



# ENAR 2020 SPRING MEETING

WITH IMS & SECTIONS OF ASA  
March 22-25, 2020  
JW Marriott Nashville  
Nashville, TN

**PRELIMINARY PROGRAM  
AND SCIENTIFIC PROGRAM**



# WELCOME

I am thrilled to welcome you to the ENAR 2020 Spring Meeting in Nashville! I would like to extend a special welcome to our first-time attendees and look forward to your return for future meetings and your future involvement in ENAR!

The ENAR 2020 Spring Meeting will be held at the JW Marriott Nashville. Nashville's foundation was built on music. It is the common thread connecting the life and soul of the city and its people. Nashville is home to the Grand Ole Opry, Ryman Auditorium, Country Music Hall of Fame, and many honkey tonks where you can enjoy great music, food and drink.

The four-day meeting, **March 22-25, 2020**, will host biostatistics students, researchers, and practitioners, from academia, government, and industry. The meeting will expose attendees to the latest developments in methods, software, and applications through the Scientific and Educational programs. The meetings also provide a great opportunity for professional networking, meeting new people, connecting job seekers with employers, and reconnecting with friends and colleagues. Our exhibitors and vendors will give you opportunities to check out the latest textbooks and see demonstrations of new software.

ENAR is committed to fostering a culture of inclusion, professionalism and civil discourse that cultivates an environment where ideas are exchanged openly and freely with mutual respect and trust. ENAR has adopted a **Meeting Conduct Policy** intended to guide all attendees at ENAR's annual Spring Meeting and attendees will be required to assent to the policy as part of registration.

The ENAR Spring Meeting is only possible through the efforts of many hard-working volunteers. Thanks to all of the volunteers for helping make the ENAR Spring Meeting a success!

## SCIENTIFIC PROGRAM

Through the leadership of the Program Chair Juned Siddique (Northwestern University) and Associate Program Chair Chenguang Wang (Johns Hopkins University), and contributions from many of you, the Program Committee (consisting of 10 ASA section representatives and 4 at-large ENAR members) has assembled a diverse and exciting invited program. The sessions cover a wide range of topics, including modern graphical modeling, complex innovative clinical trial design, electronic health records data, machine learning, neuroimaging, wearable/mobile technology, data integration, causal inference, survival outcomes, spatial modeling, environmental health, and statistical modeling in Alzheimer's disease. The IMS Program Chair Sunduz Keles (University of Wisconsin, Madison) has also put together complementary sessions on causal inference with genetic data, statistical methods for single-cell omics analysis, microbiome data analysis, precision medicine, and asymmetrical statistical learning.

Poster sessions play a prominent role at the ENAR Spring Meeting, and continue to be a vital part of the program. In addition to contributed and invited posters, the ENAR 2020 Spring Meeting will continue contributed SPEED poster sessions, in which presenters give a two-minute elevator speech on the highlights of their posters. As in 2019, these speed sessions will utilize digital poster boards, giving

presenters the opportunity for more interactive posters. Monday, March 23rd will feature the thematically grouped contributed speed poster sessions. Each session will feature two invited posters from well-known researchers and will run parallel with the rest of the sessions in the scientific program. As in previous years, the regular contributed posters will be featured during the Opening Mixer on Sunday evening. This year, poster presenters will be assigned one-hour slots to be available at their poster, giving everyone a chance to view the amazing research on display. Posters in this session will be eligible to win an award as part of the popular ENAR Regional Advisory Board's poster competition!

## EDUCATIONAL PROGRAM

Our educational program provides many opportunities to learn new statistical techniques, to develop new computational skills, and to discuss the latest research or career development skills with leading experts. The Educational Advisory Committee has assembled an engaging suite of short courses, tutorials and roundtables covering a wide range of topics from renowned instructors.

Short course topics include design and analysis in platform & basket trials and in SMART, multivariate meta-analysis, using NIMBLE for MCMC, working with electronic health records (EHRs), implementing Bayesian adaptive designs, and statistical networks in biology. Tutorial topics include disease risk modelling and causal inference in R, methods for geometric functional data, difference in difference studies, integrating 'omics and imaging data, and creating R packages. Roundtable luncheons provide a more focused discussion with distinguished statisticians from academia, government and industry. Topics range from reviewing and writing grants, working in government and a medical school, publishing and reviewing manuscripts, data science, and mentoring. Be sure to take a look and sign up for something interesting!

I would like to extend a special thanks to the members of the Educational Advisory Committee – Lynn Eberly (University of Minnesota), Jason Roy (Rutgers), Veera Baladandayuthapani (University of Michigan), and Haoda Fu (Eli Lilly) for their support and guidance in helping to put together an outstanding educational program.

## PRESIDENTIAL INVITED ADDRESS

I am thrilled to announce that the 2020 ENAR Presidential Invited Address will be given by **Dr. Sharon-Lise Normand**. Dr. Normand is a statistician whose work has made impactful contributions to health services and regulatory policy, particularly in the areas of cardiovascular disease and mental health. Methodologically, these contributions have been accomplished via Bayesian hierarchical models and Bayesian approaches for causal inference. Her contributions have been recognized in the statistics community (ASA fellow), the medical community (American College of Cardiology fellow), and the broader scientific community (AAAS fellow).

To learn more about Dr. Normand and her Invited Address, please see page 13.

## ADDITIONAL MEETING ACTIVITIES

The ENAR 2020 Spring Meeting will feature several other activities in addition to the scientific and educational programs. On Sunday, March 22nd, there will be the **Fostering Diversity in Biostatistics Workshop**, organized by Felicia R. Simpson (Winston-Salem State University) and Loni Philip Tabb, (Drexel University). Dr. Adrian Coles (Eli Lilly) will serve as this year's keynote speaker. This workshop has been very popular and impactful and registration typically fills up quickly. Please be sure to register early if you are interested in attending!

Students, recent graduates, and other young professionals should plan to attend the Networking Mixer on Monday evening and the Tuesday luncheon event organized by the **Council for Emerging and New Statisticians (CENS)**. These are great opportunities for our "younger" members to meet new people, learn about CENS and become more engaged with ENAR. Attendees seeking employment and prospective employers have the opportunity to connect via the **Career Placement Center**.

Tuesday evening will feature our second annual **ENAR Sponsor and Exhibitor Mixer**. You will be able to peruse the latest books and software while joining the sponsors and exhibitors for the reception in the exhibition area after the last Tuesday session. It will be a great opportunity to catch up with friends, collaborators, and colleagues. After the mixer, you will have time to walk around and dine in a great Nashville restaurant. The Local Arrangements Committee, chaired by Cindy Chen (Vanderbilt University), will provide recommendations for attendees.

*We hope to see you in Nashville for the 2020 ENAR Spring Meeting!*

**Mike Daniels,**  
ENAR 2020 President







*Advancing biological and life science through the development of quantitative theories and the application, development and dissemination of effective mathematical and statistical techniques.*



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ENAR 2020 Spring Meeting  
With IMS & Sections of ASA  
March 22-25 | JW Marriott Nashville | Nashville, TN





## GENERAL INFORMATION

### Location:

JW Marriott Nashville  
201 8th Avenue South | Nashville, TN 37203  
Phone: (615) 291-8600

<https://www.jwnashvillehotel.com>

<https://book.passkey.com/go/ENAR>

### ENAR SPRING MEETING CONDUCT POLICY

As a professional organization composed of diverse individuals, ENAR is committed to fostering a culture of inclusion, professionalism and civil discourse that cultivates an environment where ideas are exchanged openly and freely with mutual respect and trust. ENAR is committed to creating a safe professional environment for participants at all stages of their careers, and especially for our more junior members. ENAR has adopted a Meeting Conduct Policy intended to guide all attendees at ENAR's annual Spring Meeting including, but not limited to, conference attendees, guests, staff, contractors, vendors, exhibitors, and participants in scientific sessions, workshops, tutorials, roundtables, short courses, tours, and other social events offered in conjunction with the ENAR Spring Meeting. Attendees of the annual Spring Meeting should expect a welcoming professional atmosphere that is free of discrimination, harassment and retaliation of any kind for any reason. All attendees of the Spring Meeting must agree to comply fully and freely with the Meeting Conduct Policy, the contents of which are subject to change at the discretion of the ENAR Executive Committee.

Inappropriate, unprofessional, or threatening behavior will not be tolerated at our meetings. This includes threatening physical or verbal interactions, deliberate intimidation, stalking, sexual images in public spaces, unauthorized or inappropriate photography or recording, inappropriate or unwanted physical contact, unwelcome sexual attention, or verbal harassment. Verbal harassment includes comments relating to race, ethnicity, religion, gender, gender identity or expression, sexual orientation, disability, veteran status, or other protected statuses, and will not be tolerated in our community.

Meeting Registration Fees:	By Jan 15	After Jan 15
ENAR/WNAR/IBS Member	\$450	\$525
ASA Member (Not a member of ENAR/WNAR/IBS)	\$600	\$675
IMS Member (Not a member of ENAR/WNAR/IBS) (\$470-\$20 IMS contribution: \$450)	\$450	\$525
Student Member	\$170	\$180
Guest (Adults and Children 13+ years old)	\$100	\$110
Non-member (of any participating society)	\$650	\$725
Student Non-member	\$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, 2020.

### SHORT COURSES

The ENAR 2020 meeting will begin with an excellent set of short courses on Sunday, March 22. Please refer to the chart below 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 82 or the electronic registration form available on the ENAR website.

Short Course Registration Fees				
	By Jan 15		After Jan 15	
	Half Day	Full Day	Half Day	Full Day
Member	\$250	\$350	\$275	\$375
Non-Member	\$325	\$425	\$350	\$450

See Pages 70-71 for Short Course Details

**Register for Two Half-Day Courses and Save!**

Savings Information Provided on page 70

### TUTORIALS

Tutorials are offered on both 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 January 15, 2020) and \$85 for non-members (\$95 after January 15, 2020). The student registration fee for the tutorials is \$40 (\$50 after January 15, 2020). Be sure to register in advance, since tutorials will be closed once they are full.

### ROUNDTABLE LUNCHEONS

This year, the roundtable luncheons will be held on Monday, March 23, from 12:15 to 1:30pm. Space for each roundtable is limited and pre-registration is highly recommended. The fee is \$45 per person and includes lunch. For full descriptions of the roundtable discussion topics, please refer to page 74.

### NEW MEMBER RECEPTION, OPENING MIXER, AND POSTER SESSION

A new member reception will be held from 7:30 to 8:00pm on Sunday, March 22. All new ENAR members are cordially invited to attend. The Opening Mixer and Poster Session will take place from 8:00 to 11:00pm on Sunday, March 22.

### 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 2020 Spring Meeting is to improve the networking experience for all attendees. CENS will organize lunches on Tuesday, March 24, for groups of attendees, who 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 MIXER

All are invited to attend the CENS mixer on Monday, March 23, from 5:30 to 6:30pm. Registration is not required – so please plan to attend!

## SPONSOR & EXHIBITOR MIXER

All attendees are invited to attend the Sponsor & Exhibitor mixer on Tuesday, March 24, from 6:00 to 7:00pm. Registration is not required – so please plan to attend!

## CAREER PLACEMENT SERVICES

ENAR will conduct a job placement service at the 2020 Spring Meeting. Additional information regarding the placement center is located on page 80.

## PROGRAM OPTIONS

At the 2020 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 fee) containing all session and speaker names, session times, and locations (please refer to the registration form on page 82 and select this option when registering)

Note: The larger final program & abstract program is not printed but can be freely downloaded from the ENAR website.

## ROOM RESERVATIONS

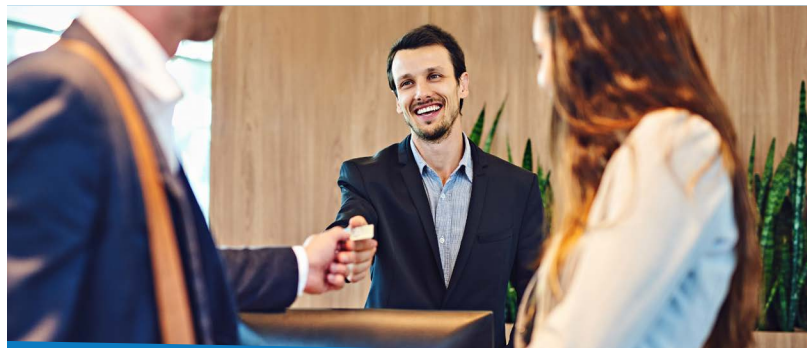
ENAR has negotiated a group hotel room rate of \$239 for single and double occupancy rooms. All reservations must be made by February 21, 2020. To receive this special ENAR meeting rate, you must make your reservations directly with the JW Marriott Nashville at (615) 291-8600 or (800) 320-5744 or online at <https://book.passkey.com/go/ENAR>. If reserving a room by phone be sure to mention that you are with the ENAR 2020 Spring Meeting. Please make your reservations early, as all hotel rooms are reserved on a first-come, first-served basis.

## IMPORTANCE OF STAYING AT THE JW MARRIOTT NASHVILLE

Your patronage of the official ENAR Spring Meeting hotel enables us to secure the meeting space at a greatly reduced cost, which helps keep the cost of the meetings and your registration fee down. With your cooperation, ENAR will continue to be successful in negotiating good contracts for the Spring Meeting and maintaining the programs and activities you have requested.

## PARKING AT THE JW MARRIOTT NASHVILLE

Valet parking is available on-site for a fee of \$42 daily, with in/out privileges. Please note the hotel does not offer self-parking on-site, however, guests may elect to self-park at off-property locations such as the Music City Center next to the hotel.



## HOTEL & TRANSPORTATION

JW Marriott Nashville  
201 8th Avenue South | Nashville, TN 37203  
Phone: (615) 291-8600

For reservations:  
<https://book.passkey.com/go/ENAR>

## TRANSPORTATION

The JW Marriott Nashville is approximately 8 miles from the airport and is conveniently located near many public transportation options. Estimated taxi fare from the airport to the meeting hotel is approximately \$30.

Public Transportation-Route 18 is a public transportation bus system between the Airport and downtown, which costs \$2 one way.

## 2020 ENAR MEETING MOBILE APP

Take advantage of our Spring Meeting mobile app; accessible on your iPhone, iPad, or Android! 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

# WELCOME TO NASHVILLE!

Named for Francis Nash, a general of the Continental Army during the American Revolutionary War, the city was founded in 1779. The city grew quickly due to its strategic location as a port on the Cumberland River and, in the 19th century, a railroad center. Nashville seceded with Tennessee during the American Civil War; in 1862 it was the first state capital in the Confederacy to fall to Union troops. After the war, the city reclaimed its position and developed a manufacturing base. Today, Nashville is known as Music City.

If cities had soundtracks, Nashville's would be like no others. It would be a mix of music's past, present and future with cuts of country, bluegrass, rock, pop, Americana, gospel, classical, jazz and blues, all blending and overlapping in perfect harmony. Live music can be heard when walking through almost any neighborhood, with open mic nights featuring talent you'd expect to pay good money to hear. The city has experienced significant growth in the last few years, as the healthcare industry and the growing appeal of tourism have led to the development of new neighborhoods and the revitalization of old ones, as well as a booming food and beer scene. You won't have any trouble filling your trip with the sights, sounds, and tastes of Nashville.

## LANDMARKS AND TOURS

### RYMAN AUDITORIUM

When you walk through the doors of historic Ryman Auditorium, one thing becomes clear right away: this isn't just another nightly music venue, and it's so much more than a daytime tourist stop. This place is hallowed ground. This is the exact spot where bluegrass was born—where Johnny Cash met June Carter, where souls were saved and a slice of history was nearly lost. It was right here that country music found an audience beyond its own back porch, and countless careers took off as deals were signed on napkins and paper scraps backstage. Open daily for tours and shows, right in the heart of Music City.

### TENNESSEE STATE CAPITOL AND LEGISLATIVE PLAZA

Designed by architect William Strickland and built in the Greek Revival architecture style that models a Greek temple, the Tennessee State Capitol is one of 12 capitol buildings in the U.S. that does not have a dome. The Capitol sits on the hilltop site once occupied by the Holy Rosary Cathedral, which was the first Roman Catholic cathedral in Nashville. On the grounds of the Capitol are two statues of U.S. presidents: Andrew Jackson and Andrew Johnson. President James K. Polk is buried in a tomb on the Capitol grounds, along with his wife, Sarah Childress Polk. Other monuments include a Tennessee Holocaust Memorial, the Sam Davis Memorial, and Sen. Edward Ward Carmack Memorial. Across the street, check out Legislative Plaza, where you'll find a statue dedicated to the Women of the Confederacy, a monument to Tennesseans, who served in the Korean War, and to the south Vietnam Veterans Park.

### TENNESSEE STATE MUSEUM

Situated on the bottom floors of the James K. Polk building downtown is the Tennessee State Museum. It depicts the history of the state of Tennessee, starting from pre-colonization and going into the 20th century. With more than 120,000 square feet (11,148 square meters) of space among three floors, the museum includes both permanent and changing exhibits that display paintings, weapons, furniture, uniforms, and battle flags from the Civil War. Larger exhibits include a painting gallery, a reproduction of a historic print shop, and a grist mill. There's also a museum store where visitors can purchase handmade crafts and Tennessee memorabilia.

### THE PARTHENON

Standing as the centerpiece in Nashville's Centennial Park, the Parthenon is a full-scale replica of the Parthenon in Athens, Greece. Come inside to see the 42-foot gilded sculpture of Athena, the permanent display of American paintings from the Cowan Collection, the history of the Nashville Parthenon dating back to the 1897 Tennessee Centennial Exposition, and a variety of temporary shows and exhibitions! The entrance is located on the ground level of the East side of the building.

### THE GRAND OLE OPRY

Take a trip to the historic Grand Ole Opry, located next to the Opryland Resort and Convention Center, about 20 minutes from the JW Marriot. You can take a backstage tour of the Opry's 18 themed dressing rooms, learn behind-the-scenes secrets, and just maybe step foot in "The Circle", the center of the Grand Ole Opry and the most sacred space in country music.





## HISTORY & ART MUSEUMS

### ANDREW JACKSON'S HERMITAGE

The Hermitage, Home of President Andrew Jackson, is one of the largest and most visited presidential homes in the United States, and recently named the #1 historic house in Tennessee. Today, The Hermitage is a 1,120-acre National Historic Landmark with more than 30 historic buildings, that welcomes some 200,000 annual visitors, including 30,000 school children, from all 50 states and many foreign countries. Visit Andrew Jackson's Hermitage to witness "The Duel: The Art of the Southern Gentleman." This 30-minute visitor experience will answer questions about dueling followed by an ACTUAL demonstration by onsite historic re-enactors. "The Duel" takes place every Thursday through Sunday throughout the day, free with paid admission. The Hermitage is about 15 miles from the JW Marriot.

### BELLE MEADE PLANTATION

Belle Meade Plantation is a non-profit historic site located in Nashville. Established in 1807, Belle Meade was revered as the greatest thoroughbred stud farm in the United States. It was home to Iroquois, the first American bred horse to win the Epsom Derby and the great foundation sire, Bonnie Scotland, whose descendants include Secretariat, Seattle Slew, Native Dancer, Big Brown and California Chrome. Belle Meade was owned and operated by the Harding-Jackson family for nearly a century from 1807 until 1906. Today, their home is restored to its turn-of-the-century appearance, along with several original outbuildings. The Plantation is about 20 minutes from the JW Marriot by car.

### BELMONT MANSION

Belmont Mansion is the largest house museum in Tennessee and one of a few whose history revolves around the life of a woman: Adelia Acklen. We host visitors seven days a week for tours and are open as a rental venue for weddings and events. Tours may be purchased online or at the door. Belmont Mansion, and Belmont campus, are about 10 minutes from the JW Marriot by car.

### THE FRIST

If you're in the mood to view some art in a gorgeous setting, look no further than the Frist Art Museum. Situated in a classic art deco building, the museum houses a rotating schedule of exhibitions from local, regional, national, and international sources. The Frist is a family-friendly environment, with the Martin ArtQuest Gallery providing more than 30 interactive art-making stations and free admission for youth 18 and under.



## PARKS

### CENTENNIAL PARK (MIDTOWN)

Smack dab in the middle of the hustle and bustle of offices, restaurants, and streets, Centennial is the perfect place to take a short walk on a lunch break. It is also home to the Parthenon replica, giving people educational benefits, along with their dose of vitamin D. Its convenient location also makes it a prime spot for events and activities. It is home to several festivals, fairs, and music series. On any given weekend, the park is full of music, food, and fun. With all of this activity, it is not the best for wildlife or nature viewing, and finding a secluded, quiet spot free of frisbees or college kids may be a challenge.

### BICENTENNIAL CAPITOL MALL STATE PARK (DOWNTOWN)

This 19-acre park in the heart of Nashville serves as a monument to the bicentennial celebration of the State of Tennessee. This park offers plenty of opportunities to learn about the long history of Tennessee, while having a great experience in a beautiful green space. More information on this park and many more can be found at the Tennessee State Parks website. While in the area, consider checking out the Nashville Farmer's Market, located next door to the park. It's a great spot to grab lunch or a coffee to go!

### CUMBERLAND PARK (EAST NASHVILLE)

Located on the East side of the river, Cumberland Park was completely renovated to become a go-to attraction for Nashvillians. There are a lot of features in this park, including an outdoor amphitheater for events, a rock climbing wall, water features, green space for kids to play and much more. The park is a short 1.5 mile walk from the JW Marriot.

### SEVIER PARK (12 SOUTH)

A small park in a growing neighborhood, Sevier Park has the best of both worlds. It's fun and lively, but hardly ever crowded! With Las Palatas and Burger Up nearby, hunger won't be an issue either. There is a small playground area and a creek down below in the shadow of the pre-Civil War Sunnyside Mansion. The mansion invites the new growth of the 12 South neighborhood in its historic front yard. This park is about 4 miles from the JW Marriot.



## LOCAL CUISINE AND RESTAURANTS

### (BY NEIGHBORHOOD)

Nashville's dining scene is exploding thanks to a combination of chef-driven restaurants and classic dining spots offering up Nashville Hot Chicken, barbecue, and Meat & Three fare. Below are some top local picks, organized by neighborhood. For more information, and to find your favorite flavor, check out <https://www.visitmusiccity.com/things-to-do/food-drink>. For a more in-depth look at the different neighborhoods in Nashville, visit [www.nashvilleguru.com/neighborhoods](http://www.nashvilleguru.com/neighborhoods).



### DOWNTOWN

Home to honky tonks, live music, and more boot shops than you could ever need, Downtown Nashville is the heart of "Nashvegas" energy. With more than 60 bars and restaurants, it's hard to go wrong here if you're looking for a fun evening. For a great view, consider Acme Feed & Seed, with multiple floors of dining options and a great rooftop bar overlooking the river. If you're looking for name recognition, consider Jason Aldean's Kitchen + Rooftop Bar, or Tootsies Orchid Lounge for a slice of honky tonk history.

### SOBRO ("SOUTH OF BROADWAY")

Just steps from Broadway lies the SoBro neighborhood, a quieter area with a lot of new developments. Check out Bajo Sexto Taco for a quick and tasty lunch, Martin's Bar-B-Que Joint for a classic plate of Nashville BBQ, or Tennessee Brew works for live music and delicious burgers. If you're looking for some activities to go with your meal, check out Pinewood Social, featuring vintage bowling lanes and an extensive craft cocktail selection to accompany your meal.

### THE GULCH

Located just a short walk from the JW Marriot, The Gulch is a small, upscale neighborhood full of great food and shops. In particular, they're known for Arnold's Country Kitchen (the quintessential Meat & Three experience, open Monday – Friday). For an upscale dinner, consider Chauhan Ale & Masala House (Indian cuisine with a Southern flair), Sambuca (American food, live music), or Sunda (Southeast Asian cuisine, with ample seating for larger groups).

### GERMANTOWN

A quiet neighborhood just north of Downtown, Germantown features brick sidewalks, ample greenery, and easy street parking in a family-friendly atmosphere. There are more than 15 dining options to be found, including casual options like Red Bicycle Coffee and Crepes and Von Elrod's Beer Hall and Kitchen (with delicious soft pretzels and an extensive German and Belgian beer list), as well as more upscale dinner options like 5th & Taylor (American cuisine, reservation required) and Geist (set in an old blacksmith shop, with upscale Southern cuisine and a champagne garden).

### MIDTOWN

For an area that's a little more relaxed and less touristy, consider Midtown, located near Vanderbilt University and popular among locals and students. Here you'll find Hattie B's, one of the most popular Nashville Hot Chicken joints. If the line is long, consider other Hattie B's in the area. Consider using their order-ahead option to avoid the line! In this neighborhood you'll also find several delicious restaurants with a Southern flair, like The Row or Tavern. For a nicer meal, check out Union Common for duck fat French fries and steak, or Patterson House for a speakeasy cocktail experience.

### HILLSBORO VILLAGE

The neighborhood of Hillsboro Village, conveniently located just south of Vanderbilt University campus, is a great spot to do some shopping and grab a coffee or a bite to eat. The Pancake Pantry is a favorite among visitors, but be sure to get there early to beat the line! Fido is a great spot for coffee, and serves a delicious all-day breakfast menu that's popular among Vanderbilt and Belmont students alike.

### 12 SOUTH

If you're in the area to check out the Belmont Mansion, walk on down to the 12 South neighborhood! The street features some great shopping (including Reese Witherspoon's boutique, Draper James) as well as excellent options for eating. Consider Frothy Monkey for coffee and breakfast favorites, Five Daughters Bakery for delicious cronuts (donuts made from layered croissant dough), or Christie Cookie Co. for a fresh-baked cookie and milk. For dinner, look no further than Edley's Bar-B-Que, with incredibly tasty pulled pork, fried pickles, and jalapeño cornbread. In the mood for lighter fare? Check out Epice Lebanese Bistro for stuffed grape leaves, lentil soup, and traditional grilled chicken and lamb skewers.



## SPECIAL THANKS

### Program Chair

**Juned Siddique**, Northwestern University

### Associate Program Chair

**Chenguang Wang**, Johns Hopkins University

### IMS Program Chair

**Sunduz Keles**, University of Wisconsin, Madison

### Digital Program Coordinator

**David Aaby**, Northwestern University

### Local Arrangements Chair

**Cindy Chen**, Vanderbilt University

### ASA Section Representatives – Program Committee

**Veronica Berrocal**, University of California at Irvine  
ASA Statistics in Epidemiology Section

**Hongyuan Cao**, University of Missouri  
ASA Mental Health Statistics Section

**Susmita Datta**, University of Florida  
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**Donatello Telesca**, UCLA  
ASA Section on Bayesian Statistics

**Zheyu Wang**, Johns Hopkins University  
ASA Biometrics Section

**Ying Wei**, Columbia University,  
ASA Statistical Learning and Data Mining Section

### ENAR At-Large Members – Program Committee

**Lauren Balmert**, Northwestern University

**Hwanhee Hong**, Duke University

**Jonathan Schildcrout**, Vanderbilt University

**Cory Zigler**, University of Texas at Austin

### ENAR Executive Committee

**Michael Daniels**, President

**Brent Coull**, President-Elect

**Sarah Ratcliffe**, Past President

**Brisa Sánchez**, Secretary

**Renee Moore**, Treasurer

**RECOM Chair:** Michael Daniels

**RAB Chair:** Leslie McClure

### Educational Advisory Committee

**Veera Baladandayuthapani**, University of Michigan

**Lynn Eberly**, University of Minnesota

**Haoda Fu**, Eli Lilly

**Jason Roy**, Rutgers University

### 2020 ENAR Student Awards

**Jeffrey S. Morris**, University of Pennsylvania

### ENAR Fostering Diversity in Biostatistics Workshop

**Felicia R. Simpson**, Winston-Salem State University

**Loni Philip Tabb**, Drexel University

### ENAR Staff

**Shannon Taylor**, Executive Director

**Leah Sibilis**, Event Director

**Tayler Kenney**, Event Specialist

**Amber Darcy**, Event Specialist

**Laura Stapleton**, Administrative/Membership Manager

## PRESIDENTIAL INVITED SPEAKER



### Sharon-Lise Normand, Ph.D.

S. James Adelstein Professor of Health Care Policy (Biostatistics)  
Department of Health Care Policy, Harvard Medical School  
Department of Biostatistics, Harvard T.H. Chan School of Public Health



### MEDICAL PRODUCT, HEALTHCARE DELIVERY, AND ROAD SAFETY POLICIES: SEEMINGLY UNRELATED REGULATORY QUESTIONS

The evaluations of medical product effectiveness and safety, the quality of hospital care, and the safety of U.S. roadways involve the use of large, complex observational data to make policy decisions. Careful design and analysis of such data are critical given the large populations impacted. While increasing access to data of increased size and type permit, in theory, richer evaluations, study design should assume a more prominent role. This talk will describe three different policy problems: the impact of the hospital readmission reduction program, the effectiveness of seemingly similar drug eluting coronary stents, and the safety of U.S. motor carriers. Statistical issues common across these problems, including clustered data, multiple treatments, multiple outcomes, high-dimensional data, and lack of randomization, are highlighted and solutions discussed.

### BIOGRAPHY

**Sharon-Lise Normand** is the S. James Adelstein Professor of Health Care Policy (biostatistics) in the Department of Health Care Policy at Harvard Medical School and in the Department of Biostatistics at the Harvard Chan School of Public Health. Dr. Normand earned her BSc (1984) and MSc (1985) degrees in statistics from the University of Western Ontario and her PhD (1990) in biostatistics from the University of Toronto. Dr. Normand's research focuses on the development of statistical methods for health services and regulatory policy research, primarily using Bayesian and causal inference approaches, including assessment of quality of health care, provider profiling, diffusion of medical technologies, and regulatory science. She has developed a long line of research on methods for the analysis of patterns of treatment and quality of care for patients with cardiovascular disease and with mental disorders in particular.

Dr. Normand has developed analytical approaches for comparing hospitals and physicians using outcomes and process-based measures. Since 2002, she served as director of Mass-DAC, the data-coordinating center responsible for collecting, analyzing, and reporting on the quality of care for adults discharged following a cardiac procedure from all non-federal hospitals in Massachusetts. She is serves as the director of the Medical Device Epidemiology Network (MDEpiNet) Methodology Center, a public-private partnership aimed at medical device evaluation. MDEpiNet partners with the FDA's Center for Device and Radiological Health and the Science and Infrastructure Center at Weill Cornell Medical School. Her focus is on the development of statistical approaches to active medical device surveillance, valid inferences from distributed networks, and the improvement of causal inference in the presence of high dimensional data.

On the mental health side, Dr. Normand is leading an NIMH-funded study to estimate the value of publicly funded mental health care for patients with serious mental illness. She is also undertaking an observational study to estimate causal dose "outcomes" curves in the context of understanding weight gain associated with cumulative antipsychotic drug exposure among subjects with schizophrenia for numerous different antipsychotics.

Dr. Normand was elected fellow of the American Statistical Association, fellow of the American Association for the Advancement of Science, fellow of the American College of Cardiology, and Associate Member of the Society of Thoracic Surgeons. She served as the 2010 President of the Eastern North American Region of the International Biometrics Society; was inaugural co-chair of the PCORI Methodology Committee; co-chairs a Committee on National Statistics/National Academy of Sciences panel reviewing the Safety Measurement System of the Compliance, Safety, Accountability program run by the Federal Motor Carrier Safety Administration; and served on several National Academy of Sciences Committees, including the Committee of Applied and Theoretical Statistics (CATS) focusing on the intersections of statistics and computer science for big data. Dr. Normand received ASA's Health Policy Statistics Section Long Term Excellence Award, the Outstanding Lifetime Achievement Award from the American Heart Association, the L. Adrienne Cupples Award for Excellence in Teaching, Research, and Service in Biostatistics from Boston University, and the Mosteller Statistician of the Year from the Boston Chapter of the ASA.

# PROGRAM SUMMARY

## Sunday, March 22

7:30 a.m.—6:30 p.m.	<b>Conference Registration</b>
8:00 a.m.—5:00 p.m.	<b>Short Courses</b> <b>SC1:</b> Implementing Bayesian Adaptive Designs: From Theory to Practice <b>SC2:</b> Practical solutions for working with electronic health records data <b>SC3:</b> Design and Analysis of Sequential, Multiple Assignment, Randomized Trials for small and large samples
8:00 a.m.—12:00 p.m.	<b>Short Courses</b> <b>SC4:</b> Programming with hierarchical statistical models: Using the BUGS-compatible NIMBLE system for MCMC and more <b>SC6:</b> Statistical Network Analysis with Applications to Biology
10:30 a.m.—6:30 p.m.	<b>Fostering Diversity in Biostatistics Workshop</b>
1:00 p.m.—5:00 p.m.	<b>Short Courses</b> <b>SC5:</b> Multivariate meta-analysis methods <b>SC7:</b> Trial Design and Analysis Using Multisource Exchangeability Models
3:00 p.m.—6:00 p.m.	<b>Exhibits Open</b>
4:00 p.m.—6:30 p.m.	<b>Career Placement Services</b>
4:30 p.m.—7:00 p.m.	<b>ENAR Executive Committee Meeting</b>
7:30 p.m.—8:00 p.m.	<b>New Member Reception</b>
8:00 p.m.—11:00 p.m.	<b>Opening Mixer and Poster Session</b> <ol style="list-style-type: none"> <li>1. Posters: Imaging Data Analysis</li> <li>2. Posters: Survival Analysis/Competing Risks</li> <li>3. Posters: Machine Learning and High-Dimensional Data</li> <li>4. Posters: Personalized Medicine and Biomarkers</li> <li>5. Posters: Cancer Applications</li> <li>6. Posters: Clinical Trials</li> <li>7. Posters: Diagnostics/Prediction/Agreement</li> <li>8. Posters: Adaptive Design/Experimental Design</li> <li>9. Posters: Bayesian Methods</li> <li>10. Posters: Causal Inference and Clinical Trials</li> <li>11. Posters: Genomics/Proteomics</li> <li>12. Posters: Functional Data/High Dimensional</li> <li>13. Posters: Bayesian, Clustered Data, Hypothesis Testing</li> <li>14. Posters: High-Dimensional Data, Missing Data and More</li> <li>15. Posters: Consulting, Education, Policy, Epidemiology</li> <li>16. Posters: Genetics, Computation</li> <li>17. Posters: Meta-Analysis, Missing Data and More</li> </ol>

## Monday, March 23

7:30 a.m.—5:00 p.m.	<b>Conference Registration</b>
7:30 a.m.—5:00 p.m.	<b>Speaker Ready Room</b>
8:30 a.m.—5:30 p.m.	<b>Exhibits Open</b>
8:30 a.m.—10:15 a.m.	<b>Tutorial</b> <b>T1:</b> Statistical methods for geometric functional data



## Monday, March 23 (continued)

8:30 a.m.—10:15 a.m.	<b>Scientific Program</b> <ul style="list-style-type: none"> <li>18. Modern Functional Data Analysis</li> <li>19. Distributed and Privacy-Preserving Methods for Electronic Health Records Data</li> <li>20. Innovative Statistical Methods in Environmental Mixture Analysis</li> <li>21. Mentoring Throughout a Lifetime: Considerations for Mentors and Mentees at all Career Stages</li> <li>22. Innovative Statistical Approaches for High-Dimensional Omic and Microbiomic Data</li> <li>23. Bayesian Nonparametrics for Causal Inference and Missing Data</li> <li>24. Contributed Papers: Variable Selection: How to Choose?</li> <li>25. Contributed Papers: Functional Data Analysis</li> <li>26. Contributed Papers: Penalized and Other Regression Models with Applications</li> <li>27. Contributed Papers: Methods for Neuroimaging Data: Get the Picture?</li> <li>28. Contributed Papers: Causal Effect Estimation</li> </ul>
9:30 a.m.—4:30 p.m.	<b>Career Placement Services</b>
10:15 a.m.—10:30 a.m.	<b>Refreshment Break with Our Exhibitors</b>
10:30 a.m.—12:15 p.m.	<b>Tutorial</b> <b>T2: Disease Risk Modeling and Visualization using R</b>
10:30 a.m.—12:15 p.m.	<b>Scientific Program</b> <ul style="list-style-type: none"> <li>29. New Perspectives on Data Integration in Genome-Wide Association Studies</li> <li>30. Advances in Causal Inference and Joint Modeling with Survival and Complex Longitudinal Data</li> <li>31. Opportunities and Challenges in the Analysis and Integration of Large-Scale Biobank Data</li> <li>32. Compositional Nature of Microbiome Data: Challenges and New Methods</li> <li>33. Statistical Modeling in Alzheimer's Disease</li> <li>34. Recent Advances in Bayesian Methods for Spatial-Temporal Processes</li> <li>35. Speed Posters: EHR Data, Epidemiology, Personalized Medicine, Clinical Trials</li> <li>36. Contributed Papers: Adaptive Designs for Clinical Trials</li> <li>37. Contributed Papers: Bayesian Semiparametric and Nonparametric Methods</li> <li>38. Contributed Papers: Statistical Methods in Cancer Research</li> <li>39. Contributed Papers: Network Analysis: Connecting the Dots</li> <li>40. Contributed Papers: Policies and Politics: Statistical Analyses of Health Outcomes in the Real World</li> <li>41. Contributed Papers: Statistical Considerations for Optimal Treatment</li> </ul>
12:15 p.m.—1:30 p.m.	<b>Roundtable Luncheons</b>
12:30 p.m.—4:30 p.m.	<b>Regional Advisory Board (RAB) Luncheon Meeting (by Invitation Only)</b>
1:45 p.m.—3:30 p.m.	<b>Tutorial</b> <b>T3: Integration of Genetics and Imaging Data in Scientific Studies</b>
1:45 p.m.—3:30 p.m.	<b>Scientific Program</b> <ul style="list-style-type: none"> <li>42. Causal Inference with Genetic Data</li> <li>43. Recent Advances in Statistical Methods for Single-Cell Omics Analysis</li> <li>44. Recent Advances in Microbiome Data Analysis</li> <li>45. Novel Methods to Evaluate Surrogate Endpoints</li> <li>46. Recent Advances in the Uncertainty Estimation and Properties of Bayesian Additive Regression Trees</li> <li>47. Current Developments in Analyzing EHR and Biobank Data</li> <li>48. Speed Posters: Causal Inference/Longitudinal Data/High-Dimensional Data/Massive Data</li> <li>49. Contributed Papers: Statistical Methods for Omics Data Analysis</li> <li>50. Contributed Papers: Observational and Historical Data Analysis: The Rest is History</li> <li>51. Contributed Papers: Immunotherapy Clinical Trial Design and Analysis</li> <li>52. Contributed Papers: Machine Learning and Statistical Relational Learning</li> <li>53. Contributed Papers: Time Series and and Recurrent Event Data</li> <li>54. Contributed Papers: Massive Data: A Giant Problem?</li> </ul>
3:30 p.m.—3:45 p.m.	<b>Refreshment Break with Our Exhibitors</b>
3:45 p.m.—5:30 p.m.	<b>Tutorial</b> <b>T4: Causal Inference Using the R TWANG Package for Mediation and Continuous Exposures</b>

## Monday, March 23 (continued)

3:45 p.m.—5:30 p.m.

**Scientific Program**

- 55. Human Microbiome Studies: Novel Methods and New Studies
- 56. Bayesian Approaches for Complex Innovative Clinical Trial Design
- 57. Achieving Real-World Evidence from Real-World Data: Recent Developments and Challenges
- 58. Novel Spatial Modeling Approaches for Air Pollution Exposure Assessment
- 59. Innovations in Two Phase Sampling Designs with Applications to EHR Data
- 60. Recent Approaches to Multivariate Data Analysis in the Health Sciences
- 61. Speed Posters: Imaging Data/Survival Analysis/Spatio-Temporal
- 62. Contributed Papers: Imaging and Streaming Data Analysis
- 63. Contributed Papers: Causal Inference and Propensity Score Methods
- 64. Contributed Papers: Longitudinal Data and Joint Models of Longitudinal and Survival Data
- 65. Contributed Papers: Personalized Medicine and Biomarkers
- 66. Contributed Papers: Statistical Genetics: Single-Cell Sequencing Data
- 67. Contributed Papers: Semiparametric and Nonparametric Methods and Applications

5:30 p.m.—6:30 p.m.

**CENS Networking Mixer**

6:30 p.m.—7:30 p.m.

**President's Reception (by Invitation Only)**

## Tuesday, March 24

7:30 a.m.—5:00 p.m.

**Conference Registration**

7:30 a.m.—5:00 p.m.

**Speaker Ready Room**

8:30 a.m.—5:30 p.m.

**Exhibits Open**

8:30 a.m.—10:15 a.m.

**Scientific Program**

- 68. Challenges and Opportunities in Methods for Precision Medicine
- 69. Recent Developments in Risk Estimation and Biomarker Modeling with a Focus in Alzheimer's Disease
- 70. Clinical Trial Designs in a New Era of Immunotherapy: Challenges and Opportunities
- 71. The Three M's: Meetings, Memberships, and Money!
- 72. Recent Advances in Joint Modeling of Longitudinal and Survival Data
- 73. Recent Advances in Network Meta-Analysis with Flexible Bayesian Approaches
- 74. Contributed Papers: Electronic Health Records Data Analysis
- 75. Contributed Papers: Rebel Without a Cause: Sessions on Causal Inference
- 76. Contributed Papers: Hypothesis Testing: Knowledge is Power
- 77. Contributed Papers: Missing (Data) in Action
- 78. Contributed Papers: Back to the Future: Prediction and Prognostic Modeling
- 79. Contributed Papers: M&M: Measurement Error and Modeling

9:30 a.m.—3:30 p.m.

**Career Placement Services**

10:15 a.m.—10:30 a.m.

**Refreshment Break with Our Exhibitors**

10:30 a.m.—12:15 p.m.

80. Presidential Invited Address

12:30 p.m.—4:30 p.m.

**Regional Committee Luncheon Meeting (by Invitation Only)**

1:45 p.m.—3:30 p.m.

**Tutorial****T5: Fundamentals of difference-in-differences studies**

1:45 p.m.—3:30 p.m.

**Scientific Program**

- 81. Statistical Analysis of Biological Shapes
- 82. Improving the Development and Validation of Screening Tests for Rare Diseases
- 83. Causal Inference and Harmful Exposures
- 84. Statistical Methods for Emerging Data in Environmental Health Research
- 85. Bayesian Analysis in Functional Brain Imaging
- 86. Human Data Interaction: Gaining an Understanding of the Data Science Pipeline
- 87. Contributed Papers: Spatial and Spatial-Temporal Data Analysis
- 88. Contributed Papers: Early Phase Clinical Trials and Biomarkers
- 89. Contributed Papers: Electronic Health Records Data Analysis and Meta-Analysis
- 90. Contributed Papers: Small Things that Make a Big Difference: Microbiome Analysis
- 91. Contributed Papers: Statistical Genetics: Sequencing Data Analysis
- 92. Contributed Papers: Robust Modeling and Inference

**Tuesday, March 24 (continued)**

3:30 p.m.—3:45 p.m.	<b>Refreshment Break with Our Exhibitors</b>
3:45 p.m.—5:30 p.m.	<b>Tutorial</b> <b>T6: R package development</b>
3:45 p.m.—5:30 p.m.	<b>Scientific Program</b> 93. High Dimensional Methods for Mechanistic Integration of Multi-Type Omics 94. New Weighting Methods for Causal Inference 95. Using Machine Learning to Analyze Randomized Trials: Valid Estimates and Confidence Intervals Without Model Assumptions 96. Recent Developments in Semiparametric Transformation Models 97. Innovations in Statistical Neuroscience 98. Artificial Intelligence for Prediction of Health Outcomes 99. Contributed Papers: Latent Variables and Processes 100. Contributed Papers: Time-to-Event Data Analysis: Survival of the Fittest 101. Contributed Papers: Risky Business: Diagnostics, ROC, and Prediction 102. Contributed Papers: Interval-Censored and Multivariate Survival Data 103. Contributed Papers: Graphical Models and Applications 104. Contributed Papers: Support Vector Machines, Neural Networks and Deep Learning
5:30 p.m.—7 p.m.	<b>ENAR Business Meeting and Sponsor/Exhibitor Mixer</b> – Open to all ENAR Members

**Wednesday, March 25**

7:30 a.m.—12:00 p.m.	<b>Speaker Ready Room</b>
7:30 a.m.—9:00 a.m.	<b>Planning Committee (by Invitation Only)</b>
8:00 a.m.—12:30 p.m.	<b>Conference Registration</b>
8:00 a.m.—12:00 p.m.	<b>Exhibits Open</b>
8:30 a.m.—10:15 a.m.	<b>Scientific Program</b> 105. Advances in Statistical Modeling for Multi-omics Data Integration 106. Causal Inference and Network Dependence: From Peer Effects to the Replication Crisis in Epidemiology 107. Flexible Spatio-Temporal Models for Environmental and Ecological Processes 108. Recent Advances in Neuroimaging Analytics 109. Novel Tensor Methods for Complex Biomedical Data 110. Integrative Analysis of Clinical Trials and Real-World Evidence Studies 111. Contributed Papers: Clustered Data Methods 112. Contributed Papers: Subgroup Analysis 113. Contributed Papers: Functional Data Analysis: Below the Surface 114. Contributed Papers: HIV, Infectious Disease and More 115. Contributed Papers: Clinical Trial Design and Analysis 116. Contributed Papers: Multivariate and High-Dimensional Data Analysis
10:15 a.m.—10:30 a.m.	<b>Refreshment Break with Our Exhibitors</b>
10:30 a.m.—12:15 p.m.	<b>Scientific Program</b> 117. Asymmetrical Statistical Learning for Binary Classification 118. Recent Advances and Opportunities in Large Scale & Multi-Omic Single-Cell Data Analysis 119. Novel Statistical Methods for Complex Interval-Censored Survival Data 120. Modern Graphical Modeling of Complex Biomedical Systems 121. Highly Efficient Designs and Valid Analyses for Resource Constrained Studies 122. Statistical Analysis of Tracking Data from Personal Wearable Devices 123. Contributed Papers: Meta-Analysis Methods 124. Contributed Papers: Longitudinal Data Analysis 125. Contributed Papers: High Dimensional Data Analysis: The BIG Picture 126. Contributed Papers: Clinical “Trials and Tribulations” 127. Contributed Papers: Count Data: The Thought that Counts



# SCIENTIFIC PROGRAM

Sunday, March 22

## POSTER PRESENTATIONS

### 1. POSTERS: IMAGING DATA ANALYSIS

Sponsor: ENAR

#### 1a. Time Varying Estimation of Tensor-on-Tensor Regression with Application in fMRI Data

Pratim Guha Niyogi\* and Tapabrata Maiti, Michigan State University

#### 1b. Estimation of Fiber Orientation Distribution through Blockwise Adaptive Thresholding

Seungyong Hwang\*, Thomas Lee, Debashis Paul and Jie Peng, University of California, Davis

#### 1c. Estimating Dynamic Connectivity Correlates of PTSD Resilience Using MultiModal Imaging

Jin Ming\*, Suprateek Kundu and Jennifer Stevens, Emory University

#### 1d. Towards an Automatic Detection Method of Chronic Active Lesions

Carolyn Lou\*, Jordan D. Dworkin and Alessandra Valcarcel, University of Pennsylvania; Martina Absinta and Pascal Sati, National Institute of Neurological Disorders and Stroke, National Institutes of Health; Kelly Clark, University of Pennsylvania; Daniel Reich, National Institute of Neurological Disorders and Stroke, National Institutes of Health

#### 1e. A Bayesian Mixture Model for Lesion Detection and Clustering in MS

Jordan D. Dworkin\*, Melissa L. Martin, Arman Oganisian and Russell T. Shinohara, University of Pennsylvania

#### 1f. Seeing Very Small Things: Applications of Mixture Modeling and Extreme Value Distributions in Microscopic Image Analysis

Miranda L. Lynch\* and Sarah E.J. Bowman, Hauptman-Woodward Medical Research Institute

### 2. POSTERS: SURVIVAL ANALYSIS/COMPETING RISKS

Sponsor: ENAR

#### 2a. Functional Additive Cox Model

Erjia Cui\*, Andrew Leroux and Ciprian Crainiceanu, Johns Hopkins University

#### 2b. Gene-Based Association Analysis of Survival Traits via Functional Regression based Mixed Effect Cox Models for Related Samples

Ruzong Fan\*, Georgetown University Medical Center; Chi-yang Chiu, University of Tennessee Health Science Center; Bingsong Zhang, Shuqi Wang and Jingyi Shao, Georgetown University Medical Center; M'Hamed Lajmi Lakhal-Chaieb, Université Laval; Richard J. Cook, University of Waterloo; Alexander F. Wilson and Joan E. Bailey-Wilson, Computational and Statistical Genomic Branch of the National Human Genome Research Institute, National Institutes of Health; Momiao Xiong, University of Texas Health Science Center at Houston

#### 2c. Regression Model for the Lifetime Risk using Pseudo-Values

Sarah C. Conner\* and Ludovic Trinquart, Boston University School of Public Health

#### 2d. Proportional Subdistribution Hazards Model with Covariate-Adjusted Censoring Weight for Clustered Competing Risks Data

Manoj Khanal\*, Soyoung Kim and Kwang Woo Ahn, Medical College of Wisconsin

#### 2e. A Unified Power Series Class of Cure Rate Survival Models for Spatially Clustered Data

Sandra Hurtado Rua\*, Cleveland State University; Dipak Dey, University of Connecticut

#### 2f. Optimizing Incremental Cost-Effective Ratios for Censored Survival Time and Cost

Xinyuan Dong\*, University of Washington

#### 2g. An EM Algorithm in Fitting the Generalized Odds-Rate Model to Right Censored Data

Ennan Gu\*, University of South Carolina

### 3. POSTERS: MACHINE LEARNING AND HIGH-DIMENSIONAL DATA

Sponsor: ENAR

#### 3a. Distributed Quadratic Inference Functions for Integrating Studies with High-Dimensional Repeated Measures

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

#### 3b. Statistical Inference for the Word2vec Natural Language Processing Algorithm Applied to Electronic Health Records

Brian L. Egleston\*, Stan Taylor, Michael Lutz and Richard J. Bleicher, Fox Chase Cancer Center; Slobodan Vucetic, Temple University

#### 3c. Neural Network Survival Model for Cardiovascular Disease Prediction

Yu Deng\*, Northwestern University; Lei Liu, Washington University, St. Louis; HongMei Jiang, Kho Abel, Yishu Wei, Norrina Allen, John Wilkins, Kiang Liu, Donald Lloyd-Jones and Lihui Zhao, Northwestern University

**3d. Applying Statistical Learning Algorithms on the Prediction of Response to Immune Checkpoint Blockade Therapy**

Tiantian Zeng\* and Chi Wang, University of Kentucky

**3e. Integrative Biclustering for Characterization of Biomarker and Phenotype Associations**

Weijie Zhang\*, University of Minnesota

**3f. Testing Presence-Absence Association in the Microbiome Using LDM and PERMANOVA**

Andrea N. Lane\*, Emory University; Glen Satten, Centers for Disease Control and Prevention; Yijuan Hu, Emory University

**3g. Feature Selection for Support Vector Regression Using a Genetic Algorithm**

Shannon B. McKearnan\*, David M. Vock and Julian Wolfson, University of Minnesota

**3h. Statistical Inferences for F1-scores in Multi-Class Classification Problems**

Kouji Yamamoto\*, Yokohama City University; Kanae Takahashi, Osaka City University; Aya Kuchiba, National Cancer Center, National Institutes of Health; Tatsuki Koyama, Vanderbilt University Medical Center

**4. POSTERS: PERSONALIZED MEDICINE AND BIOMARKERS****Sponsor: ENAR****4a. Individualized Treatment Effect Estimation using Auto-Encoder and Conditional Generative Adversarial Networks**

Yuanyuan Liu\* and Momiao Xiong, University of Texas Health Science Center at Houston

**4b. Weighted Sparse Additive Learning for ITR Estimation under Covariate Space Sparsity**

Jinchun Zhang\*, New York University

**4c. One-Step Value Difference Test for the Existence of a Subgroup with a Beneficial Treatment Effect Using Random Forests**

Dana Johnson\*, Wenbin Lu and Marie Davidian, North Carolina State University

**4d. Selecting Optimal Cut-Points for Early-Stage Detection in K-class Diseases Diagnosis Based on Concordance and Discordance**

Jing Kersey\*, Hani Samawi, Jingjing Yin, Haresh Rochani and Xinyan Zhang, Georgia Southern University

**4e. Designing and Analyzing Clinical Trials for Personalized Medicine via Bayesian Models**

Chuanwu Zhang\*, Matthew S. Mayo, Jo A. Wick and Byron J. Gajewski, University of Kansas Medical Center

**4f. Some Improved Tests for the Assessment of Bioequivalence and Biosimilarity**

Rabab Elnaïem\* and Thomas Mathew, University of Maryland, Baltimore County

**4g. Fusing Continuous and Time-Integrated Data for Estimating Personal Air Pollution Exposures**

Jenna R. Krall\* and Anna Z. Pollack, George Mason University

**4h. Value of Biostatistical Support in a Hospital Quality Improvement Department**

Henry John Domenico\*, Daniel W. Byrne and Li Wang, Vanderbilt University Medical Center

**4i. Prediction of Intervention Effects in Healthcare Systems**

Emily A. Scott\*, Johns Hopkins Bloomberg School of Public Health; Zhenke Wu, University of Michigan; Elizabeth Colantuoni, Johns Hopkins Bloomberg School of Public Health; Sarah Kachur, Johns Hopkins HealthCare; Scott L. Zeger, Johns Hopkins Bloomberg School of Public Health

**5. POSTERS: CANCER APPLICATIONS****Sponsor: ENAR****5a. Comparison of Several Bayesian Methods for Basket Trials when a Control of Subgroup-Wise Error Rate is Required**

Gakuto Ogawa\* and Shogo Nomura, National Cancer Center, Japan

**5b. Gene Profile Modeling and Integration for EWOC Phase I Clinical Trial Design while Fully Utilizing all Toxicity Information**

Feng Tian\* and Zhengjia (Nelson) Chen, Rollins School of Public Health, Emory University

**5c. A Pan-Cancer and Polygenic Bayesian Hierarchical Model for the Effect of Somatic Mutations on Survival**

Sarah Samorodnitsky\*, University of Minnesota; Katherine A. Hoadley, University of North Carolina, Chapel Hill; Eric F. Lock, University of Minnesota

**5d. A Novel GENomic NETwork CORrelation Merging System (GENECOMS) to Investigate the Relation between Differentially Expressed Methylation Regions and Gene Modules in Bladder Cancer**

Shachi Patel\* and Jeffrey Thompson, University of Kansas Medical Center

# SCIENTIFIC PROGRAM

(CONTINUED)

## 5e. Comparing the Performance of Phase I/II Oncology Trial Designs in Low-Toxicity Rate Situations

Ryo Takagi\* and Isao Yokota, Hokkaido University Hospital

## 5f. Advantage of Using a Finite-Sample Correction when Designing Clinical Trials in Rare Diseases

Audrey Mauguen\*, Memorial Sloan Kettering Cancer Center

## 5g. Implementation of Clusterability Testing Prior to Clustering

Naomi Brownstein\*, Moffitt Cancer Center

## 5h. A Probabilistic Model for Leveraging Intratumor Heterogeneity Information to Enhance Estimation of the Temporal Order of Pathway Mutations during Tumorigenesis

Menghan Wang\*, Chunming Liu, Arnold Stromberg and Chi Wang, University of Kentucky

## 5i. Functional Clustering via Weighted Dirichlet Process Modeling with Breast Cancer Genomics Data

Wenyu Gao\* and Inyoung Kim, Virginia Tech

## 6. POSTERS: CLINICAL TRIALS

Sponsor: ENAR

### 6a. Sample Size Determination Method that Accounts for Selection Probability of the Maximum Tolerated Dose in Phase I Oncology Trials

Yuta Kawatsu\*, Jun Tsuchida, Shuji Ando and Takashi Sozu, Tokyo University of Science; Akihiro Hirakawa, The University of Tokyo

### 6b. The Scale Transformed Power Prior with Applications to Studies with Different Endpoints

Brady Nifong\*, Matthew A. Psioda and Joseph G. Ibrahim, University of North Carolina, Chapel Hill

### 6c. Design and Analysis for Three-Arm Clinical Trials with Intra-Individual Right-Left Data

Ryunosuke Machida\*, National Cancer Center, Japan; Kentaro Sakamaki, Yokohama City University, Japan; Aya Kuchiba, National Cancer Center, Japan

### 6d. An Estimation of Efficacy of Potential Drug in Multiple Diseases with Discriminating Heterogeneity in Treatment Effects in Basket Trials

Shun Hirai\*, Jun Tsuchida, Shuji Ando and Takashi Sozu, Tokyo University of Science; Akihiro Hirakawa, The University of Tokyo

## 6e. Longitudinal Study of Opioid Treatment on Hamilton Depression Rating Scale Using a Negative Binomial Mixed Model

Kesheng Wang\*, West Virginia University; Wei Fang, West Virginia Clinical and Translational Science Institute; Toni DiChiacchio, West Virginia University; Chun Xu, University of Texas Rio Grande Valley; Ubolrat Piamjariyakul, West Virginia University

## 6f. Group Sequential Analysis for Sequential Multiple Assignment Randomized Trials

Liwen Wu\*, Junyao Wang and Abdus S. Wahed, University of Pittsburgh

## 6g. Incorporating Truncation Information from Phase I Clinical Studies into Phase II Designs

Li-Ching Huang\* and Fei Ye, Vanderbilt University Medical Center; Yi-Hsuan Tu, Independent Scholar; Chia-Min Chen, Nanhua University, Taiwan; Yu Shyr, Vanderbilt University Medical Center

## 6h. Replicability of Treatment Effects in Meta-Analyses

Kirsten R. Voorhies\*, Brown University; Iman Jaljuli and Ruth Heller, Tel-Aviv University; Orestis A. Panagiotou, Brown University

## 7. POSTERS: DIAGNOSTICS/PREDICTION/ AGREEMENT

Sponsor: ENAR

### 7a. A Resampling Perspective on Evaluation of Diagnosis Accuracy: An Appendicitis Example

Calvin S. Elder\*, St. Jude Children's Research Hospital; Yousef El-Gohary, Center of Colorectal and Pelvic Reconstruction; Hui Zhang, Northwestern University; Li Tang, St. Jude Children's Research Hospital

### 7b. Improving the Performance of Polygenic Risk Score with Rare Genetic Variants

Hongyan Xu\* and Varghese George, Augusta University

### 7c. A Domain Level Index to Enhance the Prediction Accuracy of Pathogenic Variants

Hua-Chang Chen\* and Qi Liu, Vanderbilt University Medical Center

### 7d. The Cornelius Project - Randomizing Real-Time Predictive Models Embedded in the Electronic Health Record to Assess Impact on Health Outcomes

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

### 7e. Privacy-Preserving Outcome Prediction

Lamin Juwara\*, McGill University



**7f. Interpretable Clustering of Hierarchical Dependent Binary Data: A Doubly-Multi-Resolution Approach**

Zhenke Wu\*, Yuqi Gu, Mengbing Li and Gongjun Xu,  
University of Michigan

**7g. Estimation and Construction of Confidence Intervals for the Cutoff-Points of Continuous Biomarkers Under the Euclidean Distance in Trichotomous Settings**

Brian Mosier\* and Leonidas Bantis, University of Kansas  
Medical Center

**7h. Confidence Interval of the Mean and Upper Tolerance Limit for Zero-Inflated Gamma Data**

Yixuan Zou\* and Derek S. Young, University of Kentucky

**7i. Predictive Performance of Physical Activity Measures for 1-year up to 5-year All-Cause Mortality in NHANES 2003-2006**

Lucia Tabacu\*, Old Dominion University; Mark Ledbetter,  
Lynchburg University; Andrew Leroux and Ciprian Crainiceanu,  
Johns Hopkins University

**8. POSTERS: ADAPTIVE DESIGN/EXPERIMENTAL DESIGN**

Sponsor: ENAR

**8a. An Empirical Bayesian Basket Trial Design Accounting for Uncertainties of Homogeneity and Heterogeneity of Treatment Effect among Subpopulations**

Junichi Asano\*, Pharmaceuticals and Medical Devices Agency; Akihiro Hirakawa, The University of Tokyo

**8b. Lessons Learned in Developing an Interdisciplinary Collaboration Between Biostatistics and Forensic Nursing**

Yesser Sebeh\*, Georgia State University; Katherine Scafide, George Mason University; Matthew J. Hayat, Georgia State University

**8c. Response-Adaptive Randomization in a Two-Stage Sequential Multiple Assignment Randomized Trial**

Junyao Wang\*, University of Pittsburgh

**8d. Integrated Multiple Adaptive Clinical Trial Design Involving Sample Size Re-Estimation and Response-Adaptive Randomization for Continuous Outcomes**

Christine M. Orndahl\* and Robert A. Perera, Virginia Commonwealth University

**8e. Design of a Calibrated Experiment**

Blaza Toman\* and Michael A. Nelson, National Institute of Standards and Technology (NIST)

**8f. Modified Q-learning with Generalized Estimating Equations for Optimizing Dynamic Treatment Regimes with Repeated-Measures Outcomes**

Yuan Zhang\*, David Vock and Thomas Murray,  
University of Minnesota

**8g. Development of a Spatial Composite Neighborhood SES Measure**

Shanika A. De Silva\*, Melissa Meeker, Yasemin Algur and Victoria Ryan, Drexel University; Leann Long, University of Alabama at Birmingham; Nyesha Black, Noire Analytics; Leslie A. McClure, Drexel University

**8h. Estimating Disease Prevalence with Potentially Misclassified Dorfman Group Testing Data**

Xichen Mou\*, University of Memphis; Joshua M. Tebbs and Dewei Wang, University of South Carolina

**9. POSTERS: BAYESIAN METHODS**

Sponsor: ENAR

**9a. Bayesian Spatial Analysis of County-Level Drug Mortality Rates in Virginia**

Jong Hyung Lee\* and Derek A. Chapman, Virginia Commonwealth University

**9b. Robust Partial Reference-Free Cell Composition Estimation in Tissue Expression Profiles**

Ziyi Li\* and Zhenxing Guo, Emory University; Ying Cheng, Yunnan University; Peng Jin and Hao Wu, Emory University

**9c. Multivariate Space-Time Disease Mapping via Quantification of Disease Risk Dependency**

Daniel R. Baer\* and Andrew B. Lawson, Medical University of South Carolina

**9d. Bayesian Envelope in Logistic Regression**

Minji Lee\* and Zhihua Su, University of Florida

**9e. Bayesian Kinetic Modeling for Tracer-Based Metabolomic Data**

Xu Zhang\*, Ya Su, Andrew N. Lane, Arnold Stromberg, Teresa W-M. Fan and Chi Wang, University of Kentucky

# SCIENTIFIC PROGRAM

(CONTINUED)

## 9f. Forecasting Glaucoma Progression using Bayesian Structural Time Series Analysis

Manoj Pathak\*, Murray State University

## 9g. A Three-Groups Bayesian Approach to GWAS Data with Application to Parkinson's Disease

Vivian Cheng\* and Daisy Philtrou, The Pennsylvania State University; Ben Shaby, Colorado State University

## 9h. Improving Estimation of Gene Expression Differences via Integrative Modeling of Transcriptomic and Genetic Data

Xue Zou\*, William H. Majoros and Andrew S. Allen, Duke University

## 9i. Reliable Rates and the Effect of Prior Information with an Application to the County Health Rankings & Roadmaps Program

Guangzi Song\*, Harrison Quick and Loni Philip Tabb, Drexel University

## 10. POSTERS: CAUSAL INFERENCE AND CLINICAL TRIALS

Sponsor: ENAR

### 10a. The Importance of Propensity Score Estimation to Achieve Balance in Covariates

Hulya Kocyigit\*, University of Georgia

### 10b. Performance of Instrumental Variable and Mendelian Randomization Estimators for Count Data

Phillip Allman\*, Hemant Tiwari, Inmaculada Aban and Dustin Long, University of Alabama at Birmingham; Todd MacKenzie, Dartmouth College; Gary Cutter, University of Alabama at Birmingham

### 10c. Improve Power Analysis in Clinical Trials with Multiple Primary Endpoints: An Application of Parametric Graphical Approaches to Multiple Comparison

Zhe Chen\* and Ih Chang, Biogen

### 10d. Two-Stage Randomized Trial for Testing Treatment Effect for Time to Event Data

Rouba A. Chahine\*, Inmaculada Aban and Dustin Long, University of Alabama at Birmingham

### 10e. Estimating Power for Clinical Trials with Patient Reported Outcomes Endpoints using Item Response Theory

Jinxiang Hu\* and Yu Wang, University of Kansas Medical Center

### 10f. Bayesian Multi-Regional Clinical Trials Using Model Averaging

Nathan W. Bean\*, Matthew A. Psioda and Joseph G. Ibrahim, University of North Carolina, Chapel Hill

## 10g. Constructing Causal Methylation Network by Additive Noise Model

Shudi Li\*, Rong Jiao and Momiao Xiong, University of Texas Health Science Center at Houston

## 10h. Detecting Intervention Effects in a Randomized Trial within a Social Network

Shaina J. Alexandria\*, Michael G. Hudgens and Allison E. Aiello, University of North Carolina, Chapel Hill

## 11. POSTERS: GENOMICS/PROTEOMICS

Sponsor: ENAR

### 11a. Kernel-Based Genetic Association Analysis for Microbiome Phenotypes

Hongjiao Liu\*, University of Washington; Michael C. Wu, Fred Hutchinson Cancer Research Center

### 11b. True Source of Inflated Zeros in Single Cell Transcriptomics

Tae Kim\* and Mengjie Chen, University of Chicago

### 11c. Estimating Cell Type Composition Using Isoform-Level Gene Expression Data

Hillary M. Heiling\* and Douglas R. Wilson, University of North Carolina, Chapel Hill; Wei Sun, Fred Hutchinson Cancer Research Center; Naim Rashid and Joseph G. Ibrahim, University of North Carolina, Chapel Hill

### 11d. EWAS of Kidney Function Identifies Shared and Ethnic-Specific Loci

Anna Batorsky\*, University of North Carolina, Chapel Hill; Mi Kyeong Lee and Stephanie J. London, National Institute of Environmental Health Sciences, National Institutes of Health; Josyf C. Mychaleckyj, University of Virginia; Andrew Marron, Eric A. Whitsel and Nora Franceschini, University of North Carolina, Chapel Hill; Charles E. Breeze, Altius Institute for Biomedical Sciences & University College London

### 11e. Deconvolutional Mixture Modeling to Account for Cell Type Composition in Tissue Samples

Zachary P. Brehm\*, University of Rochester; Marc K. Halushka, Johns Hopkins University; Matthew N. McCall, University of Rochester

### 11f. Developing a Computational Framework for Precise TAD Boundary Prediction using Genomic Elements

Spiro C. Stilianoudakis\* and Shumei Sun, Virginia Commonwealth University

**11g. Parsing Latent Factors in High-Dimensional Classification on Genomic Data**

Yujia Pan\* and Johann Gagnon-Bartsch, University of Michigan

**11h. Estimation of Metabolomic Networks with Gaussian Graphical Models**

Katherine Hoff Shutta\* and Subhajit Naskar, University of Massachusetts, Amherst; Kathryn M. Rexrode, Harvard Medical School; Denise M. Scholtens, Northwestern University; Raji Balasubramanian, University of Massachusetts, Amherst

**11i. Weighted Kernel Method for Integrative Metabolomic and Metagenomic Pathway Analysis**

Angela Zhang\*, University of Washington; Michael C. Wu, Fred Hutchinson Cancer Research Center

**12. POSTERS: FUNCTIONAL DATA/HIGH DIMENSIONAL****Sponsor: ENAR****12a. Dimension Reduction Methods for Multilevel Neural Firing Rate Data**

Angel Garcia de la Garza\* and Jeff Goldsmith, Columbia University

**12b. Amplitude-Phase Separation of Trace-Variogram and its Applications in Spatial Functional Data Analysis**

Xiaohan Guo\* and Sebastian Kurtek, The Ohio State University; Karthik Bharath, University of Nottingham

**12c. Free-Living Walking Strides Segmentation in Wrist-Worn Accelerometry Data**

Marta Karas\*, Johns Hopkins Bloomberg School of Public Health; Ryan T. Roemmich, Johns Hopkins School of Medicine; Ciprian M. Crainiceanu, Johns Hopkins Bloomberg School of Public Health; Jacek K. Urbanek, Johns Hopkins School of Medicine

**12d. Variable Selections for High-Dimensional Unsupervised Learning with Applications in Genomics and Regulatory Pathway Analysis**

Zhipeng Wang\* and David Scott, Rice University

**12e. Integrative Analysis and Prediction Method for Identifying Subgroup-Specific Omics Biomarkers**

Jessica Butts\* and Sandra Safo, University of Minnesota

**12f. A Novel FWER Controlling Procedure for Data with Generalized Reduced Rank Correlation Structure**

Jiatong Sui\* and Xing Qiu, University of Rochester

**12g. Analyzing Accelerometer Data with Probability Magnitude Graphs**

Margaret Banker\* and Peter X.K. Song, University of Michigan

**12h. Normalization of Minute-Level Activity Counts from Chest- and Wrist-Worn Accelerometers: An Example of Actiheart, Actiwatch, and Actigraph**

Vadim Zipunnikov\*, Johns Hopkins University; Jiawei Bai, Johns Hopkins Bloomberg School of Public Health

**13. POSTERS: BAYESIAN, CLUSTERED DATA, HYPOTHESIS TESTING****Sponsor: ENAR****13a. Bayesian Mechanism for Categorical Data with Data Augmentation Strategy**

Arinjita Bhattacharyya\*, Subhadip Pal, Riten Mitra and Shesh N. Rai, University of Louisville

**13b. False Coverage Rate-Adjusted Smoothed Bootstrap Simultaneous Confidence Intervals for Selected Parameters**

Jing Sun\*, Santu Ghosh and Varghese George, Augusta University

**13c. A State-Space Approach in Handling Challenges Associated with Longitudinal Continuous Neuropsychological Outcomes**

Alicia S. Chua\*, Boston University School of Public Health; Yorghos Tripodis, Boston University School of Public Health &amp; Boston University School of Medicine

**13d. Combining Dependent P-values with a Quantile-Based Approach**

Yu Gu\*, Michael P. McDermott and Xing Qiu, University of Rochester

**13e. Bayesian Estimation for Parameters of Nonlinear Multilevel Models under Burr Distributions**

Mohan D. Pant\*, Ismail E. Moudén and Jiangtao Luo, Eastern Virginia Medical School

**13f. A Flexible and Nearly Optimal Sequential Testing Approach to Randomized Testing: QUICK-STOP**

Julian Erik Hecker\*, Brigham and Women's Hospital and Harvard Medical School; Ingo Ruczinski, Johns Hopkins Bloomberg School of Public Health; Michael M. Cho and Edwin Silverman, Brigham and Women's Hospital and Harvard Medical School; Brent Coull and Christoph Lange, Harvard T.H. Chan School of Public Health

**13g. A Weighted Jackknife Approach Using Linear Model-Based Estimates for Clustered Data**

Yejin Choi\*, University of New Mexico; Ruofei Du, University of New Mexico Comprehensive Cancer Center

# SCIENTIFIC PROGRAM

(CONTINUED)

## 14. POSTERS: HIGH-DIMENSIONAL DATA, MISSING DATA AND MORE

Sponsor: ENAR

### 14a. Predicting Latent Contacts from Self-Reported Social Network Data via Outcome Misclassification Adjustment

Qiong Wu\*, Tianzhou Ma and Shuo Chen, University of Maryland

### 14b. Validate Surrogate Endpoints with Continuous and Survival Setup

Idris Demirsoy\*, Florida State University; Helen Li, Regeneron Pharmaceutical

### 14c. New Two-Step Test for Mediation Analysis with Sets of Biomarkers

Andriy Derkach\*, Memorial Sloan Kettering Cancer Center; Joshua Sampson, National Cancer Institute, National Institutes of Health; Simina Boca, Georgetown University Medical Center

### 14d. Meta-Analysis of Binary or Continuous Outcomes Combining Individual Patient Data and Aggregate Data

Neha Agarwala\* and Anindya Roy, University of Maryland, Baltimore County

### 14e. A Post-Processing Algorithm for Building Longitudinal Medication Dose Data from Extracted Medication Information Using Natural Language Processing from Electronic Health Records

Elizabeth McNeer\*, Cole Beck, Hannah L. Weeks, Michael L. Williams, Nathan T. James and Leena Choi, Vanderbilt University Medical Center

### 14f. Power and Sample Size Analysis using Various Statistical Methods in a Tumor Xenograft Study

Sheau-Chiann Chen\* and Gregory D. Ayers, Vanderbilt University Medical Center; Rebecca L. Shattuck-Brandt and Ann Richmond, Vanderbilt University, Department of Veterans Affairs and Tennessee Valley Healthcare System; Yu Shyr, Vanderbilt University Medical Center

### 14g. Estimation and Outliers for Overdispersed Multinomial Data

Barry William McDonald\*, Massey University

### 14h. Partial Least Squares Regression-Based Framework for Incomplete Observations in Environmental Mixture Data Analysis

Ruofei Du\*, University of New Mexico Comprehensive Cancer Center

### 14i. Marginalized Zero-Inflated Negative Binomial Regression Model with Random Effects: Estimating Overall Treatment Effect on Lesion Counts among Multiple Sclerosis Patients (CombiRx Trial)

Steve B. Ampah\*, Lloyd J. Edwards, Leann D. Long, Byron C. Jaeger and Nengjun Yi, University of Alabama at Birmingham

## 15. POSTERS: CONSULTING, EDUCATION, POLICY, EPIDEMIOLOGY

Sponsor: ENAR

### 15a. Semiparametric Shape Restricted Mixed Effect Regression Spline with Application on US Urban Birth Cohort Study Data and State-Wide Prenatal Screening Program Data

Qing Yin\*, University of Pittsburgh

### 15b. Development and Validation of Models to Predict Foodborne Pathogen Presence and Fecal Indicator Bacteria Levels in Agricultural Water using GIS-Based, Data-Driven Approaches

Daniel L. Weller\* and Tanzy Love, University of Rochester; Alexandra Belias and Martin Wiedmann, Cornell University

### 15c. Accounting for Competing Risks in Estimating Hospital Readmission Rates

John D. Kalbfleisch\* and Kevin Zhi He, University of Michigan; Douglas E. Schaubel, University of Pennsylvania; Wenbo Wu, University of Michigan

### 15d. A New Framework for Cost-Effectiveness Analysis with Time-Varying Treatment and Confounding

Nicholas A. Illenberger\*, University of Pennsylvania; Andrew J. Spieker, Vanderbilt University Medical Center; Nandita Mitra, University of Pennsylvania

### 15e. Rethinking the Introductory Biostatistics Curriculum for Non-Biostatisticians

Emily Slade\*, University of Kentucky

### 15f. Establishing Successful Collaboration in a Competitive Environment: Case Studies from a Healthcare Setting

Jay Mandrekar\*, Mayo Clinic

### 15g. Likelihood Ratios to Compare the Statistical Performance of Multiple Tests in Simulation Studies

Qiuxi Huang\*, Boston University School of Public Health

### 15h. Impact of a Biostatistics Department on an Academic Medical Center

Li Wang\*, Henry Domenico and Daniel W. Byrne, Vanderbilt University Medical Center



**16. POSTERS: GENETICS, COMPUTATION****Sponsor: ENAR****16a. Heterogeneity-Aware and Communication-Efficient Distributed Statistical Analysis**

Rui Duan\*, University of Pennsylvania; Yang Ning, Cornell University; Yong Chen, University of Pennsylvania

**16b. False Discovery Rate Computation and Illustration**

Megan C. Hollister\* and Jeffrey D. Blume, Vanderbilt University Medical Center

**16c. A Modified Genomic Control Method for Genetic Association Analysis Using a Stratified, Cluster Sample**

Donald Malec\*, John Pleis, Rong Wei, Bill Cai, Yulei He, Hee-Choon Shin and Guangyu Zhang, National Center for Health Statistics

**16d. Semiparametric Functional Approach with Link Uncertainty**

Young Ho Yun\*, Virginia Tech

**16e. Multi-Ethnic Phenotype Prediction via Effective Modeling of Genetic Effect Heterogeneity**

Lina Yang\* and Dajiang Liu, The Pennsylvania State University College of Medicine

**16f. High Dimensional Sparse Regression with Auxiliary Data on the Features**

Constanza Rojo\* and Pixu Shi, University of Wisconsin, Madison; Ming Yuan, Columbia University; Sunduz Keles, University of Wisconsin, Madison

**16g. A Unified Linear Mixed Model for Simultaneous Assessment of Familial Relatedness and Population Structure**

Tao Wang\*, Medical College of Wisconsin; Paul Livermore Auer and Regina Manansala, University of Wisconsin, Milwaukee; Andrea Rau, GABI, INRA, AgroParisTech and Université Paris-Saclay, France; Nick Devogel, Medical College of Wisconsin

**16h. Cubic Kernel Method for Implicit T Central Subspace**

Weihang Ren\* and Xiangrong Yin, University of Kentucky

**16i. ODAH: A One-Shot Distributed Algorithm for Estimating Semi-Continuous Outcomes using EHR Data in Multiple Sites**

Mackenzie J. Edmondson\*, Chongliang Luo and Rui Duan, University of Pennsylvania; Mitchell Maltenfort and Christopher Forrest, Children's Hospital of Philadelphia; Yong Chen, University of Pennsylvania

**17. POSTERS: META-ANALYSIS, MISSING DATA AND MORE****Sponsor: ENAR****17a. Multiple Imputation of Missing Covariates in Meta-Regression using Multivariate Imputation by Chained Equations**

Amit K. Chowdhry\* and Michael P. McDermott, University of Rochester Medical Center

**17b. Test-Inversion Confidence Intervals for Estimands in Contingency Tables Subject to Equality Constraints**

Qiansheng Zhu\* and Joseph B. Lang, University of Iowa

**17c. Bayesian Cumulative Probability Models for Continuous and Mixed Outcomes**

Nathan T. James\*, Bryan E. Shepherd, Leena Choi, Yuqi Tian and Frank E. Harrell, Jr., Vanderbilt University

**17d. R-Squared and Goodness of Fit in the Linear Mixed Model: A Cautionary Tale**

Boyi Guo\* and Byron C. Jaeger, University of Alabama at Birmingham

**17e. On the Optimality of Group Testing Estimation**

Sarah Church\* and Md S. Warasi, Radford University

**17f. Bayesian Wavelet-Packet Historical Functional Linear Models**

Mark J. Meyer\*, Georgetown University; Elizabeth J. Malloy, American University; Brent A. Coull, Harvard T. H. Chan School of Public Health

**17g. EMBVS: An EM-Bayesian Approach for Analyzing High-Dimensional Clustered Mixed Outcomes**

Yunusa Olufadi\* and E. Olusegun George, University of Memphis

**17h. Generalized Additive Dynamic Effect Change Models: An Interpretable Extension of GAM**

Yuan Yang\*, Jian Kang and Yi Li, University of Michigan

**17i. A Functional Generalized Linear Mixed Model for Estimating Dose Response in Longitudinal Studies**

Madeleine E. St. Ville\*, Clemson University; Andrew W. Bergen, Oregon Research Institute; Carolyn M. Ervin, BioRealm; Christopher McMahan, Clemson University; James W. Baurley, BioRealm; Joe Bible, Clemson University

# SCIENTIFIC PROGRAM

MONDAY, MARCH 23

8:30—10:15 a.m.

## 18. MODERN FUNCTIONAL DATA ANALYSIS

Sponsor: IMS

Organizer: Meng Li, Rice University

Chair: Meng Li, Rice University

8:30 **Minimax Powerful Functional Analysis of Covariance Tests for Longitudinal Genome-Wide Association Studies**

Yehua Li\*, University of California, Riverside

8:55 **Bayesian Function-on-Scalars Regression for High-Dimensional Data**

Daniel R. Kowal\* and Daniel C. Bourgeois, Rice University

9:20 **Modern Functional Data Analysis for Biosciences**

Ana-Maria Staicu\* and Alex Long, North Carolina State University; Meredith King, Northrop Grumman

9:45 **Mean and Covariance Estimation for Functional Snippets**

Jane-Ling Wang\*, University of California, Davis; Zhenhua Lin, National University of Singapore

10:10 **Floor Discussion**

## 19. DISTRIBUTED AND PRIVACY-PRESERVING METHODS FOR ELECTRONIC HEALTH RECORDS DATA

Sponsors: ENAR, ASA Section on Statistics in Defense and National Security, ASA Health Policy Statistics Section

Organizer: Lu Tang, University of Pittsburgh

Chair: Joyce Chang, University of Pittsburgh

8:30 **Communication Efficient Federated Learning from Multiple EHRs Databases**

Changgee Chang\*, Zhiqi Bu and Qi Long, University of Pennsylvania

8:55 **Adaptive Noise Augmentation for Privacy-Preserving Empirical Risk Minimization**

Fang Liu\* and Yinan Li, University of Notre Dame

9:20 **Generating Poisson-Distributed Differentially Private Synthetic Data**

Harrison Quick\*, Drexel University

9:45 **dblink: Distributed End-to-End Bayesian Entity Resolution**

Rebecca Steorts\*, Duke University; Neil Marchant and Ben Rubinstein, University of Melbourne; Andee Kaplan, Colorado State University; Daniel Elazar, Australian Bureau of Statistics

10:10 **Floor Discussion**

## 20. INNOVATIVE STATISTICAL METHODS IN ENVIRONMENTAL MIXTURE ANALYSIS

Sponsors: ENAR, ASA Biometrics Section, ASA Section on Statistics and the Environment, ASA Section on Statistical Learning and Data Science

Organizer: Shanshan Zhao, National Institute of Environmental Health Sciences, National Institutes of Health

Chair: Ling-Wan Chen, National Institute of Environmental Health Sciences, National Institutes of Health

8:30 **Group Inverse-Gamma Gamma Shrinkage for Estimation and Selection in Multipollutant Models**

Jonathan Boss\*, University of Michigan; Jyotishka Datta, University of Arkansas; Sehee Kim and Bhramar Mukherjee, University of Michigan

8:55 **Bayesian Copula Regression for Inference on Dose-Response Curves**

Federico H. Ferrari\*, Duke University; Stephanie M. Engel, University of North Carolina, Chapel Hill; David B. Dunson and Amy H. Herring, Duke University

9:20 **Do Males Matter? A Couple-Based Statistical Model for Association Between Environmental Exposures to Pollutants and Infertility**

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

9:45 **Accommodating Assay Limit-of-Detection in Environmental Mixture Analysis**

Jason P. Fine\*, University of North Carolina, Chapel Hill; Ling-Wan Chen and Shanshan Zhao, National Institute of Environmental Health Sciences, National Institutes of Health

10:10 **Floor Discussion**

## 21. MENTORING THROUGHOUT A LIFETIME: CONSIDERATIONS FOR MENTORS AND MENTEES AT ALL CAREER STAGES

Sponsors: ENAR, ENAR Regional Advisory Board (RAB)

Organizer: Naomi Brownstein, Moffitt Cancer Center

Chair: Emily Butler, GlaxoSmithKline

8:30 **Panel Discussion:**

Leslie McClure, Drexel University  
Brian Millen, Eli Lilly and Company  
Dionne Price, U.S. Food and Drug Administration  
Manisha Desai, Stanford University

10:10 **Floor Discussion**

## 22. INNOVATIVE STATISTICAL APPROACHES FOR HIGH-DIMENSIONAL OMIC AND MICROBIOMIC DATA

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

**Organizer:** Subharup Guha, University of Florida

**Chair:** Zhigang Li, University of Florida

8:30 **Advances and Challenges in Single Cell RNA-Seq Analysis**  
Susmita Datta\*, University of Florida; Michael Sekula and Jeremy Gaskins, University of Louisville

8:55 **Predicting DNA Methylation from Genetic Data Lacking Racial Diversity Using Shared Classified Random Effects**  
J. Sunil Rao\* and Hang Zhang, University of Miami; Melinda Aldrich, Vanderbilt University Medical Center

9:20 **Sparse Generalized Dirichlet Distributions for Microbiome Compositional Data**  
Jyotishka Datta\*, University of Arkansas; David B. Dunson, Duke University

9:45 **Bayesian Nonparametric Differential Analysis for Dependent Multigroup Data with Application to DNA Methylation Analyses**  
Subharup Guha\*, University of Florida; Chiyu Gu, Monsanto Company; Veerabhadran Baladandayuthapani, University of Michigan

10:10 **Floor Discussion**

## 23. BAYESIAN NONPARAMETRICS FOR CAUSAL INFERENCE AND MISSING DATA

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

**Organizer:** Antonio Linero, Florida State University

**Chair:** Yinpu Li, Florida State University

8:30 **Bayesian Nonparametric Models to Address Positivity Assumption Violations in Causal Inference**  
Jason Roy\*, Rutgers University

8:55 **Sensitivity Analysis using Bayesian Additive Regression Trees**  
Nicole Bohme Carnegie\*, Montana State University; Vincent Dorie, Columbia University; Masataka Harada, Fukuoka University; Jennifer Hill, New York University

9:20 **Variable Selection in Bayesian Nonparametric Models for High-Dimensional Confounding**  
Michael J. Daniels\* and Kumaresh Dhara, University of Florida; Jason Roy, Rutgers University

9:45 **Accelerated Bayesian G-Computation Algorithms**  
Antonio R. Linero\*, University of Texas, Austin

10:10 **Floor Discussion**

## 24. CONTRIBUTED PAPERS: VARIABLE SELECTION: HOW TO CHOOSE?

**Sponsor:** ENAR

**Chair:** Nicole B. Carnegie, Montana State University

8:30 **Sparse Nonparametric Regression with Regularized Tensor Product Kernel**  
Hang Yu\*, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University; Donglin Zeng, University of North Carolina, Chapel Hill

8:45 **Pursuing Sources of Heterogeneity in Mixture Regression**  
Yan Li\*, University of Connecticut; Chun Yu, Jiangxi University of Finance and Economics; Yize Zhao, Yale University; Weixin Yao, University of California, Riverside; Robert H. Aseltine and Kun Chen, University of Connecticut

9:00 **An Investigation of Fully Relaxed Lasso and Second-Generation P-Values for High-Dimensional Feature Selection**  
Yi Zuo\* and Jeffrey D. Blume, Vanderbilt University School of Medicine

9:15 **Adaptive Lasso for the Cox Regression with Interval Censored and Possibly Left Truncated Data**  
Chenxi Li\*, Michigan State University; Daewoo Pak, University of Texas MD Anderson Cancer Center; David Todem, Michigan State University

9:30 **Variable Selection for Model-Based Clustering of Functional Data**  
Tanzy Love\*, University of Rochester; Kyra Singh, Google; Eric Hernady, Jacob Finkelstein and Jacqueline Williams, University of Rochester

9:45 **Inconsistency in Multiple Regression Model Specifications**  
Changyong Feng\*, Bokai Wang and Hongyue Wang, University of Rochester; Xin M. Tu, University of California, San Diego

10:00 **C2pLasso: The Categorical-Continuous Pliable Lasso to Identify Brain Regions Affecting Motor Impairment in Huntington Disease**  
Rakheon Kim\*, Texas A&M University; Samuel Mueller, University of Sidney; Tanya Pamela Garcia, Texas A&M University

# SCIENTIFIC PROGRAM

(CONTINUED)

## 25. CONTRIBUTED PAPERS: FUNCTIONAL DATA ANALYSIS

**Sponsor: ENAR**

**Chair: Owais Gilani, Bucknell University**

8:30	<b>Covariate-Adjusted Hybrid Principal Components Analysis for EEG Data</b> Aaron Wolfe Scheffler*, University of California, San Francisco; Abigail Dickinson, Shafali Jeste and Damla Senturk, University of California, Los Angeles
8:45	<b>Evidence-Based Second-Generation P-values on Functional Magnetic Resonance Imaging Data</b> Ya-Chen Lin* and Valerie F. Welty, Vanderbilt University; Jeffrey D. Blume, Kimberly M. Albert, Brian D. Boyd, Warren D. Taylor and Hakmook Kang, Vanderbilt University Medical Center
9:00	<b>Modeling Non-Linear Time Varying Dependence with Application to fMRI Data</b> Ivor Cribben*, Alberta School of Business
9:15	<b>Average Treatment Effect Estimation with Functional Confounders</b> Xiaoke Zhang* and Rui Miao, The George Washington University
9:30	<b>Model-based Statistical Depth with Applications to Functional Data</b> Weilong Zhao* and Zishen Xu, Florida State University; Yun Yang, University of Illinois at Urbana-Champaign; Wei Wu, Florida State University
9:45	<b>Bayesian Inference for Brain Activity from Multi-Resolution Functional Magnetic Resonance Imaging</b> Andrew Whiteman*, Jian Kang and Timothy Johnson, University of Michigan
10:00	<b>Floor Discussion</b>

## 26. CONTRIBUTED PAPERS: PENALIZED AND OTHER REGRESSION MODELS WITH APPLICATIONS

**Sponsor: ENAR**

**Chair: Saryet Kucukemiroglu, U.S. Food and Drug Administration**

8:30	<b>On More Efficient Logistic Regression Analysis via Extreme Ranking</b> Hani Samawi*, Georgia Southern University
8:45	<b>Penalized Models for Analysis of Multiple Mediators</b> Daniel J. Schaid* and Jason P. Sinnwell, Mayo Clinic
9:00	<b>Fitting Equality-Constrained, L1-Penalized Models with Inexact ADMM to Find Gene Pairs</b> Lam Tran*, Lan Luo and Hui Jiang, University of Michigan

9:15	<b>A Comparative Analysis of Penalized Linear Mixed Models in Structured Genetic Data</b> Anna Reisetter* and Patrick Breheny, University of Iowa
9:30	<b>A Two-Stage Kernel Machine Regression Model for Integrative Analysis of Alpha Diversity</b> Runzhe Li* and Ni Zhao, Johns Hopkins Bloomberg School of Public Health
9:45	<b>Penalized Semiparametric Additive Modeling for Group Testing Data</b> Karl B. Gregory*, Dewei Wang, University of South Carolina; Chris S. McMahan, Clemson University
10:00	<b>Penalized Likelihood Logistic Regression with Rare Events-An Application to the Regeneration Dynamics of Pine Species in Oak-Pine Forest Types</b> Dilli Bhatta*, University of South Carolina Upstate

## 27. CONTRIBUTED PAPERS: METHODS FOR NEUROIMAGING DATA: GET THE PICTURE?

**Sponsor: ENAR**

**Chair: Hao Wang, Johns Hopkins University School of Medicine**

8:30	<b>Letting the LaxKAT Out of the Bag: Packaging, Simulation, and Neuroimaging Data Analysis for a Powerful Kernel Test</b> Jeremy S. Rubin*, University of Maryland, Baltimore County; Simon Vandekar, Vanderbilt University; Lior Rennert, Clemson University; Mackenzie Edmonson, and Russell T. Shinohara, University of Pennsylvania
8:45	<b>Comparison of Two Ways of Incorporating the External Information via Linear Mixed Model Design with Application in Brain Imaging</b> Maria Paleczny*, Institute of Mathematics of the Jagiellonian University
9:00	<b>Interpretable Classification Methods for Brain-Computer Interface P300 Speller</b> Tianwen Ma*, Jane E. Huggins and Jian Kang, University of Michigan
9:15	<b>Copula Random Field with Application to Massive Neuroimaging Data Analysis</b> Jie He*, Jian Kang and Peter X.-K. Song, University of Michigan
9:30	<b>Neural Networks Guided Independent Component Analysis with Application to Neuroimaging</b> Daiwei Zhang*, University of Michigan; Ying Guo, Emory University; Jian Kang, University of Michigan



9:45	<b>Removal of Scanner Effects in Covariance of Neuroimaging Measures</b> Andrew Chen*, Haochang Shou and Russell T. Shinohara, University of Pennsylvania
10:00	<b>Classifying Brain Edema with Low-Resolution MRI</b> Danni Tu* and Dylan Small, University of Pennsylvania; Manu S. Goyal, Washington University School of Medicine, St. Louis; Theodore Satterthwaite, Kelly Clark and Russell T. Shinohara, University of Pennsylvania

**28. CONTRIBUTED PAPERS: CAUSAL EFFECT ESTIMATION****Sponsor: ENAR****Chair: Jan De Neve, Ghent University**

8:30	<b>Assessing Exposure Effects on Gene Expression</b> Sarah A. Reifeis*, Michael G. Hudgens, Karen L. Mohlke and Michael I. Love, University of North Carolina, Chapel Hill
8:45	<b>Sensitivity of Clinical Trial Estimands under Imperfect Compliance</b> Heng Chen*, Southern Methodist University; Daniel F. Heitjan, Southern Methodist University and University of Texas, Southwestern
9:00	<b>Borrowing from Supplemental Sources to Estimate Causal Effects from a Primary Data Source</b> Jeffrey A. Boatman*, David M. Vock and Joseph S. Koopmeiners, University of Minnesota
9:15	<b>Estimating Causal Treatment Effects: A Bayesian Inference Approach Adopting Principal Stratification with Strata Predictive Covariates</b> Duncan C. Rotich*, University of Kansas Medical Center; Bin Dong, Janssen Research & Development; Jeffrey A. Thompson, University of Kansas Medical Center
9:30	<b>Estimating Causal Effects in the Presence of Positivity Violations</b> Yaqian Zhu* and Nandita Mitra, University of Pennsylvania; Jason Roy, Rutgers University
9:45	<b>Estimating Causal Effect of Multiple Treatments with Censored Data in Observational Studies</b> Youfei Yu*, Min Zhang and Bhramar Mukherjee, University of Michigan
10:00	<b>Floor Discussion</b>

**MONDAY, MARCH 23****10:15 a.m.—10:30 a.m.****REFRESHMENT BREAK WITH OUR EXHIBITORS****MONDAY, MARCH 23****10:30 a.m.—12:15 p.m.****29. NEW PERSPECTIVES ON DATA INTEGRATION IN GENOME-WIDE ASSOCIATION STUDIES****Sponsor: IMS****Organizer: Qiongshi Lu, University of Wisconsin, Madison****Chair: Hyunseng Kang, University of Wisconsin, Madison**

10:30	<b>TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits</b> Jingjing Yang*, Emory University School of Medicine; Sini Nagpal, Georgia Institute of Technology; Xiaoran Meng and Shizhen Tang, Emory University School of Public Health; Gregory C. Gibson, Georgia Institute of Technology; David A. Bennett, Rush University Medical Center; Philip L. De Jager, Columbia University; Aliza P. Wingo, Atlanta VA Medical Center; Thomas S. Wingo and Michael P. Epstein, Emory University School of Medicine
10:55	<b>Integrating Gene Expression Regulatory Variation Across Populations and Tissues to Understand Complex Traits</b> Heather E. Wheeler*, Loyola University Chicago
11:20	<b>Transcriptome-Wide Transmission Disequilibrium Analysis Identifies Novel Risk Genes for Autism Spectrum Disorder</b> Qiongshi Lu*, Kunling Huang and Yuchang Wu, University of Wisconsin, Madison
11:45	<b>Model Checking and More Powerful Inference in Transcriptome-Wide Association Studies</b> Wei Pan*, University of Minnesota
12:10	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

(CONTINUED)

## 30. ADVANCES IN CAUSAL INFERENCE AND JOINT MODELING WITH SURVIVAL AND COMPLEX LONGITUDINAL DATA

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

**Organizer:** Zhigang Li, University of Florida

**Chair:** James O'Malley, Dartmouth College

**10:30 Causal Proportional Hazards Estimation with a Binary Instrumental Variable**  
Limin Peng\* and Behzad Kianian, Emory University;  
Jung In Kim and Jason Fine, University of North Carolina, Chapel Hill

**11:00 Joint Modeling of Zero-Inflated Longitudinal Microbiome and Time-to-Event Data**  
Huili Li\*, Jiyuan Hu and Chan Wang, New York University; Martin Blaser, Rutgers University

**11:30 Causal Comparative Effectiveness Analysis of Dynamic Continuous-Time Treatment Initiation Rules with Sparsely Measured Outcomes and Death**  
Liangyuan Hu\*, Icahn School of Medicine at Mount Sinai; Joseph W. Hogan, Brown University

**12:00 Discussant:**  
Joseph Hogan, Brown University

## 31. OPPORTUNITIES AND CHALLENGES IN THE ANALYSIS AND INTEGRATION OF LARGE-SCALE BIOBANK DATA

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section in Statistics in Epidemiology, ASA Statistics in Genomics and Genetics Section

**Organizer:** Ryan Sun, University of Texas MD

**Anderson Cancer Center**

**Chair:** Ryan Sun, University of Texas MD Anderson Cancer Center

**10:30 Empowering GWAS Analysis with Missing Data Using Surrogate Phenotypes in Biobanks**  
Xihong Lin\*, Harvard University; Zachary McCaw, Google

**10:55 Fast and Efficient Generalized Estimating Equations for Fitting Non-Linear Model to Biobank Scale Data**  
Nilanjan Chatterjee\* and Diptavo Dutta, Johns Hopkins University

**11:20 Modeling Functional Enrichment Improves Polygenic Prediction Accuracy in UK Biobank and 23andMe Data Sets**  
Carla Marquez-Luna\*, Icahn School of Medicine at Mount Sinai; Steven Gazal, Harvard T.H. Chan School of Public Health; Po-Ru Loh, Brigham and Women's Hospital and Harvard Medical School; Samuel S. Kim, Massachusetts Institute of Technology; Nicholas Furlotte and Adam Auton, 23andMe Inc; Alkes L. Price, Harvard T.H. Chan School of Public Health

## Handling Sampling and Selection Bias in Association Studies Embedded in Electronic Health Records

**11:45**  
Bhramar Mukherjee\* and Lauren J. Beesley, University of Michigan

**12:10 Floor Discussion**

## 32. COMPOSITIONAL NATURE OF MICROBIOME DATA: CHALLENGES AND NEW METHODS

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section in Statistics in Epidemiology, ASA Statistics in Genomics and Genetics Section

**Organizer:** Michael Sohn, University of Rochester

**Chair:** Michael Sohn, University of Rochester

**10:30 Association Testing for Longitudinal Multiomics Data**  
Anna M. Plantinga\*, Williams College

**11:00 Scalable Inference for Count Compositional Microbiome Data**  
Justin D. Silverman\*, Duke University

**11:30 Robust and Powerful Differential Composition Tests on Clustered Microbiome Data**  
Zhengzheng Tang\* and Guanhua Chen, University of Wisconsin, Madison

**12:00 Discussant:**  
Hongzhe Li, University of Pennsylvania

## 33. STATISTICAL MODELING IN ALZHEIMER'S DISEASE

**Sponsors:** ENAR, ASA Health Policy Statistics Section

**Organizer:** Guoqiao Wang, Washington University in St. Louis

**Chair:** Chengjie Xiong, Washington University in St. Louis

**10:30 Bent Lines and Quantiles in Longitudinal Modeling of Alzheimer's Progression**  
Rick Chappell\*, University of Wisconsin, Madison

**10:55 Partly Conditional Modeling for Ordinal Outcomes with Application to Alzheimer's Disease Progression**  
Dandan Liu\* and Jacquelyn Neal, Vanderbilt University

**11:20 Leveraging Disease Progression Modeling to Improve Clinical Trial Design in Alzheimer's Disease**  
Barbara Wendelberger\*, Melanie Quintana and Scott Berry, Berry Consultants

**11:45 Integrative Modeling and Dynamic Prediction of Alzheimer's Disease**  
Sheng Luo\*, Duke University; Kan Li, Merck & Co., Inc.

**12:00 Floor Discussion**

### 34. RECENT ADVANCES IN BAYESIAN METHODS FOR SPATIAL-TEMPORAL PROCESSES

**Sponsors:** ENAR, ASA Bayesian Statistical Science Section, ASA Section in Statistics in Epidemiology  
**Organizer:** Zehang Li, Yale School of Public Health  
**Chair:** Joshua L. Warren, Yale University

10:30	<b>Multivariate Disease Mapping using Directed Acyclic Graph Autoregressive Models</b> Abhi Datta*, Johns Hopkins University
10:55	<b>Modeling Heroin-Related EMS Calls in Space and Time</b> Zehang Richard Li*, Forrest Crawford and Gregg Gonsalves, Yale School of Public Health
11:20	<b>Bayesian Spatial Prediction of Collective Efficacy Across an Urban Environment</b> Catherine Calder*, University of Texas, Austin
11:45	<b>Estimating Subnational Variation in Health Indicators in a Low- and Medium-Income Countries Setting</b> Jon Wakefield*, University of Washington
12:00	<b>Floor Discussion</b>

### 35. SPEED POSTERS: EHR DATA, EPIDEMIOLOGY, PERSONALIZED MEDICINE, CLINICAL TRIALS

**Sponsor:** ENAR  
**Chair:** Chenguang Wang, Johns Hopkins University

#### 35a. INVITED POSTER: Extending Difference-in-Difference Methods to Test the Impact of State-Level Marijuana Laws on Substance Use Using Published Prevalence Estimates

Christine M. Mauro\* and Melanie M. Wall, Columbia University Mailman School of Public Health

#### 35b. INVITED POSTER: Methods of Analysis when an Outcome Variable is a Prediction with Berkson Error

Pamela A. Shaw\*, University of Pennsylvania; Paul Gustafson, University of British Columbia; Daniela Sotres-Alvarez, University of North Carolina, Chapel Hill; Victor Kipnis, National Cancer Institute, National Institutes of Health; Laurence Freedman, Gertner Institute for Epidemiology and Health Policy Research, Sheba Medical Center

#### 35c. Confidence Intervals for the Youden Index and Its Optimal Cut-Off Point in the Presence of Covariates

Xinjie Hu\*, Gengsheng Qin and Chenxue Li, Georgia State University; Jinyuan Chen, Lanzhou University

#### 35d. Critical Window Variable Selection for Pollution Mixtures

Joshua L. Warren\*, Yale University

#### 35e. Learning Individualized Treatment Rules for Multiple-Domain Latent Outcomes

Yuan Chen\*, Columbia University; Donglin Zeng, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University

#### 35f. Semi-Parametric Efficient Prediction of Binary Outcomes when Some Predictors are Incomplete via Post-Stratification

Yaqi Cao\*, University of Pennsylvania; Sebastien Haneuse, Harvard T.H. Chan School of Public Health; Yingye Zheng, Fred Hutchinson Cancer Research Center; Jinbo Chen, University of Pennsylvania

#### 35g. Optimal Sampling Plans for Functional Linear Regression Models

Hyungmin Rha\*, Ming-Hung Kao and Rong Pan, Arizona State University

#### 35h. Optimal Experimental Design for Big Data: Applications in Brain Imaging

Eric W. Bridgeford\*, Shangsi Wang, Zeyi Wang, Brian Caffo and Joshua Vogelstein, Johns Hopkins University

#### 35i. New Statistical Learning for Evaluating Nested Dynamic Treatment Regimes with Test-and-Treat Observational Data

Ming Tang\*, Lu Wang and Jeremy M.G. Taylor, University of Michigan

#### 35j. A Sequential Strategy for Determining Confidence in Individual Treatment Decisions in Personalized Medicine

Nina Orwitz\*, Eva Petkova and Thaddeus Tarpey, New York University

#### 35k. Hidden Analyses: A Systematic Framework of Data Analyses Prior to Statistical Modeling and Recommendations for More Transparent Reporting

Marianne Huebner\*, Michigan State University; Werner Vach, University Hospital Basel, Switzerland; Saskia le Cessie, Leiden University Medical Center, Netherlands; Carsten Schmidt, University Medicine of Greifswald, Germany; Lara Lusa, University of Primorska, Slovenia

#### 35l. A Bayesian Adaptive Design for Early Phase Biomarker Discovery Study

Yi Yao\*, Ying Yuan and Liang Li, University of Texas MD Anderson Cancer Center

#### 35m. Association Between Tooth Loss and Cancer Mortality: NHANES 1999-2015

Xiaobin Zhou\*, Agnes Scott College; Kelli O'Connell and Mengmeng Du, Memorial Sloan Kettering Cancer Center

# SCIENTIFIC PROGRAM

(CONTINUED)

## 36. CONTRIBUTED PAPERS: ADAPTIVE DESIGNS FOR CLINICAL TRIALS

**Sponsor: ENAR**

**Chair: Jingshu O. Wang, The University of Chicago**

**10:30 Keyboard Design for Phase I Drug-Combination Trials**  
Haitao Pan\*, St. Jude Children's Research Hospital;  
Ruitao Lin and Ying Yuan, University of Texas MD  
Anderson Cancer Center

**10:45 Interim Adaptive Decision-Making for Small n Sequential Multiple Assignment Randomized Trial**  
Yan-Cheng Chao\* and Thomas M. Braun, University of  
Michigan; Roy N. Tamura, University of South Florida;  
Kelley M. Kidwell, University of Michigan

**11:00 Bayesian Adaptive Enrichment Trial Design for Continuous Predictive Biomarkers with Possibly Non-Linear or Non-Monotone Effects**  
Yusha Liu\*, Rice University; Lindsay Ann Renfro,  
University of Southern California

**11:15 Robust Blocked Response-Adaptive Randomization Designs**  
Thevaa Chandereng\* and Rick Chappell, University of  
Wisconsin, Madison

**11:30 Streamlined Hyperparameter Tuning in Mobile Health**  
Marianne Menictas\*, Harvard University

**11:45 A Two-Stage Sequential Design for Selecting the t Best Treatments**  
Mingyue Wang\* and Pinyuen Chen, Syracuse University

**12:00 Adaptive Monitoring: Optimal Burn-in to Control False Discoveries Allowing Unlimited Monitoring**  
Jonathan J. Chipman\*, Huntsman Cancer Institute,  
University of Utah; Jeffrey D. Blume and Robert A.  
Greevy, Jr., Vanderbilt University

## 37. CONTRIBUTED PAPERS: BAYESIAN SEMIPARAMETRIC AND NONPARAMETRIC METHODS

**Sponsor: ENAR**

**Chair: Ana-Maria Staicu, North Carolina State University**

**10:30 Heterogeneity Pursuit for Spatial Point Process with Applications: A Bayesian Semiparametric Recourse**  
Jieying Jiao\*, Guanyu Hu and Jun Yan, University of  
Connecticut

**10:45 A Bayesian Finite Mixture Model-Based Clustering Method with Variable Selection for Identifying Disease Phenotypes**  
Shu Wang\*, University of Florida

**11:00 A Bayesian Nonparametric Model for Zero-Inflated Outcomes: Prediction, Clustering, and Causal Estimation**  
Arman Oganisian\* and Nandita Mitra, University of  
Pennsylvania; Jason A. Roy, Rutgers University

**11:15 Longitudinal Structural Topic Models for Estimating Latent Health Trajectories using Administrative Claims Data**  
Mengbing Li\* and Zhenke Wu, University of Michigan

**11:30 Novel Semiparametric Bayesian Methods for the Competing Risks Data with Length-Biased Sampling**  
Tong Wang\*, Texas A&M University

**11:45 A Bayesian Nonparametric Approach for Estimating Causal Effects for Longitudinal Data**  
Kumaresh Dhara\* and Michael J. Daniels,  
University of Florida

**12:00 Floor Discussion**

## 38. CONTRIBUTED PAPERS: STATISTICAL METHODS IN CANCER RESEARCH

**Sponsor: ENAR**

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

**10:30 Identifying Gene-Environment Interactions Using Integrative Multidimensional Omics Data for Cancer Outcomes**  
Yaqing Xu\*, Yale University; Mengyun Wu, Shanghai  
University of Finance and Economics; Shuangge Ma,  
Yale University

**10:45 Bayesian Modeling of Metagenomic Sequencing Data for Discovering Microbial Biomarkers in Colorectal Cancer Detection**  
Shuang Jiang\*, Southern Methodist University;  
Qiwei Li, University of Texas, Dallas; Andrew Y. Koh,  
Guanghua Xiao and Xiaowei Zhan, University of Texas  
Southwestern Medical Center

**11:00 Propensity Score Methods in the Presence of Missing Covariates**  
Kay See Tan\*, Memorial Sloan Kettering Cancer Center

**11:15 Pathway-Structured Predictive Modeling for Multi-Level Drug Response in Multiple Myeloma**  
Xinyan Zhang\*, Georgia Southern University; Bingzong  
Li and Wenzhuo Zhuang, Soochow University; Nengjun  
Yi, University of Alabama at Birmingham

**11:30 Integrative Network Based Analysis of Metabolomic and Transcriptomic Data for Understanding Biological Mechanism of Lung Cancer**  
Christopher M. Wilson\*, Brooke L. Fridley and Doug  
W. Cress, Moffitt Cancer Center; Farnoosh Abbas  
Aghabazadeh, Princess Margaret Cancer Centre



11:45	<b>A General Framework for Multi-Gene, Multi-Cancer Mendelian Risk Prediction Models</b> Jane W Liang*, Harvard T.H. Chan School of Public Health; Gregory Idos, Christine Hong and Stephen B. Gruber, University of Southern California Norris Comprehensive Cancer Center; Giovanni Parmigiani and Danielle Braun, Dana-Farber Cancer Institute
12:00	<b>The Impact of Design Misspecification in Oncology Trials with Survival Endpoint</b> Tyler Zemla* and Jennifer Le-Rademacher, Mayo Clinic

### 39. CONTRIBUTED PAPERS: NETWORK ANALYSIS: CONNECTING THE DOTS

**Sponsor: ENAR**

**Chair: Maiying Kong, University of Louisville**

10:30	<b>Bayesian Assessment of Homogeneity and Consistency for Network Meta-Analysis</b> Cheng Zhang*, Hao Li and Ming-Hui Chen, University of Connecticut; Joseph G. Ibrahim, University of North Carolina, Chapel Hill; Arvind K. Shah and Jianxin Lin, Merck & Co., Inc.
10:45	<b>Bayesian Community Detection for Multiple Networks</b> Luoying Yang* and Zhengwu Zhang, University of Rochester Medical Center
11:00	<b>Semi-Parametric Bayes Regression with Network Valued Covariates</b> Xin Ma*, Suprateek Kundu and Jennifer Stevens, Emory University
11:15	<b>Scalable Network Estimation with L0 Penalty</b> Junghi Kim*, U.S. Food and Drug Administration; Hongtu Zhu, University of North Carolina, Chapel Hill; Xiao Wang, Purdue University; Kim-Anh Do, University of Texas MD Anderson Cancer Center
11:30	<b>Disease Prediction by Integrating Marginally Weak Signals and Local Predictive Gene/Brain Networks</b> Yanming Li*, University of Michigan
11:45	<b>Scalar-on-Network Regression Via Gradient Boosting</b> Emily Morris* and Jian Kang, University of Michigan
12:00	<b>Floor Discussion</b>

### 40. CONTRIBUTED PAPERS: POLICIES AND POLITICS: STATISTICAL ANALYSES OF HEALTH OUTCOMES IN THE REAL WORLD

**Sponsor: ENAR**

**Chair: Ciprian M. Crainiceanu, Johns Hopkins University**

10:30	<b>The Challenges of Electronic Health Record Use to Estimate Individualized Type 2 Diabetes Treatment Strategies</b> Erica EM Moodie* and Gabrielle Simoneau, McGill University
10:45	<b>Incorporating Statistical Methods to Address Spatial Confounding in Large EHR Data Studies</b> Jennifer Bobb* and Andrea Cook, Kaiser Permanente Washington
11:00	<b>A Spatial Causal Analysis of Wildland Fire-Contributed PM2.5 Using Numerical Model Output</b> Alexandra E. Larsen*, Duke University School of Medicine; Shu Yang and Brian J. Reich, North Carolina State University; Ana Rappold, U.S. Environmental Protection Agency
11:15	<b>Propensity Score Matching with Time-Varying Covariates: An Application in the Prevention of Recurrent Preterm Birth</b> Erinn M. Hade*, Giovanni Nattino, Heather A. Frey and Bo Lu, The Ohio State University
11:30	<b>A Bayesian Spatio-Temporal Abundance Model for Surveillance of the Opioid Epidemic</b> David M. Kline*, The Ohio State University; Lance A. Waller, Emory University; Staci A. Hepler, Wake Forest University
11:45	<b>Health Co-Benefits of the Implementation of Global Climate Mitigation Commitments</b> Gavin Shaddick*, University of Exeter
12:00	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

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## 41. CONTRIBUTED PAPERS: STATISTICAL CONSIDERATIONS FOR OPTIMAL TREATMENT

Sponsor: ENAR

Chair: Andrada E. Ivanescu, Montclair State University

10:30	<b>Optimal Treatment Regime Estimation using Pseudo Observation with Censored Data</b> Taehwa Choi* and Sangbum Choi, Korea University
10:45	<b>Boosting Algorithms for Estimating Optimal Individualized Treatment Rules</b> Duzhe Wang*, University of Wisconsin, Madison; Haoda Fu, Eli Lilly and Company; Po-Ling Loh, University of Wisconsin, Madison
11:00	<b>Capturing Heterogeneity in Repeated Measures Data by Fusion Penalty</b> Lili Liu*, Shandong University and Washington University in St. Louis; Lei Liu, Washington University in St. Louis
11:15	<b>Optimal Individualized Decision Rules Using Instrumental Variable Methods</b> Hongxiang Qiu* and Marco Carone, University of Washington; Ekaterina Sadikova, Maria Petukhova and Ronald C. Kessler, Harvard Medical School; Alex Luedtke, University of Washington
11:30	<b>Sample Size and Timepoint Tradeoffs for Comparing Dynamic Treatment Regimens in a Longitudinal SMART</b> Nicholas J. Seewald* and Daniel Almirall, University of Michigan
11:45	<b>Floor Discussion</b>

## MONDAY, MARCH 23

12:15 p.m. — 1:30 p.m.

### ROUNDTABLE LUNCHEONS

## MONDAY, MARCH 23

1:45 p.m. — 3:30 p.m.

## 42. CAUSAL INFERENCE WITH GENETIC DATA

Sponsor: IMS

Organizer: Qingyuan Zhao, University of Cambridge

Chair: Richard Charnigo, University of Kentucky

1:45	<b>Estimating Causal Relationship for Complex Traits with Weak and Heterogeneous Genetic Effects</b> Jingshu Wang*, The University of Chicago; Qingyuan Zhao, University of Cambridge; Jack Bowden, Gibran Hemani and George Davey Smith, University of Bristol; Nancy R. Zhang and Dylan Small, University of Pennsylvania
2:15	<b>Distinguishing Genetic Correlation from Causation in GWAS</b> Luke J. O'Connor*, Broad Institute; Alkes L. Price, Harvard T.H. Chan School of Public Health
2:45	<b>Robust Methods with Two-Sample Summary Data Mendelian Randomization</b> Hyunseung Kang*, University of Wisconsin, Madison
3:15	<b>Discussant:</b> Qingyuan Zhao, University of Cambridge

## 43. RECENT ADVANCES IN STATISTICAL METHODS FOR SINGLE-CELL OMICS ANALYSIS

Sponsor: IMS

Organizer: Yuchao Jiang, University of North Carolina, Chapel Hill

Chair: Rhonda Bacher, University of Florida

1:45	<b>Fast and Accurate Alignment of Single-Cell RNA-seq Samples Using Kernel Density Matching</b> Mengjie Chen*, Yang Li and Qi Zhan, The University of Chicago
2:10	<b>Novel Computational Methods for Analyzing Single Cell Multi-Omics Data</b> Wei Chen*, University of Pittsburgh
2:35	<b>DNA Copy Number Profiling: From Bulk to Single-Cell Sequencing</b> Yuchao Jiang*, University of North Carolina, Chapel Hill
3:00	<b>Statistical Analysis of Spatial Expression Pattern for Spatially Resolved Transcriptomic Studies</b> Xiang Zhou*, Shiquan Sun and Jiaqiang Zhu, University of Michigan
3:25	<b>Floor Discussion</b>

**44. RECENT ADVANCES IN MICROBIOME DATA ANALYSIS****Sponsor:** IMS**Organizer:** Anru Zhang, University of Wisconsin, Madison**Chair:** Chi Zhang, Indiana University

1:45	<b>Incorporating Auxiliary Information to Improve Microbiome-Based Prediction Models</b> Michael C. Wu*, Fred Hutchinson Cancer Research Center
2:10	<b>Estimation and inference with non-random missing data and latent factors</b> Christopher McKennan*, University of Pittsburgh
2:35	<b>Statistical Methods for Tree Structured Microbiome Data</b> Hongyu Zhao*, Yale University; Tao Wang and Yaru Song, Shanghai Jiao Tong University; Can Yang, Hong Kong University of Science and Technology
3:00	<b>High-Dimensional Log-Error-in-Variable Regression with Applications to Microbial Compositional Data Analysis</b> Anru Zhang*, Pixu Shi and Yuchen Zhou, University of Wisconsin, Madison
3:25	<b>Floor Discussion</b>

**45. NOVEL METHODS TO EVALUATE SURROGATE ENDPOINTS****Sponsors:** ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section**Organizer:** Ludovic Trinquart, Boston University School of Public Health**Chair:** Michael LaValley, Boston University School of Public Health

1:45	<b>Using a Surrogate Marker for Early Testing of a Treatment Effect</b> Layla Parast*, RAND; Tianxi Cai, Harvard University; Lu Tian, Stanford University
2:10	<b>Mediation Analysis with Illness-Death Model for Right-Censored Surrogate and Clinical Outcomes</b> Isabelle Weir*, Harvard T.H. Chan School of Public Health; Jennifer Rider and Ludovic Trinquart, Boston University
2:35	<b>Incorporating Patient Subgroups During Surrogate Endpoint Validation</b> Emily Roberts*, Michael Elliott and Jeremy MG Taylor, University of Michigan

**Assessing a Surrogate Predictive Value: A Causal Inference Approach**

3:00	Ariel Alonso Abad*, University of Leuven; Wim Van der Elst, Janssen Pharmaceutica; Geert Molenberghs, University of Leuven
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**3:25 Floor Discussion****46. RECENT ADVANCES IN THE UNCERTAINTY ESTIMATION AND PROPERTIES OF BAYESIAN ADDITIVE REGRESSION TREES****Sponsors:** ENAR, IMS, ASA Bayesian Statistical Science Section, ASA Section on Statistical Learning and Data Science**Organizer:** Yaoyuan Vincent Tan, Rutgers School of Public Health  
**Chair:** Chanmin Kim, Boston University School of Public Health

1:45	<b>Heteroscedastic BART via Multiplicative Regression Trees</b> Matthew T. Pratola*, The Ohio State University; Hugh A. Chipman, Acadia University; Edward I. George, University of Pennsylvania; Robert E. McCulloch, Arizona State University
2:10	<b>Bayesian Nonparametric Modeling with Tree Ensembles for Predicting Patient Outcomes</b> Robert E. McCulloch*, Arizona State University; Rodney Sparapani, Purushottam Laud and Brent Logan, Medical College of Wisconsin
2:35	<b>Bayesian Decision Tree Ensembles in Fully Nonparametric Problems</b> Yinpu Li*, Florida State University; Antonio Linero, University of Texas, Austin; Junliang Du, Florida State University
3:00	<b>On Theory for BART</b> Veronika Rockova* and Enakshi Saha, The University of Chicago
3:25	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

(CONTINUED)

## 47. CURRENT DEVELOPMENTS IN ANALYZING EHR AND BIOBANK DATA

**Sponsor:** ENAR

**Organizer:** Xue Zhong, Vanderbilt University

**Chair:** Xue Zhong, Vanderbilt University

1:45	<b>Adventures with Large Biomedical Datasets: Diseases, Medical Records, Environment and Genetics</b> Andrey Rzhetsky*, The University of Chicago
2:10	<b>Association Analysis of Biobank Scale Data Using Minimal Sufficient Statistics</b> Dajiang Liu*, Penn State College of Medicine
2:35	<b>Use of Electronic Health Records and a Biobank for Pharmacogenomic Studies: Promises and Challenges</b> Leena Choi*, Vanderbilt University Medical Center
3:00	<b>Assessing the Progress of Alzheimer's Disease Via Electronic Medical Records</b> Zhijun Yin*, Vanderbilt University Medical Center
3:25	<b>Floor Discussion</b>

## 48. SPEED POSTERS: CAUSAL INFERENCE/ LONGITUDINAL DATA/HIGH-DIMENSIONAL DATA/MASSIVE DATA

**Sponsor:** ENAR

**Chair:** Yong Lin, Rutgers University

<b>48a. INVITED POSTER: Bipartite Causal Inference with Interference for Evaluating Air Pollution Regulations</b> Corwin M. Zigler*, University of Texas, Austin and Dell Medical School
<b>48b. Doubly Robust Estimation of Causal Effects with Covariate-Balancing Propensity Score and Machine-Learning-Based Outcome Prediction</b> Byeong Yeob Choi*, University of Texas Health Science Center at San Antonio
<b>48c. Percentile-Based Residuals for Model Assessment</b> Sophie Berube*, Abhirup Datta, Chenguang Wang, Qingfeng Li and Thomas A. Louis, Johns Hopkins Bloomberg School of Public Health
<b>48d. Change-Point Detection in Multivariate Time Series</b> Tong Shen*, University of California, Irvine; Xu Gao, Google; Hernando Ombao, King Abdullah University of Science and Technology; Zhaoxia Yu, University of California, Irvine

## 48e. Approaches for Modeling Spatially Varying Associations Between Multi-Modal Images

Alessandra M. Valcarcel\*, University of Pennsylvania; Simon N. Vandekar, Vanderbilt University; Tinashe Tapera, Azeez Adebimpe and David Roalf, University of Pennsylvania; Armin Raznahan, National Institute of Mental Health, National Institutes of Health; Theodore Satterthwaite, Russell T. Shinohara and Kristin Linn, University of Pennsylvania

## 48f. Generalizing Trial Findings using Nested Trial Designs with Sub-Sampling of Non-Randomized Individuals

Sarah E. Robertson\* and Issa J. Dahabreh, Brown University; Miguel A. Hernan, Harvard University; Ashley L. Buchanan, University of Rhode Island; Jon A. Steingrimsson, Brown University

## 48g. Causal Inference with Multiple Mediators in a Survival Context

Hui Zeng\* and Vernon Michael Chinchilli, The Pennsylvania State University

## 48h. Adjusting for Compliance in SMART Designs

William Jeremy Artman\*, Ashkan Ertefaie and Brent Johnson, University of Rochester

## 48i. Statistical Inference for Cox Proportional Hazards Model with a Diverging Number of Covariates

Lu Xia\*, University of Michigan; Bin Nan, University of California, Irvine; Yi Li, University of Michigan

## 48j. Bayesian Focal-Area Detection for Multi-Class Dynamic Model with Application to Gas Chromatography

Byung-Jun Kim\*, Virginia Tech

## 48k. The Survivor Separable Effects

Mats Julius Stensrud\* and Miguel Hernan, Harvard T. H. Chan School of Public Health; Jessica Julius Young, Harvard Medical School

## 48l. Adjusted Cox Scores for GWAS and PheWAS Screening in R

Elizabeth A. Sigworth\*, Ran Tao, Frank Harrell and Qingxia Chen, Vanderbilt University

## 48m. Microbiome Quantile Regression

Myung Hee Lee\*, Weill Cornell Medical College



**49. CONTRIBUTED PAPERS: STATISTICAL METHODS FOR OMICS DATA ANALYSIS****Sponsor: ENAR****Chair: Yehua Li, University of California, Riverside**

1:45	<b>Mean-Correlation Relationship Biases Co-Expression Analysis</b> Yi Wang* and Stephanie C. Hicks, Johns Hopkins Bloomberg School of Public Health; Kasper D. Hansen, Johns Hopkins Bloomberg School of Public Health and McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins School of Medicine
2:00	<b>Efficient Detection and Classification of Epigenomic Changes Under Multiple Conditions</b> Pedro L. Baldoni*, Naim U. Rashid and Joseph G. Ibrahim, University of North Carolina, Chapel Hill
2:15	<b>BREM-SC: A Bayesian Random Effects Mixture Model for Clustering Single Cell Multi-Omics Data</b> Xinjun Wang*, Zhe Sun, Yanfu Zhang, Heng Huang, Kong Chen, Ying Ding and Wei Chen, University of Pittsburgh
2:30	<b>Co-Localization Between Sequence Constraint and Epigenomic Information Improves Interpretation of Whole Genome Sequencing Data</b> Dangqing Xu*, Chen Wang and Krzysztof Kiryluk, Columbia University; Joseph D. Buxbaum, Icahn School of Medicine at Mount Sinai; Iuliana Ionita-Laza, Columbia University
2:45	<b>Covariate Adaptive False Discovery Rate Control with Applications to Epigenome-Wide Association Studies</b> Jun Chen*, Mayo Clinic; Xianyang Zhang, Texas A&M University
3:00	<b>Estimation of Cell-Type Proportions in Complex Tissue</b> Gregory J. Hunt*, William & Mary; Johann A. Gagnon-Bartsch, University of Michigan
3:15	<b>Floor Discussion</b>

**50. CONTRIBUTED PAPERS: OBSERVATIONAL AND HISTORICAL DATA ANALYSIS: THE REST IS HISTORY****Sponsor: ENAR****Chair: Paul J. Rathouz, University of Texas, Austin**

1:45	<b>Identifying the Optimal Timing of Surgery from Observational Data</b> Xiaofei Chen* and Daniel F. Heitjan, Southern Methodist University and University of Texas Southwestern Medical Center; Gerald Greil and Haekyung Jeon-Slaughter, University of Texas Southwestern Medical Center
2:00	<b>Historical Control Borrowing in Adaptive Designs “To Borrow or Not to Borrow?”</b> Nusrat Harun*, Cincinnati Children’s Hospital Medical Center; Mi-Ok Kim, University of California, San Francisco; Maurizio Macaluso, Cincinnati Children’s Hospital Medical Center
2:15	<b>Weighted F Test and Weighted Chi-Square Test for Multiple Group Comparisons in Observational Studies</b> Maiying Kong*, Xiaofang Yan and Qi Zheng, University of Louisville
2:30	<b>Bayesian Probability of Success of Clinical Trials for the Generalized Linear Model Using Historical Data</b> Ethan M. Alt*, Matthew A. Psioda and Joseph G. Ibrahim, University of North Carolina, Chapel Hill
2:45	<b>Borrowing Strength from Auxiliary Variables and Historical Data for Counties with very Small Sample Sizes or No Data</b> Hui Xie*, Deborah B. Rolka and Lawrence Barker, Centers for Disease Control and Prevention
3:00	<b>Adaptive Combination of Conditional Treatment Effect Estimators Based on Randomized and Observational Data</b> David Cheng*, VA Boston Healthcare System; Ross Prentice, University of Washington School of Public Health and Community Medicine; Tianxi Cai, Harvard T.H. Chan School of Public Health
3:15	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

(CONTINUED)

## 51. CONTRIBUTED PAPERS: IMMUNOTHERAPY CLINICAL TRIAL DESIGN AND ANALYSIS

**Sponsor: ENAR**

**Chair: Ming-Hui Chen, University of Connecticut**

1:45	<b>Time-to-Event Model-Assisted Designs to Accelerate and Optimize Early-Phase Immunotherapy Trials</b> Ruitao Lin*, University of Texas MD Anderson Cancer Center
2:00	<b>Designing Cancer Immunotherapy Trials with Delayed Treatment Effect Using Maximin Efficiency Robust Statistics</b> Xue Ding* and Jianrong Wu, University of Kentucky
2:15	<b>Cancer Immunotherapy Trial Design with Cure Rate and Delayed Treatment Effect</b> Jing Wei* and Jianrong Wu, University of Kentucky
2:30	<b>Cancer Immunotherapy Trial Design with Long-Term Survivors</b> Jianrong Wu* and Xue Ding, University of Kentucky
2:45	<b>Evaluate the Properties of Cure Model in the Context of Immuno-oncology Trials</b> Quyen Duong* and Jennifer Le-Rademacher, Mayo Clinic
3:00	<b>Phase I/II Dose-Finding Interval Design for Immunotherapy</b> Yeonhee Park*, Medical University of South Carolina
3:15	<b>Floor Discussion</b>

## 52. CONTRIBUTED PAPERS: MACHINE LEARNING AND STATISTICAL RELATIONAL LEARNING

**Sponsor: ENAR**

**Chair: Mohan D. Pant, Eastern Virginia Medical School**

1:45	<b>Merging versus Ensembling in Multi-Study Machine Learning: Theoretical Insight from Random Effects</b> Zoe Guan* and Giovanni Parmigiani, Harvard T.H. Chan School of Public Health, Dana-Farber Cancer Institute; Prasad Patil, Boston University
2:00	<b>Informative Dynamic ODE-based-Network Learning (IDOL) from Steady Data</b> Chixiang Chen*, Ming Wang and Rongling Wu, The Pennsylvania State University

## Examining the Regulatory Use of Machine Learning for Drug Safety Studies

2:15

Jae Joon Song\*, Hana Lee and Tae Hyun Jung, U.S. Food and Drug Administration

## Mixture Proportion Estimation in Positive-Unlabeled Learning

2:30

James Patrick Long\*, University of Texas MD Anderson Cancer Center; Zhenfeng Lin, Microsoft

## Unsupervised Learning of Disease Heterogeneity and Patient Subgroups using Diagnosis Codes in Electronic Medical Records

2:45

Yaomin Xu\*, Vanderbilt University Medical Center

## Deep Learning for Cell Painting Image Analysis

3:00

Yuting Xu\*, Andy Liaw and Shubing Wang, Merck & Co., Inc.

## Model Building Methods in Machine Learning for Clinical Outcome Prediction

3:15

Jarcy Zee\* and Qian Liu, Arbor Research Collaborative for Health; Laura H. Mariani, University of Michigan; Abigail R. Smith, Arbor Research Collaborative for Health

## 53. CONTRIBUTED PAPERS: TIME SERIES AND RECURRENT EVENT DATA

**Sponsor: ENAR**

**Chair: S. Yaser Samadi, Southern Illinois University**

## Integer-Valued Autoregressive Process with Flexible Marginal and Innovation Distributions

1:45

Matheus Bartolo Guerrero\*, King Abdullah University of Science and Technology; Wagner Barreto-Souza, Universidade Federal de Minas Gerais; Hernando Ombao, King Abdullah University of Science and Technology

## Analysis of N-of-1 Trials Using Bayesian Distributed Lag Model with AR(p) Error

2:00

Ziwei Liao\*, Ying Kuen Cheung and Ian Kronish, Columbia University; Karina Davidson, Feinstein Institute for Medical Research

## An Estimating Equation Approach for Recurrent Event Models with Non-Parametric Frailties

2:15

Lili Wang\*, University of Michigan; Douglas E. Schaebel, University of Pennsylvania

## Shape-Preserving Prediction for Stationary Functional Time Series

2:30

Shuhao Jiao\* and Hernando Ombao, King Abdullah University of Science and Technology

2:45	<b>A Class of Dynamic Additive-Multiplicative Models for Recurrent Event Data</b> Russell S. Stocker*, Indiana University of Pennsylvania
3:00	<b>Causal Dependence between Multivariate Time Series</b> Yuan Wang*, Washington State University; Louis Scharf, Colorado State University
3:15	<b>Floor Discussion</b>

#### 54. CONTRIBUTED PAPERS: MASSIVE DATA: A GIANT PROBLEM?

**Sponsor:** ENAR

**Chair:** Sharon M. Lutz, Harvard Medical School and Harvard Pilgrim Health Care Institute

1:45	<b>Irreproducibility in Large-Scale Drug Sensitivity Data</b> Zoe L. Rehnberg* and Johann A. Gagnon-Bartsch, University of Michigan
2:00	<b>A New Integrated Marked Point Process Approach to Analyze Highly Multiplexed Cellular Imaging Data</b> Coleman R. Harris*, Qi Liu, Eliot McKinley, Joseph Roland, Ken Lau, Robert Coffey and Simon Vandekar, Vanderbilt University Medical Center
2:15	<b>Comparison of Methods to Analyze Clustered Time-to-Event Data with Competing Risks</b> Yuxuan Wang*, Guanqun Meng, Wenhan Lu, Zehua Pan, Can Meng, Erich Greene, Peter Peduzzi and Denise Esserman, Yale Center for Analytical Sciences
2:30	<b>False Discovery Rates for Second-Generation p-Values in Large-Scale Inference</b> Valerie Welty* and Jeffrey Blume, Vanderbilt University
2:45	<b>Drives of Inpatient Readmissions: Insights from Analysis of National Inpatient Database</b> Haileab Hilafu* and Bogdan Bichescu, University of Tennessee
3:00	<b>Large Scale Hypothesis Testing with Reduced Variance of the False Discovery Proportion</b> Olivier Thas*, I-BioStat, Data Science Institute, Hasselt University, Belgium, Ghent University, Belgium and University of Wollongong, Australia; Stijn Hawinkel, Ghent University, Belgium; Luc Bijnen, Janssen Pharmaceuticals
3:15	<b>Floor Discussion</b>

#### MONDAY, MARCH 23

**3:30 p.m. — 3:45 p.m.**

#### REFRESHMENT BREAK WITH OUR EXHIBITORS

#### MONDAY, MARCH 23

**3:45 p.m. — 5:30 p.m.**

#### 55. HUMAN MICROBIOME STUDIES: NOVEL METHODS AND NEW STUDIES

**Sponsors:** ENAR, IMS, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section

**Organizer:** Ni Zhao, Johns Hopkins Bloomberg School of Public Health

**Chair:** Ni Zhao, Johns Hopkins Bloomberg School of Public Health

3:45	<b>A Novel Method for Compositional Analysis of the Microbiome Data</b> Yijuan Hu*, Emory University
4:10	<b>Estimating the Overall Contribution of Human Oral Microbiome to the Risk of Developing Cancers Based on Prospective Studies</b> Jianxin Shi*, National Cancer Institute, National Institutes of Health
4:35	<b>Multi-Group Analysis of Compositions of Microbiomes with Bias Correction (MANCOM-BC)</b> Shyamal D. Peddada* and Huang Lin, University of Pittsburgh
5:00	<b>A Powerful Microbial Group Association Test Based on the Higher Criticism Analysis for Sparse Microbial Association Signals</b> Ni Zhao* and Hyunwook Koh, Johns Hopkins University
5:25	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

(CONTINUED)

## 56. BAYESIAN APPROACHES FOR COMPLEX INNOVATIVE CLINICAL TRIAL DESIGN

**Sponsors:** ENAR, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Statistical Consulting Section, ASA Biopharmaceutical Section

**Organizer:** Joseph Ibrahim, University of North Carolina, Chapel Hill

**Chair:** Brady Nifong, University of North Carolina, Chapel Hill

3:45 **Bayesian Clinical Trial Design using Historical Data that Inform the Treatment Effect**  
Joseph G. Ibrahim\* and Matthew A. Psioda, University of North Carolina, Chapel Hill

4:10 **Advanced Hierarchical Modeling in Clinical Trials**  
Kert Viele\*, Berry Consultants

4:35 **Bayesian Sequential Monitoring of Clinical Trials**  
Matthew Austin Psioda\* and Evan Kwiatkowski, University of North Carolina, Chapel Hill; Mat Soukup and Eugenio Andraca-Carrera, U.S. Food and Drug Administration

5:00 **Bayesian Clinical Trial Designs using SAS**  
Fang Chen\*, SAS Institute Inc.; Guanghan Frank Liu, Merck & Co. Inc.

5:25 **Floor Discussion**

## 57. ACHIEVING REAL-WORLD EVIDENCE FROM REAL-WORLD DATA: RECENT DEVELOPMENTS AND CHALLENGES

**Sponsors:** ENAR, ASA Biometrics Section

**Organizer:** Haiwen Shi, U.S. Food and Drug Administration

**Chair:** Haiwen Shi, U.S. Food and Drug Administration

3:45 **Real-World Data and Analytics for Regulatory Decision-Making: FDA/CDRH Experience**  
Lilly Yue\*, U.S. Food and Drug Administration

4:15 **RWD, EHRs, PROs; Using Data to Inform the Patient Trajectory and Experience**  
Warren A. Kibbe\*, Duke University

4:45 **Addressing Confounding in Real-World Evidence using Propensity Scores**  
John D. Seeger\*, Optum

5:15 **Discussant:**  
Lisa LaVange, University of North Carolina, Chapel Hill

## 58. NOVEL SPATIAL MODELING APPROACHES FOR AIR POLLUTION EXPOSURE ASSESSMENT

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

**Organizer:** Yawen Guan, University of Nebraska, Lincoln

**Chair:** Kate Calder, The Ohio State University

3:45 **Spatiotemporal Data Fusion Model for Air Pollutants in the Near-Road Environment using Mobile Measurements and Dispersion Model Output**  
Owais Gilani\*, Bucknell University; Veronica J. Berrocal, University of California, Irvine; Stuart A. Batterman, University of Michigan

4:10 **Multi-Resolution Data Fusion of Air Quality Model Outputs for Improved Air Pollution Exposure Assessment: An Application to PM2.5**  
Veronica J. Berrocal\*, University of California, Irvine

4:35 **Multivariate Spectral Downscaling for PM2.5 Species**  
Yawen Guan\*, University of Nebraska, Lincoln; Brian Reich, North Carolina State University; James Mulholland, Georgia Institute of Technology; Howard Chang, Emory University

5:00 **Functional Regression for Predicting Air Pollution Concentrations from Spatially Misaligned Data**  
Meredith Franklin\* and Khang Chau, University of Southern California

5:25 **Floor Discussion**

## 59. INNOVATIONS IN TWO PHASE SAMPLING DESIGNS WITH APPLICATIONS TO EHR DATA

**Sponsors:** ENAR, ASA Biometrics Section

**Organizer:** Pamela Shaw, University of Pennsylvania

**Chair:** Bryan Shepherd, Vanderbilt University

3:45 **Optimal and Nearly-Optimal Designs for Studies with Measurement Errors**  
Gustavo G. C. Amorim\*, Bryan E. Shepherd, Ran Tao and Sarah C. Lotspeich, Vanderbilt University Medical Center; Pamela A. Shaw, University of Pennsylvania; Thomas Lumley, University of Auckland

4:15 **The Mean Score and Efficient Two-Phase Sampling for Discrete-Time Survival Models with Error Prone Exposures**  
Kyunghee Han\*, University of Pennsylvania; Thomas Lumley, University of Auckland; Bryan E. Shepherd, Vanderbilt University Medical Center; Pamela A. Shaw, University of Pennsylvania



4:45	<b>Two-Phase Designs Involving Incomplete Life History Processes</b> Richard J. Cook*, University of Waterloo
5:15	<b>Discussant:</b> Jianwen Cai, University of North Carolina, Chapel Hill
<b>60. RECENT APPROACHES TO MULTIVARIATE DATA ANALYSIS IN THE HEALTH SCIENCES</b>	
Sponsors: ENAR, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Section on Statistics in Epidemiology, ASA Statistics in Genomics and Genetics Section, ASA Health Policy Statistics Section Organizer: Brian Neelon, Medical University of South Carolina Chair: Christopher Schmid, Brown University	
3:45	<b>A Multivariate Discrete Failure Time Model for the Analysis of Infant Motor Development</b> Brian Neelon*, Medical University of South Carolina
4:10	<b>Incorporating a Bivariate Neighborhood Effect of a Single Neighborhood Identifier in a Hierarchical Model</b> James O'Malley*, Dartmouth College; Peter James, Harvard T.H. Chan School of Public Health; Todd A. MacKenzie and Jinyoung Byun, Dartmouth College; SV Subramanian, Harvard T.H. Chan School of Public Health; Jason B. Block, Harvard Pilgrim Health Care
4:35	<b>hubViz: A Bayesian Model for Hub-Centric Visualization of Multivariate Binary Data</b> Dongjun Chung*, The Ohio State University; Jin Hyun Nam, Medical University of South Carolina; Ick Hoon Jin, Yonsei University
5:00	<b>On Nonparametric Estimation of Causal Networks with Additive Faithfulness</b> Kuang-Yao Lee*, Temple University; Tianqi Liu, Google; Bing Li, The Pennsylvania State University; Hongyu Zhao, Yale University
5:25	<b>Floor Discussion</b>

## 61. SPEED POSTERS: IMAGING DATA/SURVIVAL ANALYSIS/SPATIO-TEMPORAL

**Sponsor:** ENAR

**Chair:** Layla Parast, RAND

### 61a. INVITED POSTER: A Geometric Approach Towards Evaluating fMRI Preprocessing Pipelines

Martin Lindquist\*, Johns Hopkins Bloomberg School of Public Health

### 61b. Non-Parametric Estimation of Spearman's Rank Correlation with Bivariate Survival Data

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

### 61c. Nonparametric Tests for Semi-Competing Risks Data under Markov Illness-Death Model

Jing Li\* and Giorgos Bakoyannis, Indiana University; Ying Zhang, University of Nebraska Medical Center; Sujuan Gao, Indiana University

### 61d. Parsimonious Covariate Selection for Interval Censored Data

Yi Cui\*, State University of New York at Albany; Xiaoxue Gu, North Dakota State University; Bo Ye, State University of New York at Albany

### 61e. Identifying Amenity Typologies in the Built Environment: A Bayesian Non-Parametric Approach

Adam T. Peterson\*, University of Michigan; Veronica Berrocal, University of California, Irvine; Brisa Sánchez, Drexel University

### 61f. Estimation of a Buffering Window in Functional Linear Cox Regression Models for Spatially-Defined Environmental Exposure

Jooyoung Lee\*, Harvard T.H. Chan School of Public Health; Donna Spiegelman, Yale School of Public Health; Molin Wang, Harvard T.H. Chan School of Public Health

### 61g. An Alternative Sensitivity Analysis for Informative Censoring

Patrick O'Connor\*, Chiu-Hsieh Hsu, Denise Roe and Chengcheng Hu, University of Arizona; Jeremy M.G. Taylor, University of Michigan

### 61h. Displaying Survival of Patient Groups Defined by Covariate Paths: Extensions of the Kaplan-Meier Estimator

Melissa Jay\*, University of Iowa; Rebecca Betensky, New York University

# SCIENTIFIC PROGRAM

(CONTINUED)

## 61i. Semiparametric Transformation Model for Clustered Competing Risks Data

Yizeng He\* and Soyoung Kim, Medical College of Wisconsin; Lu Mao, University of Wisconsin, Madison; Kwang Woo Ahn, Medical College of Wisconsin

## 61j. Partial Linear Single Index Mean Residual Life Models

Peng Jin\* and Mengling Liu, New York University School of Medicine

## 61k. Evaluating the Diagnostic Accuracy of a New Biomarker for Prostate Cancer: Challenges in Small Samples

Joshua I. Banks\*, Jungreem Woo, Sandra Santasusagna, Benjamin Leiby and Josep Domingo-Domenech, Thomas Jefferson University

## 61l. Identifying Spatio-Temporal Variation in Breast Cancer Incidence Among Different Age Cohorts Using Bayesian Hierarchical Modeling

Amy E. Hahn\*, Jacob Oleson and Paul Romitti, University of Iowa

## 61m. One-to-One Feature Matching with Application to Multi-Level Modeling

David Degras\*, University of Massachusetts, Boston

## 62. CONTRIBUTED PAPERS: IMAGING AND STREAMING DATA ANALYSIS

Sponsor: ENAR

Chair: Daniel Kowal, Rice University

### 3:45 Generalizable Two-Stage PCA for Confounding Adjustment

Sarah M. Weinstein\*, Kristin A. Linn\*, and Russell T. Shinohara\*, University of Pennsylvania

### 4:00 Permutation-Based Inference for Spatially Localized Signals in Longitudinal MRI Data

Jun Young Park\* and Mark Fiecas, University of Minnesota

### 4:15 Geostatistical Modeling of Positive Definite Matrices: An Application to Diffusion Tensor Imaging

Zhou Lan\*, The Pennsylvania State University; Brian Reich, North Carolina State University; Joseph Guinness, Cornell University; Dipankar Bandyopadhyay, Virginia Commonwealth University

### 4:30 Length Penalized Probabilistic Principal Curve with Application to Pharmacologic Colon Imaging Study

Huan Chen\*, Johns Hopkins Bloomberg School of Public Health

### 4:45 Image-on-Scalar Regression Via Interpretable Regularized Reduced Rank Regression

Tianyu Ding\*, Dana Tudorascu, Annie Cohen and Robert Krafty, University of Pittsburgh

### 5:00 Automatic Transformation and Integration to Improve Visualization and Discovery of Latent Effects in Imaging Data

Johann A. Gagnon-Bartsch\*, University of Michigan; Gregory J. Hunt, William & Mary

### 5:15 Floor Discussion

## 63. CONTRIBUTED PAPERS: CAUSAL INFERENCE AND PROPENSITY SCORE METHODS

Sponsor: ENAR

Chair: Wei Chen, University of Pittsburgh

### 3:45 Generalizing Randomized Trial Findings to a Target Population using Complex Survey Population Data

Benjamin Ackerman\*, Catherine R. Lesko and Elizabeth A. Stuart, Johns Hopkins Bloomberg School of Public Health

### 4:00 Weak-Instrument Robust Tests in Two-Sample Summary-Data Mendelian Randomization

Sheng Wang\* and Hyunseung Kang, University of Wisconsin, Madison

### 4:15 Propensity Score Matching Methods in Unbalanced Studies with Optimal Caliper Choice

Ziliang Zhu\*, University of North Carolina, Chapel Hill; Toshio Kimura, Regeneron Pharmaceuticals, Inc.; Xinyi He, Agios Pharmaceuticals, Inc.; Zhen Chen, Regeneron Pharmaceuticals, Inc.

### 4:30 Mendelian Randomization with Statistical Warranty of All Core Assumptions

Zhiguang Huo\*, University of Florida

### 4:45 Improved Propensity Score for Matching

Ernesto Ulloa\*, Marco Carone and Alex Luedtke, University of Washington

### 5:00 A Likelihood Ratio Test for Multi-Dimensional Mediation Effects

Wei Hao\* and Peter X.K. Song, University of Michigan

### 5:15 Floor Discussion

#### 64. CONTRIBUTED PAPERS: LONGITUDINAL DATA AND JOINT MODELS OF LONGITUDINAL AND SURVIVAL DATA

**Sponsor: ENAR**

**Chair: Liang Li, University of Texas MD Anderson Cancer Center**

3:45	<b>Estimation of the Joint Distribution of Survival Time and Mark Variable in the Presence of Dependent Censoring</b> Busola O. Sanusi*, Michael G. Hudgens and Jianwen Cai, University of North Carolina, Chapel Hill
4:00	<b>A Multilevel Mixed Effects Varying Coefficient Model with Multilevel Predictors and Random Effects for Modeling Hospitalization Risk in Patients on Dialysis</b> Yihao Li*, University of California, Los Angeles; Danh V. Nguyen, University of California, Irvine; Esra Kurum, University of California, Riverside; Connie M. Rhee, University of California, Irvine; Yanjun Chen, University of California, Irvine Institute of Clinical and Translational Science; Kamyar Kalantar-Zadeh, University of California, Irvine; Damla Senturk, University of California, Los Angeles
4:15	<b>Structural Joint Modeling of Longitudinal and Survival Data</b> Bryan Blette*, University of North Carolina, Chapel Hill; Peter Gilbert, Fred Hutchinson Cancer Research Center; Michael Hudgens, University of North Carolina, Chapel Hill
4:30	<b>Bayesian Models for Joint Longitudinal and Competing Risks Data</b> Allison KC Furgal*, Ananda Sen and Jeremy M.G. Taylor, University of Michigan
4:45	<b>Joint Model for Survival and Multivariate Sparse Functional Data with Application to a Study of Alzheimer's Disease</b> Cai Li*, Yale University; Luo Xiao, North Carolina State University
5:00	<b>Bayesian Semiparametric Joint Models to Study Growth and Islet Autoimmunity in Subjects at High Risk for Type 1 Diabetes</b> Xiang Liu*, Roy Tamura, Kendra Vehik and Jeffrey Krischer, University of South Florida
5:15	<b>Marginal Inference in Transition Models with Generalized Estimating Equations: What is Being Estimated?</b> Danping Liu*, National Cancer Institute, National Institutes of Health; Joe Bible, Clemson University; Paul S. Albert, National Cancer Institute, National Institutes of Health; Bruce G. Simons-Morton, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health

#### 65. CONTRIBUTED PAPERS: PERSONALIZED MEDICINE AND BIOMARKERS

**Sponsor: ENAR**

**Chair: Dong-Yun Kim, National Heart, Lung, and Blood Institute, National Institutes of Health**

3:45	<b>Synergistic Self-Learning of Individualized Dietary Supplement Rules from Multiple Health Benefit Outcomes</b> Yiwan Zhou* and Peter X.K. Song, University of Michigan
4:00	<b>Integrative Network Learning for Multi-Modality Biomarker Data</b> Shanghong Xie*, Columbia University; Donglin Zeng, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University
4:15	<b>An Optimal Design of Experiments Approach to Closed-Loop Target-Controlled Induction of Anesthesia for Robustness to Interpatient PK/PD Variability: A Simulation Study</b> Ryan T. Jarrett* and Matthew S. Shotwell, Vanderbilt University
4:30	<b>Utilization of Residual Lifetime Quantiles to Optimize Personalized Biomarker Screening Intervals</b> Fang-Shu Ou* and Phillip J. Schulte, Mayo Clinic; Martin Heller, Private Practitioner
4:45	<b>Precision Medicine Using MixedBART for Repeated Measures</b> Charles K. Spanbauer* and Rodney Sparapani, Medical College of Wisconsin
5:00	<b>A Statistical Method to Estimate Sleep Duration from Actigraphy Data</b> Jonggyu Baek*, University of Massachusetts Medical School; Margaret Banker, Erica C. Jansen and Karen E. Peterson, University of Michigan; E. Andrew Pitchford, Iowa State University; Peter X. K. Song, University of Michigan
5:15	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

(CONTINUED)

## 66. CONTRIBUTED PAPERS: STATISTICAL GENETICS: SINGLE-CELL SEQUENCING DATA

Sponsor: ENAR

Chair: Qing Pan, The George Washington University

3:45	<b>SMNN: Batch Effect Correction for Single-Cell RNA-seq Data via Supervised Mutual Nearest Neighbor Detection</b> Gang Li*, Yuchen Yang, Huijun Qian and Kirk C. Wilhelmsen, University of North Carolina, Chapel Hill; Yin Shen, University of California, San Francisco; Yun Li, University of North Carolina, Chapel Hill
4:00	<b>Multiple Phenotype-Multiple Genotype Testing with Principal Components</b> Andy Shi*, Harvard University; Ryan Sun, University of Texas MD Anderson Cancer Center; Xihong Lin, Harvard University
4:15	<b>Single-Cell ATAC-seq Signal Extraction and Enhancement with SCATE</b> Zhicheng Ji*, Weiqiang Zhou and Hongkai Ji, Johns Hopkins University
4:30	<b>A Neural Network Based Dropout Correction for Single-Cell RNA-Seq Data with High Sparsity</b> Lingling An*, Xiang Zhang and Siyang Cao, University of Arizona
4:45	<b>A Novel Surrogate Variable Analysis Framework in Large-Scale Single-Cell RNA-seq Data Integration</b> Chao Huang*, Yue Julia Wang and Madison Layfield, Florida State University
5:00	<b>Robust Normalization of Single-Cell RNA-seq Data using Local Smoothing and Median Ratio</b> Chih-Yuan Hsu*, Qi Liu and Yu Shyr, Vanderbilt University Medical Center
5:15	<b>Subpopulation Identification for Single-Cell RNA-Sequencing Data Using Functional Data Analysis</b> Kyungmin Ahn* and Hironobu Fujiwara, RIKEN Center for Biosystems Dynamics Research, Japan

## 67. CONTRIBUTED PAPERS: SEMIPARAMETRIC AND NONPARAMETRIC METHODS AND APPLICATIONS

Sponsor: ENAR

Chair: Aaron W. Scheffler, University of California, San Francisco

3:45	<b>A Semiparametric Alternative Method to Conditional Logistic Regression for Combining Biomarkers under Matched Case-Control Studies</b> Wen Li* and Ruosha Li, University of Texas Health Science Center at Houston; Ziding Feng, Fred Hutchinson Cancer Research Center; Jing Ning, University of Texas MD Anderson Cancer Center
4:00	<b>Exponential and Super-Exponential Convergence of Misclassification Probabilities in Nonparametric Modeling</b> Richard Charnigo* and Cidambi Srinivasan, University of Kentucky
4:15	<b>Zero-Inflated Quantile Rank-Score Based Test (ZIQRank) with Application to scRNA-seq Differential Gene Expression Analysis</b> Wodan Ling*, Fred Hutchinson Cancer Research Center; Ying Wei, Columbia University; Wenfei Zhang, Sanofi
4:30	<b>A Nonparametric MC-SIMEX Method</b> Lili Yu*, Congjian Liu, Jingjing Yin and Jun Liu, Georgia Southern University
4:45	<b>Nonparametric Regression for Error-Prone Homogeneous Pooled Data</b> Dewei Wang*, University of South Carolina
5:00	<b>Testing for Uniform Stochastic Ordering among k Populations</b> Chuan-Fa Tang*, University of Texas, Dallas; Dewei Wang, University of South Carolina
5:15	<b>k-Tuple Partially Rank-Ordered Set Sampling</b> Kaushik Ghosh* and Marvin C. Javier, University of Nevada, Las Vegas



**TUESDAY, MARCH 24****8:30 a.m. — 10:15 a.m.****68. CHALLENGES AND OPPORTUNITIES IN METHODS FOR PRECISION MEDICINE****Sponsor:** IMS**Organizer** Yingqi Zhao, Fred Hutchinson Cancer Research Center**Chair:** Xinyuan Dong, University of Washington

8:30 **Subgroup-Effects Models (SGEM) for Analysis of Personal Treatment Effects**  
Peter X.K. Song\*, Ling Zhou and Shiquan Sun, University of Michigan; Haoda Fu, Eli Lilly and Company

8:55 **Kernel Optimal Orthogonality Weighting for Estimating Effects of Continuous Treatments**  
Michele Santacatterina\*, Cornell University

9:20 **Inference on Individualized Treatment Rules from Observational Studies with High-Dimensional Covariates**  
Yingqi Zhao\* and Muxuan Liang, Fred Hutchinson Cancer Research Center; Young-Geun Choi, Sookmyung University; Yang Ning, Cornell University; Maureen Smith, University of Wisconsin, Madison

9:45 **Integrative Analysis of Electronic Health Records for Precision Medicine**  
Yuanjia Wang\*, Columbia University; Jitong Luo and Donglin Zeng, University of North Carolina, Chapel Hill

10:10 **Floor Discussion**

**69. RECENT DEVELOPMENTS IN RISK ESTIMATION AND BIOMARKER MODELING WITH A FOCUS IN ALZHEIMER'S DISEASE****Sponsors:** ENAR, ASA Biometrics Section, ASA Health Policy Statistics Section, ASA Mental Health Statistics Section**Organizer:** Zheyu Wang, Johns Hopkins University**Chair:** Danping Liu, National Cancer Institute, National Institutes of Health

8:30 **Analyzing Semi-Competing Risks Data as a Longitudinal Bivariate Process**  
Sebastien Haneuse\*, Harvard T.H. Chan School of Public Health; Daniel Nevo, University of Tel Aviv

8:55 **Biomarker Models for Early Alzheimer's Disease Risk Prediction Before Symptoms Appear**  
Zheyu Wang\*, Johns Hopkins University

9:20 **A Statistical Test on the Ordering of Changes in Biomarkers for Preclinical Alzheimer's Disease**  
Chengjie Xiong\*, Washington University in St. Louis

9:45 **Changepoint Estimation for Biomarkers of Alzheimer's Disease**  
Laurent Younes\*, Johns Hopkins University

10:10 **Floor Discussion**

**70. CLINICAL TRIAL DESIGNS IN A NEW ERA OF IMMUNOTHERAPY: CHALLENGES AND OPPORTUNITIES****Sponsors:** ENAR, ASA Biometrics Section, ASA Biopharmaceutical Section**Organizer:** Yeonhee Park, Medical University of South Carolina**Chair:** Yeonhee Park, Medical University of South Carolina

8:30 **Immune-Oncology Agents: Endpoints and Designs**  
Hao Wang\* and Gary Rosner, Johns Hopkins University School of Medicine

8:55 **Adaptive Dose Finding Based on Safety and Feasibility in Early-Phase Clinical Trials of Adoptive Cell Immunotherapy**  
Nolan A. Wages\* and Camilo E. Fadul, University of Virginia

9:20 **Novel Bayesian Phase I/II Designs for Identifying Safe and Efficacious Treatments for Immunotherapy**  
J. Jack Lee\*, University of Texas MD Anderson Cancer Center

9:45 **Impact of Design Misspecification in Immuno-Oncology Trials**  
Jennifer Le-Rademacher\*, Quyen Duong, Tyler Zemla and Sumithra J. Mandrekar, Mayo Clinic

10:10 **Floor Discussion**

# SCIENTIFIC PROGRAM

(CONTINUED)

## 71. THE THREE M'S: MEETINGS, MEMBERSHIPS, AND MONEY!

**Sponsors:** CENS, ENAR

**Organizers:** Jing Li, Richard M. Fairbanks School of Public Health, Indiana University and Hannah Weeks, Vanderbilt University

**Chair:** Will A. Eagan, Purdue University

### Panel Discussion:

- 8:30 Jeff Goldsmith, Columbia University  
Donna LaLonde, American Statistical Association  
Nandita Mitra, University of Pennsylvania Perelman School of Medicine  
Sarah Ratcliffe, University of Virginia

10:00 **Floor Discussion**

## 72. RECENT ADVANCES IN JOINT MODELING OF LONGITUDINAL AND SURVIVAL DATA

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Defense and National Security, ASA Section on Statistics and the Environment, ASA Section on Statistics in Epidemiology, ASA Health Policy Statistics Section, ASA Mental Health Statistics Section

**Organizer:** Abdus Sattar, Case Western Reserve University

**Chair:** Jeffrey Alberto, Case Western Reserve University

### Assessing Importance of Biomarkers: A Bayesian Joint Modeling Approach of Longitudinal and Survival Data with Semicompeting Risks

- 8:30 Ming-Hui Chen\* and Fan Zhang, University of Connecticut; Xiuyu Julie Cong, Boehringer Ingelheim (China) Investment Co., Ltd.; Qingxia Chen, Vanderbilt University

### Inference with Joint Models Under Misspecified Random Effects Distributions

- 8:55 Sanjoy Sinha\*, Carleton University; Abdus Sattar, Case Western Reserve University

### Personalized Decision Making for Biopsies in Prostate Cancer Active Surveillance Programs

- 9:20 Dimitris Rizopoulos\*, Erasmus University Medical Center

### Quantifying Direct and Indirect Effect for Longitudinal Mediator and Survival Outcome Using Joint Modeling Approach

- 9:45 Cheng Zheng\*, University of Wisconsin, Milwaukee; Lei Liu, Washington University in St. Louis

10:10 **Floor Discussion**

## 73. RECENT ADVANCES IN NETWORK META-ANALYSIS WITH FLEXIBLE BAYESIAN APPROACHES

**Sponsors:** ENAR, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Section on Statistics in Epidemiology, ASA Health Policy Statistics Section

**Organizer:** Hwanhee Hong, Duke University School of Medicine

**Chair:** Roland Matsouaka, Duke University School of Medicine

### Data-Adaptive Synthesis of Historical Information through Network-Meta-Analytic-Predictive Priors

- 8:30 Jing Zhang\*, University of Maryland; Hwanhee Hong, Duke University School of Medicine; Yong Chen, University of Pennsylvania; Cher Dallal, University of Maryland

### Bayesian Flexible Hierarchical Skew Heavy-Tailed Multivariate Meta Regression Models for Individual Patient Data with Applications

- 9:00 Sung Duk Kim\*, National Cancer Institute, National Institutes of Health; Ming-Hui Chen, University of Connecticut; Joseph G. Ibrahim, University of North Carolina, Chapel Hill; Arvind K. Shah and Jianxin Lin, Merck Research Laboratories

### Bayesian Network Meta-Analysis for Estimating Population Treatment Effects

- 9:30 Hwanhee Hong\*, Duke University School of Medicine

### Discussant:

- 10:00 Christopher Schmid, Brown University School of Public Health

## 74. CONTRIBUTED PAPERS: ELECTRONIC HEALTH RECORDS DATA ANALYSIS

**Sponsor:** ENAR

**Chair:** Adam Ciarleglio, George Washington University

### Estimating Individualized Treatment Rules for Multicategory Type 2 Diabetes Treatments Using Electronic Health Records

- 8:30 Jitong Lou\*, University of North Carolina, Chapel Hill; Yuanjia Wang, Columbia University; Lang Li, The Ohio State University; Donglin Zeng, University of North Carolina, Chapel Hill

### Modeling Heterogeneity and Missing Data in Electronic Health Records

- 8:45 Rebecca Anthopolos\*, New York University; Qixuan Chen and Ying Wei, Columbia University Mailman School of Public Health

### Modeling Valid Drug Dosage in the Presence of Conflicting Information Extracted from Electronic Health Records

- 9:00 Michael L. Williams\*, Hannah L. Weeks, Cole Beck, Elizabeth McNeer and Leena Choi, Vanderbilt University Medical Center

9:15	<b>Case Contamination in Electronic Health Records-Based Case-Control Studies</b> Jill Schnall*, Lu Wang, Scott Damrauer, Michael Levin and Jinbo Chen, University of Pennsylvania
9:30	<b>Quantile Rank Test for Dynamic Heterogeneous Genetic Effect in Longitudinal Electronic Health Record Analysis</b> Tianying Wang*, Ying Wei, Iuliana Ionita-Laza, Zixu Wang and Chunhua Weng, Columbia University
9:45	<b>Leveraging Electronic Health Data for Embedded Pragmatic Clinical Trials within Health Care Systems: Lessons Learned from the NIH Collaboratory</b> Andrea J. Cook*, Kaiser Permanente Washington Health Research Institute
10:00	<b>Floor Discussion</b>

## 75. CONTRIBUTED PAPERS: REBEL WITHOUT A CAUSE: SESSIONS ON CAUSAL INFERENCE

Sponsor: ENAR

Chair: Kesheng Wang, West Virginia University

8:30	<b>A New Method for Estimating a Principal Stratum Causal Effect Conditioning on a Post-Treatment Intermediate Response</b> Xiaoqing Tan*, University of Pittsburgh; Judah Abberbock, GlaxoSmithKline; Priya Rastogi and Gong Tang, University of Pittsburgh
8:45	<b>Detecting Heterogeneous Treatment Effect with Instrumental Variables</b> Michael W. Johnson*, University of Wisconsin, Madison; Jiongyi Cao, The University of Chicago; Hyunseung Kang, University of Wisconsin, Madison
9:00	<b>A Groupwise Approach for Inferring Heterogeneous Treatment Effects in Causal Inference</b> Chan Park* and Hyunseung Kang, University of Wisconsin, Madison
9:15	<b>Estimating Complier Quantile Causal Treatment Effects with Randomly Censored Data and A Binary Instrumental Variable</b> Bo Wei* and Limin Peng, Emory University; Mei-jie Zhang, Medical College of Wisconsin; Jason Fine, University of North Carolina, Chapel Hill

9:30	<b>Causal Effects in Twin Studies: The Role of Interference</b> Bonnie Smith* and Elizabeth Ogburn, Johns Hopkins Bloomberg School of Public Health; Saonli Basu and Matthew McGue, University of Minnesota; Daniel Scharfstein, Johns Hopkins Bloomberg School of Public Health
9:45	<b>Causal Inference from Self-Controlled Case Series Studies Using Targeted Maximum Likelihood Estimation</b> Yaru Shi*, Fang Liu and Jie Chen, Merck & Co., Inc.
10:00	<b>Caution Against Examining the Role of Reverse Causality in Mendelian Randomization</b> Sharon M. Lutz* and Ann C. Wu, Harvard Medical School and Harvard Pilgrim Health Care Institute; Christoph Lange, Harvard T.H. Chan School of Public Health

## 76. CONTRIBUTED PAPERS: HYPOTHESIS TESTING: KNOWLEDGE IS POWER

Sponsor: ENAR

Chair: Daniel J. Schaid, Mayo Clinic

8:30	<b>A Score Based Test for Functional Linear Concurrent Regression</b> Rahul Ghosal* and Arnab Maity, North Carolina State University
8:45	<b>Differential Expression Analysis in Single-Cell RNA Sequencing with G-modeling-based Two-Sample Test</b> Jingyi Zhai* and Hui Jiang, University of Michigan
9:00	<b>Detect with BERET</b> Duyeol Lee*, Kai Zhang and Michael R. Kosorok, University of North Carolina, Chapel Hill
9:15	<b>Resampling-Based Stepwise Multiple Testing Procedures with Applications to Clinical Trial Data</b> Jiwei He* and Feng Li, U.S. Food and Drug Administration; Yan Gao, The University of Illinois at Chicago; Mark Rothmann, U.S. Food and Drug Administration

# SCIENTIFIC PROGRAM

(CONTINUED)

9:30	<b>Global and Simultaneous Hypothesis Testing for High-Dimensional Logistic Regression Models</b> Rong Ma*, T. Tony Cai and Hongzhe Li, University of Pennsylvania
9:45	<b>Hypothesis Testing to Determine if Two Penalties Are Better Than One: Should Second Order Terms have the Same Penalty as Main Effects?</b> Todd A. MacKenzie*, Iben Rickett, Jiang Gui and Kimon Bekelis, Dartmouth College
10:00	<b>Floor Discussion</b>

## 77. CONTRIBUTED PAPERS: MISSING (DATA) IN ACTION

**Sponsor: ENAR**

**Chair: Jason Roy, Rutgers University**

8:30	<b>Identifying Treatment Effects using Trimmed Means when Data are Missing Not at Random</b> Alex J. Ocampo*, Harvard University
8:45	<b>A Bayesian Multivariate Skew-Normal Mixture Model for Longitudinal Data with Intermittent Missing Observations: An Application to Infant Motor Development</b> Carter Allen* and Brian Neelon, Medical University of South Carolina; Sara E. Benjamin-Neelon, Johns Hopkins Bloomberg School of Public Health
9:00	<b>Estimation, Variable Selection and Statistical Inference in a Linear Regression Model under an Arbitrary Missingness Mechanism</b> Chi Chen* and Jiwei Zhao, State University of New York at Buffalo
9:15	<b>Influence Function Based Inference in Randomized Trials with Non Monotone Missing Binary Outcomes</b> Lamar Hunt* and Daniel O. Scharfstein, Johns Hopkins Bloomberg School of Public Health
9:30	<b>Multiple Imputation Variance Estimation in Studies with Missing or Misclassified Inclusion Criteria</b> Mark J. Giganti*, Center for Biostatistics in AIDS Research; Bryan E. Shepherd, Vanderbilt University
9:45	<b>Missing Data in Deep Learning</b> David K. Lim*, Naim U. Rashid and Joseph G. Ibrahim, University of North Carolina, Chapel Hill
10:00	<b>An Approximated Expectation-Maximization Algorithm for Analysis of Data with Missing Values</b> Gong Tang*, University of Pittsburgh

## 78. CONTRIBUTED PAPERS: BACK TO THE FUTURE: PREDICTION AND PROGNOSTIC MODELING

**Sponsor: ENAR**

**Chair: Dongjun Chung, Medical University of South Carolina**

8:30	<b>High Dimensional Classified Mixed Model Prediction</b> Mengying Li* and J. Sunil Rao, University of Miami
8:45	<b>Connecting Population-Level AUC and Latent Scale-Invariant R-square via Semiparametric Gaussian Copula and Rank Correlations</b> Debangana Dey* and Vadim Zipunnikov, Johns Hopkins Bloomberg School of Public Health
9:00	<b>Artificial Intelligence and Agent-Based Modeling - Prediction and Simulation Issue</b> Nicolas J. Savy* and Philippe Saint-Pierre, Toulouse Institute of Mathematics
9:15	<b>Improving Survival Prediction Using a Novel Feature Selection and Feature Reduction Framework Based on the Integration of Clinical and Molecular Data</b> Lisa Neums*, Richard Meier, Devin C. Koestler and Jeffrey A. Thompson, University of Kansas Medical Center and University of Kansas Cancer Center
9:30	<b>Quantile Regression for Prediction of High-Cost Patients</b> Scott S. Coggeshall*, VA Puget Sound
9:45	<b>Joint Prediction of Variable Importance Rank from Binary and Survival Data via Adaptively Weighted Random Forest</b> Jihwan Oh* and John Kang, Merck & Co., Inc.
10:00	<b>External Validation Study of SMART Vascular Event Prediction Model Using UK Primary Care Data Between 2000-2017</b> Laura H. Gunn*, University of North Carolina, Charlotte & Imperial College London; Ailsa McKay, Azeem Majeed and Kosh Ray, Imperial College London



**79. CONTRIBUTED PAPERS: M&M: MEASUREMENT ERROR AND MODELING****Sponsor:** ENAR**Chair:** Mark Meyer, Georgetown University

**Statistical Analysis of Data Reproducibility Measures**  
 8:30 Zeyi Wang\* and Eric Bridgeford, Johns Hopkins Bloomberg School of Public Health; Joshua T. Vogelstein, Johns Hopkins University; Brian Caffo, Johns Hopkins Bloomberg School of Public Health

**An Approximate Quasi-Likelihood Approach to Analyzing Error-Prone Failure Time Outcomes and Exposures**  
 8:45 Lillian A. Boe\* and Pamela A. Shaw, University of Pennsylvania

**Improving the Efficiency of Generalized Raking Estimators to Address Correlated Covariate and Failure-Time Outcome Error**  
 9:00 Eric J. Oh\*, University of Pennsylvania; Thomas Lumley, University of Auckland; Bryan E. Shepherd, Vanderbilt University; Pamela A. Shaw, University of Pennsylvania

**Surrogate-Assisted Subsampling in Logistic Regression with Outcome Misclassification**  
 9:15 Chongliang Luo\*, Arielle Marks-Anglin and Yong Chen, University of Pennsylvania

**Impact of Design Considerations in Sensitivity to Time Recording Errors in Pharmacokinetic Modeling**  
 9:30 Hannah L. Weeks\* and Matthew S. Shotwell, Vanderbilt University

9:45 **Floor Discussion**

**TUESDAY, MARCH 24****10:15 a.m. — 10:30 a.m.****REFRESHMENT BREAK WITH OUR EXHIBITORS****TUESDAY, MARCH 24****10:30 a.m. — 12:15 p.m.****80. PRESIDENTIAL INVITED ADDRESS****Sponsor:** ENAR**Organizer/Chair:** Michael J. Daniels, University of Florida

10:30 **Introduction**

10:35 **Distinguished Student Paper Awards**

**Medical Product, Healthcare Delivery, and Road Safety Policies: Seemingly Unrelated Regulatory Questions**

10:45 **Sharon-Lise Normand, Ph.D.**, S. James Adelstein Professor of Health Care Policy (Biostatistics), Department of Health Care Policy, Harvard Medical School, Department of Biostatistics, Harvard T.H. Chan School of Public Health

# SCIENTIFIC PROGRAM

(CONTINUED)

**TUESDAY, MARCH 24**

**1:45 p.m. — 3:30 p.m.**

## 81. STATISTICAL ANALYSIS OF BIOLOGICAL SHAPES

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

**Organizer:** Anuj Srivastava, Florida State University

**Chair:** Anuj Srivastava, Florida State University

1:45	<b>Manifold-Valued Data Analysis of Brain Networks</b> Ian L. Dryden*, Simon P. Preston and Katie E. Severn, University of Nottingham
2:10	<b>Shape Analysis for Mitochondria Data</b> Todd Ogden*, Columbia University; Ruiyi Zhang, Florida State University; Martin Picard, Columbia University; Anuj Srivastava, Florida State University
2:35	<b>Geometric Methods for Image-Based Statistical Analysis of Shape and Texture of Glioblastoma Multiforme Tumors</b> Sebastian Kurtek*, The Ohio State University; Karthik Bharath, University of Nottingham; Veera Baladandayuthapani and Arvind Rao, University of Michigan
3:00	<b>Fiber Bundles in Probabilistic Models</b> Lorin Crawford*, Brown University; Bruce Wang, Princeton University; Timothy Sudijono, Brown University; Henry Kirveslahti, Duke University; Tingran Gao, The University of Chicago; Doug M. Boyer and Sayan Mukherjee, Duke University
3:25	<b>Floor Discussion</b>

## 82. IMPROVING THE DEVELOPMENT AND VALIDATION OF SCREENING TESTS FOR RARE DISEASES

**Sponsor:** ENAR, ASA Section on Medical Devices and Diagnostics

**Organizer:** Gene Pennello, U.S. Food and Drug Administration

**Chair:** Norberto Pantoja-Galicia, U.S. Food and Drug Administration

1:45	<b>From Prediction to Policy: Risk Stratification to Improve the Efficiency of Early Detection for Cancer</b> Ruth Etzioni*, Fred Hutchinson Cancer Research Center
2:10	<b>A Simple Framework to Identify Optimal Cost-Effective Risk Thresholds for a Single Screen: Comparison to Decision Curve Analysis</b> Hormuzd Katki*, National Cancer Institute, National Institutes of Health; Ionut Bebu, The George Washington University

2:35	<b>Sample Weighted Semiparametric Estimation of Cause-Specific Cumulative Risk and Incidence Using Left or Interval-censored Data from Electronic Health Records</b> Noorie Hyun*, Medical College of Wisconsin; Hormuzd A. Katki and Barry I. Graubard, National Cancer Institute, National Institutes of Health
3:00	<b>A Statistical Review: Why Average Weighted Accuracy, not Accuracy or AUC?</b> Qing Pan*, Yunyun Jiang and Scott Evans, The George Washington University
3:25	<b>Floor Discussion</b>

## 83. CAUSAL INFERENCE AND HARMFUL EXPOSURES

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics and the Environment, ASA Section on Statistics in Epidemiology, ASA Health Policy Statistics Section

**Organizer:** Maria Cuellar, University of Pennsylvania

**Chair:** Daniel Malinsky, Johns Hopkins University

1:45	<b>Envisioning Hypothetical Interventions on Occupational Exposures to Protect Worker Health: Applications of the Parametric G-formula</b> Andreas M. Neophytou*, Colorado State University
2:10	<b>A Causal Inference Framework for Cancer Cluster Investigations Using Publicly Available Data</b> Rachel C. Nethery* and Yue Yang, Harvard T.H. Chan School of Public Health; Anna J. Brown, The University of Chicago; Francesca Dominici, Harvard T.H. Chan School of Public Health
2:35	<b>Estimating the Effects of Precinct Level Policing Policies Through Causal Inference with Interference</b> Joseph Antonelli* and Brenden Beck, University of Florida
3:00	<b>Exploring Evidence of Residual Confounding in Tropical Cyclone Epidemiology Using a Negative Exposure Control Analysis</b> Brooke Anderson*, Colorado State University; Meilin Yan, Peking University
3:25	<b>Floor Discussion</b>

#### 84. STATISTICAL METHODS FOR EMERGING DATA IN ENVIRONMENTAL HEALTH RESEARCH

**Sponsors:** ENAR, ASA Section on Statistics and the Environment, ASA Section on Statistics in Epidemiology  
**Organizer:** Jenna Krall, George Mason University  
**Chair:** Jenna Krall, George Mason University

1:45	<b>Bayesian Joint Modeling of Chemical Structure and Dose Response Curves</b> Kelly R. Moran*, David Dunson and Amy H. Herring, Duke University
2:10	<b>Source-Specific Exposure Assessment by using Bayesian Spatial Multivariate Receptor Modeling</b> Eun Sug Park*, Texas A&M Transportation Institute
2:35	<b>The Impact of Complex Social and Environmental Mixtures on Educational Outcomes in Young Children</b> Kathy B. Ensor*, Rice University; Mercedes Bravo, Research Triangle Institute and Rice University; Daniel Kowal, Henry Leong and Marie Lynn Miranda, Rice University
3:00	<b>Accounting for Mixtures in Risk Assessment</b> Chris Gennings*, Icahn School of Medicine at Mount Sinai
3:25	<b>Floor Discussion</b>

#### 85. BAYESIAN ANALYSIS IN FUNCTIONAL BRAIN IMAGING

**Sponsors:** ENAR, IMS, ASA Bayesian Statistical Science Section, ASA Biometrics Section, ASA Section on Statistics in Imaging, ASA Mental Health Statistics Section  
**Organizer:** Donatello Telesca, University of California, Los Angeles  
**Chair:** Donatello Telesca, University of California, Los Angeles

1:45	<b>Functional Regression Methods for Functional Neuroimaging</b> Jeffrey Scott Morris*, University of Pennsylvania; Hongxiao Zhu, Virginia Tech University; Michelle Miranda, University of Victoria; Neel Desai, Rice University; Veera Baladandayuthapani, University of Michigan; Philip Rausch, Humboldt University
2:10	<b>A Grouped Beta Process Model for Multivariate Resting-State EEG Microstate Analysis on Twins</b> Mark Fiecas*, University of Minnesota; Brian Hart, UnitedHealthGroup; Stephen Malone, University of Minnesota

#### Bayesian Analysis of Multidimensional Functional Data

2:35 John Shamshoian\*, Donatello Telesca and Damla Senturk, University of California, Los Angeles

#### Encompassing Semiparametric Bayesian Inference for Stationary Points in Gaussian Process Regression Models with Applications to Event-Related Potential Analysis

3:00 Meng Li\*, Cheng-Han Yu and Marina Vannucci, Rice University

3:25 **Floor Discussion**

#### 86. HUMAN DATA INTERACTION: GAINING AN UNDERSTANDING OF THE DATA SCIENCE PIPELINE

**Sponsors:** ENAR, ASA Section on Statistical Learning and Data Science  
**Organizer:** Jeff Leek, Johns Hopkins Bloomberg School of Public Health  
**Chair:** Jeff Leek, Johns Hopkins Bloomberg School of Public Health

1:45 **Tools for Analyzing R Code the Tidy Way**  
Lucy D'Agostino McGowan\*, Wake Forest University

2:10 **Domain Specific Languages for Data Science**  
Hadley Wickham\*, RStudio

2:35 **The Challenges of Analytic Workflows: Perspectives from Data Science Educators**  
Sean Kross\*, University of California, San Diego

3:00 **Building A Software Package in Tandem with Machine Learning Methods Research Can Result in Both More Rigorous Code and More Rigorous Research**  
Nick Stayer\*, Vanderbilt University

3:25 **Floor Discussion**

# SCIENTIFIC PROGRAM

(CONTINUED)

## 87. CONTRIBUTED PAPERS: SPATIAL AND SPATIAL-TEMPORAL DATA ANALYSIS

Sponsor: ENAR

Chair: Fridtjof Thomas, University of Tennessee Health Science Center

1:45	<b>Bayesian Spatial-Temporal Accelerated Failure Time Models for Survival Data from Cancer Registries</b> Ming Wang*, The Pennsylvania State University; Zheng Li, Novartis; Lijun Zhang, The Pennsylvania State University; Yimei Li, University of Pennsylvania; Vern M. Chinchilli, The Pennsylvania State University
2:00	<b>Where did All the Good Fish Go? Spatio- Temporal Modelling of Research Vessel Data with R</b> Ethan Lawler* and Joanna Mills Flemming, Dalhousie University
2:15	<b>Assessing Meteorological Drivers of Air Pollution in the Eastern United States via a Bayesian Quantile Regression Model with Spatially Varying Coefficients</b> Stella Coker Watson Self*, University of South Carolina; Christopher S. McMahan, Brook Russell and Derek Andrew Brown, Clemson University
2:30	<b>Spatio-Temporal Mixed Effects Single Index Models</b> Hamdy F. F. Mahmoud*, Virginia Tech and Assiut University, Egypt; Inyoung Kim, Virginia Tech
2:45	<b>Bayesian Spatial Blind Source Separation via Thresholded Gaussian Processes</b> Ben Wu*, University of Michigan; Ying Guo, Emory University; Jian Kang, University of Michigan
3:00	<b>Incorporating Spatial Structure into Bayesian Spike-and-Slab Lasso GLMs</b> Justin M. Leach*, Inmaculada Aban and Nengjun Yi, University of Alabama at Birmingham
3:15	<b>Floor Discussion</b>

## 88. CONTRIBUTED PAPERS: EARLY PHASE CLINICAL TRIALS AND BIOMARKERS

Sponsor: ENAR

Chair: Lingling An, University of Arizona

1:45	<b>Building an Allostatic Load Scale using Item Response Theory</b> Shelley H. Liu*, Kristen Dams-O'Connor and Julie Spicer, Icahn School of Medicine at Mount Sinai
2:00	<b>Subgroup-Specific Dose Finding in Phase I Clinical Trials Based on Time to Toxicity Allowing Adaptive Subgroup Combination</b> Andrew G. Chapple*, Louisiana State University; Peter F. Thall, University of Texas MD Anderson Cancer Center
2:15	<b>Evaluation of Continuous Monitoring Approach in Early Phase Oncology Trial</b> Suhyun Kang* and Jingyi Liu, Eli Lilly and Company
2:30	<b>PA-CRM: A Continuous Reassessment Method for Pediatric Phase I Trials with Concurrent Adult Trials</b> Yimei Li*, University of Pennsylvania; Ying Yuan, University of Texas MD Anderson Cancer Center
2:45	<b>Two-Stage Enrichment Clinical Trial Design with Adjustment for Misclassification in Predictive Biomarkers</b> Yong Lin*, Weichung Joe Shih and Shou-En Lu, Rutgers University
3:00	<b>Incorporating Real-World Evidence or Historical Data to Improve Phase I Clinical Trial Designs</b> Yanhong Zhou*, Ying Yuan and J. Jack Lee, University of Texas MD Anderson Cancer Center
3:15	<b>Density Estimation Based on Pooled Biomarkers using Dirichlet Process Mixtures</b> Zichen Ma*, University of South Carolina



**89. CONTRIBUTED PAPERS: ELECTRONIC HEALTH RECORDS DATA ANALYSIS AND META-ANALYSIS****Sponsor: ENAR****Chair: Jung-Ying Tzeng, North Carolina State University**

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|------|--|
| 1:45 | <b>The Impact of Covariance Priors on Arm-Based Bayesian Network Meta-Analyses with Binary Outcomes</b><br>Zhenxun Wang*, University of Minnesota; Lifeng Lin, Florida State University; James S. Hodges and Haitao Chu, University of Minnesota   |
| 2:00 | <b>A Bayesian Multivariate Meta-Analysis of Prevalence Data</b><br>Lianne Siegel* and Kyle Rudser, University of Minnesota; Siobhan Sutcliffe, Washington University School of Medicine; Alayne Markland, University of Alabama at the Birmingham VA Medical Center; Linda Brubaker and Sheila Gahagan, University of California, San Diego; Ann E. Stapleton, University of Washington; Haitao Chu, University of Minnesota |
| 2:15 | <b>An Augmented Estimation Procedure for EHR-based Association Studies Accounting for Differential Misclassification</b><br>Jiayi Tong* and Jing Huang, University of Pennsylvania; Jessica Chubak, Kaiser Permanente Washington Health Research Institute; Xuan Wang, Zhejiang University; Jason H. Moore, Rebecca Hubbard and Yong Chen, University of Pennsylvania  |
| 2:30 | <b>Testing Calibration of Risk Prediction Models Using Positive-Only EHR Data</b><br>Lingjiao Zhang*, University of Pennsylvania; Yanyuan Ma, The Pennsylvania State University; Daniel Herman and Jinbo Chen, University of Pennsylvania  |
| 2:45 | <b>Bias Reduction Methods for Propensity Scores Estimated from Mismeasured EHR-Derived Covariates</b><br>Joanna Grace Harton*, Rebecca A. Hubbard and Nandita Mitra, University of Pennsylvania  |

**Bayesian Network Meta-Regression for Partially Collapsed Ordinal Outcomes: Latent Counts Approach**

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|------|---|
| 3:00 | Yeongjin Gwon*, University of Nebraska Medical Center; Ming-Hui Chen, University of Connecticut; Mo May, Xun Jiang and Amy Xia, Amgen Inc.; Joseph Ibrahim, University of North Carolina, Chapel Hill |
|------|---|

**Efficient and Robust Methods for Causally Interpretable Meta-Analysis: Transporting Inferences From Multiple Randomized Trials to a Target Population**

- |      |   |
|------|---|
| 3:15 | Issa J. Dahabreh*, Jon A. Steingrimsdottir and Sarah E. Robertson, Brown University; Lucia C. Petito, Northwestern University; Miguel A. Hernán, Harvard University |
|------|---|

**90. CONTRIBUTED PAPERS: SMALL THINGS THAT MAKE A BIG DIFFERENCE: MICROBIOME ANALYSIS****Sponsor: ENAR****Chair: Olivier Thas, Ghent University, Hasselt University and University of Wollongong**

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|------|---|
| 1:45 | <b>Robust Inter-Taxa Dependency Estimation for High-Dimensional Microbiome Data</b><br>Arun A. Srinivasan*, The Pennsylvania State University; Danning Li, Jilin University; Lingzhou Xue and Xiang Zhan, The Pennsylvania State University |
| 2:00 | <b>Analysis of Compositions of Microbiomes with Bias Correction</b><br>Huang Lin* and Shyamal Das Peddada, University of Pittsburgh   |
| 2:15 | <b>Zero-Inflated Poisson Factor Model with Application to Microbiome Absolute Abundance Data</b><br>Tianchen Xu*, Columbia University; Ryan T. Demmer, University of Minnesota; Gen Li, Columbia University                                 |

# SCIENTIFIC PROGRAM

(CONTINUED)

2:30	<b>Zero-Inflated Topic Models for Human Microbiome Data</b> Rebecca A. Deek* and Hongzhe Li, University of Pennsylvania	2:45	<b>A Systematic Evaluation of Single-Cell RNA-seq Imputation Methods</b> Wenpin Hou*, Zhicheng Ji, Hongkai Ji and Stephanie C. Hicks, Johns Hopkins University
2:45	<b>Bayesian Modeling of Microbiome Count Data for Network Analysis</b> Qiwei Li*, University of Texas, Dallas; Shuang Jiang, Southern Methodist University; Xiaowei Zhan, University of Texas Southwestern Medical Center	3:00	<b>A Comprehensive Evaluation of Preprocessing Methods for Single-Cell RNA Sequencing Data</b> Shih-Kai Chu*, Qi Liu and Yu Shyr, Vanderbilt University Medical Center
3:00	<b>Sparse Kernel RV for Identifying Genomic Features Related to Microbiome Community Composition</b> Nanxun Ma*, University of Washington; Anna Plantinga, Williams College; Michael C. Wu, Fred Hutchinson Cancer Research Center	3:15	<b>Fast Clustering for Single-Cell RNA-seq Data using Mini-Batch k-Means</b> Stephanie C. Hicks*, Johns Hopkins Bloomberg School of Public Health; Ruoxi Liu, Johns Hopkins University; Yuwei Ni, Weill Cornell Medical College; Elizabeth Purdom, University of California, Berkeley; Davide Risso, University of Padova
3:15	<b>A Bayesian Semiparametric Approach to Wild-Type Distribution Estimation: Accounting for Contamination and Measurement Error (BayesACME)</b> Will A. Eagan* and Bruce A. Craig, Purdue University	<b>92. CONTRIBUTED PAPERS: ROBUST MODELING AND INFERENCE</b>	
<b>91. CONTRIBUTED PAPERS: STATISTICAL GENETICS: SEQUENCING DATA ANALYSIS</b>		<b>Sponsor: ENAR</b> <b>Chair: Julia Wrobel, Colorado School of Public Health</b>	
1:45	<b>IncDIFF: A Novel Quasi-Likelihood Method for Differential Expression Analysis of Non-Coding RNA</b> Qian Li*, University of South Florida; Xiaoqing Yu, Ritu Chaudhary, Robbert J. Slebos, Christine Chung and Xuefeng Wang, Moffitt Cancer Center	1:45	<b>Robust Estimation with Outcome Misclassification and Covariate Measurement Error in Logistic Regression</b> Sarah C. Lotspeich*, Bryan E. Shepherd and Gustavo G.C. Amorim, Vanderbilt University Medical Center; Pamela A. Shaw, University of Pennsylvania; Ran Tao, Vanderbilt University Medical Center
2:00	<b>ASEP: Gene-based Detection of Allele-Specific Expression in a Population by RNA-seq</b> Jiaxin Fan* and Jian Hu, University of Pennsylvania Perelman School of Medicine; Chenyi Xue, Hanrui Zhang and Muredach P. Reilly, Columbia University; Rui Xiao and Mingyao Li, University of Pennsylvania Perelman School of Medicine	2:00	<b>Implementing Interventions to Combat the Opioid Epidemic During a Rising Tide of Activities Aimed at Improving Patient Outcomes: Evaluating the Robustness of Parallel-Group and Stepped-Wedge Cluster Randomized Trials to Confounding from External Events</b> Lior Rennert*, Clemson University
2:15	<b>A Sparse Negative Binomial Classifier with Covariate Adjustment for RNA-seq Data</b> Md Tanbin Rahman*, University of Texas MD Anderson Cancer Center; Hsin-En Huang, An-Shun Tai and Wen-Ping Hsieh, National Tsing Hua University; George Tseng, University of Pittsburgh	2:15	<b>Robust Statistical Models for Impact Injury Risk Estimation</b> Anjishnu Banerjee* and Narayan Yoganandan, Medical College of Wisconsin
2:30	<b>A Functional Regression Based Approach for Gene-Based Association Testing of Quantitative Trait in Family Studies</b> Chi-Yang Chiu*, University of Tennessee Health Science Center	2:30	<b>Joint Testing of Donor/Recipient Genetic Matching Scores and Recipient Genotype has Robust Power for Finding Genes Associated with Transplant Outcomes</b> Victoria L. Arthur*, University of Pennsylvania Perelman School of Medicine; Sharon Browning, University of Washington; Bao-Li Chang and Brendan Keating, University of Pennsylvania; Jinbo Chen, University of Pennsylvania Perelman School of Medicine

2:45	<b>A Robust Bayesian Copas Selection Model for Detecting and Correcting Publication Bias</b> Ray Bai*, Yong Chen and Mary Regina Boland, University of Pennsylvania
3:00	<b>Estimation of Knots in Linear Spline Models</b> Guangyu Yang*, University of Michigan, Ann Arbor; Baqun Zhang, Shanghai University of Finance and Economics; Min Zhang, University of Michigan, Ann Arbor
3:15	<b>Floor Discussion</b>

**TUESDAY, MARCH 24****3:30 p.m. — 3:45 p.m.****REFRESHMENT BREAK WITH OUR EXHIBITORS****TUESDAY, MARCH 24****3:45 p.m. — 5:30 p.m.****93. HIGH DIMENSIONAL METHODS FOR MECHANISTIC INTEGRATION OF MULTI-TYPE OMICS****Sponsor:** IMS**Organizer:** Qi Zhang, University of Nebraska, Lincoln**Chair:** Min Jin Ha, University of Texas MD Anderson Cancer Center

3:45	<b>Integrating Heterogeneous Longitudinal Omics Data with Personalized Dynamic Network Analysis</b> Xing Qiu*, University of Rochester; Leqin Wu, Jinan University; Ya-xiang Yuan, Chinese Academy of Sciences; Hulin Wu, University of Texas Health Science Center at Houston
4:10	<b>INFIMA Leverages Multi-Omic Model Organism Data to Identify Target Genes for Human GWAS Variants</b> Sunduz Keles* and Chenyang Dong, University of Wisconsin, Madison
4:35	<b>Nonlinear Moderated Mediation Analysis with Genetical Genomics Data</b> Yuehua Cui* and Bin Gao, Michigan State University; Xu Liu, Shanghai University of Finance and Economics
5:00	<b>High Dimensional Mediation Analysis for Causal Gene Selection</b> Qi Zhang*, University of Nebraska, Lincoln
5:25	<b>Floor Discussion</b>

**94. NEW WEIGHTING METHODS FOR CAUSAL INFERENCE****Sponsors:** ENAR, IMS, ASA Biometrics Section, ASA Section on Statistics in Epidemiology**Organizer:** Roland Matsouaka, Duke University**Chair:** Hwanhee Hong, Duke University

3:45	<b>Propensity Score Weighting for Causal Inference with Multiple Treatments</b> Fan Li*, Yale School of Public Health; Fan Li, Duke University
4:10	<b>Methods for Balancing Covariates when Estimating Heterogeneous Treatment Effects in Observational Data</b> Laine Thomas* and Fan Li, Duke University; Daniel Wojdyla, Duke Clinical Research Institute; Siyun Yang, Duke University
4:35	<b>Flexible Regression Approach to Propensity Score Analysis and its Relationship with Matching and Weighting</b> Liang Li*, University of Texas MD Anderson Cancer Center; Huzhang Mao, Eli Lilly and Company
5:00	<b>Robust Inference when Combining Probability and Non-Probability Samples with High-Dimensional Data</b> Shu Yang*, North Carolina State University; Jae Kwang Kim, Iowa State University; Rui Song, North Carolina State University
5:25	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

(CONTINUED)

## 95. USING MACHINE LEARNING TO ANALYZE RANDOMIZED TRIALS: VALID ESTIMATES AND CONFIDENCE INTERVALS WITHOUT MODEL ASSUMPTIONS

**Sponsors:** ENAR, IMS, ASA Biometrics Section, ASA Section on Statistical Learning and Data Science

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

**Chair:** Bingkai Wang, Johns Hopkins University

### 3:45 Performance Evaluation of Flexible Strategies for Estimating HIV Vaccine Efficacy

Alex Luedtke\*, University of Washington

### 4:10 Inference for Model-Light Machine Learning in Precision Medicine

Michael Kosorok\*, University of North Carolina, Chapel Hill

### 4:35 Synthetic Difference in Differences

David A. Hirshberg\*, Stanford University; Dmitry Arkhangelsky, CEMFI, Madrid; Susan Athey, Guido Imbens and Stefan Wager, Stanford University

### 5:00 Machine Learning Versus Standard Methods for Covariate Adjustment: Performance Comparison Across 10 Completed Randomized Trials

Michael M. Rosenblum\*, Johns Hopkins Bloomberg School of Public Health

### 5:25 Floor Discussion

## 96. RECENT DEVELOPMENTS IN SEMIPARAMETRIC TRANSFORMATION MODELS

**Sponsors:** ENAR, ASA Biometrics Section

**Organizer:** Chun Li, Case Western Reserve University

**Chair:** Gustavo Amorim, Vanderbilt University Medical Center

### 3:45 Semiparametric Regression Models for Indirectly Observed Outcomes

Jan De Neve\* and Heideinde Dehaene, Ghent University

### 4:15 Addressing Outcome Detection Limits using Semiparametric Cumulative Probability Models

Bryan E. Shepherd\* and Yuqi Tian, Vanderbilt University

### 4:45 Cumulative Probability Models for Big Data

Chun Li\*, Case Western Reserve University

### 5:15 Discussant:

Frank Harrell, Vanderbilt University

## 97. INNOVATIONS IN STATISTICAL NEUROSCIENCE

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

**Organizer:** Jeff Goldsmith, Columbia University

**Chair:** Jeff Goldsmith, Columbia University

### 3:45 A Study of Longitudinal Trends in Time-Frequency Transformations of EEG Data During a Learning Experiment

Damla Senturk\*, Joanna Boland, Shafali Jeste and Donatello Telesca, University of California, Los Angeles

### 4:10 Improved Diagnostics and Prognostics using MRI in Multiple Sclerosis

Russell Shinohara\*, University of Pennsylvania

### 4:35 Intensity Warping for Multisite MRI Harmonization

Julia L. Wrobel\*, Colorado School of Public Health; Melissa Martin and Taki Shinohara, University of Pennsylvania; Jeff Goldsmith, Columbia University

### 5:00 Bayesian Approaches for Estimating Dynamic Functional Network Connectivity in fMRI Data

Michele Guindani\*, University of California, Irvine

### 5:25 Floor Discussion

## 98. ARTIFICIAL INTELLIGENCE FOR PREDICTION OF HEALTH OUTCOMES

**Sponsors:** ENAR, ASA Biometrics Section, ASA Health Policy Statistics Section, ASA Section on Statistical Learning and Data Science

**Organizer:** Lihui Zhao, Northwestern University

**Chair:** Lei Liu, Washington University in St. Louis

### 3:45 Distributed Learning from Multiple EHR Databases for Predicting Medical Events

Qi Long\*, University of Pennsylvania; Ziyi Li, Emory University; Kirk Roberts and Xiaoqian Jiang, University of Texas Health Science Center at Houston

### 4:10 Deep Learning with Time-to-Event Outcomes

Jon Steingrimsson\*, Samantha Morrison and Constantine Gatsonis, Brown University

### 4:35 A Scalable Discrete-Time Survival Model for Neural Networks

Balasubramanian Narasimhan\*, Stanford University

### 5:00 Deep Learning for Dynamic Prediction of Cardiovascular Events

Lihui Zhao\*, Northwestern University

### 5:25 Floor Discussion

**99. CONTRIBUTED PAPERS: LATENT VARIABLES AND PROCESSES****Sponsor: ENAR****Chair: Donglin Zeng, University of North Carolina, Chapel Hill**

- |      |  |
|------|--|
| 3:45 | <b>Modeling the Effects of Multiple Exposures with Unknown Group Memberships: A Bayesian Latent Variable Approach</b><br>Alexis E. Zavez*, University of Rochester Medical Center; Emeir M. McSorley, Ulster University; Sally W. Thurston, University of Rochester Medical Center             |
| 4:00 | <b>A Time-Dependent Structural Model Between Latent Classes and Competing Risks Outcomes</b><br>Teng Fei*, John Hanfelt and Limin Peng, Emory University   |
| 4:15 | <b>Dirichlet Depths for Point Process</b><br>Kai Qi*, Yang Chen and Wei Wu, Florida State University   |
| 4:30 | <b>Acknowledging the Dilution Effect in Group Testing Regression: A New Approach</b><br>Stefani C. Mokalled*, Christopher S. McMahan and Derek A. Brown, Clemson University; Joshua M. Tebbs, University of South Carolina; Christopher R. Bilder, University of Nebraska, Lincoln             |
| 4:45 | <b>Modeling Brain Waves as a Mixture of Latent Processes</b><br>Guillermo Cuauhtemotzin Granados Garcia* and Hernando Ombao, King Abdullah University of Science and Technology; Mark Fiecas, University of Minnesota; Babak Shahbaba, University of California, Irvine                        |
| 5:00 | <b>A Method to Flexibly Incorporate Covariates in Latent Class Analysis with Application to Mild Cognitive Impairment</b><br>Grace Kim* and John Hanfelt, Emory University Rollins School of Public Health   |
| 5:15 | <b>Exploration of Misspecification in Latent Class Trajectory Analysis (LCTA) and Growth Mixture Modeling (GMM): Error Structure Matters</b><br>Megan L. Neely*, Jane Pendergast and Bida Gu, Duke University; Natasha Dmitreava, Duke University Medical Center; Carl Pieper, Duke University |

**100. CONTRIBUTED PAPERS: TIME-TO-EVENT DATA ANALYSIS: SURVIVAL OF THE FITTEST****Sponsor: ENAR****Chair: Richard Chappell, University of Wisconsin, Madison**

- |      |  |
|------|--|
| 3:45 | <b>Survival Analysis under the Cox Proportional Hazards Model with Pooled Covariates</b><br>Paramita Saha Chaudhuri* and Lamin Juwara, McGill University   |
| 4:00 | <b>Quantile Association Regression on Bivariate Survival Data</b><br>Ling-Wan Chen*, National Institute of Environmental Health Sciences, National Institutes of Health; Yu Cheng and Ying Ding, University of Pittsburgh; Ruosha Li, University of Texas Health Science Center at Houston |
| 4:15 | <b>Restricted Mean Survival Time as a Function of Restriction Time</b><br>Yingchao Zhong*, University of Michigan; Douglas E. Schaebel, University of Pennsylvania   |
| 4:30 | <b>Quantile Regression on Cause-Specific Inactivity Time</b><br>Yichen Jia* and Jong-Hyeon Jeong, University of Pittsburgh   |
| 4:45 | <b>Relaxing the Independence Assumption in Relative Survival Analysis: A Parametric Approach</b><br>Reuben Adatorwovor* and Jason Fine, University of North Carolina at Chapel Hill; Aurelien Latouche, Conservatoire National des Arts et Métiers and Institut Curie, St-Cloud, France    |
| 5:00 | <b>Estimation of Effect Measures in Survival Analysis that Allow Causal Interpretation</b><br>Kjetil Røysland*, University of Oslo   |
| 5:15 | <b>Floor Discussion</b>  |



# SCIENTIFIC PROGRAM

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## 101. CONTRIBUTED PAPERS: RISKY BUSINESS: DIAGNOSTICS, ROC, AND PREDICTION

Sponsor: ENAR

Chair: Gong Tang, University of Pittsburgh

3:45	<b>NMADiaT: An R package for Network Meta-Analysis of Multiple Diagnostic Tests</b> Boyang Lu*, University of Minnesota; Qinshu Lian, Genentech; James S. Hodges and Haitao Chu, University of Minnesota
4:00	<b>Informative Back-End Screening</b> Michael R. Stutz* and Joshua M. Tebbs, University of South Carolina
4:15	<b>Patient-Reported Outcome (PRO) Assessment in Diagnostic Devices: A Novel Approach</b> Saryet Kucukemiroglu* and Manasi Sheth, U.S. Food and Drug Administration
4:30	<b>A Placement-Value Based Approach to Concave ROC Curves</b> Soutik Ghosal* and Zhen Chen, Eunice Kennedy Shriver National Institute of Child Health and Human Development, National Institutes of Health
4:45	<b>Inference in ROC Curves for Two-Phase Nested Case-Control Biomarker Studies</b> Leonidas E. Bantis*, University of Kansas Medical Center; Ziding Feng, Fred Hutchinson Cancer Research Center
5:00	<b>Diagnostic Evaluation of Quantitative Features of Functional Markers</b> Jeong Hoon Jang*, Indiana University; Amita K. Manatunga, Emory University
5:15	<b>Evaluation of Multiple Diagnostic Tests using Multi-Institutional Data with Missing Components</b> Jiasheng Shi*, Children's Hospital of Philadelphia; Jing Huang, University of Pennsylvania and The Children's Hospital of Philadelphia; Yong Chen, University of Pennsylvania

## 102. CONTRIBUTED PAPERS: INTERVAL-CENSORED AND MULTIVARIATE SURVIVAL DATA

Sponsor: ENAR

Chair: Jianxin Shi, National Cancer Institute, National Institutes of Health

3:45	<b>A Divide-and-Combine Approach of Multivariate Survival Analysis in Big Data</b> Wei Wang* and Shou-En Lu, Rutgers University; Jerry Q. Cheng, New York Institute of Technology
4:00	<b>Nonparametric Inference for Nonhomogeneous Multi-State Processes Based on Clustered Observations</b> Giorgos Bakoyannis*, Indiana University
4:15	<b>Flexible, Unified Approach for Analyzing Arbitrarily-Censored and/or Left-Truncated Interval-Censored Data</b> Prabhashi Withana Gamage*, James Madison University; Christopher McMahan, Clemson University; Lianming Wang, University of South Carolina
4:30	<b>Potential Intransitivity of Win-Ratio Preferences: Is it a Problem and What Do We Do About It?</b> David Oakes*, University of Rochester
4:45	<b>Bayesian Analysis of Multivariate Survival Data Based on Vine Copulas</b> Guanyu Hu*, University of Connecticut; Dooti Roy, Boehringer Ingelheim; Dipak Dey, University of Connecticut
5:00	<b>Non-parametric estimation in an illness-death model with component-wise censoring</b> Anne Eaton*, University of Minnesota
5:15	<b>Floor Discussion</b>

**103. CONTRIBUTED PAPERS: GRAPHICAL MODELS AND APPLICATIONS****Sponsor: ENAR****Chair: Russell Stocker, Indiana University of Pennsylvania**

3:45	<b>Inference of Large Modified Poisson-Type Graphical Models: Application to RNA-seq Data in Childhood Atopic Asthma Studies</b> Rong Zhang*, University of Pittsburgh; Juan C. Celedon and Wei Chen, UPMC Children's Hospital of Pittsburgh; Zhao Ren, University of Pittsburgh
4:00	<b>Assisted Estimation of Gene Expression Graphical Models</b> Huangdi Yi*, Yale School of Public Health; Yifan Sun, Renmin University of China; Qingzhao Zhang, Xiamen University; Yang Li, Renmin University of China; Shuangge Ma, Yale School of Public Health
4:15	<b>Directed Acyclic Graph Assisted Methods for Estimating Average Treatment Effect</b> Jingchao Sun*, Maiying Kong, Scott Davis Duncan and Subhadip Pal, University of Louisville
4:30	<b>Gene Network Analysis Based on Single Cell RNA Sequencing Data</b> Meichen Dong* and Fei Zou, University of North Carolina, Chapel Hill
4:45	<b>Selection and Estimation of Conditional Graphical Models</b> Stephen Salerno* and Yi Li, University of Michigan
5:00	<b>Joint Estimation of the Two-Level Gaussian Graphical Models across Multiple Classes</b> Inyoung Kim*, Virginia Tech; Liang Shan, University of Alabama at Birmingham
5:15	<b>Floor Discussion</b>

**104. CONTRIBUTED PAPERS: SUPPORT VECTOR MACHINES, NEURAL NETWORKS AND DEEP LEARNING****Sponsor: ENAR****Chair: Tanzy M. Love, University of Rochester**

3:45	<b>ForgeNet: A Graph Deep Neural Network Model Using Tree-Based Ensemble Classifiers for Feature Graph Construction</b> Yunchuan Kong* and Tianwei Yu, Emory University
4:00	<b>GWAS-Based Deep Learning for Survival Prediction</b> Tao Sun*, Wei Chen and Ying Ding, University of Pittsburgh
4:15	<b>An Inferential Framework for Individualized Minimal Clinically Importance Difference with a Linear Structure</b> Zehua Zhou* and Jiwei Zhao, State University of New York at Buffalo
4:30	<b>Deep Neural Networks for Survival Analysis Using Pseudo Values</b> Lili Zhao*, University of Michigan; Feng Dai, Merck & Co., Inc.
4:45	<b>Neural Networks for Clustered and Longitudinal Data using Mixed Effects Models</b> Francesca Mandel* and Ian Barnett, University of Pennsylvania
5:00	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

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## WEDNESDAY, MARCH 25

8:30 a.m. — 10:15 a.m.

### 105. ADVANCES IN STATISTICAL MODELING FOR MULTI-OMICS DATA INTEGRATION

**Sponsor:** IMS

**Organizer:** Sunyoung Shin, University of Texas, Dallas

**Chair:** Sunyoung Shin, University of Texas, Dallas

**Gene-Set Integrative Omics Analysis Using Tensor-Based Association Tests**

8:30 Jung-Ying Tzeng\*, North Carolina State University; Meng Yang, The SAS Institute; Wenbin Lu, North Carolina State University; Jeff Miecznikowski, University of Buffalo; Sheng-Mao Chang, National Cheng-Kung University

**Radiogenomic Analysis of Lower Grade Gliomas Incorporating Tumor Heterogeneity in Imaging Through Densities**

8:55 Shariq Mohammed\*, University of Michigan; Sebastian Kurtek, The Ohio State University; Karthik Bharath, University of Nottingham; Arvind Rao and Veerabhadran Baladandayuthapani, University of Michigan

**Bayesian Regression and Clustering Models to Incorporate Multi-Layer Overlapping Group Structure in Multi-Omics Applications**

9:20 George Tseng\*, University of Pittsburgh

**Graphical Models for Data Integration and Mediation Analysis**

9:45 Min Jin Ha\*, University of Texas MD Anderson Cancer Center; Veera Baladandayuthapani, University of Michigan

10:10 **Floor Discussion**

### 106. CAUSAL INFERENCE AND NETWORK DEPENDENCE: FROM PEER EFFECTS TO THE REPLICATION CRISIS IN EPIDEMIOLOGY

**Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology, ASA Health Policy Statistics Section

**Organizer:** Corwin Zigler, University of Texas, Austin and Dell Medical School

**Chair:** Corwin Zigler, University of Texas, Austin and Dell Medical School

**Social Network Dependence, the Replication Crisis, and (in)valid Inference**

8:30 Elizabeth L. Ogburn\*, Johns Hopkins University

**Nonparametric Identification of Causal Intervention Effects Under Contagion**

8:55 Forrest W. Crawford\* and Xiaoxuan Cai, Yale School of Public Health; Wen Wei Loh, University of Ghent

**Bayesian Auto-g-Computation of Network Causal Effects: Incarceration and Infection in a High Risk Network**

9:20 Isabel R. Fulcher\*, Harvard Medical School; Eric J. Tchetgen Tchetgen, University of Pennsylvania; Ilya Shpitser, Johns Hopkins University

**Heterogeneous Causal Effects under Network Interference**

9:45 Laura Forastiere\*, Yale University; Costanza Tortú and Falco Bargagli-Stoffi, IMT Lucca, Italy

10:10 **Floor Discussion**

### 107. FLEXIBLE SPATIO-TEMPORAL MODELS FOR ENVIRONMENTAL AND ECOLOGICAL PROCESSES

**Sponsor:** ENAR, ASA Section on Statistics and the Environment

**Organizer:** Alexandra Schmidt, McGill University

**Chair:** Alexandra Schmidt, McGill University

**Evaluating Proxy Influence in Assimilated Paleoclimate Reconstructions - Testing the Exchangeability of Two Ensembles of Spatial Processes**

8:30 Bo Li\* and Trevor Harris, University of Illinois at Urbana-Champaign; Nathan Steiger and Jason Smerdon, Columbia University; Naveen Narisetty, University of Illinois at Urbana-Champaign; J. Derek Tucker, Sandia National Lab

**Fusing Multiple Existing Space-Time Categorical Land Cover Datasets**

8:55 Amanda S. Hering\*, Baylor University; Nicolás Rodríguez-Jeangros and John E. McCray, Colorado School of Mines

**Inverse Reinforcement Learning for Animal Behavior from Environmental Cues**

9:20 Toryn L.J. Schafer\* and Christopher K. Winkle, University of Missouri

**High-dimensional multivariate Geostatistics: A Bayesian Matrix-Normal Approach**

9:45 Lu Zhang\* and Sudipto Banerjee, UCLA-Fielding School of Public Health

10:10 **Floor Discussion**

**108. RECENT ADVANCES IN NEUROIMAGING ANALYTICS****Sponsors:** ENAR, ASA Biometrics Section**Organizer:** Zainab Albar, Case Western Reserve University School of Medicine and Quantitative Health Sciences**Chair:** Abdus Sattar, Case Western Reserve University School of Medicine and Quantitative Health Sciences

8:30	<b>Covariance Regression in Brain Imaging</b> Brian S. Caffo*, Johns Hopkins University; Yi Zhao, Indiana University Purdue University Indianapolis; Bingkai Wang, Johns Hopkins University; Xi (Rossi) Luo, University of Texas Health Science Center at Houston
8:55	<b>Bayesian Modeling of Multiple Structural Connectivity Networks During the Progression of Alzheimer's Disease</b> Christine Peterson*, The University of Texas MD Anderson Cancer Center
9:20	<b>Modeling Lead-Lag Dynamics in High Dimensional Time Series</b> Hernando Ombao* and Chee-Ming Ting, King Abdullah University of Science and Technology; Marco Pinto, Oslo Metropolitan University
9:45	<b>Modeling Positive Definite Matrices in Diffusion Tensor Imaging</b> Dipankar Bandyopadhyay*, Virginia Commonwealth University; Zhou Lan, The Pennsylvania State University; Brian J. Reich, North Carolina State University
10:10	<b>Floor Discussion</b>

**109. NOVEL TENSOR METHODS FOR COMPLEX BIOMEDICAL DATA****Sponsors:** ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section, ASA Section on Statistical Learning and Data Science, ICOSA**Organizer:** Gen Li, Columbia University**Chair:** Gen Li, Columbia University

8:30	<b>Generalized Tensor Regression with Covariates on Multiple Modes</b> Miaoyan Wang*, Zhuoyan Xu and Jiaxin Hu, University of Wisconsin, Madison
8:55	<b>Co-Manifold Learning on Tensors</b> Eric Chi*, North Carolina State University

9:20	<b>Nonparametric Regression for Brain Imaging Data Analysis</b> Weining Shen*, University of California, Irvine
9:45	<b>Brain Regions Identified as Being Associated with Verbal Reasoning through the Use of Imaging Regression via Internal Variation</b> Xuan Bi*, University of Minnesota; Long Feng and Heping Zhang, Yale University
10:10	<b>Floor Discussion</b>

**110. INTEGRATIVE ANALYSIS OF CLINICAL TRIALS AND REAL-WORLD EVIDENCE STUDIES****Sponsors:** ENAR, IMS, ASA Biometrics Section**Organizer:** Shu Yang, North Carolina State University**Chair:** Shu Yang, North Carolina State University

8:30	<b>On Using Electronic Health Records to Improve Optimal Treatment Rules in Randomized Trials</b> Peng Wu*, Columbia University and Visa Inc.; Donglin Zeng, University of North Carolina, Chapel Hill; Haoda Fu, Eli Lilly and Company; Yuanjia Wang, Columbia University
8:55	<b>Making Use of Information Contained in Existing Black-Box-Type Risk Calculators</b> Peisong Han*, Jeremy M.G. Taylor and Bhramar Mukherjee, University of Michigan
9:20	<b>Integrative Analysis of Randomized Clinical Trials with Real World Evidence Studies</b> Lin Dong*, Wells Fargo Bank; Shu Yang, North Carolina State University
9:45	<b>Risk Projection for Time-to-Event Outcome Leveraging External Summary Statistics with Source Individual-Level Data</b> Jiayin Zheng*, Li Hsu and Yingye Zheng, Fred Hutchinson Cancer Research Center
10:10	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

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## 111. CONTRIBUTED PAPERS: CLUSTERED DATA METHODS

Sponsor: ENAR

Chair: Sanjoy K. Sinha, Carleton University

8:30	<b>Modeling Tooth-Loss using Inverse Probability Censoring Weights in Longitudinal Clustered Data with Informative Cluster Size</b> Aya A. Mitani*, Harvard T. H. Chan School of Public Health; Elizabeth K. Kaye, Boston University Henry M. Goldman School of Dental Medicine; Kerrie P. Nelson, Boston University School of Public Health
8:45	<b>Partially Pooled Propensity Score Models for Average Treatment Effect Estimation with Multilevel Data</b> Youjin Lee*, University of Pennsylvania; Trang Nguyen and Elizabeth Stuart, Johns Hopkins Bloomberg School of Public Health
9:00	<b>Outcome-Guided Disease Subtyping for High-Dimensional Omics Data</b> Peng Liu*, Lu Tang and George Tseng, University of Pittsburgh
9:15	<b>The Impact of Sample Size Re-Estimation using Baseline ICC in Cluster Randomized Trials: A Simulation Study</b> Kaleab Z. Abebe*, Kelley A. Jones, Taylor Paglisotti and Elizabeth Miller, University of Pittsburgh; Daniel J. Tancredi, University of California, Davis
9:30	<b>Hypothesis Testing for Community Detection in Network Data</b> Chetkar Jha*, Mingyao Li and Ian Barnett, University of Pennsylvania
9:45	<b>On the Interplay Between Exposure Misclassification and Informative Cluster Size</b> Glen McGee*, Harvard University; Marianthi-Anna Kioumourtzoglou, Columbia University; Marc G. Weisskopf, Sebastien Haneuse and Brent A. Coull, Harvard University
10:00	<b>An Alternative to the Logistic GLMM with Normal Random Effects for Estimating Dose Response in the Presence of Extreme Between Subject Heterogeneity</b> Joe Bible* and Christopher McMahan, Clemson University

## 112. CONTRIBUTED PAPERS: SUBGROUP ANALYSIS

Sponsor: ENAR

Chair: Sheng Luo, Duke University

8:30	<b>Inference on Selected Subgroups in Clinical Trials</b> Xinzhou Guo*, Harvard University; Xuming He, University of Michigan
8:45	<b>A Simultaneous Inference Procedure to Identify Subgroups in Targeted Therapy Development with Time-to-Event Outcomes</b> Yue Wei*, University of Pittsburgh; Jason Hsu, The Ohio State University; Ying Ding, University of Pittsburgh
9:00	<b>Cross-Platform Omics Prediction (CPOP) Procedure Enables Precision Medicine</b> Kevin Y.X. Wang*, The University of Sydney; Varsha Tembe and Gullietta Pupo, Melanoma Institute Australia and The University of Sydney; Garth Tarr and Samuel Mueller, The University of Sydney; Graham Mann, Melanoma Institute Australia and The University of Sydney; Jean Y.H. Yang, The University of Sydney
9:15	<b>Bayesian Subgroup Analysis in Regression using Mixture Models</b> Yunju Im* and Aixin Tan, University of Iowa
9:30	<b>Adaptive Subgroup Identification in Phase I-II Clinical Trials</b> Alexandra M. Curtis* and Brian J. Smith, University of Iowa; Andrew G. Chapple, Louisiana State University School of Public Health
9:45	<b>Identifying Effect Modifiers and Subgroups that May Benefit from Treatment when the Number of Covariates is Large</b> John A. Craycroft*, Maiying Kong and Subhadip Pal, University of Louisville
10:00	<b>Floor Discussion</b>



**113. CONTRIBUTED PAPERS: FUNCTIONAL DATA ANALYSIS: BELOW THE SURFACE****Sponsor: ENAR****Chair: Lihui Zhao, Northwestern University**

8:30	<b>Imaging Genetics: Where the Statistics of fMRI and Genome-Wide Association Studies Collide</b> Kristen N. Knight*, University of Georgia
8:45	<b>Bayesian Quantile Monotone Single-Index Model for Bounded Response Using Functional and Scalar Predictors</b> Bradley B. Hupf*, Debajyoti Sinha, Eric Chicken and Greg Hajcak, Florida State University
9:00	<b>Sparse Log-Contrast Regression with Functional Compositional Predictors: Linking Gut Microbiome Trajectory in Early Postnatal Period to Neurobehavioral Development of Preterm Infants</b> Zhe Sun*, Wanli Xu and Xiaomei Cong, University of Connecticut; Gen Li, Columbia University; Kun Chen, University of Connecticut
9:15	<b>Principle ERP Reduction and Analysis</b> Emilie Campos*, Chad Hazlett, Patricia Tan, Holly Truong, Sandra Loo, Charlotte DiStefano, Shafali Jeste and Damla Senturk, University of California, Los Angeles
9:30	<b>Approaches for Extending Multiple Imputation to Handle Scalar and Functional Data</b> Adam Ciarleglio*, The George Washington University
9:45	<b>Statistical Analysis of Heart Rate Variability from Electrocardiogram Data</b> Andrada E. Ivanescu*, Montclair State University; Naresh Punjabi and Ciprian M. Crainiceanu, Johns Hopkins University
10:00	<b>Interpretable Principal Components Analysis for Multilevel Multivariate Functional Data, with Application to EEG Experiments</b> Jun Zhang* and Greg J. Siegle, University of Pittsburgh; Wendy D' Andrea, New School for Social Research; Robert T. Krafty, University of Pittsburgh

**114. CONTRIBUTED PAPERS: HIV, INFECTIOUS DISEASE AND MORE****Sponsor: ENAR****Chair: Ming Wang, The Pennsylvania State University**

8:30	<b>A Hybrid Compartment/Agent-Based Model for Infectious Disease Modeling</b> Shannon Gallagher*, National Institute of Allergy and Infectious Diseases, National Institutes of Health; William Eddy, Carnegie Mellon University
8:45	<b>Analysis of Two-Phase Studies using Generalized Method of Moments</b> Prosenjit Kundu*, Johns Hopkins Bloomberg School of Public Health; Nilanjan Chatterjee, Johns Hopkins Bloomberg School of Public Health and Johns Hopkins University School of Medicine
9:00	<b>Bias and Efficiency in Group Testing Estimation for Infectious Disease Surveillance</b> Katherine M. Bindbeutel* and Md S. Warasi, Radford University
9:15	<b>Mediation Effect Sizes for Latent Outcome Models using Explained Variance Decomposition</b> Yue Jiang*, University of North Carolina, Chapel Hill; Shanshan Zhao, National Institute of Environmental Health Sciences, National Institutes of Health; Jason Peter Fine, University of North Carolina, Chapel Hill
9:30	<b>Toward Evaluation of Disseminated Effects of Non-Randomized HIV Prevention Interventions Among Observed Networks of People who Inject Drugs</b> Ashley Buchanan*, Natallia Katenka and TingFang Lee, University of Rhode Island; M. Elizabeth Halloran, Fred Hutchinson Cancer Research Center and University of Washington; Samuel Friedman, New York University; Georgios Nikolopoulos, University of Cyprus
9:45	<b>Joint Model of Adherence to Dapivirine-containing Vaginal Ring and HIV-1 Risk</b> Qi Dong*, University of Washington; Elizabeth R. Brown and Jingyang Zhang, Fred Hutchinson Cancer Research Center
10:00	<b>The Mechanistic Analysis of Founder Virus Data in Challenge Models</b> Ana Maria Ortega-Villa* and Dean A. Follmann, National Institute of Allergy and Infectious Diseases, National Institutes of Health

# SCIENTIFIC PROGRAM

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## 115. CONTRIBUTED PAPERS: CLINICAL TRIAL DESIGN AND ANALYSIS

Sponsor: ENAR

Chair: Fang Liu, University of Notre Dame

8:30	<b>Bayesian Design of Clinical Trials for Joint Models of Longitudinal and Time-to-Event Data</b> Jiawei Xu*, Matthew A. Psioda and Joseph G. Ibrahim, University of North Carolina, Chapel Hill
8:45	<b>Statistical Support for Designing Non-Inferiority Trials: An Application to Rheumatoid Arthritis</b> Rebecca Rothwell* and Gregory Levin, U.S. Food and Drug Administration
9:00	<b>Determining Mental Health Condition Patterns in Veterans with a Lifetime PTSD Diagnosis</b> Ilaria Domenicano*, Department of Veterans Affairs Cooperative Studies Program and Yale School of Public Health; Lori L. Davis, Tuscaloosa Veterans Affairs Medical Center and University of Alabama School of Medicine; Lisa Mueller, Edith Nourse Rogers Memorial Veterans Hospital; Tassos Constantino Kyriakides, Department of Veterans Affairs Cooperative Studies Program and Yale School of Public Health
9:15	<b>Estimation of Ascertainment Bias and its Effect on Power in Clinical Trials with Time-to-Event Outcomes</b> Erich J. Greene*, Peter Peduzzi, James Dziura, Can Meng and Denise Esserman, Yale Center for Analytical Sciences
9:30	<b>Design and Analysis Considerations for Utilizing a Tailoring Function in a snSMART with Continuous Outcomes</b> Holly E. Hartman*, University of Michigan; Roy N. Tamura, University of South Florida; Matthew J. Schipper and Kelley Kidwell, University of Michigan
9:45	<b>Two-Part Proportional Mixed Effects Model for Clinical Trials in Alzheimer's Disease</b> Guoqiao Wang*, Yan Li, Chengjie Xiong, Lei Liu, Andrew Aschenbrenner, Jason Hassenstab, Eric McDade and Randall Bateman, Washington University in St. Louis
10:00	Floor Discussion

## 116. CONTRIBUTED PAPERS: MULTIVARIATE AND HIGH-DIMENSIONAL DATA ANALYSIS

Sponsor: ENAR

Chair: Qiwei Li, University of Texas, Dallas

8:30	<b>On Genetic Correlation Estimation with Summary Statistics from Genome-Wide Association Studies</b> Bingxin Zhao* and Hongtu Zhu, University of North Carolina, Chapel Hill
8:45	<b>Multivariate Association Analysis with Correlated Traits in Related Individuals</b> Souvik Seal*, University of Minnesota
9:00	<b>Grafted and Vanishing Random Subspaces</b> Matthew Corsetti* and Tanzy Love, University of Rochester
9:15	<b>Modeling Repeated Multivariate Data to Estimate Individuals' Trajectories with Application to Scleroderma</b> Ji Soo Kim*, Johns Hopkins University; Ami Shah and Laura Hummers, Johns Hopkins University School of Medicine; Scott L. Zeger, Johns Hopkins University
9:30	<b>Nonignorable Item Nonresponse in Multivariate Outcomes</b> Sijing Li* and Jun Shao, University of Wisconsin, Madison
9:45	<b>Multivariate Association Analysis with Somatic Mutation Data</b> Chad He*, Fred Hutchinson Cancer Research Center; Yang Liu, Wright State University; Ulrike Peters and Li Hsu, Fred Hutchinson Cancer Research Center
10:00	Floor Discussion

**WEDNESDAY, MARCH 25**

**10:15 a.m. — 10:30 a.m.**

**REFRESHMENT BREAK WITH OUR EXHIBITORS**

**WEDNESDAY, MARCH 25****10:30 a.m. — 12:15 p.m.****117. ASYMMETRICAL STATISTICAL LEARNING FOR BINARY CLASSIFICATION****Sponsor:** IMS**Organizer:** Jingyi Li, University of California, Los Angeles**Chair:** Anqi Zhao, National University of Singapore

	<b>Introduction to Neyman-Pearson Classification</b>
10:30	Jingyi Jessica Li*, University of California, Los Angeles; Xin Tong, University of Southern California; Yang Feng, Columbia University
	<b>A Unified View of Asymmetric Binary Classification</b>
10:55	Wei Vivian Li*, Rutgers, The State University of New Jersey; Xin Tong, University of Southern California; Jingyi Jessica Li, University of California, Los Angeles
	<b>Neyman-Pearson Classification: Parametrics and Sample Size Requirement</b>
11:20	Yang Feng*, New York University
	<b>Intentional Control of Type I Error over Unconscious Data Distortion: A Neyman-Pearson Approach to Text Classification</b>
11:45	Xin Tong*, University of Southern California; Lucy Xia, Hong Kong University of Science and Technology; Richard Zhao, The Pennsylvania State University; Yanhui Wu, University of Southern California
12:10	<b>Floor Discussion</b>

**118. RECENT ADVANCES AND OPPORTUNITIES IN LARGE SCALE & MULTI-OMIC SINGLE-CELL DATA ANALYSIS****Sponsors:** ENAR, ASA Biometrics Section, ASA Statistics in Genomics and Genetics Section**Organizer:** Rhonda Bacher, University of Florida**Chair:** Mengjie Chen, University of Chicago

	<b>Statistical Analysis of Coupled Single-Cell RNA-seq and Immune Profiling Data</b>
10:30	Hongkai Ji* and Zhicheng Ji, Johns Hopkins Bloomberg School of Public Health
	<b>Assessing Consistency of Single Cell Unsupervised Multi-Omics Methods</b>
11:00	Michael I. Love*, University of North Carolina, Chapel Hill

11:30	<b>Statistical Methods for Identifying and Characterizing Cell Populations using High-Dimensional Single-Cell Data</b> Raphael Gottardo*, Fred Hutchinson Cancer Research Center
12:00	<b>Discussant:</b> Rhonda Bacher, University of Florida

**119. NOVEL STATISTICAL METHODS FOR COMPLEX INTERVAL-CENSORED SURVIVAL DATA****Sponsors:** ENAR, ASA Biometrics Section, ASA Section on Statistics in Epidemiology**Organizer:** Sedigheh Mirzaei Salehabadi, St. Jude Children's Research Hospital**Chair:** Sedigheh Mirzaei Salehabadi, St. Jude Children's Research Hospital

	<b>Semiparametric Regression Analysis of Multiple Censored Events in Family Studies</b>
10:30	Donglin Zeng*, University of North Carolina, Chapel Hill; Fei Gao, Fred Hutchinson Cancer Research Center; Yuanjia Wang, Columbia University
	<b>AModeling Interval Censored Time to Event Outcomes with Inflation of Zeros, with Application to Pediatric HIV Studies</b>
10:55	Raji Balasubramanian*, University of Massachusetts, Amherst
	<b>Case-Cohort Studies with Multiple Interval-Censored Disease Outcomes</b>
11:20	Qingning Zhou*, University of North Carolina, Charlotte; Jianwen Cai and Haibo Zhou, University of North Carolina, Chapel Hill
	<b>Adjusting for Covariate Measurement Error in Survival Analysis under Competing Risks</b>
11:45	Sharon Xiangwen Xie* and Carrie Caswell, University of Pennsylvania
12:10	<b>Floor Discussion</b>

# SCIENTIFIC PROGRAM

(CONTINUED)

## 120. MODERN GRAPHICAL MODELING OF COMPLEX BIOMEDICAL SYSTEMS

**Sponsor:** ENAR, ASA Bayesian Statistical Science Section

**Organizer:** Lili Zhao, University of Michigan

**Chair:** Lili Zhao, University of Michigan

**10:30 A Tripartite Latent Graph for Phenotype Discovery in EHR Data**  
Peter Mueller\*, University of Texas, Austin; Yang Ni, Texas A&M University; Yuan Ji, The University of Chicago

**10:55 The Reduced PC-Algorithm: Improved Causal Structure Learning in Large Random Networks**  
Ali Shojaie\*, University of Washington

**11:20 Latent Network Estimation and Variable Selection for Compositional Data via Variational EM**  
Nathan Osborne\*, Rice University; Christine B. Peterson, MD Anderson Cancer Center; Marina Vannucci, Rice University

**11:45 Personalized Integrated Network Estimation**  
Veera Baladandayuthapani\*, University of Michigan; Min Jin Ha, University of Texas MD Anderson Cancer Center; Yang Ni, Texas A&M University; Francesco C. Stingo, University of Florence, Italy

**12:10 Floor Discussion**

## 121. HIGHLY EFFICIENT DESIGNS AND VALID ANALYSES FOR RESOURCE CONSTRAINED STUDIES

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

**Organizer:** Jonathan Schildcrout, Vanderbilt University Medical Center

**Chair:** Jonathan Schildcrout, Vanderbilt University Medical Center

**10:30 Semiparametric Generalized Linear Models for Analysis of Longitudinal Data with Biased Observation-Level Sampling**  
Paul Rathouz\*, University of Texas, Austin

**10:55 Cluster-Based Outcome-Dependent Sampling in Resource-Limited Settings: Inference in Small-Samples**  
Sara M. Sauer\*, Harvard T.H. Chan School of Public Health; Bethany Hedt-Gauthier, Harvard Medical School; Claudia Rivera-Rodriguez, University of Auckland; Sebastien Haneuse, Harvard T.H. Chan School of Public Health

## Optimal Designs of Two-Phase Studies

**11:20** Ran Tao\*, Vanderbilt University Medical Center; Donglin Zeng and Danyu Lin, University of North Carolina, Chapel Hill

## Predictive Case Control Designs for Modification Learning

**11:45** Patrick James Heagerty\*, University of Washington; Katherine Tan, Flatiron Health

**12:10 Floor Discussion**

## 122. STATISTICAL ANALYSIS OF TRACKING DATA FROM PERSONAL WEARABLE DEVICES

**Sponsors:** ENAR, ASA Section on Statistical Learning and Data Science

**Organizer:** Jonggyu Baek, University of Massachusetts Medical School

**Chair:** Peter X.K. Song, University of Michigan

## Smartphone-Based Estimation of Sleep

**10:30** Ian J. Barnett\* and Melissa Martin, University of Pennsylvania

## Quantifying Mortality Risks using Accelerometry Data Collected According to the Complex Survey Weighted Design

**11:00** Ekaterina Smirnova\*, Virginia Commonwealth University; Andrew Leroux, Johns Hopkins University; Lucia Tabacu, Old Dominion University; Ciprian Crainiceanu, Johns Hopkins University

## Circadian Rhythm for Physical Activity of Infants Under 1-year Old

**11:30** Jiawei Bai\*, Sara Benjamin-Neelon and Vadim Zipunnikov, Johns Hopkins University

## Discussant:

**12:00** Ciprian Crainiceanu, Johns Hopkins University

**123. CONTRIBUTED PAPERS: META-ANALYSIS METHODS****Sponsor: ENAR****Chair: Jing Zhang, University of Maryland**

10:30	<b>A Three-Groups Bayesian Approach for Identifying Genetic Modifiers from Disparate Data Sources, with Application to Parkinson's Disease</b> Daisy Philtrou*, The Pennsylvania State University; Benjamin Shaby, Colorado State University; Vivian Cheng, The Pennsylvania State University
10:45	<b>Multi-Trait Analysis of Rare-Variant Association Summary Statistics using MTAR</b> Lan Luo*, University of Wisconsin, Madison; Judong Shen, Hong Zhang, Aparna Chhibber and Devan V. Mehrotra, Merck & Co., Inc.; Zheng-zheng Tang, Wisconsin Institute for Discovery at University of Wisconsin, Madison
11:00	<b>Empirical Bayes Approach to Integrate Multiple External Summary-Level Information into Current Study</b> Tian Gu*, Jeremy M.G. Taylor and Bhramar Mukherjee, University of Michigan
11:15	<b>Tradeoff between Fixed-Effect and Random-Effects Meta-Analyses</b> Yipeng Wang* and Lifeng Lin, Florida State University
11:30	<b>Bayesian Approach to Assessing Publication Bias with Controlled False Positive Rate in Meta-Analyses of Odds Ratios</b> Linyu Shi* and Lifeng Lin, Florida State University
11:45	<b>A Bayesian Hierarchical CACE Model Accounting for Incomplete Noncompliance Data in Meta-Analysis</b> Jincheng (Jeni) Zhou*, Amgen; James S. Hodges and Haitao Chu, University of Minnesota
12:00	<b>Meta-Analysis of Gene Set Coexpression</b> Haocan Song*, Vanderbilt University Medical Center; Yan Guo, University of New Mexico; Fei Ye, Vanderbilt University Medical Center

**124. CONTRIBUTED PAPERS: LONGITUDINAL DATA ANALYSIS****Sponsor: ENAR****Chair: Erinn M. Hade, The Ohio State University**

10:30	<b>Regression Analysis of Sparse Asynchronous Longitudinal Data with Informative Observation Times</b> Dayu Sun*, University of Missouri; Hui Zhao, Zhongnan University of Economics and Law; Jianguo Sun, University of Missouri
10:45	<b>Modeling Continuous Longitudinal Response Data using Ordinal Regression</b> Yuqi Tian* and Bryan E. Shepherd, Vanderbilt University; Chun Li, Case Western Reserve University; Jonathan S. Schildcrout, Vanderbilt University
11:00	<b>Novel Joint Models for Identifying Determinants of Cognitive Decline in the Presence of Informative Drop-out and Observation Times</b> Kendra Davis-Plourde* and Yorghos Tripodis, Boston University
11:15	<b>Multiple Imputation of an Expensive Covariate in Outcome Dependent Sampling Designs for Longitudinal Data</b> Chiara Di Gravio*, Ran Tao and Jonathan S. Schildcrout, Vanderbilt University
11:30	<b>Real-Time Regression Analysis of Streaming Clustered Data with Possible Abnormal Data Batches</b> Lan Luo* and Peter X.K. Song, University of Michigan
11:45	<b>Modeling Disease Progression with Time-Dependent Risk Factors and Time-Varying Effects using Longitudinal Data</b> Jacquelyn E. Neal* and Dandan Liu, Vanderbilt University
12:00	<b>Informative Visit Processes in Longitudinal Data from the Health Sciences</b> Fridtjof Thomas*, University of Tennessee Health Science Center; Csaba P. Kovesdy, Memphis VA Medical Center; Yunusa Olufadi, University of Memphis



# SCIENTIFIC PROGRAM

(CONTINUED)

## 125. CONTRIBUTED PAPERS: HIGH DIMENSIONAL DATA ANALYSIS: THE BIG PICTURE

Sponsor: ENAR

Chair: Kaushik Ghosh, University of Nevada, Las Vegas

10:30	<b>Capturing Skewness and Sparsity in High Dimensions</b> Xiaoqiang Wu*, Yiyuan She and Debajyoti Sinha, Florida State University
10:45	<b>Efficient Greedy Search for High-Dimensional Linear Discriminant Analysis</b> Hannan Yang* and Quefeng Li, University of North Carolina, Chapel Hill
11:00	<b>Parallelized Large-Scale Estimation and Inference for High-Dimensional Clustered Data with Binary Outcomes</b> Wenbo Wu*, Kevin He and Jian Kang, University of Michigan School of Public Health
11:15	<b>A Generalized Framework for High-Dimensional Inference based on Leave-One-Covariate-Out LASSO Path</b> Xiangyang Cao*, Karl Gregory and Dewei Wang, University of South Carolina
11:30	<b>Iterative Algorithm to Select Vine Copula According to Expert Knowledge and Pairwise Correlations</b> Philippe Saint Pierre*, University of Toulouse; Nazih Benoumechiara, Sorbonnes University; Nicolas J. Savy, University of Toulouse
11:45	<b>Floor Discussion</b>

## 126. CONTRIBUTED PAPERS: CLINICAL 'TRIALS AND TRIBULATIONS'

Sponsor: ENAR

Chair: Rachel Nethery, Harvard T.H. Chan School of Public Health

10:30	<b>Model-Robust Inference for Clinical Trials that Improve Precision by Stratified Randomization and Adjustment for Additional Baseline Variables</b> Bingkai Wang*, Michael Rosenblum, Ryoko Susukida, Ramin Mojtabai and Masoumeh Aminesmaeili, Johns Hopkins University
10:45	<b>Dynamic Borrowing in the Presence of Treatment Effect Heterogeneity</b> Ales Kotalik* and David Vock, University of Minnesota; Eric Donny, Wake Forest School of Medicine; Dorothy Hatsukami and Joseph Koopmeiners, University of Minnesota
11:00	<b>Bayesian Methods to Compare Dose Levels to Placebo in a Small n Sequential Multiple Assignment Randomized Trial (snSMART)</b> Kimberly A. Hochstedler* and Fang Fang, University of Michigan; Roy N. Tamura, University of South Florida; Thomas M. Braun and Kelley M. Kidwell, University of Michigan
11:15	<b>Sample Size Calculation in Comparative Clinical Trials with Longitudinal Count Data: Incorporation of Misspecification of the Variance Function and Correlation Matrix</b> Masataka Igeta*, Hyogo College of Medicine; Shigeyuki Matsui, Nagoya University Graduate School of Medicine
11:30	<b>Sequential Interval Estimation of Patient Accrual Rate in Clinical Trials</b> Dongyun Kim*, National Heart Lung and Blood Institute, National Institutes of Health; Sung-Min Han, OSEHRA
11:45	<b>Statistical Analysis of Glucose Variability</b> Jiangtao Luo*, Ismail El Moudden and Mohan Pant, Eastern Virginia Medical School
12:00	<b>The Impact of Precision on Go/No-Go Decision in Proof-of-Concept Trials</b> Macaulay Okwukenye*, Brio Dexter Pharmaceuticals

## 127. CONTRIBUTED PAPERS: COUNT DATA: THE THOUGHT THAT COUNTS

**Sponsor: ENAR**

**Chair: Sandra Hurtado Rua, Cleveland State University**

10:30	<b>Probabilistic Canonical Correlation Analysis for Sparse Count Data</b> Lin Qiu* and Vernon M. Chinchilli, The Pennsylvania State University
10:45	<b>Bayesian Credible Subgroups for Count Regression and Its Application to Safety Evaluation in Clinical Studies</b> Duy Ngo*, Western Michigan University; Patrick Schnell, The Ohio State University; Shahrul Mt-Isa, MSD Research Laboratories; Jie Chen and Greg Ball, Merck & Co., Inc.; Dai Feng, AbbVie Inc.; Richard Baumgartner, Merck & Co., Inc.
11:00	<b>Analysis of Panel Count Data with Time-Dependent Coefficient and Covariate Effects</b> Yuanyuan Guo* and Jianguo Sun, University of Missouri, Columbia
11:15	<b>Semi-Parametric Generalized Linear Model for Binary Count Data with Varying Cluster Sizes</b> Xinran Qi* and Aniko Szabo, Medical College of Wisconsin
11:30	<b>Drug Safety Evaluation Using Panel Count Model</b> Yizhao Zhou*, Ao Yuan and Ming Tan, Georgetown University
11:45	<b>Measurement Error Modeling for Count Data</b> Cornelis J. Potgieter*, Texas Christian University
12:00	<b>Conditional Mutual Information Estimation for Discrete and Continuous Data with Nearest Neighbors</b> Octavio César Mesner* and Cosma Rohilla Shalizi, Carnegie Mellon University

*Denotes Student Award Winner*

## SHORT COURSES

### Short Course Registration Fees

	By January 15			After January 15		
	Half Day	Second Half Day	Full Day	Half Day	Second Half Day	Full Day
Member	\$250	\$200	\$350	\$275	\$225	\$375
Non-Member	\$325	\$290	\$425	\$350	\$315	\$450

Sunday, March 22, 2020

#### SC 1.

### Implementing Bayesian Adaptive Designs: From Theory to Practice

Full Day | 8:00 am – 5:00 pm

**Ying Yuan**, University of Texas MD Anderson Cancer Center

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

**Description:** As a statistical framework, a Bayesian approach is intuitive, logical, coherent, elegant, and adaptive in nature. It is uniquely suitable for the design and analysis of clinical trials. The learning curve of Bayesian methods, however, is steep and the complexity of Bayesian computation can be intimidating. To overcome these hurdles, this short course is designed to provide an overview of Bayesian theory and its application to adaptive clinical trials. The emphasis is on implementing such designs by turning theory into practice. Easy-to-use Shiny applications and downloadable standalone programs will be introduced to facilitate the study design, conduct, and analysis of Bayesian adaptive methods. The main application areas include adaptive dose finding, adaptive toxicity and efficacy evaluation, posterior probability and predictive probability for interim monitoring of study endpoints, outcome-adaptive randomization, hierarchical models, adaptive biomarker identification and validation, multi-arm, multi-stage designs, and platform designs, etc. Bayesian adaptive designs allow flexibility in clinical trial conduct, increase study efficiency, enhance clinical trial ethics by treating more patients with more effective treatments, increase the overall success rate for drug development and can still preserve frequentist operating characteristics by controlling type I and type II error rates. Lessons learned from real trial examples and practical considerations for conducting adaptive designs will be given.

#### SC 2.

### Practical solutions for working with electronic health records data

Full Day | 8:00 am – 5:00 pm

**Rebecca Hubbard**, 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 the general population. 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.

This short course will introduce participants to the basic structure of EHR data and analytic approaches to working with these data through a combination of lecture and hands-on exercises in R. The first part of the course 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. Participants will have the opportunity to explore a synthetic EHR-derived data set to gain familiarity with the structure of EHR data and data exploration and visualization tools for identifying data quality issues. In the second half of the course, we will discuss statistical methods to mitigate some of the data quality issues arising in EHR, including missing data and error in EHR-derived covariates and outcomes. R code will be provided for implementation of the presented methods, and hands-on exercises will be used to compare results of alternative approaches.

This short course is of interest to researchers without prior experience working with EHR data as well as more experienced individuals interested in learning practical solutions to some common analytic challenges. The overarching objective of this course is to provide participants with an introduction to the structure and content of EHR data as well as a set of practical tools to investigate and analyze this rich data resource.

#### SC 3.

### Design and Analysis of Sequential, Multiple Assignment, Randomized Trials for small and large samples

Full Day | 8:00 am – 5:00 pm

**Kelley Kidwell**, University of Michigan

**Thomas Braun**, University of Michigan

**Roy Tamura**, University of South Florida

**Description:** Sequential, multiple assignment, randomized trials (SMARTs) have been implemented in oncology, drug abuse, ADHD, obesity, depression, insomnia, autism, and smoking cessation, among other areas. A SMART is a multi-stage trial design that allows for individuals to be randomized at two or more stages based on intermediate outcomes. SMART design has primarily been focused on informing the construction of dynamic treatment regimens (DTRs) or adaptive interventions. DTRs are evidence-based treatment guidelines where treatment can be altered over time based on the individual. Most SMARTs are conducted in large samples and analyzed using frequentist methods to explore potential delayed effects and treatment interactions over time to estimate and compare DTRs. More recently, Bayesian and frequentist methods have been developed to apply the SMART design in rare diseases, or more generally, small samples to find the best overall treatment sharing information across stages. Thus, a SMART design can also be used to strengthen inference on the best single treatment. The Bayesian methods developed to analyze SMART data in small samples may also be extended to find the most effective DTRs. This short course will introduce SMART design for both large and small samples. Case studies will be used as examples and R code will be provided for practice.

## SC 4.

**Programming with hierarchical statistical models: Using the BUGS-compatible NIMBLE system for MCMC and more**

Half Day | 8:00 am – 12:00 pm

**Christopher Paciorek**, University of California, Berkeley

**Description:** NIMBLE ([r-nimble.org](http://r-nimble.org)) is a system for fitting and programming with hierarchical models in R that builds on the BUGS language for declaring models. NIMBLE provides analysts with a flexible system for using MCMC, sequential Monte Carlo, MCEM, and other techniques on user-specified models. It provides developers and methodologists with the ability to write algorithms in an R-like syntax that can be easily disseminated to users. C++ versions of models and algorithms are created for speed, but these are manipulated from R without any need for analysts or algorithm developers to program in C++. While analysts can use NIMBLE as a drop-in replacement for WinBUGS or JAGS, NIMBLE provides greatly enhanced functionality in a number of ways.

This hands-on tutorial will first show how to specify a hierarchical statistical model using BUGS syntax and fit that model using MCMC. Participants will learn how to customize the MCMC for better performance (choosing samplers and blocking schemes) and how to specify one's own statistical distributions and functions to extend the syntax of BUGS. We will demonstrate the use of NIMBLE for biostatistical methods such as semiparametric random effects models and clustering models using Bayesian nonparametric techniques. We will also demonstrate the use of NIMBLE's built-in reversible jump MCMC for variable selection and the use of NIMBLE's CAR-based spatial models.

## SC 5.

**Multivariate meta-analysis methods**

Half Day | 1:00 pm – 5:00 pm

**Haitao Chu**, University of Minnesota Twin Cities**Yong Chen**, University of Pennsylvania

**Description:** Comparative effectiveness research aims to inform health care decisions concerning the benefits and risks of different prevention strategies, diagnostic instruments and treatment options. A meta-analysis is a statistical method that combines results of multiple independent studies to improve statistical power and to reduce certain biases compared to individual studies. Meta-analysis also has the capacity to contrast results from different studies and identify patterns and sources of disagreement among those results. The increasing number of prevention strategies, assessment instruments and treatment options for a given disease condition, as well as the rapid escalation in costs, have generated a need to simultaneously compare multiple options in clinical practice using innovative and rigorous multivariate meta-analysis methods.

This short course, co-taught by Drs. Chu and Chen who have collaborated on this topic for more than a decade, will focus on most recent developments for multivariate meta-analysis methods. This short course will offer a comprehensive overview of new approaches, modeling, and applications on multivariate meta-analysis. Specifically, this short course will discuss the contrast-based and the arm-based network meta-analysis methods for multiple treatment comparisons; network meta-analysis methods for multiple diagnostic tests; multivariate extension of network meta-analysis; and multivariate meta-analysis methods estimating complier average causal effect in randomized clinical trials with noncompliance.

Case studies will be used to illustrate the principles and statistical methods introduced in this course. R codes with real examples will also be provided. This application oriented short course should be of interest to researchers who would apply up-to-date multivariate meta-analysis methods and

who are interested in developing novel methods for multivariate meta-analysis. We anticipate that it will be well-received by an interdisciplinary scientific community, and play an important role in improving the rigor and broadening the applications of multivariate meta-analysis.

## SC 6.

**Statistical Network Analysis with Applications to Biology**

Half Day | 8:00 am – 12:00 pm

**Ali Shojaie**, University of Washington**George Michailidis**, University of Florida

**Description:** Networks and network analysis methods are increasingly used by biomedical scientists and computational biologists to glean insight into cellular functions and mechanisms of disease propagation and initiation. While many approaches have been recently proposed, statistical and machine learning tools commonly play a key role in such analyses. This course provides a practical introduction to statistical network analysis methods for biological application. This short course will cover the following classes of methods: (i) statistical methods for network-structured data analysis; (ii) inference methods for undirected networks. The course will primarily focus on methods that are widely used in biological applications and, in particular, in the analysis of -omics data, as well as recent developments in statistical machine learning. Throughout, the emphasis will be on practical applications of network analysis methods, as well as their limitations, including validation of results and tools for reproducible research. Case studies using publicly available -omics data will be used to describe various statistical network analysis methods.

## SC 7.

**Trial Design and Analysis Using Multisource Exchangeability Models**

Half Day | 1:00 pm – 5:00 pm

**Joseph Koopmeiners**, University of Minnesota**Brian Hobbs**, Cleveland Clinic**Alex Kaizer**, University of Colorado

**Description:** Modern biomedical applications often call statisticians to estimate the effect of a treatment or intervention in sub-groups defined by demographic, genetic, or other participant information. This results in increasingly smaller sample sizes, which reduces power. Hierarchical modeling allows sub-group specific effects to be “shrunk” together, thus borrowing strength and increasing precision. However, standard hierarchical approaches are limited because they lack the flexibility to model complex relationships between sub-groups, where some sub-groups are exchangeable, while others are not. In this short course, we discuss trial design using multi-source exchangeability models (MEMs), which provide a flexible approach to estimating sub-group-specific effects, while accounting for complex relationships between subgroups. We provide an overview of the methodology and a comparison with standard hierarchical modeling approaches. We then discuss multi-source modeling in the context of trial design, focusing specifically on platform and basket trial designs, illustrating the advantage of multi-source trial designs vs. standard designs. The ability to incorporate other adaptive elements, such as adaptive randomization, will also be discussed. Much of the course will be illustrated via the basket package in R.

# TUTORIALS

## Tutorial Registration Fees

	By January 15	After January 15
Member	\$75	\$85
Non-Member	\$85	\$95
Student	\$40	\$50

**Monday, March 23 - Tuesday, March 24, 2020**

**T 1.**

### Statistical methods for geometric functional data

Monday, March 23 | 8:30 am – 10:15 am

**Karthik Bharath**, University of Nottingham, UK

**Sebastian Kurtsek**, The Ohio State University

**Description:** How can one quantify variation in Hippocampal shapes obtained from MRI images as 2D curves? How does one model intra-tumour heterogeneity using samples of pixel densities? Answers to such questions on functional data with rich geometric structure require methods that are at a nascent developmental stage, and are typically not part of the standard functional data toolbox.

In this tutorial, we shall introduce some modern statistical and computational tools for handling such functional data objects. The first part of the tutorial will focus on the representation of such data and computation of descriptive summaries such as averages and PCA, with numerous references to existing works and computing resources. The focus then moves to understanding the challenges involved in developing regression models involving such data objects. The last part of the tutorial will present an overview of the current state-of-the-art, and suggest future directions of research with a view towards inference.

**T 2.**

### Disease Risk Modeling and Visualization using R

Monday, March 23 | 10:30 am - 12:15 pm

**Paula Moraga**, University of Bath, UK

**Description:** Disease risk models are essential to inform public health and policy. These models can be used to quantify disease burden, understand geographic and temporal patterns, identify risk factors, and measure inequalities. In this tutorial we will learn how to estimate disease risk and quantify risk factors using areal and geostatistical data. We will also create interactive maps of disease risk and risk factors, and introduce presentation options such as interactive dashboards. We will work through two disease mapping examples using data of malaria in The Gambia and cancer in Pennsylvania, USA. We will cover the following topics:

- Model disease risk in different settings,
- Manipulate and transform point, areal and raster data using spatial packages,
- Retrieve high resolution spatially referenced environmental data using the raster package,
- Fit and interpret spatial models using Integrated Nested Laplace Approximations (INLA) (<http://www.r-inla.org/>),
- Map disease risk and risk factors using leaflet (<https://rstudio.github.io/leaflet/>) and ggplot2 (<https://ggplot2.tidyverse.org/>),

The tutorial examples will focus on health applications, but the approaches covered are also applicable to other fields that use georeferenced data including epidemiology, ecology or demography. We will provide clear descriptions of the R code for data importing, manipulation, modeling and visualization, as well as the interpretation of the results. The tutorial materials are drawn from the book 'Geospatial Health Data: Modeling and Visualization with R-INLA and Shiny' by Paula Moraga (2019, Chapman & Hall/CRC Biostatistics Series).

**T 3.**

### Integration of Genetics and Imaging Data in Scientific Studies

Monday, March 23 | 1:45 pm - 3:30 pm

**Debashis Ghosh**, Colorado School of Public Health

**Description:** In this tutorial, we will discuss issues and approaches in the consideration of combining genetics and imaging data in biological and biomedical studies. A variety of motivating examples will be described. A common life-cycle pipeline for analytics will be discussed, along with some emergent lessons that have been learned through the literature. I will also focus on the types of questions that typically asked with these data sources and the roles of regression modelling and machine learning in these contexts.

**T 4.**

### Causal Inference Using the R TWANG Package for Mediation and Continuous Exposures

Monday, March 23 | 3:45 pm - 5:30 pm

**Donna Coffman**, Temple University

**Description:** When randomized experiments are infeasible, analysts must rely on observational data in which treatment (or exposure) is not randomly assigned (e.g., in health policy research or when determining the effects of environmental exposures). In addition, knowing the mechanisms or pathways through which a treatment works requires causal inference methods because the mediator is not randomly assigned. This tutorial aims to promote the use of causal inference methods for mediation and continuous exposures using the R twang package. The twang package recently was expanded to handle mediation and continuous exposures. We will first introduce causal mediation using the potential outcomes framework and weighting methods for estimating the causal mediation effects. We then will illustrate the implementation of gradient (or generalized) boosting models (GBM) for estimating the weights using the R twang package. Next, we will introduce the generalized propensity score (GPS) for continuous exposures. We will illustrate the implementation of GBM for estimating the GPS using the R twang package. The tutorial will provide relevant statistical background knowledge of mediation, the GPS, GBM, and weighting but will focus on implementation rather than statistical theory. Attendees should have some familiarity with propensity score analysis (e.g., for binary treatments/ exposures) and regression models, but knowledge of causal mediation, GPS, and GBM is not necessary. Attendees will be provided with the R code.



T 5.

**Fundamentals of difference-in-differences studies**

Tuesday, March 24 | 1:45 pm - 3:30 pm

**Laura A. Hatfield**, Harvard Medical School**Bret Zeldow**, Harvard Medical School

**Description:** A popular design in policy and economics research, difference-in-differences contrasts a treated group's pre- to post-intervention change in outcomes to an untreated comparison group's change in outcomes over the same period. The difference between the changes in the treated and comparison groups may be interpreted as the causal effect of the intervention if one assumes that the comparison group's change is a good proxy for the treated group's counterfactual change if it had not been treated. In this tutorial, we review the fundamentals of difference-in-differences studies, including key causal assumptions and ways to assess their plausibility, selection of a good comparison group, matching and regression techniques, statistical inference, and robustness checks.

T 6.

**R package development**

Tuesday, March 24 | 3:45 pm - 5:30 pm

**John Muschelli**, Johns Hopkins University

**Description:** The jump from R programming with scripts to packages can be quite large. We hope to answer some of the basic questions of getting you started with package development answering the questions of: How do you create a basic R package? What are some R package best practices? How do I know if I can install this package? How do I depend on other packages? The tutorial will go through a simple 2-function package and describe resources to use after the course, including the R Package Development YouTube series: <https://www.youtube.com/watch?v=79s3z0gluFU&list=PLk3B5c8iCV-T4LM0mwEyWlunlunLyEqjM&index=1>



# ROUNDTABLES

Registration is required. Roundtable Registration Fee: \$45

Monday, March 23 12:15-1:30 p.m.

R 1.

## Statistical positions in government

Paul Albert, National Cancer Institute

**Description:** The federal government provides exciting career opportunities for biostatisticians. There are positions ranging from mathematical statisticians, postdoctoral fellows, and tenure-track investigators. We will discuss these different types of positions, including the different types of work and the citizen requirements. We will discuss how to locate positions and the application/interview process. Focus will be on positions at the National Institutes of Health and the Food and Drug Administration where most government biostatisticians work.

R 2.

## How Can We Improve Biostatistical Reviewing for Medical Journals?

Cynthia Garvan, University of Florida

**Description:** The scientific community is justifiably concerned about both the rigor and reproducibility of medical research. From Statistics Done Wrong (Reinhart, 2015) to findings from a recent National Academies of Sciences, Engineering, and Medicine workshop convened to address questions about the reproducibility of scientific research, lack of statistics education has been identified as a major culprit in the generation of poor science. Beyond a lack of statistics education for researchers, a lack of education for biostatistical reviewers is problematic. In this roundtable we will discuss steps needed to improve this vital contribution of the biostatistician to advance medical research.

R 3.

## Early career mentoring: What do I do now?

Lance A. Waller, Emory University

**Description:** A career in the field of Biostatistics can be rewarding but also a challenge to navigate early in one's career. Some parts of the field seem to be changing quickly, others seem to stay the same. Departments and research groups grow and shrink, scientific (and funding!) priorities shift with new technology, new discoveries, and new approaches. In this roundtable, we will consider multiple issues involved with beginning a career in Biostatistics. We will discuss the different "currencies of success" associated with careers in academic, industry, and government organizations. We will discuss communication skills, funding strategies, collaboration skills, and opportunities to contribute to the field in multiple ways. Please feel free to bring questions (or send them to the facilitator beforehand) to allow the discussion to address your needs as well as these guidelines.

R 4.

## Publish or Perish in Biostatistics

Geert Molenberghs, Hasselt University and KU Leuven, Belgium

**Description:** Like statistics and biostatistics itself, publishing in biostatistics journals is in full transition: from paper to also electronic to electronic only: what about open access? What about reproducibility and, relatedly, scientific integrity?; all of this against the background of privacy protection. Do we publish in a journal owned by a commercial publisher, in a society-owned journal, in a cooperative journal, or perhaps in no journal at all? Do we prefer a statistics or a data science journal – or is this a false dichotomy? What is the relative status of theory, theorems, methodology, modeling, data analysis, and simulations? Apart from being an author, what are the relative advantages and drawbacks of acting as referee or Associate Editor? Should we give weight to impact factors or are they ignorable?

R 5.

## Understanding the NIH Grant Review Process

Scarlett L. Bellamy, Drexel University

**Description:** Have you ever wondered what it's like to be member of an NIH study section? Have you ever wondered about the review process for grants that you have submitted or plan to submit? In this roundtable we will discuss the NIH review process, from the perspective of a current member of Biostatistical Methods and Research Design (BMRD) Study Section. Attendees should leave the discussion with a better understanding the grant review process to better inform how they might prepare future grants or as they consider service on future study sections.

R 6.

## Data Science Programs

Joel Greenhouse, Carnegie Mellon University

**Description:** Academic and online data science programs are popping up everywhere. Employers now post positions for data scientist and rarely for statisticians or data analyst. If statistical thinking is the bedrock of data science, how can we insure that statistics and good statistical thinking play a proper role in the training of the next generation of statistical scientist? What has your experience been with the emergence of data science at your University or your place of employment. These, as well as other participant generated questions will be the source of discussion for this roundtable.

R 7.

## Being a Biostatistician in a Medical Center

Bryan E. Shepherd, Vanderbilt University Medical Center

**Description:** Statisticians are in great demand in medical centers. This can be both exciting and daunting. We will discuss strategies for flourishing in a medical center, from gaining respect among medical collaborators, to identifying and pursuing interesting research projects, to protecting one's time.

R 8.

## How to navigate collaborative research

Andrea B. Troxel, NYU School of Medicine

**Description:** We will discuss best practices for working with collaborators to develop grant proposals, guidelines for effort allocation for both faculty and staff, and timelines for grant preparation. We will also discuss common roadblocks that arise, and offer tips for troubleshooting challenging situations.

R 9.

## Running a Statistical Consulting Business

Alicia Y. Toledano, Biostatistics Consulting, LLC

**Description:** Running your own consultancy has many benefits, such as choosing your clients and projects, setting your own hours, and possibly working from home. This roundtable will focus on meeting challenges and carrying out responsibilities associated with those benefits. We will discuss making decisions related to: incorporation, using an attorney to review contracts, accounting, insurance, SOPs including for quality control, and having subcontractors and/or employees. Based on time and attendees' interests, we may also discuss one or more of: 1) Deciding what projects to undertake, with respect to areas of statistical expertise and 2) project type, such as short- or long-term; papers, grants, and/or FDA submissions; 3) How to get clients; 4) Working with clients that are not local; and 5) Ensuring your continued professional development statistically, and in soft skills like working as part of an interdisciplinary team. Come with questions and/or suggestions!







# WORKSHOP & STUDENT OPPORTUNITIES

## Special Opportunities for Our Student Members

### PARTICIPATE IN STUDENT-FOCUSED ELEMENTS OF THE SCIENTIFIC PROGRAM:

The Sunday night mixer presents an ideal opportunity to network and hear about emerging research at the annual ENAR Poster session. This year we will conduct our fifth Poster Competition for the session. Prizes will be announced within topical areas in the Tuesday morning Presidential Invited Address session. A student winner will be selected within each topical area. Watch for details on entering the competition on the website when the meeting registration goes live.

### EDUCATIONAL AND PROFESSIONAL DEVELOPMENT OPPORTUNITIES:

Be sure to take advantage of the educational offerings to be held during the meeting – short courses, tutorials, and roundtable discussions (see pages 70-71).

### Don't Forget the Popular ENAR Career Placement Services!

(See page 80.)

### NETWORK WITH YOUR FELLOW STUDENTS

Back by popular demand, the **Council for Emerging and New Statisticians (CENS) Mixer** will be held the evening of Monday, March 23, 2020. This is a great way to meet and greet your fellow students from other graduate programs. Don't miss this opportunity to begin building connections with your future colleagues and friends.

Looking for more ways to plug in with other students? Check out additional CENS-sponsored activities on page 78.









## CENS



Council for Emerging and New Statisticians

### CENS EVENTS AT ENAR 2020

#### **CENS Sponsored Session: The Three M's: Meetings, Memberships, and Money!**

This panel will educate emerging and new statisticians on how to gain more from professional meetings and associations. Topics for discussion will include the benefits of joining a professional organization, means of navigating scientific sessions at a conference, developing a professional network, and obtaining funding (e.g., travel grants/awards, scholarships).

#### **Networking Mixer: Monday, March 23, 2020 from 5:30 - 6:30pm**

All students and recent graduates are invited to attend the CENS Networking Mixer. Registration is not required - so please plan to attend!

#### **Networking Lunch: Tuesday, March 24, 2020 from 12:30 - 1:30pm at local restaurants**

CENS will organize lunches 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. Participants meet at the CENS table in the Exhibition Hall at 12:15 PM before walking with their assigned group to a nearby restaurant for networking and lunch! Participation is open to all meeting attendees. If you would like to participate, please select the CENS lunch option on the registration form or email CENS at [enar.cens@gmail.com](mailto:enar.cens@gmail.com).

#### **About CENS**

CENS was formed in 2012 by ENAR's Regional Advisory Board (RAB) to help ENAR better address the needs of students and recent graduates. CENS is composed of 10 graduate students, post-doctoral fellows, or recent graduates, who are ENAR members. With the help of the RAB Liaison, CENS members collaborate to bring student/recent graduate concerns to the attention of RAB and ENAR; work to help ENAR better serve all students/recent graduates; advise and help implement ideas to enhance the benefits of ENAR membership and to increase awareness of the benefits of ENAR membership to students; organize a CENS sponsored session at each ENAR Spring Meeting; assist in planning events that help advance students' and recent graduates' education and careers; and contribute to the development of ENAR's social media presence.

#### **Join CENS**

We are actively recruiting new members! Each member is appointed to a 2-year term. Within CENS, three or four people are chosen to participate in the steering committee, which reports to the RAB chair. Members of the steering committee will serve an additional year on CENS. CENS members meet in person yearly at the ENAR Spring Meeting and participate in conference calls throughout the year to plan events and address issues as they arise. If you are interested in joining CENS, please email [enar.cens@gmail.com](mailto:enar.cens@gmail.com).

*CENS seeks to advocate for the needs and concerns of students and recent graduates in collaboration with ENAR's Regional Advisory Board. Through annual events at the ENAR Spring Meeting, CENS strives to promote the benefits of participating in the ENAR community, support the advancement of students and recent graduates, and facilitate stronger connections within the statistical community.*

# CAREER PLACEMENT SERVICES

## Hours of Operation:

<b>Sunday, March 22</b>	<b>4:00 pm – 6:30 pm</b>
<b>Monday, March 23</b>	<b>9:30 am – 4:30 pm</b>
<b>Tuesday, March 24</b>	<b>9:30 am – 3:30 pm</b>

## General Information

The ENAR Career Placement Service helps match applicants seeking employment and employers. The service includes online registration and electronic uploading and distribution of applicant and employer materials through a password-protected online web-based facility. Visit the ENAR website at <https://enar.org/meetings/spring2020/career/> to register for the placement center.

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

## Employers

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

## Employer Registration

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

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

## Interview Suites

For an additional fee, employers may reserve private interview suites each day on a first-come, first-served basis. There are a very limited number of private suites, so please reserve early.

## Employer Registration Instructions, Deadlines, and Fees

ALL employers must FULLY complete an online Employer Form located at: <https://enar.org/meetings/spring2020/career/> for each position listing. Attachments may be included.

Employer Registration Fees	By Jan. 15	After Jan. 15
Employer (3 reps/ 4 job postings)	\$1,650	\$1,725
Private Interview Room (Per 4-hour increments)	\$275	n/a
Additional Representatives (Cost per person includes conference registration)	\$520	\$620
Additional Job Postings	\$150	\$250

## 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.

## 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 Instructions, Deadlines, and Fees

ALL applicants must FULLY complete an online Applicant Form located at: <https://enar.org/meetings/spring2020/career/> for each job classification.

Applicant Registration Fees	By Jan. 15	After Jan. 15
Regular Registration	\$60	\$85
Student Registration	\$25	\$40

**Applicants PLEASE NOTE:** If you are planning to interview and participate on-site you must also register for the conference and pay the meeting registration fee.



## FAMILY FRIENDLY ACCOMMODATIONS

ENAR maintains a family-friendly environment. However, to help with logistics/planning, all family members/guests, who wish to enter any of the meeting space, must be formally registered. Children 12 years and under may be registered for free. All other adults and children 13+ years will require a \$100 guest registration (if registering prior to January 15) to attend any ENAR Spring Meeting event. If registering after January 15, the guest registration fee is \$110.

Guest registration includes access to all Scientific Program sessions, exhibit space, Opening Mixer & Poster Session, refreshment break with exhibitors and the Presidential Invited Address. Guest registration does not include admission to Short Courses, Tutorials or Roundtables, or any invite only/user-pay events.

### Child Care

Attendees with child-care needs may contact Sitter Scout (<https://www.sitter-scout.com/>) for arrangements during the ENAR Spring Meeting. Please contact Jaclyn at 860-508-766 or Cori at 802-540-0433 for arrangements.

ENAR assumes no responsibility for any child-care services and all policies are established by the child-care facility.

### New Mothers Room

If you have a child and want a private space for nursing or other infant care, please visit the ENAR registration desk.



# SPRING MEETING REGISTRATION FORM

## PLEASE PRINT OR TYPE

First Name:  MI:  Last Name:

Highest Degree: ☐ Bachelors ☐ Masters ☐ Doctorate Or Medical Degree ☐ Other

Name for badge if different:

Spouse/Guest Name For Badge:

Organization:

Mailing Address, City:  State:  ZIP Code:  Country:

Daytime Phone:  E-mail:

## 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, 2020. Requests for refunds will not be honored after February 1, 2020. **No refunds will be issued for the cancellation of short courses, tutorials, or roundtables.**

## Meeting Registration Fees:

Employer Registration Fees	By Jan. 15	After Jan. 15
<input type="checkbox"/> ENAR/WNAR/IBS Member	\$450	\$ 525
<input type="checkbox"/> ASA Member (not a member of ENAR/WNAR/IBS)	\$600	\$675
<input type="checkbox"/> IMS Member (\$470-\$20 IMS contribution: \$450) (not a member of ENAR/WNAR/IBS)	\$450	\$525
<input type="checkbox"/> Nonmember (in any participating society)	\$650*	\$725
<input type="checkbox"/> Student (With letter from major professor verifying status.)	\$170	\$180
<input type="checkbox"/> Nonmember Student (With letter from major professor verifying status.)	\$200	\$210
<input type="checkbox"/> Guest (Adults and Children 13+ years old)	\$100	\$110
<input type="checkbox"/> Children 12 and under	free	free

\* Includes membership in ENAR through December 31, 2020

## Conduct Policy

☐ I agree to comply with the ENAR Code of Conduct Policy

## Short Courses

The short courses will be held on Sunday, March 22.

(Indicate the short course number)

☐ Member (participating society): ☐ Nonmember:

☐ Full Day: \$350 (\$375 after Jan 15) ☐ Full Day: \$425 (\$450 after Jan 15)

☐ Half Day: \$250 (\$275 after Jan 15) ☐ Half Day: \$325 (\$350 after Jan 15)

☐ Second Half Day: \$200 ☐ Second Half Day: \$290  
(\$225 after Jan 15) (\$315 after Jan 15)

## Tutorials

The tutorials will be held on Monday, March 23 & Tuesday, March 24.

	Member	Nonmember	Student
T1	<input type="checkbox"/> \$75 (\$85 after Jan 15)	<input type="checkbox"/> \$85 (\$95 after Jan 15)	<input type="checkbox"/> \$40 (\$50 after Jan 15)
T2	<input type="checkbox"/> \$75 (\$85 after Jan 15)	<input type="checkbox"/> \$85 (\$95 after Jan 15)	<input type="checkbox"/> \$40 (\$50 after Jan 15)
T3	<input type="checkbox"/> \$75 (\$85 after Jan 15)	<input type="checkbox"/> \$85 (\$95 after Jan 15)	<input type="checkbox"/> \$40 (\$50 after Jan 15)
T4	<input type="checkbox"/> \$75 (\$85 after Jan 15)	<input type="checkbox"/> \$85 (\$95 after Jan 15)	<input type="checkbox"/> \$40 (\$50 after Jan 15)
T5	<input type="checkbox"/> \$75 (\$85 after Jan 15)	<input type="checkbox"/> \$85 (\$95 after Jan 15)	<input type="checkbox"/> \$40 (\$50 after Jan 15)
T6	<input type="checkbox"/> \$75 (\$85 after Jan 15)	<input type="checkbox"/> \$85 (\$95 after Jan 15)	<input type="checkbox"/> \$40 (\$50 after Jan 15)

## Roundtables

The roundtables will be held on Monday, March 23. Space is limited. Preregistration is required. Indicate the number of your 1st, 2nd, and 3rd choices:

1st:

2nd:

3rd:

Fee: ☐ \$ 45

Please make lunch vegetarian ☐ YES ☐ NO

## Council for Emerging and New Statisticians (CENS) Lunch, Tuesday, March 24:

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 only be available on the ENAR website)

The personal information ("personal data") you provide on this web page is being collected with your consent, for the exclusive purpose of permitting ENAR to facilitate your registration for the ENAR 2020 Spring Meeting and to contact and bill you in connection with that event and/or your ENAR membership status. The personal data is subject to the terms of ENAR's privacy policy (<https://www.enar.org/about/policy.cfm>). A party located in the European Union or European Economic Area wishing to exercise rights under the General Data Protection Regulation (GDPR) with respect to such personal data should contact [privacy@enar.org](mailto:privacy@enar.org).

## Membership

☐ YES, I want to renew my 2020 ENAR membership or become an ENAR member.

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

☐ Regular Member: \$ 150  
Includes *Biometric Bulletin* Newsletter and a print subscription of one journal (choose one):  
☐ *Biometrics* Journal **or** ☐ *JABES* Journal

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

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

## TOTAL PAYMENT:

### Form of Payment (if not registering online):

☐ Check\* ☐ Money Order\*

☐ Please call me to pay via credit card over the phone.

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



# ENAR MEMBERSHIP APPLICATION

## PLEASE PRINT OR TYPE

In compliance with GDPR, a new regulation for data protection and privacy, I elect to receive email communication from ENAR regarding membership, society activities, and the Spring Meeting.

Please contact the ENAR office at [enar@enar.org](mailto:enar@enar.org) if you do not wish to receive email communications.

If you are located in the European Union or European Economic Area ("EEA"), you may also have certain rights under the General Data Protection Regulation ("GDPR"). The personal information ("Personal Data") you provide on this web page to register for this event is being collected with your consent, for the exclusive purpose of permitting ENAR to facilitate your registration for the ENAR 2020 Spring Meeting and to contact you with information regarding this meeting. The data may be stored or processed outside of the EU, including in the United States, on servers of ENAR. The Personal Data is subject to the terms of ENAR's Privacy Policy. Contact ENAR at [enar@enar.org](mailto:enar@enar.org) if you have concerns regarding your Personal Data or wish to exercise any of your rights under the GDPR.

Please Check One: ☐ New Member ☐ Renewal

First Name:  MI:  Last Name:

Highest Degree: ☐ Bachelors ☐ Masters ☐ Doctorate Or Medical Degree ☐ Other

Name for badge if different:

Spouse/Guest Name For Badge:

Organization:

Mailing Address, City:  State:  ZIP Code:  Country:

Daytime Phone:  E-mail:

## Membership Type:

- ☐ Regular Member: \$ 140  
Includes electronic access to the *Biometrics Journal*, *JABES Journal* and *Biometric Bulletin* Newsletter
- ☐ Regular Member: \$150  
Includes *Biometric Bulletin* Newsletter and a print subscription of one journal (choose one):  
☐ *Biometrics Journal* **or** ☐ *JABES Journal*
- ☐ Regular Member: \$160  
Includes print subscriptions to *Biometrics Journal*, *JABES Journal*, and *Biometric Bulletin* Newsletter
- ☐ Supporting Member: \$30
- ☐ Student Member: \$20  
Includes electronic access to the *Biometrics Journal*, *JABES Journal* and *Biometric Bulletin* Newsletter

I certify that  is a full-time student.

Signature:  Title:

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

## Please Indicate Two Areas Of Interest:

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

## NATURAL RESOURCES:

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

## TOTAL PAYMENT:

### Form of Payment (if not registering online):

- ☐ Check\* ☐ Money Order\*
- ☐ Please call me to pay via credit card over the phone.

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



### Eastern North American Region (ENAR)

11130 Sunrise Valley Drive, Suite 350  
Reston, VA 20191

Tel: 703-234-4146 | Fax: 703-234-4147 | E-mail: [enar@enar.org](mailto:enar@enar.org)

## MAIL TO

ENAR  
11130 Sunrise Valley Drive  
Suite 350  
Reston, VA 20191

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## NOTES

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# NOTES



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