrera*, University of Edinburgh; Eric Peres Barbosa and Tatiana Benaglia, Universidad Estatal de Sao Paulo

4:35 Inferring Diagnostic Accuracy for Clustered Ordinal Diagnostic Groups in Three-Class or even Higher Case—Application to the Early Diagnosis of Alzheimer's Disease

Chengjie Xiong*, Jingqin Luo and Randall Bateman, Washington University in St. Louis

5:00 Translating Alzheimer's Disease Risk Polymorphisms into Functional Candidates

Yuriko Katsumata*, Peter T. Nelson, Steven Estus, David W. Fardo, University of Kentucky

5:25 Floor Discussion

97. RECENT ADVANCES IN THE ESTIMATION OF GRAPHICAL AND COVARIANCE MODELS

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

Organizer Lili Zhao, University of Michigan

Chair Lili Zhao, University of Michigan

3:45 ARMA Cholesky Factor Models for the Covariance Matrix

Michael J. Daniels*, University of Florida; Keunbaik Lee and Changryong Baek, Sungkyunkwan University

4:10 Bayesian Hierarchical Modeling for Inference of Multiple Graphical Models

Christine B. Peterson*, University of Texas MD Anderson Cancer Center; Nathan Osborne, Rice University; Francesco C. Stingo, University of Florence; Marina Vannucci, Rice University

4:35 Inferring Dynamic Functional Connectivity from Magnetoencephalography Recordings using Time-Varying State-Space Models

Nicholas J. Foti*, Adrian K.C. Lee and Emily B. Fox, University of Washington

5:00 Covariance Models for Structured Sparse Shrinkage

Peter D. Hoff*, Duke University; Maryclare Griffin, University of Washington

5:25 Floor Discussion

98. STATISTICAL METHODS FOR CANCER RADIOMICS

Sponsors ASA Section Bayesian Statistical Science Section, ASA Biometrics Section, ASA Section on Statistics in Imaging

Organizer Brian Hobbs, University of Texas MD Anderson Cancer Center

Chair Brian Hobbs, University of Texas MD Anderson Cancer Center

3:45 Development of a Multiparametric MR Classifier for Prostate Cancer

Joseph Koopmeiners*, Jin Jin, Lin Zhang, Ethan Leng and Greg Metzger, University of Minnesota

4:10 Distribution-Free Liver Cancer Detection using CT Perfusion Imaging

Yuan Wang*, Washington State University

4:35 A Bayesian Hidden Potts Mixture Model for Analyzing Lung Cancer Pathological Images

Qiwei Li* and Faliu Yi, University of Texas Southwestern Medical Center; Faming Liang, Purdue University; Xinglei Wang, Southern Methodist University; Yang Xie, Adi Gazdar and Guanghua Xiao, University of Texas Southwestern Medical Center

5:00 A Bayesian Nonparametric Approach for Cancer Radiomics: Elucidating Textural Pattern Heterogeneity of Solid Lesions

Xiao Li*, University of Texas Health Science Center at Houston and University of Texas MD Anderson Cancer Center; Brian Hobbs and Chaan Ng, University of Texas MD Anderson Cancer Center; Michele Guindani, University of California, Irvine

5:25 Floor Discussion

99. ADVANCING THE ANALYSIS OF MULTIWAY (TENSOR) DATA

Sponsors ENAR, ASA Section on Statistics in Imaging, ASA Statistical Learning and Data Mining Section

Organizer Eric Lock, University of Minnesota

Chair Eric Lock, University of Minnesota

3:45 Supervised Multiway Factorization

Gen Li*, Columbia University; Eric Lock, University of Minnesota

4:10 Supervised Modeling of Tensor Objects

Rajarshi Guhaniyogi*, University of California, Santa Cruz; Shaan Qamar, Google Inc.; David B. Dunson, Duke University

4:35 Standard Errors for Regression on Relational Data with Exchangeable Errors

Bailey K. Fosdick* and Frank W. Marrs, Colorado State University; Tyler H. McCormick, University of Washington

5:00 Covariate-Adjusted Tensor Classification in High-Dimensions

Xin Zhang*, Florida State University

5:25 Floor Discussion

100. MODERN STATISTICAL METHODS FOR THE EHR ERA

Sponsors ENAR, ASA Biometrics Section, ASA Statistical Learning and Data Mining Section

Organizers Dandan Liu and Qingxia Chen, Vanderbilt University Medical Center

Chair Dandan Liu, Vanderbilt University Medical Center

3:45 Quantile Decision Trees and Forest with its Application for Predicting the Risk (Post-Traumatic Stress Disorder) PTSD after Experienced an Acute Coronary Syndrome

Ying Wei*, Columbia University

4:10 Distributed Learning from Multiple EHR Databases: Contextual Embedding Models for Medical Events

Qi Long*, University of Pennsylvania; Ziyi Li, Emory University; Xiaoqian Jiang, University of California, San Diego

4:35 Learning Maternal Smoking Effect on Childhood Bronchiolitis from TennCare

Qingxia Chen*, TDavid Schlueter, Christopher Fannesbeck, Department of Biostatistics, Vanderbilt University Medical Center; Pingsheng Wu, Department of Biostatistics, Vanderbilt University Medical Center, Department of Medicine, Vanderbilt University Medical Center

5:00 Retrospective Study Designs for Longitudinal Data Obtained from a Biobank-Linked Electronic Medical Records

Jonathan S. Schildcrout*, Vanderbilt University Medical Center

5:25 Floor Discussion
**101. CONTRIBUTED PAPERS:
ADAPTIVE DESIGN/ADAPTIVE RANDOMIZATION IN CLINICAL TRIALS**

Sponsor ENAR

Chair Michael A. Rosenblum, Johns Hopkins Bloomberg School of Public Health

3:45 A Novel Bayesian Phase I/II Dose/Schedule-Finding Design Based on Biological Mechanism

Xiao Su* and Yisheng Li, University of Texas MD Anderson Cancer Center

4:00 Adaptive Designs in Multi-Reader Multi-Case Clinical Trials of Imaging Devices

Zhipeng Huang*, Weijie Chen, Frank Samuelson and Lucas Tcheuko, U.S. Food and Drug Administration

4:15 A Bayesian Precision Medicine Design for Phase II/III Clinical Trials with Multiple Treatments

Liangcai Zhang*, Rice University; Suyu Liu and Ying Yuan, University of Texas MD Anderson Cancer Center

4:30 Comparative Review of Toxicity Probability Interval Designs for Phase I Clinical Trials

Heng Zhou*, University of Texas MD Anderson Cancer Center; Thomas A. Murray, Department of Biostatistics, The University of Minnesota; Haitao Pan, Department of Biostatistics, St. Jude Children's Research Hospital; Ying Yuan, Department of Biostatistics, University of Texas MD Anderson Cancer Center

4:45 Group-Sequential Strategies in Clinical Trials with Bivariate Time-to-Event Outcomes

Toshimitsu Hamasaki*, National Cerebral and Cardiovascular Center; Scott Evans, Harvard School of Public Health; Tomoyuki Sugimoto, Kagoshima University; Koko Asakura, National Cerebral and Cardiovascular Center

5:00 Floor Discussion
**102. CONTRIBUTED PAPERS:
FUNCTIONAL REGRESSION MODELS**

Sponsor ENAR

Chair Matthew Reimherr, The Pennsylvania State University

3:45 Bayesian ANOVA Modeling for Functional Data

Yu Yue*, Baruch College, The City University of New York; David Bolin, Chalmers University of Technology, Sweden; Havard Rue, Norwegian University of Science and Technology, Norway; Xiao-Feng Wang, Cleveland Clinic Lerner Research Institute

4:00 Multivariate Functional Response Regression

Hongxiao Zhu*, Virginia Tech; Jeffrey S. Morris, University of Texas MD Anderson Cancer Center; Fengrong Wei; University of West Georgia; Dennis D. Cox, Rice University

4:15 Two Sample Tests for Longitudinal Functional Data

Saebitna Oh*, Arnab Maity and Ana-Maria Staicu, North Carolina State University

4:30 Generalized Functional Linear Models in the Presence of Missing Data with Application to a Renal Study

Will Zhu*, Emory University; Qi Long, University of Pennsylvania; Amita Manatunga, Emory University

4:45 Functional Variable Selection in Low-Dimensional Internal Musculoskeletal Biomechanical (LIMB) Model

Md Nazmul Islam*, Jonathan Stallings, Ana-Maria Staicu and He Huang, North Carolina State University

5:00 Floor Discussion**103. CONTRIBUTED PAPERS:
ANALYSIS OF ROC CURVES**

Sponsor ENAR

Chair Jiarui Lu, University of Pennsylvania

3:45 A Covariate-Adjusted Classification Model for Multiple Biomarkers in Disease Screening and Diagnosis

Suizhi Yu* and Wei-Wen Hsu, Kansas State University

4:00 A Model-Free Framework to Determining the Covariate-Adjusted Youden Index and its Associated Cut-Point

Jiwei Zhao*, State University of New York at Buffalo

4:15 New Applications of Kullback-Leibler Information as a Measure of Diagnostic Accuracy and its Relation to Common ROC Indices

Jingjing Yin*, Hani Samawi, Xinyan Zhang, Lili Yu, Haresh Rochani and Robert Vogel, Georgia Southern University

4:30 Measuring Accuracy of Biomarkers Under Tree or Umbrella Ordering

Yingdong Feng* and Lili Tian, State University of New York at Buffalo

4:45 Statistical Inference of Two Classifiers by Area under the ROC Curve with Empirical Likelihood

Xue Ding* and Mai Zhou, University of Kentucky

5:00 Assessing Predictive Value of Risk Factors in Large-Scale Prospective Observational Studies

Xiang Liu*, Kendra Vehik and Jeffrey Krischer, University of South Florida

5:25 Floor Discussion**104. CONTRIBUTED PAPERS:
JOINT MODELS FOR SURVIVAL AND LONGITUDINAL DATA****Sponsor** ENAR**Chair** Lu Mao, University of Wisconsin, Madison**3:45 Effect of Adherence on AIDS Related Outcomes in HIV Patients - A Likelihood Based Approach to Correct for Misclassification in a Cox Proportional Hazards Model**

Varadan Sevilimedu* and Shuangge Ma, Yale School of Public Health; Tassos Kyriakides, Department of Veteran Affairs

4:00 Joint Analysis of Multiple Longitudinal Processes with Skewness and Excess of Zeroes and a Discrete Survival Time: An Application to Fecundity Data

Sedigheh Mirzaei Salehabadi*, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health; Somak Chatterjee and Subrata Kundu, The George Washington University; Rajeshwari Sundaram, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

4:15 Applying Survival Analysis and Count Models to Twitter Data

Congjian Liu*, Jingjing Yin, Chun Hai (Isaac) Fung and Lindsay Mulligan, Georgia Southern University

4:30 On the Landmark Survival Model for Dynamic Prediction of Event Occurrence using Longitudinal Data

Yayuan Zhu*, Liang Li and Xuelin Huang, University of Texas MD Anderson Cancer Center

4:45 Floor Discussion**105. CONTRIBUTED PAPERS:
BIOMARKERS****Sponsor** ENAR**Chair** Ning Leng, Genentech**3:45 Robust $\Delta\Delta$ ct Estimate**

Arun Kumar*, Livanova USA Inc; Daniel Lorand, Novartis Pharma AG

4:00 Association of Biomarkers with Progressive Disease States

Julia E. Crook (Kelsall)*, Mayo Clinic

4:15 A Latent Class Approach for Joint Modeling of a Time-to-Event Outcome and Multiple Longitudinal Biomarkers Subject to Limits of Detection

Menghan Li* and Lan Kong, The Pennsylvania State University

4:30 Nonparametric Conditional Density Estimation for Biomarkers based on Pooled Assessments

Xichen Mou*, Dewei Wang and Joshua M. Tebbs, University of South Carolina

4:45 A Bayesian Screening Approach for Hepatocellular Carcinoma using Multiple Longitudinal Biomarkers

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

5:00 Floor Discussion**106. CONTRIBUTED PAPERS:
BAYESIAN METHODS FOR GENETICS AND GENOMICS****Sponsor** ENAR**Chair** Ziyi Li, Emory University**3:45 Negative Binomial Bayesian Generalized Linear Model for Analyzing High-Dimensional OTU Count Data**

Amanda H. Pendegraft*, Nengjun Yi and Boyi Guo, University of Alabama at Birmingham

4:00 Knowledge-Guided Bayesian Variable Selection in Support Vector Machines for Structured High-Dimensional Data

Wenli Sun*, Changgee Chang and Qi Long, University of Pennsylvania

4:15 The Spike-and-Slab Lasso Cox Model for Survival Prediction and Associated Genes Detection

Xinyan Zhang*, Georgia Southern University; Zaixiang Tang and Yueping Shen, Soochow University; Nengjun Yi, University of Alabama at Birmingham

4:30 A Bayesian Framework for Rewiring the Topological Network of Intratumoral Cells

Lin Qiu*, Vernon M. Chinchilli and Rongling Wu, The Pennsylvania State University

4:45 Bayesian Indicator Variable Selection Model to Incorporate Multi-Layer Overlapping Group Structure in Multi-Omics Applications

Li Zhu*•, University of Pittsburgh; Zhiguang Huo, University of Florida; Tianzhou Ma and George Tseng, University of Pittsburgh

5:00 Floor Discussion**WEDNESDAY MARCH 28****8:30 am - 10:15 am**

107. UNCOVERING HETEROGENEITY IN LONGITUDINAL DATA: CLUSTERING AND MIXTURE MODELING

Sponsors ASA Biometrics Section, ASA Mental Health Statistics Section

Organizer Laura Hatfield, Harvard Medical School

Chair Brian Hobbs, University of Texas MD An-derson Cancer Center

8:30 Tree-Based Clustering of Longitudinal Childhood Growth

Brianna Heggeseth*, Williams College

8:55 Clustering Discrete State Trajectories of Varying Lengths: Health Care Utilization Patterns

Laura A. Hatfield*, Harvard Medical School; Megan S. Schuler, RAND Corporation; Nina R. Joyce, Brown University; Elizabeth B. Lamont and Haiden A. Huskamp, Harvard Medical School

9:20 Clustering Longitudinal Data

Paul D. McNicholas*, McMaster University

9:45 Semi-Parametric Mixture Modeling of Longitudinal Data: Implications for Identifying Heterogeneous Treatment Effects

Amelia M. Haviland* and Hilary Wolfendale, Carnegie Mellon University

10:10 Floor Discussion

108. STATISTICAL METHODS FOR CANCER - OMIC DATA

Sponsors ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section

Organizer Wei Sun, Fred Hutchinson Cancer Research Center

Chair Yi-Juan Hu from Emory University

8:30 A Multi-View Spectral Clustering Method to Analyze Diverse 'Omics Data Sets

Hongyu Zhao* and Seyoung Park, Yale University; Hao Xu, Sichuan University

9:00 PRECISE - PeRsonalizEd Cancer-speClfic Integrated Network Estimation

Kim-Anh Do*, Min Jin Ha and Veera Baladandayuthapani, University of Texas MD Anderson Cancer Center

9:30 Using eQTLs to Discover Novel Genetic Loci for Complex Diseases

Li Hsu*, Wei Sun and Vicky Wu, Fred Hutchinson Cancer Research Center

10:00 Discussant:

Wei Sun, Fred Hutchinson Cancer Research Center

109. GEOMETRIC APPROACHES TO FUNCTIONAL DATA ANALYSIS FOR BIOMEDICAL APPLICATIONS

Sponsors ENAR, ASA Biometrics Section, ASA Section on Statistics in Imaging, IMS
Organizers Sebastian Kurtek, The Ohio State University and Karthik Bharath, University of Nottingham
Chair Sarah Janse, The Ohio State University

8:30 Statistical Summarization, Principal Modes and Shape Modeling for Simplified Neuronal Trees

Adam G. Duncan*, Eric Klassen and Anuj Srivastava, Florida State University

8:55 Modeling Multi-Way Functional Data Under Weak Separability, with Application to Brain Functional Connectivity

Kehui Chen* and Brian Lynch, University of Pittsburgh

9:20 Sampling Warping Functions for Curve Registration

Karthik Bharath*, University of Nottingham; Sebastian Kurtek, The Ohio State University

9:45 Radiologic Image-Based Statistical Shape Analysis of Brain Tumors

Sebastian Kurtek*, The Ohio State University; Karthik Bharath, University of Nottingham; Arvind U.K. Rao and Veera Baladandayuthapani, University of Texas MD Anderson Cancer Center

10:10 Floor Discussion

II. RANDOMIZATION INFERENCE: A BACK TO THE FUTURE PERSPECTIVE

Sponsors ENAR, IMS
Organizer Peng Ding, University of California, Berkeley
Chair Fan Li, Duke University

8:30 Randomization Inference with General Interference and Censoring

Michael G. Hudgens*, University of North Carolina, Chapel Hill; Wen Wei Loh, Ghent University

9:00 Beyond the Sharp Null: Randomization Inference, Bounded Null Hypotheses, and Confidence Intervals for Maximum Effects

Luke W. Miratrix*, Harvard University; Devin Caughey, Massachusetts Institute of Technology; Allan Dafoe, Yale University

9:30 Rerandomization and ANCOVA

Peng Ding*, University of California, Berkeley

10:00 Discussant:

Dylan Small, University of Pennsylvania

III. FRONTIERS IN HIGH-DIMENSIONAL DATA & BIG DATA ANALYSIS

Sponsors ENAR, IMS
Organizer Song Rui, North Carolina State University
Chair Wenbin Lu, North Carolina State University

8:30 Measurement Error—Not just a Nuisance

Len Stefanski*, North Carolina State University

8:55 Hypothesis Testing on Linear Structures of High Dimensional Covariance Matrix

Runze Li*, The Pennsylvania State University; Shurong Zheng, Northeast Normal University; Zhao Chen, The Pennsylvania State University; Hengjian Cui, Capital Normal University

9:20 Large-Scale Inference with Graphical Nonlinear Knockoffs

Yingying Fan* and Emre Demirkaya, University of Southern California; Gaorong Li, Beijing University of Technology; Jinchi Lv, University of Southern California

9:45 Network Membership Estimation by Mixed-SCORE

Jiashun Jin*, Carnegie Mellon University; Tracy Ke, University of Chicago; Shengming Luo, Carnegie Mellon University

10:10 Floor Discussion

II.2. CONTRIBUTED PAPERS: FUNCTIONAL CONNECTIVITY AND NETWORKS

Sponsor ENAR

Chair Simon Vandekar, University of Pennsylvania

8:30 Latent Source Separation for Multi-Subject Brain Networks

Ben Wu*, Emory University; Jian Kang, University of Michigan; Ying Guo, Emory University

8:45 A Spatial-Temporal Model for Detecting the Effect of Cocaine Dependence on Brain Connectivity

Jifang Zhao*, Montserrat Fuentes, Liangsuo Ma, Frederick Gerard Moeller and Qiong Zhang, Virginia Commonwealth University

9:00 Evidence-Based Inference on Resting State Functional Connectivity

Allison E. Hainline* and Hakmook Kang, Vanderbilt University

9:15 Latent Classes of Resting-State Functional Connectivity and Their Association with Clinical Features

Xin Ma*, Ying Guo, Limin Peng and Amita Manatunga, Emory University

9:30 Spectral Domain Copula-Based Dependence Models with Application to Brain Signals

Charles Fontaine* and Hernando Ombao, King Abdullah University of Science and Technology

9:45 Modeling Dynamic Brain Connectivity

Marco Antonio Pinto Orellana* and Ting Chee-Ming, King Abdullah University of Science and Technology; Jeremy Skipper, University College London; Steven Small, University of California, Irvine; Hernando Ombao, King Abdullah University of Science and Technology

10:00 A Novel Hierarchical Independent Component Modeling Framework with Application to Longitudinal fMRI Study

Yikai Wang*• and Ying Guo, Emory University

II3. CONTRIBUTED PAPERS: INDIVIDUALIZED TREATMENT RULES

Sponsor ENAR

Chair Shu Yang, North Carolina State University

8:30 Hypothesis Testing's on Individualized Treatment Rules from High-Dimensional Observational Studies

Young-Geun Choi*, Fred Hutchinson Cancer Research Center; Yang Ning, Cornell University; Yingqi Zhao, Fred Hutchinson Cancer Research Center

8:45 Matched Learning (M-Learning) for Estimating Optimal Individualized Treatment Rules with an Application to Electronic Health Records

Peng Wu*•, Columbia University; Donglin Zeng, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University

9:00 Sequential Outcome-Weighted Multicategory Learning for Estimating Optimal Individualized Treatment Rules

Xuan Zhou*, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University; Donglin Zeng, University of North Carolina, Chapel Hill

9:15 Semiparametric Single-Index Models for Optimal Treatment Regimes with Potentially Censored Outcomes

Jin Wang*, Donglin Zeng and Danyu Lin, University of North Carolina, Chapel Hill

9:30 Lasso for Modeling Treatment Covariate Interactions

Yu Du*, Johns Hopkins University; Ravi Varadhan, Johns Hopkins School of Medicine

9:45 Floor Discussion

II4. CONTRIBUTED PAPERS: METABOLOMICS AND PROTEOMICS

Sponsor ENAR

Chair Tian Ge, Harvard Medical School

8:30 Bayesian Latent Class Models for Identifying Circadian Patterns in High-Dimensional Longitudinal Metabolomics Data

Sung Duk Kim* and Paul S. Albert, National Cancer Institute, National Institutes of Health

8:45 Bayesian Nonparametric Matching of Cell Lines to Tumor Samples

Chiyu Gu* and Subharup Guha, University of Missouri; Veerabhadran Baladandayuthapani, University of Texas MD Anderson Cancer Center

9:00 Missing Data Imputation for Mass Spectrometry Metabolomics Data using a 2-Step LASSO Approach

Qian Li*, University of South Florida; Brooke L. Fridley, Moffitt Cancer Center; Chengpeng Bi, Roger Gaedigk and Steven Leeder, Children's Mercy Hospital

9:15 A Two-Part Semi-Parametric Model for Zero-Inflated Metabolomics and Proteomics Data

Yuntong Li*, University of Kentucky

9:30 Floor Discussion**II5. CONTRIBUTED PAPERS:
BAYESIAN HIGH DIMENSIONAL DATA AND VARIABLE SELECTION****Sponsor** ENAR**Chair** Yu Yue, Baruch College, The City University of New York**8:30 High Dimensional Posterior Consistency in Bayesian Vector Autoregressive Models**

Satyajit Ghosh*, Kshitij Khare and George Michailidis, University of Florida

8:45 MORETreeS: A Flexible Method for Multi-Outcome Regression with Tree-Structured Shrinkage

Emma G. Thomas*, Giovanni Parmigiani, Francesca Dominici and Lorenzo Trippa, Harvard University

9:00 High-Dimensional Posterior Consistency for Hierarchical Non-Local Priors in Regression

Xuan Cao*, Malay Ghosh and Kshitij Khare, University of Florida

9:15 From Mixed-Effects Modeling to Spike and Slab Variable Selection: A Bayesian Regression Model for Group Testing Data

Chase Joyner* and Christopher McMahan, Clemson University; Joshua Tebbs, University of South Carolina; Christopher Bilder, University of Nebraska-Lincoln

9:30 Robust Bayesian Variable Selection for Modeling Mean Medical Costs

Grace Yoon*, Texas A&M University; Wenxin Jiang, Northwestern University; Lei Liu, Washington University in St. Louis; Ya-Chen Tina Shih, University of Texas MD Anderson Cancer Center

9:45 Bayesian Variable Selection for Multi-Outcome Models Through Shared Shrinkage

Debamita Kundu*, Jeremy Gaskins and Ritendranath Mitra, University of Louisville

10:00 Floor Discussion

II6. CONTRIBUTED PAPERS: METHODS FOR SURVIVAL ANALYSIS

Sponsor ENAR

Chair Leah Suttner, University of Pennsylvania

8:30 Empirical Comparison of the Breslow Estimator and the Kalbfleisch-Prentice Estimator for Survival Functions

Fang Xia*, Xuelin Huang and Jing Ning, University of Texas MD Anderson Cancer Center; Jack D. Kalbfleisch, University of Michigan

8:45 Time-Varying Proportional Odds Model for Mega-Analysis of Clustered Event Times

Tanya Garcia*, Texas A&M University; Karen Marder and Yuanjia Wang, Columbia University

9:00 Cox Regression for Right-Truncated Data

Bella Vakulenko-Lagun*, Harvard University; Micha Mandel, Hebrew University of Jerusalem; Rebecca A. Betensky, Harvard University

9:15 Modeling Negatively Skewed Survival Data in AFT and Correlated Frailty Models using the RSTG Distribution

Sophia D. Waymyers*, Francis Marion University; Hrishikesh Chakraborty, Duke Clinical Research Institute

9:30 Integrative Survival Analysis with Uncertain Event Records with Application in a Suicide Risk Study

Wenjie Wang*, University of Connecticut; Robert Aseltine, UConn Health; Kun Chen and Jun Yan, University of Connecticut

9:45 New Modeling of Recurrent Events Data Subject to Terminal Events

Bo Wei* and Limin Peng, Emory University; Zhumin Zhang and Huichuan Lai, University of Wisconsin, Madison

10:00 OptBand: Optimal Confidence Bands for Functions to Characterize Time-to-Event Distributions

Sam Tracy* and Tom Chen, Harvard School of Public Health; Hajime Uno, Harvard Medical School

II7. CONTRIBUTED PAPERS: VARIABLE SUBSET AND MODEL SELECTION

Sponsor ENAR

Chair Natasha Sahr, Medical College of Wisconsin

8:30 Weak Signals in High-Dimension Regression: Detection, Estimation and Prediction

Yanming Li*, University of Michigan; Hyokyoung Grace Hong, Michigan State University; S. Ejaz Ahmed, Brock University, Canada; Yi Li, University of Michigan

8:45 Variable Selection and Prediction in Two-Part Regression Modeling for Semicontinuous Data

Seongtae Kim*, North Carolina A&T State University

9:00 Gaussian Process Selections in Semiparametric Regression for Multi-Pathway Analysis

Jiali Lin* and Inyoung Kim, Virginia Tech

9:15 Variable Screening for High Dimensional Time Series

Kashif Yousuf*, Columbia University

9:30 Examining the Vanishing Tetrad Number as an Index of the Complexity of SEM Models

Hangcheng Liu* and Robert A. Perera, Virginia Commonwealth University

9:45 Floor Discussion

II.8. CONTRIBUTED PAPERS: METHODS FOR SINGLE-CELL ANALYSIS

Sponsor ENAR

Chair Anqi Zhu, University of North Carolina, Chapel Hill

8:30 ZINB-WaVE: A General and Flexible Method for the Supervised and Unsupervised Analysis of Single-Cell RNA-Seq

Davide Risso*, Weill Cornell Medicine; Fanny Perraudeau, University of California, Berkeley; Svetlana Gribkova, Université Paris Diderot; Sandrine Dudoit, University of California, Berkeley; Jean-Philippe Vert, MINES ParisTech

8:45 Identifying Differential Alternative Splicing Events using Single-Cell RNA Sequencing Data

Yu Hu*, University of Pennsylvania Perelman School of Medicine; Nancy Zhang, University of Pennsylvania; Mingyao Li, University of Pennsylvania Perelman School of Medicine

9:00 A Bayesian Hierarchical Model for Clustering Droplet-Based Single Cell Transcriptomic Data from Multiple Individuals

Zhe Sun*, Li Zhu and Ying Ding, University of Pittsburgh; Wei Chen, Children's Hospital of Pittsburgh of UPMC, University of Pittsburgh; Ming Hu, Cleveland Clinic Foundation

9:15 Interrogation of Human Hematopoietic Traits at Single-Cell and Single-Variant Resolution

Caleb A. Lareau*, Harvard University

9:30 Penalized Latent Dirichlet Allocation Model in Single Cell RNA Sequencing

Xiaotian Wu*• and Zhijin Wu, Brown University; Hao Wu, Emory University

9:45 Gene Co-Expression Network Estimation from Single-Cell RNA-Sequencing Data

Jihwan Oh*, Changgee Chang, Mingyao Li and Qi Long, University of Pennsylvania

10:00 Floor Discussion**WEDNESDAY MARCH 28****10:15 am - 10:30 am REFRESHMENT BREAK WITH OUR EXHIBITORS****WEDNESDAY MARCH 28****10:30 am - 12:15 pm****II9. MODERN HIERARCHICAL APPROACHES TO STATISTICAL MODELING****Sponsors** ENAR, IMS**Organizer** Liang Feng, University of Illinois at Urbana-Champaign**Chair** Tingting Zhang, University of Virginia**10:30 Nonparametric SURE Estimates for Compound Decision Problems**

Dave Zhao*, University of Illinois at Urbana-Champaign

10:55 Smoothness and Sparsity Adaptive Bayesian Tree Ensemble Method for High-Dimensional Nonparametric Regression

Yun Yang* and Antonio Linero, Florida State University

11:20 Spatial Analysis using Sparse Cholesky Factors

Abhirup Datta*, Johns Hopkins University; Sudipto Banerjee, University of California, Los Angeles; James S. Hodges, University of Minnesota

11:45 Bayesian Modeling of Infant's Growth Dynamics with Prenatal Exposure to Environmental Toxicants

Peter X.K. Song* and Jonggyu Baek, University of Michigan; Bin Zhu, National Cancer Institute, National Institutes of Health

12:10 Floor Discussion

I20. ADVANCES AND INNOVATIVE APPLICATIONS OF JOINT MODELING TO PUBLIC HEALTH RESEARCH

Sponsors ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology
Organizer Rajeshwari Sundaram, Eunice Kenne-dy Shriver National Institute of Child Health and Human Development, National Institutes of Health
Chair Ling Ma, Clemson University

10:30 **Statistical Challenges in Obstetrics: Predicting Poor Pregnancy Outcomes from Multivariate Longitudinal Fetal Growth Data**

Paul S. Albert*, National Cancer Institute, National Institutes of Health

10:55 **Joint Analysis of Multiple Longitudinal and Survival Data Measured on Nested Time-Scales: An Application to Predicting Infertility**

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

11:20 **Personalized Biopsy Schedule for Prostate Cancer Patients using Joint Models**

Dimitris Rizopoulos*, Anirudh Tomer, Ewout Steyerberg and Monique Roobol, Erasmus MC

11:45 **Dealing with Covariates Measured at Dependent Follow-Up Visits in the Estimation of Cox Models**

Yifei Sun*, Columbia University; Chung-Yu Huang, University of California, San Francisco

12:10 **Floor Discussion**

I21. STATISTICS AND INFORMATICS: STRONGER TOGETHER

Sponsors ENAR, ASA Biometrics Section, ASA Statistical Learning and Data Mining Section
Organizer Erinn Hade, The Ohio State University
Chair David Kline, The Ohio State University

10:30 **Fostering Collaboration between Biostatistics, Bioinformatics, and Biomedical Informatics**

Lance A. Waller*, Emory University

10:55 **Life on the Edge: Interfacing Biostatistics and Bioinformatics**

Kevin R. Coombes*, The Ohio State University

11:20 **Using Data to Defeat Antibiotic Resistance**

Erinn M. Hade*, Yuan Gao, Protiva Rahman, Courtney Dewart, Mark Lustberg, Kurt Stevenson, Emily Patterson, Awa Mbodj, Arnab Nandi and Courtney Hebert, The Ohio State University

11:45 **Moving a Paralyzed Hand: A Biomedical Big Data Success Story**

Nicholas D. Skomrock*, Michael A. Schwemmer and David A. Friedenber, Battelle Memorial Institute

12:10 **Floor Discussion**

122. RECENT DEVELOPMENTS IN STATISTICAL ANALYSIS OF BRAIN DATA**Sponsors** ENAR, IMS**Organizer** Tingting Zhang, University of Virginia**Chair** Feng Liang, University of Illinois at Urbana Champaign**10:30 Statistical Modeling of Brain Connectivity using Multimodal Neuroimaging**

Ying Guo* and Yingtian Hu, Emory University

10:55 Calcium Imaging: State-of-the-Art and Future Challenges

Jordan Rodu*, University of Virginia

11:20 Human Seizures Couple Across Spatial Scales through Traveling Wave Dynamics

Mark Kramer*, Boston University; Louis-Emmanuel Martinet and Emad Eskandar, Massachusetts General Hospital; Wilson Truccolo, Brown University; Uri Eden, Boston University; Sydney Cash, Massachusetts General Hospital

11:45 A Low-Rank Multivariate General Linear Model for Multi-Subject fMRI Data and a Non-Convex Optimization Algorithm for Brain Response Comparison

Tingting Zhang*, Minh Pham, Marlen Z. Gonzalez and James A. Coan, University of Virginia

12:10 Floor Discussion**123. STATISTICAL MODELING TO ADDRESS HUMAN RIGHTS ISSUES****Sponsors** ENAR, IMS**Organizer** Kristian Lum, Human Rights Data Analysis Group**Chair** Mehmet Kocak, University of Tennessee Health Science Center**10:30 Estimating the Number of Fatal Victims of the Peruvian Internal Armed Conflict, 1980-2000: New Analyses and Results**

Daniel Manrique-Vallier*, Indiana University; Patrick Ball, Human Rights Data Analysis Group; David Sulmont, Pontificia Universidad Catolica del Peru

10:55 Statistics and Justice: Issues in Forensic Feature Comparisons

Robin Mejia*, Carnegie Mellon University

11:20 Accounting for Record Linkage Uncertainty in Population Size Estimation

Mauricio Sadinle*, University of Washington

11:45 The Causal Impact of Bail on Case Outcomes for Indigent Defendants

Kristian Lum*, Human Rights Data Analysis Group

12:10 Floor Discussion

124. CONTRIBUTED PAPERS: LATENT VARIABLES

Sponsor ENAR

Chair Brisa N. Sánchez, University of Michigan

10:30 Mixed Membership Regression Models for Estimating Autoimmune Disease Patient Subsets

Zhenke Wu*, University of Michigan; Livia Casciola-Rosen and Antony Rosen, Johns Hopkins University School of Medicine; Scott L. Zeger, Johns Hopkins University

10:45 Constructing Targeted Latent Variables using Longitudinal Data to Develop a More Sensitive Clinical Endpoint for Progressive Multiple Sclerosis

Christopher R. Barbour* and Mark Greenwood, Montana State University; Bibiana Bielekova and Peter Kosa, National Institute of Neurological Disorders and Stroke, National Institutes of Health

11:00 Acknowledging the Dilution Effect in Group Testing Regression: A New Approach

Stefani Mokalled* and Christopher McMahan, Clemson University; Joshua Tebbs, University of South Carolina; Christopher Bilder, University of Nebraska-Lincoln

11:15 Predicting Disease Risk by Transformation Models in the Presence of Unspecified Subgroup Membership

Qianqian Wang*, University of South Carolina; Yanyuan Ma, The Pennsylvania State University; Yuanjia Wang, Columbia University

11:30 Modeling Rater Diagnostic Skills in Binary Classification Processes

Don Edwards* and Xiaoyan Lin, University of South Carolina; Hua Chen, Oklahoma Medical Foundation; Kerrie Nelson, Boston University

11:45 A Gamma-Frailty Proportional Hazards Model for Bivariate Interval-Censored Data

Prabhashi W. Withana Gamage* and Christopher S. McMahan, Clemson University; Lianming Wang, University of South Carolina; Wanzhu Tu, Indiana University School of Medicine

12:00 Floor Discussion

125. CONTRIBUTED PAPERS: CAUSAL INFERENCE IN SURVIVAL ANALYSIS

Sponsor ENAR

Chair Michael G. Hudgens, University of North Carolina, Chapel Hill

10:30 Targeted Minimum Loss-Based Estimation with Interval-Censored Time-to-Event Outcomes

Oleg Sofrygin*, University of California, Berkeley and Kaiser Permanente; Mark J. van der Laan, University of California, Berkeley; Romain Neugebauer, Kaiser Permanente

10:45 Instrumental Variable Analysis with Censored Data in the Presence of Many Weak Instruments

Ashkan Ertefaie*, University of Rochester; Anh Nguyen, University of Michigan; David Harding, University of California, Berkeley; Jeffrey Morenoff, University of Michigan; Wei Yang, University of Pennsylvania

11:00 Instrumental Variable Structural Nested Cumulative Failure Time Models for Comparing the Risk of Fracture with Antiepileptic Drugs

Alisa J. Stephens-Shields*, University of Pennsylvania; Xu Han, Temple University; Marshall Joffe, Dylan Small and Wei Yang, University of Pennsylvania

11:15 Weighted Estimators of the Complier Average Causal Effect on Restricted Mean Survival Time with Observed Instrument-Outcome Confounders

Sai Hurrish Dharmarajan* and Douglas E. Schaebel, University of Michigan

11:30 Weighted Log-Rank Tests Adjusted for Non-Random Treatment Allocation and Dependent Censoring

Chenxi Li*, Michigan State University

11:45 Matching Methods for Evaluating the Effect of a Time-Dependent Treatment on the Survival Function

Danting Zhu* and Douglas Schaebel, University of Michigan

12:00 Floor Discussion**I26. CONTRIBUTED PAPERS:
ELECTRONIC HEALTH RECORDS**

Sponsor ENAR

Chair Jihui Lee, Columbia University

10:30 Scalable Bayesian Nonparametric Clustering and Classification

Yang Ni* and Peter Mueller, University of Texas, Austin; Yuan Ji, University of Chicago

10:45 Outcome Identification in Electronic Health Records using Predictions from an Enriched Dirichlet Process Mixture

Bret Zeldow*, Alisa Stephens-Shields and Jason A. Roy, University of Pennsylvania

11:00 Challenges in Jointly Modelling Irregular Visit Process and Outcome Process in Observational Studies: Review and Extension

Janie Coulombe*, Robert Platt and Erica E.M. Moodie, McGill University

11:15 Risk Prediction in Current Status Data using Partial and Imperfect Information from Electronic Medical Records

Stephanie Fulane Chan*, Xuan Wang and Tianxi Cai, Harvard University

11:30 Accounting for Dependent Errors in Predictors and Time-to-Event Outcomes using Validation Samples and Electronic Health Records

Mark J. Giganti*, Vanderbilt University; Pamela A. Shaw, University of Pennsylvania; Guanhua Chen, University of Wisconsin, Madison; Sally S. Bebawy, Megan M. Turner and Timothy R. Sterling, Vanderbilt University School of Medicine; Bryan E. Shepherd, Vanderbilt University

11:45 Floor Discussion**127. CONTRIBUTED PAPERS:
METHODS FOR RNA-SEQ DATA**

Sponsor ENAR

Chair Rhonda Bacher, University of Wisconsin, Madison

10:30 A Method for Mitigating the Adverse Impact of Batch Effects in Sample Pattern Detection

Teng Fei*, Emory University; Tengjiao Zhang and Weiyang Shi, Tongji University; Tianwei Yu, Emory University

10:45 Cell Type-Aware Differential Expression Analysis for RNA-Seq Data

Chong Jin*, University of North Carolina, Chapel Hill; Wei Sun, Fred Hutchinson Cancer Research Center; Mengjie Chen, University of Chicago; Danyu Lin, University of North Carolina, Chapel Hill

11:00 PennSeq2: Efficient Quantification of Isoform-Specific Gene Expression from RNA-Seq Data using Weighted Likelihood Method

Jian Hu*, Mingyao Li and Yu Hu, University of Pennsylvania Perelman School of Medicine

11:15 Gene Selection and Identifiability Analysis of RNA Deconvolution Model using Profile Likelihood

Shaolong Cao*, Zeya Wang and Wenyi Wang, University of Texas MD Anderson Cancer Center

11:30 Application of t priors to Sequence Count Data: Removing the Noise and Preserving Large Differences

Anqi Zhu*, Michael I. Love and Joseph G. Ibrahim, University of North Carolina, Chapel Hill

11:45 GLMM-seq: Gene-Based Detection of Allele-Specific Expression by RNA-seq

Jiaxin Fan*, Rui Xiao, Mingyao Li and Jian Hu, University of Pennsylvania Perelman School of Medicine

12:00 Floor Discussion

128. CONTRIBUTED PAPERS: MULTIPLE TESTING

Sponsor ENAR

Chair Abhisek Saha, UT MD Anderson Cancer Center

10:30 Statistical Considerations of MCP-Mod in Applying to Multi-Regional Dose-Response Studies Including Japanese Population

Toshifumi Sugitani* and Yusuke Yamaguchi, Astellas Pharma Inc.

10:45 Choice of Multiple Comparison Procedures for Study with Multiple Objectives

Bin Dong*, Janssen Research & Development

11:00 Quasi-Bayesian Multiple Confidence Interval Procedure Maintaining FWCR

TaeHo Kim* and Edsel A. Pena, University of South Carolina

11:15 A Unified Framework for Weighted Parametric Multiple Test Procedures

Dong Xi*, Ekkehard Glimm, Willi Maurer and Frank Bretz, Novartis

11:30 An Efficient FWER Controlling Procedure for Data with Reduced Rank Structure

Xing Qiu* and Jiatong Sui, University of Rochester

11:45 Bias Correction for Nonparametric Tests

Duchwan Ryu*, Northern Illinois University; Yoonsung Jung, Prairie View A&M University; Seong Keon Lee, Sungshin University

12:00 Floor Discussion

129. CONTRIBUTED PAPERS: CANCER GENOMICS

Sponsor ENAR

Chair Paul Little, Lineberger Comprehensive Cancer Center

10:30 Unsupervised Clustering and Variable Selection for RNA-seq Data

David K.T. Lim*, Naim Rashid and Joseph Ibrahim, University of North Carolina, Chapel Hill

10:45 Structured Variable Selection of Gene-Environment Interactions in Cancer Prognosis

Guotao Chu*, Yin hao Du, Jie Ren and Cen Wu, Kansas State University

11:00 Modeling Between-Study Heterogeneity for Reproducible Gene Signature Selection and Clinical Prediction

Naim Rashid*, Quefeng Li and Joseph G. Ibrahim, University of North Carolina, Chapel Hill

11:15 Impact of Non-Hierarchical Model Structure and Inheritance Mode on Detecting SNP-SNP Interactions

Hui-Yi Lin*, Louisiana State University Health Sciences Center; Po-Yu Huang, Industrial Technology Research Institute, Taiwan; Jong Park, Moffitt Cancer Center & Research Institute

11:30 Monte Carlo Expectation Maximization Algorithm for the Heterogeneous Deconvolution of Mixed Tumor Ex-pression

Rongjie Liu*, Rice University; Hongtu Zhu and Wenyi Wang, University of Texas MD Anderson Cancer Center

11:45 Semiparametric Analysis of Complex Polygenic Gene-Environment Interactions in Case-Control Studies

Alexander Asher*, Texas A&M University; Odile Stalder, University of Bern; Liang Liang, Harvard University; Raymond J. Carroll, Texas A&M University; Yanyuan Ma, The Pennsylvania State University; Nilanjan Chatterjee, Johns Hopkins University

12:00 Floor Discussion

	RECEIVED BY FEB 1 ST			RECEIVED AFTER FEB 1 ST		
	HALF DAY	2 ND HALF DAY	FULL DAY	HALF DAY	2 ND HALF DAY	FULL DAY
MEMBER	\$225	\$190	\$325	\$250	\$215	\$350
NONMEMBER	\$275	\$240	\$375	\$300	\$265	\$400

SUNDAY, MARCH 25, 2018

SCI. Bayesian Adaptive Clinical Trials

Full Day | 8:00 am – 5:00 pm

Scott Berry, Berry Consultants

Description: This course focuses on the innovative uses of Bayesian adaptive clinical trials. The application of Bayesian statistics to flexible adaptive trials is becoming a powerful innovation within the clinical trials industry. This is evidenced by the currently proposed FDA work in PDUFA VI:

“To facilitate the advancement and use of complex adaptive, Bayesian, and other novel clinical trial designs, FDA will conduct the following activities during PDUFA VI: a. FDA will develop the staff capacity to enable processes to facilitate appropriate use of these types of methods. This staff will support the computationally intensive review work necessary to evaluate complex adaptive, Bayesian, and other novel clinical trial designs, with a particular focus on clinical trial designs for which simulations are necessary to evaluate the operating characteristics.”

This demonstrates the increased desire and demand for FDA to be able to evaluate Bayesian Adaptive clinical trials. The course will focus on the specific strengths of the Bayesian approach and present numerous examples of trials in phase I, II, and III in the clinical trials space. Examples from a wide variety of therapeutic areas such as cardiovascular, neurology, pain, oncology, and rare disease will be discussed. The course will present examples from drugs and devices.

The course will discuss the Bayesian approach with the strengths and weaknesses it brings embedded in trial design, the software needs for using the Bayesian approach and for building adaptive trials, and the receptivity of these approaches to multiple stakeholders.

SC2. Machine Learning for Biomarker Discovery

Full Day | 8:00 am – 5:00 pm

Noah Simon, University of Washington

Description: We will present a number of supervised learning methods that can be applied to Biomedical Big Data: In particular we will cover penalized approaches to regression and classification; as well as support vector machines, and tree-based methods.

We will consider the analysis of "high-dimensional" data sets from genomics, transcriptomics, metabolomics, proteomics, and other fields. These data are typically characterized by a huge number of molecular measurements (such as genes) and a relatively small number of samples (such as patients). In addition, we will discuss the use of these tools in the development of prognostic and predictive biomarkers. Throughout the course, we will focus on common pitfalls in the supervised analysis of Biomedical Big Data and how to avoid them.

This course assumes some previous exposure to linear regression and statistical hypothesis testing.

SC3. An Introduction to the Joint Modeling of Longitudinal & Survival Data, with Applications in R

Full Day | 8:00 am – 5:00 pm

Dmitri Rizopoulos, Erasmus University Medical Center

Description: In follow-up studies different types of outcomes are typically collected for each subject. These include longitudinally measured responses (e.g., biomarkers), and the time until an event of interest occurs (e.g., death, dropout). Often these outcomes are separately analyzed, but in many occasions it is of scientific interest to study their association. This type of research question has given rise in the class of joint models for longitudinal and time-to-event data. These models constitute an attractive paradigm for the analysis of follow-up data that is mainly applicable in two settings: First, when focus is on a survival outcome and we wish to account for the effect of endogenous time-dependent covariates measured with error, and second, when focus is on the longitudinal outcome and we wish to correct for non-random dropout.

This full-day course is aimed at applied researchers and graduate students, and will provide a comprehensive introduction into this modeling framework. We will explain when these models should be used in practice, which are the key assumptions behind them, and how they can be utilized to extract relevant information from the data. Emphasis is given on applications, and after the end of the course participants will be able to define appropriate joint models to answer their questions of interest.

This course assumes knowledge of basic statistical concepts, such as standard statistical inference using maximum likelihood, and regression models. In addition, basic knowledge of R would be beneficial but is not required. Participants are required to bring their own laptop with the battery fully charged. Before the course instructions will be sent for installing the required software.

The primary target audience includes statisticians working in applied environments where hierarchical modelling

and survival analysis are key issues; this would include biostatisticians working in the pharmaceutical industry, regulatory agencies, or academic centers.

SC4. Neuroimaging Analysis within R

Half Day | 8:00 am – 12:00 pm

John Muschelli, Johns Hopkins Bloomberg School of Public Health

Kristin Linn, University of Pennsylvania

Description: In the neuroimaging community, there is a diverse and large set of software tools currently being used by analysts and researchers. There have been great strides in standardizing the syntax for multiple pieces of software such as nypipe in Python, yet many of these languages do not have the statistical sophistication demanded to solve cutting-edge neuroimaging problems. R is a programming language that has the state of the art statistical tools that are relevant to imaging analysis. Already, a number of neuroimaging researchers use R as their primary language, and we believe this community will grow rapidly in the future.

With the rapid and increasing number of open-access neuroimaging datasets, such as the Alzheimer's Disease Neuroimaging Initiative (ADNI) and the Human Connectome Project (HCP), there is a void for an analysis framework that (1) is reproducible and can deal with high-dimensional data structures, (2) is open-access and accessible to a large community, and (3) provides the best environment to perform fast and advanced statistical methods needed for such complex data. The R programming language satisfies 1, 2, and 3. In this tutorial, we will provide tutorials on how to use R for structural magnetic resonance imaging (MRI) analysis. We will show how to perform entire image analysis in R, from the scans in raw image format to the statistical analysis after image pre-processing, with an emphasis on reproducibility by using a single programming language. This course will use a real multiple sclerosis dataset and will show the steps of going from the raw image files to performing multiple sclerosis lesion classification with a number of classifiers

entirely in R. In this hands-on tutorial, attendees will be given instructions for setup and data before the course, so that they are able to follow along and perform the analysis during the tutorial.

The topics to be cover in the course are as follows:

- (a) Introduction to the Statistical Software R (JM)
- (b) Read and Write Images (JM)
- (c) Visualization (JM and JPF)
- (d) Inhomogeneity Correction (JPF)
- (e) Brain Extraction (JM)
- (f) Image Segmentation (JPF)
- (g) Coregistration Within and Between MRI Studies (JM)
- (h) Intensity Normalization (JPF)
- (i) Harmonization of multi-site datasets (JPF)

Only within recent years has it become possible to perform entire image analysis completely and reproducibly in R. New R packages such as ANTsR (<http://stnava.github.io/ANTsR/>) and fsR (<https://cran.r-project.org/web/packages/fsR/index.html>) have made this possible. R is a powerful and open source statistical software that many members of ENAR already use for post-processing statistical analysis; yet members may be unaware of the new and powerful potential of R for image preprocessing, allowing for the creation of a streamline reproducible pipeline for entire image analysis. This tutorial is designed to educate and instruct in a step-by-step manner how to perform an entire image analysis in R, and should be a useful exercise for researchers interested in any type of imaging data, not just MRI. In addition, if time permits, we will show how we can use several statistical methods from existing R packages to attack the crucial problem of harmonizing datasets coming from different imaging sites.

SC5. Causal Inference Using Structural Nested Mean Models

Half Day | 8:00 am – 12:00 pm

Judith Lok, Harvard T.H. Chan School of Public Health

Description: Structural nested models allow investigators to estimate the causal effect of a time-varying treatment in the presence of confounding mechanisms. When a time-varying treatment is repeatedly adapted to evolving prognostic factors and the value of the prognostic factors is affected by prior treatment, the effect of the treatment cannot simply be estimated by conditioning on the patient characteristics. This treatment-confounder feedback is common in observational studies. The course will describe g-estimation of Structural Nested Mean Models (SNMMs) using single-robust and doubly robust estimators. I will present methods for estimating and testing the parameters of SNMMs. I will also cover coarse Structural Nested Mean Models, and illustrate these methods with an application to the effect of antiretroviral treatment in HIV-positive patients.

SC6. Reproducible Research with R & RStudio

Half Day | 1:00 pm – 5:00 pm

Keith A. Baggerly, The University of Texas M.D. Anderson Cancer Center

Description: In recent years, it has become apparent that sizeable numbers of papers in the biomedical literature are neither replicable (we can't get similar results with new samples) nor reproducible (we can't even get the reported results starting from the same data). Some problematic cases have even affected patient care.

In partial response to the situation, the National Institutes of Health (NIH) rolled out a "Rigor and Reproducibility Initiative" in 2016, placing more emphasis on how these issues are addressed in studies they fund. Journals are similarly beginning to ask for more documentation.

But, just as the pressure to work more reproducibly is increasing, tools which make it easier to do so are being introduced, lowering barriers to entry.

In this short course, we will:

- discuss some examples motivating the shift to RR
- survey the simple nature of the most common problems
- discuss organizing data as projects
- use RStudio, knitr, and R Markdown to illustrate
- the use of literate programming to interleave
- text describing the analyses with the code
- producing the results
- use RStudio, devtools, and roxygen2 to construct
- a basic R package
- survey other commonly used tools and give pointers
- how they might be used and where to learn more

This course presumes some working knowledge of R. Attendees are requested to bring laptops with recent versions of R and RStudio installed, as well as the R packages knitr, R Markdown, devtools, roxygen2, and RTools (this last is for Windows PCs; it's required to compile R packages).

Suggested references include:

- Reproducible Research with R and RStudio (2e) by Christopher Gandrud
- R Packages by Hadley Wickham

SC7. Survival for Precision Medicine

Half Day | 1:00 pm – 5:00 pm

Lu Tian, Stanford University School of Medicine

Haoda Fu, Eli Lilly

Description: The idea of precision medicine is to use patient's specific characteristics, such as genetic make-up, biomarker profile, clinical history, environmental exposure, etc., to guide clinical decision making for effective prevention and treatment. Recent advances in

high-throughput and information technologies can easily and robustly generate a large amount data to characterize individual patients, offering extraordinary opportunities to develop and promote precision medicine in daily clinical practice. The development of such a smart and targeted strategy needs to be empirically data-driven and the corresponding challenges in the statistical front are huge, mainly because analyzing heterogeneous treatment effect/associations, i.e., interaction, is much more difficult than analyzing the homogeneous counterparts, i.e., main effect.

The goal of this course to introduce recently developed statistical and machine learning techniques for precision medicine. Most of the course will focus on how to optimally assign treatment to patients according to his or her personal characteristics in the context of two-arm randomized clinical trial. However, we will also discuss extensions to multi-arm trials and observational studies. Specifically, we will cover the following topics: the casual inference framework for personalized treatment effect based on counterfactual outcomes; estimation of optimal treatment selection rule including subgroup analysis, tree-based method, regression modeling, modified covariates approach, Q-learning and outcome weighted learning; and validation and statistical inference of the optimal treatment selection strategy. We will also discuss the computational perspective of the aforementioned methods including dimension reduction via regularization and applications of machine learning methods. We will provide examples for how to construct and evaluate estimated optimal treatment regimes in R.

There is no requirement for prior exposure to precision medicine or machine learning methods, but graduate-level statistical knowledge of basic methods such as regression, interactions, and analysis of randomized clinical trials is expected.

	RECEIVED BY FEB 1 ST	RECEIVED AFTER FEB 1 ST
MEMBER	\$75	\$85
NONMEMBER	\$85	\$95
STUDENT	\$40	\$50

MONDAY, MARCH 26, 2018 – TUESDAY, MARCH 27, 2018

TI. Micro-randomized Trials for Constructing Mobile Health Interventions

Monday, March 26 | 10:30 am – 12:15 pm

Susan Murphy, Harvard University

Description: Mobile devices along with wearable sensors make possible the ability to deliver treatments anytime and anywhere. These mobile interventions are being employed across a variety of health fields, including to support HIV medication adherence, encourage physical activity and healthier eating as well as to support recovery in addictions. The treatments in the mobile intervention are often time-varying and might be delivered many times across 100s or 1000s or more time points. In this tutorial we discuss a type of factorial trial design, namely the (stratified) micro-randomized trial, for use in constructing mobile interventions. We discuss primary hypotheses for these factorial designs and how to determine the sample size so as to test these hypotheses with a given power. We will also review secondary analyses that can be used to estimate and test interaction effects between time-varying context (e.g., location, current stress classification, time of day, mood and ambient noise) and time-varying treatments. These discussions will be made concrete by using three real-life micro-randomized trials (namely in physical activity, smoking cessation and encouraging adherence) to clarify ideas and analyses.

T2. Design & Analysis of Medical Studies Using Electronic Health Records Data

Monday, March 26 | 1:45 pm – 3:30 pm

Rebecca Hubbard, Perelman School of Medicine, University of Pennsylvania

Yong Chen, Perelman School of Medicine, University of Pennsylvania

Description: The widespread adoption of electronic health records (EHR) as a means of documenting medical care has created a vast resource for the study of health conditions, interventions, and outcomes in routine clinical practice. Using EHR data for research facilitates the efficient creation of large research databases, execution of pragmatic clinical trials, and study of rare diseases. Despite these advantages, there are many challenges for research conducted using EHR data. To make valid inference, statisticians must be aware of data generation, capture, and availability issues and utilize appropriate study designs and statistical analysis methods to account for these issues.

In this tutorial, we will discuss topics related to the design and analysis of research studies using EHR data. In the first part of the tutorial we will cover issues related to the structure and quality of EHR data, including data types and methods for extracting variables of interest; sources of missing data; error in covariates and outcomes extracted from EHR data; and data capture considerations such as informative visit processes and medical records coding procedures. In the second half of the tutorial, we will discuss statistical methods that mitigate some of these

issues, including missing data and error in EHR-derived covariates and outcomes. We will also discuss cutting-edge methods developed to address unique challenges in the EHR context such as privacy-preserving computation in the context of distributed research networks. The overarching objective of this tutorial is to provide participants with an introduction to the structure and content of EHR data as well as a set of appropriate tools to investigate and analyze this rich data resource.

T3. Overview of the FDA Draft Guidance on Multiple Endpoints

Monday, March 26 | 3:45 pm – 5:30 pm

Jeff Maca, QuintilesIMS, Inc.

Description: The FDA released a draft guidance document for industry “Multiple Endpoints in Clinical Trials” in January, 2017. This draft guidance aims to share statistical methods and the agencies thinking on issues which can occur in studies which have multiple endpoints. The guidance document also shares methods for handling the issues which arise in such studies. This tutorial will give an overview of the content of the guidance document, with examples of the common multiplicity methodologies, as well as an introduction to the graphical methodology (Bretz, 2009)

T4. Fast & Easy RNA-seq Computational Workflow Using Bioconductor

Tuesday, March 27 | 8:30 am – 10:15 am

Michael Love, University of North Carolina Gillings School of Public Health

Description: Here we walk through an end-to-end gene-level RNA-seq differential expression workflow using Bioconductor packages and other open source software. We will start from the FASTQ files, show how to generate gene quantifications using Salmon and to import these data into R. We perform exploratory data analysis (EDA) for quality assessment and to explore the relationship between samples, perform differential gene expression analysis using different statistical packages, and visually explore the results. Additionally, we will point to (but not

cover) new methods and workflows being developed for single-cell analysis.

T5. Multi-Modal Imaging: Promises & Pitfalls

Tuesday, March 27 | 1:45 pm – 3:30 pm

Martin Lindquist, Johns Hopkins Bloomberg School of Public Health

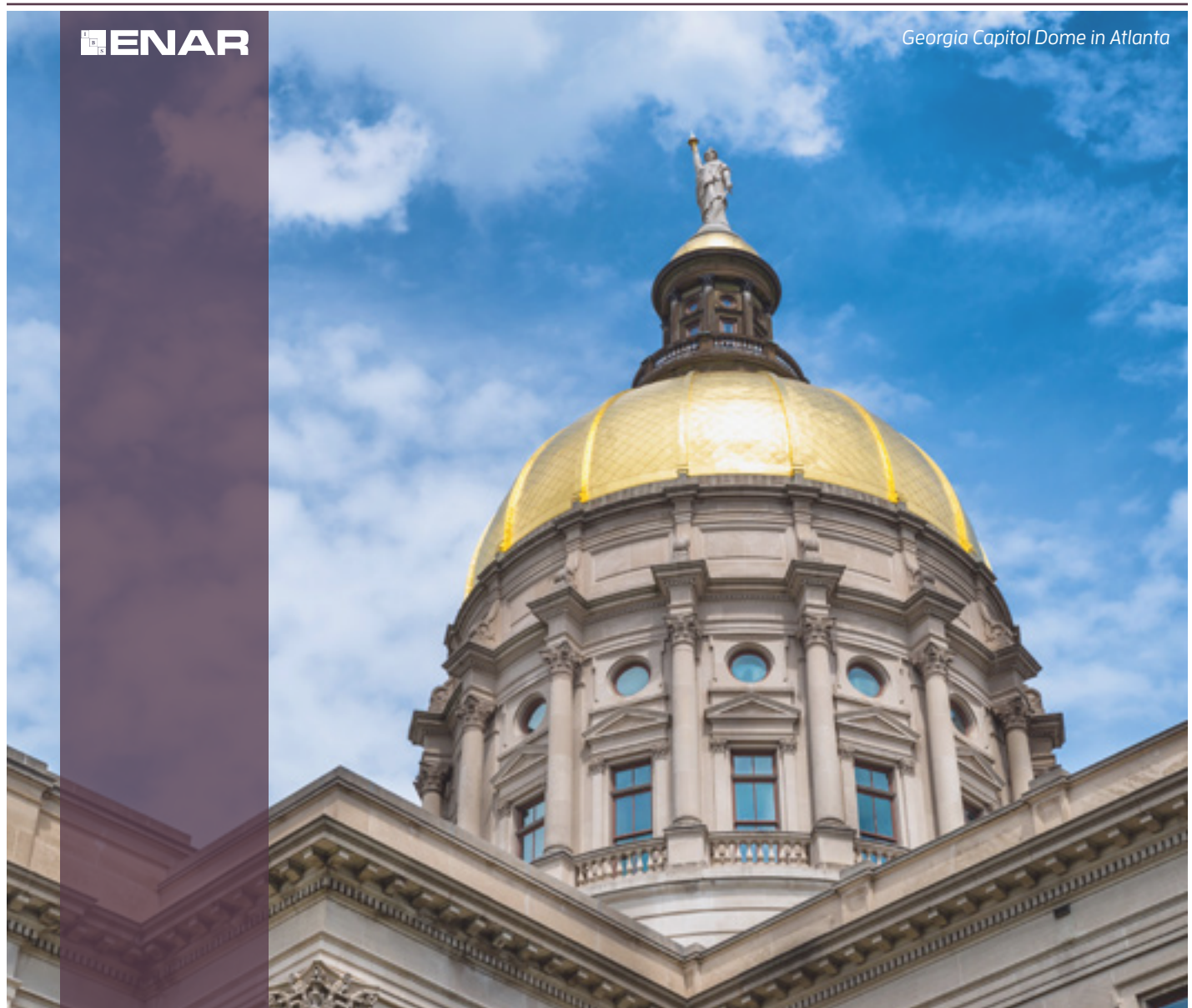
Description: All methods used for human neuroimaging have their own limitations and strengths. Therefore the current trend is toward increasingly interdisciplinary approaches that use multiple methodologies to overcome some of the limitations of each method used in isolation. For example, fMRI data are increasingly combined with EEG and MEG data to improve temporal precision, among other benefits. Neuroimaging data is also being combined with transcranial magnetic stimulation to integrate the powerful ability of neuroimaging to observe brain activity with the ability afforded by TMS to manipulate brain function and examine causal effects. In addition, integrating genetics with brain imaging is seen as a way to study how a particular subset of polymorphisms may affect functional brain activity. Each of these multi-modal approaches promise to be important topics of future research, and to fully realize their promise, novel statistical techniques will be needed. Here we discuss these promises, as well as challenges that need to be addressed.

T6. Integrative Analyses of High-throughput Multi-platform Genomics Data

Tuesday, March 27 | 3:45 pm – 5:30 pm

Veera Baladandayuthapani, The University of Texas M.D. Anderson Cancer Center

Description: Due to rapid technological advances, various types of genomic, epigenomic, transcriptomic, and proteomic data with different sizes, formats, and structures have become available. Each of these distinct data types provides a different, partly independent and complementary, high-resolution view of various biological processes. Modeling and inference in such studies is challenging,



not only due to high dimensionality, but also due to presence of structured dependencies (e.g. pathway/regulatory mechanisms, serial and spatial correlations etc.). Integrative analyses of these multi-domain data combined with patients' clinical outcomes can help us understand the complex biological processes that characterize a disease, as well as how these processes relate to the eventual pro-

gression and development of a disease. This tutorial will cover integrative statistical and computational frameworks that acknowledge and exploit these inherent complex structural relationships for both biomarker discovery and clinical prediction to aid translational medicine. These approaches will be illustrated using several biomedical case examples, especially in oncology.

REGISTRATION IS REQUIRED | FEE: \$40

MONDAY, MARCH 26 | 12:15 pm – 1:30 pm

RI. Obtaining Grant Funding for Your Research

Michelle Dunn, Data Collaboratory

Description: For some academic positions, research funding is nice; for others it's essential. If finding and obtaining grants is important to your career, this roundtable is for you. We will talk about finding biostatistics grant funding opportunities from NIH as well as other sources. You will come away with tips that will save precious time.

R2. Effective Interdisciplinary Collaborations

Reneé Moore, Emory University Rollins School of Public Health

Description: Many of us, statisticians, find that the greatest joy in our work is making meaningful contributions to the application of our choice (e.g. medicine, public health, business) as a part of interdisciplinary research teams. Being an effective member of these teams is analogous to sewing together the relevant pieces to make a beautiful quilt. To be an effective member one, obviously, must have strong analytical skills and be able to communicate the statistical methodology, but also one must have strong interpersonal skills and develop a collaborative approach to address the needs of the interdisciplinary team. We will discuss key elements for effectively enhancing interdisciplinary experiences, successful leadership as part of a research team, and how to address common challenges that arise in this environment. In addition, we will discuss the incorporation of training students and interns while weaving together the pieces to be an effective member of interdisciplinary collaborations.

R3. Wearable & Implantable Technology

Ciprian Crainiceanu, Johns Hopkins University Bloomberg School of Public Health

Description: The round table will focus on the many aspects of wearable and implantable technology measurements and their application to health studies. This is in response to the explosion of studies utilizing various types of devices including accelerometers, heart and glucose monitors, GPS, and ecological momentary assessment (EMA) devices. We will discuss recent developments in the area, potential for funding applications, and strategies for using WIT to reduce bias and measurement error in observational studies and clinical trials.

R4. Practical Issues in Clinical Trial Design & Analysis

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

Description: This roundtable will focus on methods for dealing with practical considerations that arise in the process of clinical trial design, conduct, and analysis. Depending on the attendees' interests, we will discuss a variety of recent developments, including designs discussed in the 2016 book 'Bayesian Designs for Phase I-II Clinical Trials' by Yuan, Nguyen and Thall, as well as new utility-based designs for randomized trials and personalized medicine.

R5. Career Opportunities for Statisticians at the CDC

Timothy Green, Centers for Disease Control and Prevention

Description: The Centers for Disease Control and Prevention (CDC) employs more than 400 mathematical and health statisticians across six coordinating offices, the Center for Global Health and the National Institute for Occupational Safety and Health. CDC statisticians serve a critical role in supporting the Agency's mission through the compilation, analysis, and interpretation of statistical information used to inform public health activities. Using

a multidisciplinary approach to investigate public health problems, statisticians serve as technical experts in the development of study designs, data collection systems, software and analytic methodologies. In this roundtable, we will discuss different roles of statisticians at CDC. We will examine opportunities at various career stages and discuss potential career trajectories within the Agency.

R6. Grant Proposal IOI for Statisticians

Debashis Ghosh, Colorado School of Public Health

Description: In the current funding climate for grant-sponsoring organizations such as NIH and NSF, research grants of all types have become more competitive than ever before. This roundtable will focus on strategies and resources for researchers to be able to submit competitive research methodology grants for these mechanisms. In addition, review processes for various grant mechanisms will be described.

R7. Statistics and Connections: Opportunities and Challenges for Statistics for Studying how Neurons, Organisms and People Communicate

Brian Caffo, Johns Hopkins University Bloomberg School of Public Health

Description: In this roundtable we will discuss the development of statistical tools for studying connections. Connectivity dominates brain studies from functional neuroimaging studies to the microscopic study of individual neurons. Connectivity similarly dominates our daily behavior and human connections of all sorts. Several parallel efforts address the statistical problems of connectivity including: random graphs, graphical models and covariance modeling. In this roundtable we discuss the emerging field of connectomics and both the unique and common aspects of different applied connectivity settings. We will further discuss statistical challenges and ways that statisticians can have a large impact on this field.

R8. Modeling and Inference for Spatial-Temporal BIG DATA

Sudipto Banerjee, University of California at Los Angeles

Description: With the growing capabilities of Geographic Information Systems (GIS) and user-friendly software, statisticians today routinely encounter geographically referenced data containing observations from a large number of spatial locations and time points. Over the last decade, a variety of models have been proposed for researchers to better understand the complex nature of spatial and temporal variability. However, their computational complexity renders such models unfeasible for massive data sets. This roundtable will discuss and offer solutions to some of the challenges facing spatial statisticians and GIS analysts with regard to analyzing massive amounts of spatial data. Recent research and developments will be discussed and emphasis will be accorded to practical implementation, the state of current software and tools, and the different types of inferential questions being posed to spatial statisticians today.

R9. Identifying the Non-Identifiable: Non-Progressive Cancers in Screened Populations

Yu Shen, The University of Texas M.D. Anderson Cancer Center

Ruth Etzioni, Fred Hutchinson Cancer Research Center

Description: Over the past decades, some cancer screening programs such as mammography in breast cancer and colonoscopy in colon cancer, among others, have been considered powerful weapons to prolong survival and increase cure. At the same time, however, the debate about the potential harm due to overdiagnosis has also attracted attention. Though several cancer screening studies have been conducted for breast, lung, colon and prostate, estimation of the cancer natural history and overdiagnosis can be extremely challenging due to various biases and an unobservable disease process in the screening cohort. In this roundtable lunch, we will discuss study designs, data sources, methodological challenges and opportunities in the area of cancer screening with a particular focus on leveraging available data to learn about heterogeneity of the underlying disease progression process.

SPECIAL OPPORTUNITIES FOR STUDENTS

- » **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 fourth 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.
- » **Educational & 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 105-113)
Don't forget the popular ENAR Career Placement Services! (see pages 115-116)
- » **Network with Your Fellow Students:** The CENS mixer will be held the evening of Monday, March 26, 2018. This is a great way to meet and greet students from other graduate programs. Don't miss this opportunity to begin building connections with your future colleagues and friends.



HOURS

Sunday, March 25: 4:00 pm to 6:30 pm

Monday, March 26: 9:30 am to 4:30 pm

Tuesday, March 27: 9:30 am to 3:30 pm

General Information: The ENAR 2018 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 to register for the placement center: www.enar.org/meetings/spring2018/career/index.cfm.

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. There are a very limited number of private suites, so please reserve early.

EMPLOYER REGISTRATION	BY FEB 1 ST	AFTER FEB 1 ST
Employer <i>3 reps/4 job postings</i>	\$1,600	\$1,695
Private Interview Room <i>per 4-hour increments</i>	\$275	n/a
Additional Representatives <i>cost per person includes conference registration</i>	\$500	\$600
Additional Job Postings	\$100	\$200

Employer Registration Instructions, Deadlines, & Fees: All employers must **FULLY** complete an online Employer Form located at: www.enar.org/meetings/spring2018/career/index.cfm for each position listing. Attachments may be included.



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.

APPLICANT REGISTRATION	BY FEB 1 ST	AFTER FEB 1 ST
Regular Registration	\$50	\$75
Student Registration	\$25	\$40

NOTE: 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 Instructions, Deadlines, & Fees:

All applicants must **FULLY** complete an online Applicant Form located at: www.enar.org/meetings/spring2018/career/index.cfm for each job classification.

PLEASE PRINT OR TYPE

FULL NAME (FIRST/MIDDLE INITIAL/LAST) _____

HIGHEST DEGREE: BACHELORS MASTERS DOCTORATE OR MEDICAL DEGREE OTHER

BADGE NAME (IF DIFFERENT THAN ABOVE) _____ SPOUSE/GUEST BADGE NAME _____

ORGANIZATION _____

MAILING ADDRESS (STREET ADDRESS) _____

CITY _____ STATE _____ ZIPCODE _____ COUNTRY _____

DAYTIME PHONE _____ FAX _____

EMAIL _____

MEMBERSHIP IN PARTICIPATING SOCIETIES: (check all that apply)

- ENAR WNAR ASA IMS IBS

CANCELLATION POLICY: Registration fees, less a \$100 administrative fee, will be refunded if written notice is received by February 1, 2018. Requests for refunds will not be honored after February 1, 2018. **No refunds will be issued for the cancellation of short courses, tutorials, or roundtables.**

MEETING REGISTRATION FEES:

<input type="checkbox"/> ENAR WNAR IBS Member	\$ 420 (\$495 after 2/1)
<input type="checkbox"/> ASA Member <i>not an ENAR/WNAR/IBS member</i>	\$ 560 (\$635 after 2/1)
<input type="checkbox"/> IMS Member <i>not an ENAR/WNAR/IBS member</i> *\$440-\$20 IMS contribution: \$420	\$ 420 (\$495 after 2/1)
<input type="checkbox"/> Nonmember <i>in any participating society</i> *Includes membership in ENAR through December 31, 2018	\$ 610 (\$685 after 2/1)
<input type="checkbox"/> Student <i>w/ letter from major professor verifying status</i>	\$ 165 (\$175 after 2/1)
<input type="checkbox"/> Nonmember Student <i>w/ letter from major professor verifying status</i>	\$ 200 (\$210 after 2/1)
<input type="checkbox"/> Guest	\$ 95 (\$105 after 2/1)

SHORT COURSES: Short courses will be held on **Sunday, March 25.**

Indicate the Short Course Number(s): _____

- | | |
|-----------------------------------------------------------------------|-----------------------------------------------------------------------|
| <input type="checkbox"/> Member <i>in participating society</i> | <input type="checkbox"/> Nonmember* |
| <input type="checkbox"/> Full Day: \$325 (\$350 after 2/1) | <input type="checkbox"/> Full Day: \$375 (\$400 after 2/1) |
| <input type="checkbox"/> Half Day: \$225 (\$250 after 2/1) | <input type="checkbox"/> Half Day: \$275 (\$300 after 2/1) |
| <input type="checkbox"/> 2nd Half Day: \$190 (\$215 after 2/1) | <input type="checkbox"/> 2nd Half Day: \$240 (\$265 after 2/1) |

TUTORIALS: Tutorials will be held on **Monday, March 26 & Tuesday, March 27.**

Member	Nonmember	Student
T1 <input type="checkbox"/> \$75 (\$85 after 2/1)	<input type="checkbox"/> \$85 (\$95 after 2/1)	<input type="checkbox"/> \$40 (\$50 after 2/1)
T2 <input type="checkbox"/> \$75 (\$85 after 2/1)	<input type="checkbox"/> \$85 (\$95 after 2/1)	<input type="checkbox"/> \$40 (\$50 after 2/1)
T3 <input type="checkbox"/> \$75 (\$85 after 2/1)	<input type="checkbox"/> \$85 (\$95 after 2/1)	<input type="checkbox"/> \$40 (\$50 after 2/1)
T4 <input type="checkbox"/> \$75 (\$85 after 2/1)	<input type="checkbox"/> \$85 (\$95 after 2/1)	<input type="checkbox"/> \$40 (\$50 after 2/1)
T5 <input type="checkbox"/> \$75 (\$85 after 2/1)	<input type="checkbox"/> \$85 (\$95 after 2/1)	<input type="checkbox"/> \$40 (\$50 after 2/1)
T6 <input type="checkbox"/> \$75 (\$85 after 2/1)	<input type="checkbox"/> \$85 (\$95 after 2/1)	<input type="checkbox"/> \$40 (\$50 after 2/1)

ROUNDTABLES: The roundtables will be held on **Monday, March 26.** Space is limited.

Preregistration is required. Indicate the number of your 1st, 2nd, and 3rd choices:

- Fee: **\$40** | Please make lunch vegetarian: Yes No
- 1st _____ 2nd _____ 3rd _____



COUNCIL FOR EMERGING AND NEW STATISTICIANS (CENS) LUNCH:

The Lunch will be held on **Tuesday, March 27.** 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 (\$10.00)

Note that the full Final Program & Abstract book will be available on the ENAR website. -

ENAR MEMBERSHIP

- YES**, I want to renew my 2018 ENAR membership or become an ENAR member. **Renew by 12/31/2017 and save \$20.00 annually!**

- Regular Member: **\$120** when paid by 12/31/2017 (\$140 after 12/31/2017) Includes electronic access to the *Biometrics Journal*, *JABES* and *Biometric Bulletin Newsletter*
- Regular Member: **\$130** when paid by 12/31/2017 (\$150 after 12/31/2017) Includes *Biometric Bulletin Newsletter* and a print subscription of one journal (choose one):
 Biometrics Journal *JABES*
- Regular Member: **\$140** when paid by 12/31/2017 (\$160 after 12/31/2017) Includes *Biometric Bulletin Newsletter* and print subscriptions to *Biometrics Journal* and *JABES*
- Student Member: **\$20**
Includes electronic access to the *Biometrics Journal*, *JABES* and *Biometric Bulletin Newsletter*

TOTAL PAYMENT DUE \$

PAYMENT INFORMATION:

(Remittance accepted only in US currency, payable to ENAR)

- Enclosed is my **check** or **money order**

- Please **charge** payment to:

- VISA MasterCard Amex

CARD NO. _____ EXP. DATE _____

NAME ON CARD _____

SIGNATURE _____

FULL NAME (FIRST/MIDDLE INITIAL/LAST)		
DEGREE	TITLE	
MAILING ADDRESS		
CITY/STATE/ZIPCODE/COUNTRY		
DAYTIME PHONE	FAX	EMAIL

MEMBERSHIP TYPE

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

Regular Member **\$ 150**
Includes *Biometric Bulletin Newsletter* and a print subscription of one journal (choose one):
 Biometrics Journal *JABES*

Regular Member **\$ 160**
Includes *Biometric Bulletin Newsletter* and print subscriptions to *Biometrics Journal* and *JABES*

Supporting Member **\$ 30**

Student Member **\$ 20**
Includes electronic access to the *Biometrics Journal*, *JABES* 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.

PAYMENT INFORMATION

Enclosed is my **check**, payable to ENAR (*Remittance accepted only in US currency*)

Please **charge** payment to: VISA MasterCard Amex

CARD NO.	EXP. DATE
NAME ON CARD	SIGNATURE



Eastern North American Region (ENAR)
11130 Sunrise Valley Drive, Suite 350
Reston, Virginia 20191

T: 703.437.4377 | **F:** 703.435.4390
E: enar@enar.org

PLEASE CHECK ONE:

- New Member
 Renewal

PLEASE INDICATE TWO AREAS OF INTEREST:

- Agriculture (01)
 Animal & Veterinary Science (02)
 Clinical Trials (03)
 Epidemiology (04)
 Genetics & Heredity (05)
 Molecular Biology & Biotechnology (06)
 Toxicology (07)

NATURAL RESOURCES:

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

Return the Completed Form and Payment
via mail to:

WACHOVIA BANK/ENAR

P.O. Box 758929
Baltimore, MD 21275-8929





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