

2020 Statistical Practice in Cancer Conference Program

Day 1: Friday, February 28 – Moffitt Cancer Center, Stabile Research Building (SRB), Ted and Marty Couch Auditorium

Program will take place in the SRB, Ted & Marty Couch Auditorium unless otherwise noted

- 8:00-8:30 **REGISTRATION & CONTINENTAL BREAKFAST** SRB 1st Floor Atrium/Foyer
- 8:30-8:35 WELCOME Michael Schell, Moffitt Cancer Center
- 8:35-9:30 **KEYNOTE PRESENTATION**

Paul Scheet, PhD, MD Anderson Cancer Center Professor and Chair, Department of Epidemiology; Leader: MDACC Risk, Detection and Outcomes Program What was I doing Friday afternoon when I was interrupted? Oh yes, characterizing allelic imbalance in 11,000 tumor/normal pairs!

9:30-10:30 WORKSHOP: Introduction to Omics Analysis Tools Leslie Cope, PhD, Johns Hopkins University Associate Professor, Division of Biostatistics and Bioinformatics Co-Director, Experimental and Computational Genomics Core, Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins

- 10:30-10:45 BREAK
- 10:45-11:10 Memorial for Dr. Ken Hess Jack Lee, MD Anderson Cancer Center

11:15-11:30 **POSTER ELEVATOR TALKS**

- **1.** Jing Zhao, University of Florida Development of an R Shiny APP for Randomized Clinical Trial
- 2. Xueliang Pan, The Ohio State University Practical Considerations for the Implementation of Adaptive Designs for Oncology Phase I Dose-Finding Trials
- **3.** Y. Ann Chen, Moffitt Cancer Center ISCVA: Interactive Single Cell Visual Analytics
- 11:30-12:00 **POSTER SESSION** SRB, 1st Floor Atrium/Foyer
- 12:00-1:00 **LUNCH & NETWORKING** SRB, 1st Floor Atrium/Foyer

Program will return to the SRB, Ted & Marty Couch Auditorium

1:00-2:00	 PANEL DISCUSSION #1: Can Biostatisticians and Bioinformaticians Live Happily Ever After in the Big Data Era? <u>Moderators</u>: AC Tan: Moffitt Cancer Center; Leslie Cope: Johns Hopkins University; Stanley Pounds: St. Jude Children's Research Hospital; Mithat Gönen: Memorial Sloan-Kettering Cancer Center; Alberto Riva:
	University of Florida
2:00-2:15	BREAK
2:15-3:45	ORAL PRESENTATIONS – Omics
2:15-2:45	Christopher Wilson, Moffitt Cancer Center Integrative Network Based Analysis of Metabolomic and Transcriptomic Data for Understanding Biological Mechanism of Lung Cancer
2:45-3:15	Liang Shan, University of Alabama at Birmingham Sparse Estimation of a Two-Level Gene-Pathway Network for Predicting Breast Cancer Patients' Treatment Responses
3:15-3:45	Stanley Pounds, St. Jude Children's Research Hospital Bootstrap Evaluation of Association Matrices (BEAM): A Robust Method for Integrated Analysis of Multiple Omic Data Sets with Multiple Clinical Outcomes
3:45-4:00	BREAK
4:00-5:30	ORAL PRESENTATIONS – Analysis and Prediction
4:00-4:30	Jeremy Taylor, University of Michigan Evaluating Existing Risk Prediction Models in the Presence of Missing Covariates
4:30-5:00	Jordan Creed, Moffitt Cancer Center mediator: An R Package for Conducting Causal Mediation Analyses
5:00-5:30	Naomi Brownstein, Moffitt Cancer Center Methodological challenges that keep us statistically sharp: modeling associations between repeated patient and physician reported outcomes
5:30-6:00	NETWORKING - SRB, 1 st Floor Atrium/Foyer
6:00-7:30	DINNER (Hosted by Moffitt Cancer Center) – SRB, 1 st Floor Atrium/Foyer

Day 2: Saturday, February 29 – Moffitt Cancer Center, Stabile Research Building (SRB), Ted and Marty Couch Auditorium

Program will take place in the SRB, Ted & Marty Couch Auditorium unless otherwise noted

- 8:00-8:30 **CONTINENTAL BREAKFAST** SRB 1st Floor Atrium/Foyer
- 8:30-8:35 INTRODUCTION OF SECOND KEYNOTE SPEAKER Michael Schell, Moffitt Cancer Center
- 8:35-9:30 **KEYNOTE PRESENTATION Xiangqin Cui, PhD Emory University** Associate Professor, School of Public Health; Director VA Data Analytics Core *From Omics to EHR, Following the Research Calls (Needs)*
- 9:30-10:20 **PANEL DISCUSSION #2:** *Staying Cool in a Hot Profession: Career Development of Staff Biostatisticians* <u>Moderators:</u> Richie Reich: Moffitt Cancer Center; Dan Ayers: Vanderbilt University Medical Center; Kathy Panageas: Memorial Sloan Kettering Cancer Center; Heidi Weiss: University of Kentucky Markey Cancer Center; Sejong Bae: University of Alabama at Birmingham
- 10:20-10:30 BREAK
- 10:30-12:00 ORAL PRESENTATIONS Study Design
- 10:30-11:00 Gang Han, Texas A&M University Quantification of Heterogeneity from Pathologists in the Assessment of the PD-L1 Assay in Breast Cancer and Lung Cancer
- 11:00-11:30 **Jianrong Wu, University of Kentucky** Cancer Immunotherapy Trial Design with Long-Term Survivors
- 11:30-12:00Zhixin Wang, University of Alabama at Birmingham
A Batch Effect Adjusted Simon's Two-Stage Design for Cancer Vaccine Clinical Studies
- 12:00 CLOSING



CONFERENCE HOST & ORGANIZER



Michael J. Schell, PhD H. Lee Moffitt Cancer Center & Research Institute

Dr. Schell is a Senior Member in the Biostatistics and Bioinformatics Department at the Moffitt Cancer Center. He is also the Director of the Biostatistics Core for the Skin SPORE grant. He has over 30 years of experience in statistical analysis related to cancer research, with primary areas of expertise in clinical trials, flexible regression methods, and next-generation sequencing analysis. He authored "Identifying Key Statistical Papers From 1985-2002 Using Citation Data for Applied Biostatisticians", The American Statistician, 2010.

KEYNOTE SPEAKER



Paul Scheet, PhD The University of Texas MD Anderson Cancer Center

Paul Scheet, PhD is Professor and Chair of the Dept. of Epidemiology at The University of Texas MD Anderson Cancer Center, with joint appointments in the Dept. of Genomic Medicine and Translational Molecular Pathology. A Statistical geneticist with interests in complex disease and cancer genomics, Dr. Scheet serves as Leader of MD Anderson's CCSG "Risk, Detection and Outcomes" Program. His main research involves the development of statistical methods for the analysis of population genetic data. Specifically, he works with models for linkage disequilibrium (LD), and develops applications for taking proper account of the dependence among nearby loci. These applications include haplotype inference, missing genotype imputation, disease mapping, genotype error detection and correction, the visualization of haplotype variation, and the integration of emerging data types such as next generation DNA sequencing. For these applications, he maintains a widely-used software package called fastPHASE.



WORKSHOP SPEAKER



Leslie Cope, PhD Johns Hopkins University-Baltimore

Leslie Cope is a biostatistician and bioinformatician with expertise in the design and analysis of high-throughput genomic data. He co-directs the Johns Hopkins Kimmel Experimental Cancer Center's and Computational Genomics Core. Cope also has participated in research teams including Stand Up to Cancer and the Department of Defense's Center of Excellence in Ovarian Cancer. Cope is a member of the Epigenetics Genome Characterization program within the National Institutes of Health-funded project, The Cancer Genome Atlas (TCGA), where he leads DNA methylation data analysis and its integration with other data types for several TCGA disease working groups. His research focuses on methods for identifying and validating biomarkers, including tools for integrating multiple sources of data to take advantage of the vast stores of archival data that are now available.

POSTER ELEVATOR TALK



Jing Zhao, MS, PhD University of Florida Health Cancer Center

Jing is currently a biostatistician and a full member of the University of Florida Health Cancer Center (UFHCC). Prior to joining UFHCC, Jing has obtained both her MS degree from the Department of Statistics in 2019 and PhD in biology-related major at Iowa State University (ISU) in 2017. During the study, Jing has published seven peer reviewed papers and has been designated as one contributor nationwide patent. Solid of а statistical/biological training, practical University-wise statistical Consultant, and industry hands-on data scientist experiences has helped her to be skilled in computer applications; adept at modeling in different experimental designs using regression, general and generalized linear model, mixed model, multinomial, and non-parametric analysis; capable in data mining, modelling, and prediction based on big data. She has proved her ability in applying statistical knowledge in a variety of contexts and will keep learning and applying new knowledge on cancer research to welcome with the advent of precision medicine.



POSTER ELEVATOR TALK



Xueliang Pan, PhD The Ohio State University Xueliang (Jeff) Pan is currently a clinical assistant professor in the Center for Biostatistics within the Department of Biomedical Informatics at The Ohio State University. Prior to his faculty position, Dr. Pan served as a research scientist in the Center for Biostatistics from 2008 to 2016 and as a student consultant manager in the Statistical Consulting Service of the OSU Department of Statistics from 2005 - 2008. Dr. Pan collaborates extensively with researchers on designing clinical trials and laboratory experiments, preparing grant proposals, and analyzing clinical and experiment data. His current research focuses on the influence of missing data in clinical trials with repeated measures. The goal of his research is to develop statistical analysis methods and models for complex biological/biomechanical process and bioinformatics data. He is an author of more than 100 refereed publications in international scientific journals, and co-investigator for more 20 research grants from NIH.

POSTER ELEVATOR TALK



Y. Ann Chen, PhD H. Lee Moffitt Cancer Center & Research Institute

Dr. Chen obtained her doctoral degree in Biostatistics and Bioinformatics from Medical University of South Carolina in 2005. Between 2006 and 2008 she did a postdoctoral fellowship in Bioinformatics Program, Department of Statistics at Texas A&M University. In 2008, she joined in the department of Biostatistics and Bioinformatics at Moffitt Cancer Center. She was promoted to Associate Member with tenure in 2015. Her current research focuses on developing computational methods and tools for multi-omics integration in single cell and bulk samples for treatment and clinical-outcome prediction.



ORAL PRESENTER



Christopher Wilson, PhD H. Lee Moffitt Cancer Center & Research Institute

I am currently a postdoc working with Brooke Fridley, Xuefeng Wang, and Xiaoqing Yu at Moffitt Cancer Center and have been at Moffitt since January 2018. My research interests are integration of multiple omics data sources utilizing machine learning techniques such as multiple kernel learning, various clustering methods, and deep learning. The aim of many of these projects is to find a subset of patients that will respond to or provide proper dosage to avoid unwanted outcomes from dangerous cancer treatments. I also work on several collaborations at Moffitt where we aim to discover risk factors for time to local regional recurrence in breast cancer. I earned my PhD from Clemson University where my dissertation was focused on developing resampling schemes in order to improve kernel density and tolerance interval estimates for data for hierarchical data.

ORAL PRESENTER



Liang Shan, PhD, is a biostatistician in the Biostatistics and Bioinformatics Shared Facility (BBSF) at the University of Alabama at Birmingham. Her research interests include Gaussian Graphical model and Network Estimation, clinical trials, survival analysis, and cancer survivorship.

Liang Shan, PhD University of Alabama at Birmingham



ORAL PRESENTER



Stanley Pounds, PhD St. Jude Children's Research Hospital

ORAL PRESENTER



Jeremy Taylor, PhD University of Michigan

Stan Pounds earned a PhD in Statistics from Texas A&M University and is currently Director of the Division of the Department of **Biostatistics** for Genomics and Neuroimaging at St. Jude Children's Research Hospital. Dr. Pounds actively develops innovative statistical concepts and methods to accelerate scientific progress in clinical, translational. laboratory and pediatric cancer research. His methodological publications span a broad spectrum of topics in statistical cancer genomics, including sample size determination, data preprocessing, association analyses, and false discovery rate estimation. St. Jude executive leadership has publicly recognized these methods as essential to the success of some of the institution's most impactful biomedical research endeavors. Recently, Dr. Pounds' methods for integrative analysis of multiple omics and multiple endpoint data discovered that increased expression of the DNA methyltransferase gene DNMT3B and total genome-wide DNA methylation are poor prognostic factors for pediatric acute myeloid leukemia (AML). This insight provided compelling scientific motivation to evaluate demethylating agents in the ongoing AML16 multi-center clinical trial for pediatric AML. He is principal biostatistician of that trial and has served in that role for 12 other clinical trials. Jeremy M G Taylor PhD is the Pharmacia Professor of

Biostatistics at the University of Michigan. He obtained a Bachelor's degree in Mathematics and a Diploma in Statistics from Cambridge University and a PhD in Statistics from University of California Berkeley. He was a faculty member in the Dept. of Biostatistics and the Dept. of Radiation Oncology at UCLA from 1983-1998. He is currently a faculty member in the Dept. of Biostatistics, the Dept. of Radiation Oncology and the Dept. of Computational Medicine and the Bioinformatics and the Director of the Center for Cancer Biostatistics at the University of Michigan. He is the winner of the Michael Fry award from the Radiation Research Society, the Mortimer Spiegelman award from the American Public Health Association and the Jerome Sacks award from the National Institute of Statistical Science. He has over 370 publications and research interests in longitudinal and survival data, cure models, methods for missing data, causal inference, biomarkers, surrogate and auxiliary variables. He worked previously in AIDS research but currently mainly focusses on cancer research. He has served as the dissertation chair for 36 PhD students in Biostatistics at UCLA and the University of Michigan.



ORAL PRESENTER



Jordan Creed, Ph.D. H. Lee Moffitt Cancer Center & Research Institute

ORAL PRESENTER



Naomi Brownstein, PhD H. Lee Moffitt Cancer Center & Research Institute

Jordan Creed is a research data analyst in the Gerke Lab at Moffitt Cancer Center. She received her MPH from the University of Florida. Her work blends molecular epidemiology, bioinformatics, stastistics and data science under the umbrella of cancer research. Primary interests involve creating software tools, such as web applications and R packages, for the academic community that improve reproducibility in research and integrate causal inference and modern data science practices. The majority of her research has focused on molecular epidemiology and racial disparities in prostate and brain cancer.

Dr. Brownstein is an assistant member in the biostatistics and bioinformatics department at Moffitt Cancer Center and assistant professor at USF in the department of oncologic sciences. She joined the faculty at Moffitt in 2019 after receiving her PhD in biostatistics at the University of North Carolina at Chapel Hill, completing a postdoctoral associate at the National High Magnetic Field Lab, and serving as an assistant professor and the sole faculty biostatistician at the Florida State University College of Medicine. Through these environments, Dr. Brownstein has gained experience and interest in a variety of research areas throughout statistics, public health and medicine. Dr. Brownstein has developed statistical methods related to clusterability, survival analysis, and missing data and mentored students from the undergraduate through doctoral levels. Her primary areas of application concern cancer prevention, behavioral interventions and outcomes, patient reported outcomes, and radiation oncology. Dr. Brownstein also serves the biostatistics profession as chair of the mentoring committee of the ENAR Regional Advisory Board and as the Florida representative to the American Statistical Association Council of Chapters Governing Board.



KEYNOTE SPEAKER



Xiangqin Cui, PhD Emory University

ORAL PRESENTER



Gang Han, PhD Texas A&M University Xiangqin Cui is a Research Associate Professor who joined Emory in 2017 after spending 13 years at the University of Alabama at Birminghm. Currently, she is the funding Director of the VA Data Analytics Core, which supports the analytical needs in research and quality assurance at the Atlanta VA Medical Center. The Core's major responsibility is to assist investigators to take advantage of the vast VA electronic medical records in their research and health care quality improvements. Dr. Cui's research interests include various types of omics (transcriptomics, epigenomics, proteomics, metabolomics, and microbiome) and her newly acquired interest is EHR data analysis.

Dr. Gang Han is Associate Professor of Biostatistics in Department of Epidemiology and Biostatistics, at Texas A&M University, School of Public Health. He received his M.S. and Ph.D. in Statistics from The Ohio State University and B.S. in Computer Science from the Beijing University of Technology. He is a member of the American Statistical Association, American Public Health Association, and Institute for Operations Research and the Management Sciences. His research efforts have been in statistics theory and applications in Biomedical Research and Bioinformatics. His statistical research experiences lie in fields: 1, modeling time-to-event data for personalized cancer therapy, 2, frequentist and Bayesian hybrid inference for modeling HIV viral load, and 3, the design and analysis of computer experiments. His scientific research has been focusing on clinical trials, health epidemiology, outcome research, biomarker identification, comparative effectiveness research, and genome studies regarding next generation sequencing and SNP analysis, as well as statistical inferences based on U.S. national registration data.



ORAL PRESENTER



Jianrong Wu, PhD University of Kentucky Dr. Wu got his PhD degree from the Department of Statistics, University of Toronto in 1999 and had postdoctor training at the Fred Hutchinson Cancer Research Center. Dr. Wu had worked at the Department of Biostatistics, St. Jude Children's Research Hospital from 2002-2017. Now, Dr. Wu is a Professor of Biostatistics, Markey Cancer Center at the University of Kentucky.

ORAL PRESENTER



Zhixin Wang, PhD University of Alabama at Birmingham Zhixin Wang is a Researcher V at the Division of Preventive Medicine, University of Alabama at Birmingham. Her work is mainly focused on data analysis and batch effects in Phase II cancer clinical trials.