



**INTERNATIONAL GENETIC  
EPIDEMIOLOGY SOCIETY**

**IGES 28th ANNUAL MEETING**

October 12-14, 2019  
Hilton Americas-Houston  
Houston, Texas, USA



**ANNUAL MEETING AGENDA**

Special Programming including  
**IGES Education Workshop:  
Introduction to Mendelian randomization**  
October 12, 2019 10am-4pm



## IGES 2019 Annual Meeting Agenda

### Saturday, October 12

8:30am-6:00pm	Registration	Prefunction
10:00am-4:00pm	<b>Education Workshop: Introduction to Mendelian randomization</b> <i>Separate registration required</i> <b>Chair: Stephanie Santorico</b> Course Tutors: Kaitlin Wade, Carolina Borges, Jie Zheng	Ballroom of The Americas F
5:00pm 7:00pm	IGES Board of Directors Meeting	Meeting Room 333
7:00pm 8:00pm	Welcome Reception	Ballroom of The Americas A

### Sunday, October 13

7:00am 6:00pm	Registration	Prefunction
<b>7:00am 8:15am</b>	<b>Continental Breakfast</b>	<b>Prefunction</b>
8:30am 9:00am	Welcome and Presidential Address Inke König Celia Greenwood	Ballroom of The Americas A

#### Session 1: Polygenic scores, risk assessment and prognostic modeling

Ballroom of The Americas A

Chairs: Inke König and Brandon Coombes

	Presentation	Abstract	Author
9:00am-9:15am	Leveraging external repositories to generate calibrated rare variant gene risk scores	62	Ricky Lali
9:15am-9:30am	Progress and controversy in analysis of complex phenotypes based on genome-wide association statistics	5	David Balding
9:30am-9:45am	Identifying risk factors involved in the common versus specific liabilities to substance abuse: a genetically informed approach	101	Tabea Schoeler*
9:45am-10:00am	NSAIDs and colorectal cancer: results from genomewide gene environment interaction scans	58	Andre Kim
10:00am-10:30am	Refreshment Break		Prefunction

#### Session 2: Mediation and Mendelian randomization

Ballroom of The Americas A

Chairs: Eleanor Wheeler and James Cook

	Presentation	Abstract	Author
10:30am-11:00am	<b>Keynote Presentation:</b> <b>Identifying drug targets using human genetics at scale</b>	55	<b>Toby Johnson</b>
11:00am-11:15am	Hierarchical modeling framework for Mendelian randomization and transcriptome-wide association approaches for correlated SNPs and intermediates	52	Lai Jiang^
11:15am-11:30am	A powerful and versatile colocalization test	28	Yangqing Deng
11:30am-11:45am	An extended expression prediction approach for TWAS leveraging the cis-mediator trans-eQTL paradigm	63	Nicholas Larson
11:45am-12:00pm	Estimated total mediation effects for multiple types of high-dimensional omics in over 3500 individuals on aging-related variation in blood pressure	138	Yujie Zhao

## Sunday, October 13

**12:00pm 1:30pm Lunch on your own**

**12:00pm 1:30pm Young Investigators' Luncheon** (Ticketed Event)

**Ballroom of The Americas C**

**12:00pm 1:30pm Committee Lunches:**

Publications Committee working lunch

Meeting Room 330

Communications Committee working lunch

Meeting Room 332

ELSI Committee working lunch

Meeting Room 329

**Session 3: Genomics in diverse populations**

**Ballroom of The Americas A**

**Chairs: Corinne Engelman and Alisa Manning**

	Presentation	Abstract	Author
1:30pm-2:00pm	<b>Keynote Presentation:</b> <b>The future of genomic studies must be globally representative</b>	85	<b>Kari North</b>
2:00pm-2:15pm	eMERGE phenome-wide association study of biogeographic ancestries predicts ocular, immune system, renal, cardiometabolic, gynecological, and vector-borne disease risk	56	Jacob Keaton*
2:15pm-2:30pm	An African ancestry uterine fibroids polygenic risk score (PRS) identifies associations with other gynecologic conditions in the clinical phenome	134	Jacklyn Hellwege
2:30pm-2:45pm	The association between common risk factors for age-related disease and DNA methylation clocks in an African American population	106	Jennifer Smith
2:45pm-3:00pm	Estimation of SNP-based heritability in multi-ethnic studies	6	Saonli Basu

**3:00pm-3:15pm Poster Highlights Group A**

	Poster	Abstract	Author
	Genomic imprinting analyses reveal maternal effects to be a cause of genotypic variability in type 1 diabetes and rheumatoid arthritis	29	Inga Blunk
	Epigenetic loci for blood pressure are associated with hypertensive target organ damage in an older African American population	57	Minjung Kho
	Effects of mitochondrial DNA variants on blood biomarkers	131	Ekaterina Yonova-Doing
	A principal component approach to polygenic risk scores to avoid over and underfitting	19	Brandon Coombes
	A framework for transcriptome-wide association studies in breast cancer in diverse study populations	7	Arjun Bhattacharya

3:15pm-4:45pm Poster Session A and Refreshment Break

Ballroom of The Americas D

**Session 4: Large-scale populations, collections and challenges**

**Ballroom of The Americas A**

**Chairs: Iris Heid and Jacob Keaton**

	Presentation	Abstract	Author
4:45pm-5:00pm	A powerful gene-set analysis method identifies novel associations and improves interpretation in UK-Biobank	32	Diptavo Dutta^
5:00pm-5:15pm	Improving power and avoiding pitfalls in gene-environment interaction scans	125	Thomas Winkler*
5:15pm-5:30pm	An efficient identity by descent mapping test for biobank-scale cohorts	15	Han Chen
5:30pm-5:45pm	Genome-wide gene-smoking interaction analysis of lung function in UK Biobank	80	Carl Melbourne*
5:45pm-6:00pm	An online platform for densely imputed GWAS summary statistics	27	Marika Kaakinen

**7:30pm - 8:00 pm Cocktail Reception**

**Prefunction**

**8:00pm 10:00pm Banquet**

**Ballroom of the Americas A**

## Monday October 14

7:00am-5:30pm Registration Prefunction

**7:00am 8:15am Continental Breakfast Prefunction**

**Session 5: New aspects on statistical modeling in genetic epidemiology Ballroom of The Americas A**

Chairs: Sajay Shete and Thomas Winkler

	Presentation	Abstract	Author
<b>8:30am-8:45am</b>	<b>Best Paper Presentation</b>		
8:45am-9:00am	Allele-Specific QTL fine-mapping with PLASMA	116	Austin Wang <sup>^</sup>
9:00am-9:15am	Testing gene-environment interactions without measuring the environment	71	Qiongshi Lu
9:15am-9:30am	Ordered multinomial regression for genetic association analysis of ordinal phenotypes	39	Christopher German
9:30am-9:45am	A rare variant nonparametric linkage method for nuclear and extended pedigrees with application to late-onset Alzheimer's Disease using whole genome sequence data	64	Suzanne Leal

**9:45am-10:00am Poster Highlights Group B**

	Poster	Abstract	Author
	High-dimensional regularized regression for identifying gene-environment interactions incorporating external information	132	Natalia Zemlianskaia
	Leveraging genetic ancestry for new insights into complex traits in admixed populations	45	Andrea Horimoto
	Efficient estimation of hidden ancestry structure using summary genotype frequency data	76	Gregory Matesi
	Gene-based rare variant association tests for ancestry-matched case-control data	117	Chaolong Wang
	A gene based association test utilizing an optimally weighted combination of multiple traits	136	Xuexia Wang

10:00am-11:30am Poster Session B and Refreshment Break Ballroom of The Americas D

**Session 6: Polygenic Trait Genetics II Ballroom of The Americas A**

Chairs: Maggie Wang and Audrey Hendricks

	Presentation	Abstract	Author
11:30am-12:00pm	<b>Keynote Presentation:</b> <b>Data Integration: Data-Driven discovery from diverse data sources</b>	1	<b>Genevera Allen</b>
12:00pm-12:15pm	Addressing the missing data issue in multi-phenotype genome-wide association studies	3	Mila Anasanti <sup>^</sup>
12:15pm-12:30pm	Investigating the use of machine learning methods to build risk prediction models for complex disease	18	James Cook
12:30pm-12:45pm	Nearest-neighbor projected-distance regression to detect network interactions and control for confounders, population structure and multiple testing	79	Brett McKinney
12:45pm-1:00pm	Towards an accurate cancer diagnosis modelization: Comparison of random forest strategies	24	Ahmed Debit

**1:00pm-2:30pm Lunch on your own**

**1:00pm-2:30pm Committee Lunches**

Program Committee working lunch	Meeting Room 332
Education Committee working lunch	Meeting Room 330
Young Investigators' Committee working lunch	Meeting Room 329
Genetic Epidemiology Editorial Board working lunch	Meeting Room 328

# Monday, October 14

## Session 7: Omics: methods and applications

Ballroom of The Americas A

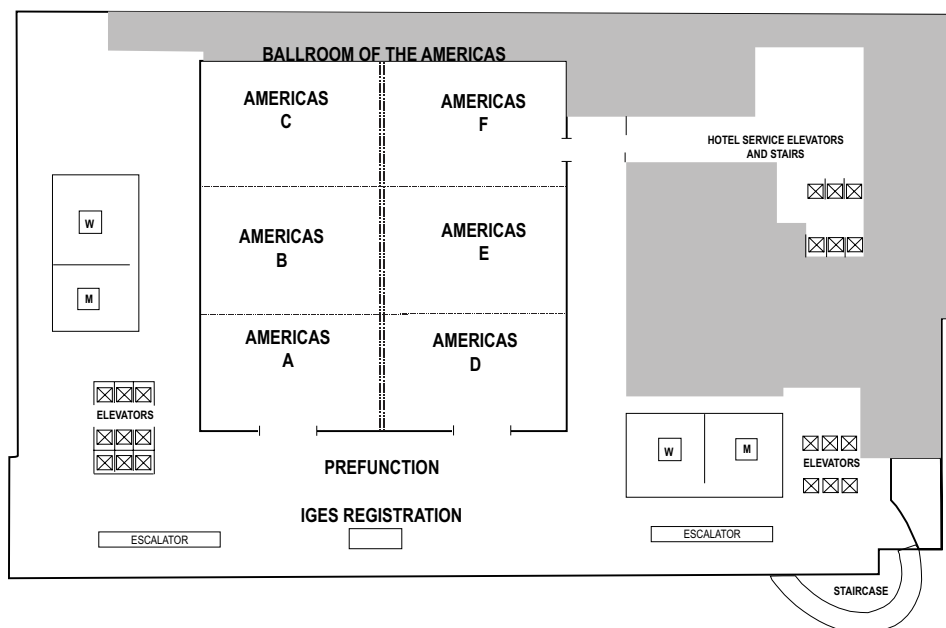
Chairs: Ching-Ti Liu and Ekaterina Yonova-Doing

	Presentation	Abstract	Author
2:30pm-3:00pm	<b>Keynote Presentation:</b> <b>Empirical Bayes methods for genetic risk prediction</b>	140	Hongyu Zhao
3:00pm-3:15pm	Detecting tumor-immunity-specific expression QTL in cancer	119	Xuefeng Wang
3:15pm-3:30pm	Multi-phenotype transcriptome-wide association study (TWAS) tests using summary statistics	36	Helian Feng
3:30pm-3:45pm	A two-stage epigenome wide association study identifies novel pancreatic cancer susceptibility loci by leveraging public controls	120	Ziqiao Wang
3:45pm-4:00pm	Exome-wide low-frequency genetic variants contribute to human craniofacial morphology	70	Dongjing Liu
4:00pm-4:30pm	Refreshment Break		Prefunction
<b>4:30pm-5:30pm</b>	<b>Business Meeting and Awards</b>		<b>Ballroom of The Americas A</b>

## Meeting Sponsors



## Level Two Map



Meeting Rooms for Committee Lunches are on Level 3 reachable by the staircase or elevator

**Meeting Wifi Network: IGES2019 Password: iges!HOU**

## Sunday, October 13

3:15pm-4:45pm		Poster Session A		Ballroom of the Americas AB			
Poster	Presenter	Poster	Presenter	Poster	Presenter	Poster	Presenter
2	Almeer, H	33	Espin-Garcia, O	67	Li, Y-J	96	Paynton, M
7	Bhattacharya, A	35	Ezquina, S	69	Lipunova, N	98	Ray, D
10	Blunk, I	38	Fundator, M	73	Luyapan, J	100	Sarnowski, C
12	Breeyear, J	41	Goldstein, A	75	Mandal, D	103	Sebro, R
14	Camargo, A	46	Horton, M	77	Mautz, B	105	Sitlani, C
17	Chikowore, T	48	Ibi, D	81	Middlebrooks, C	108	Stiemke, A
19	Coombes, B	50	Jallow, M	83	Musolf, A	110	Sun, R
21	Cordero, R	53	Jiang, R	86	Nyberg, T	112	Syed, H
23	de Andrade, M	57	Kho, M	88	Ostrom, Q	114	Tekola-Ayele, F
26	Demerais, F	60	Kraven, L	92	Park, H	118	Wang, J
30	Duchen, D	65	Leutengger, A-L	94	Pattee, J	122	Waring, S

Session 4 will start promptly at 4:45, please allow time to proceed next door and be seated.

## Monday, October 14

10:00am-11:30am		Poster Session B		Ballroom of the Americas AB			
Poster	Presenter	Poster	Presenter	Poster	Presenter	Poster	Presenter
4	Bailey-Wilson, J	34	Ewusie, J	66	Li, Q	93	Pattee, J
8	Bhattacharyya, U	37	Freitag-Wolf, S	68	Liang, Y	95	Paul, S
9	Blue, E	40	Ghosh, S	72	Lu, T	97	Piekos, J
11	Bohlender, R	42	Harbs, J	74	Mall, R	99	Saad, M
13	Caliebe, A	45	Horimoto, A	76	Matesi, G	102	Schoenbuchner, S
16	Chen, H-H	47	Howey, R	78	McGregor, K	104	Shi, B
20	Cordero, J	49	Im, HK	82	Montazeri, Z	107	Sorant, A
22	Daley, D	51	Jee, SH	84	Nolte, I	109	Sun, J
25	Deelder, W	54	John, J	87	Ochs-Balcom, H	111	Sung, Y
29	Draisma, H	59	Kiser, D	89	Oualkacha, K	113	Szymczak, S
31	Duroux, D	61	Kunji, K	91	Panyard, D	115	Van Steen, K

Session 6 will start promptly at 11:30, please allow time to proceed next door and be seated.

**Poster set-up hours**

Saturday October 12  
Sunday October 13

**Ballroom of the Americas D**

1:00pm-8:00pm  
7:00am-10:30am

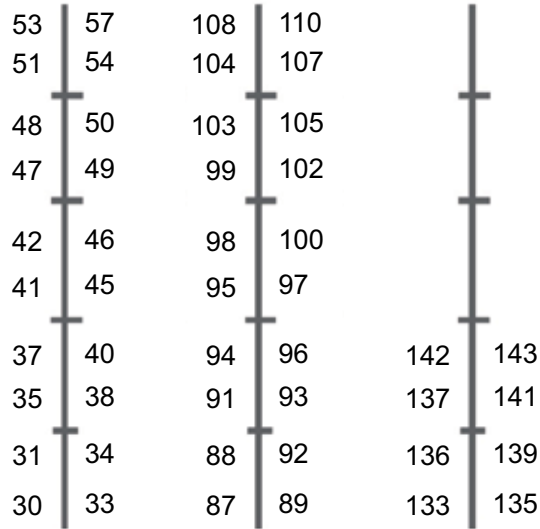
**Poster removal hours**

Monday October 14

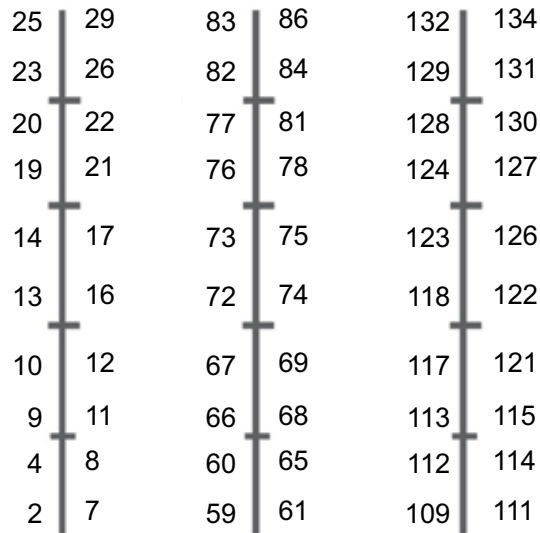
By 2:30pm

Poster	Presenter
124	Willems, E
127	Xia, X
129	Xu, J
131	Yonova-Doing, E
133	Wendel, B
135	Zhang, D
137	Zhao, K
141	Zhao, W
143	Zhu, X

**BALLROOM OF THE AMERICAS E**



Poster	Presenter
117	Wang, C
121	Wang, Z
123	Wei, W
126	Wu, C-C
128	Xu, H
130	Yang, T
132	Zemlianskaia, N
134	Zeng, Y
136	Wang, X
139	Zheng, X
142	Zhu, M



**BALLROOM OF THE AMERICAS D**



PREFUNCTION

IGES REGISTRATION

## Keynote Speakers



**Genevera Allen**

**Abstract: Data Integration: Data-driven discovery from diverse data sources**

Genevera Allen is an Associate Professor of Statistics, Electrical and Computer Engineering, and Computer Science at Rice University as well as an investigator at the Neurological Research Institute at Baylor College of Medicine. Her research interests are in developing statistical tools to help scientists understand big data by using techniques from high-dimensional inference, machine learning and convex optimization. Her applied research interests include neuro-imaging, neural recordings, and high-throughput genomics.



**Toby Johnson**

**Abstract: Identifying drug targets using human genetics at scale**

Toby Johnson is a Scientific Director at GlaxoSmithKline. His work involves developing and implementing statistical genetics tools for large scale selection and validation of drug targets, and developing requisite database infrastructure for GWAS complete summary statistics for thousands of diseases and traits. His general research interests include causal inference and Mendelian randomization, inference from summary statistics, and pharmacogenomics and biomarkers.



**Kari North**

**Abstract: The future of genomic studies must be globally representative**

Dr. North is a professor of epidemiology in the UNC Department of Epidemiology and has developed a strong multidisciplinary research program evaluating the genetic epidemiology of cardiovascular disease (CVD) and associated risk factors. At the national level, Dr. North chairs the National Institutes of Health CHSA study section, is an editorial board member of multiple prominent journals and serves in several elected leadership roles in The Obesity Society and in the American Heart Association Epidemiology Council. At UNC, Dr. North has been engaged with several interdisciplinary centers that foster collaborative research in genetics.



**Hongyu Zhao**

**Abstract: Empirical Bayes methods for genetic risk prediction**

Dr. Hongyu Zhao is the Ira V. Hiscock Professor and Chair of Biostatistics at Yale University. His research interests are the developments and applications of statistical methods in human genetics, molecular biology, drug developments, and precision medicine. Dr. Zhao is a Co-Editor of the Journal of the American Statistical Association – Theory and Methods, and was the recipient of several honors, including the Mortimer Spiegelman Award for a top statistician in health statistics by the American Public Health Association, and Pao-Lu Hsu Prize by the International Chinese Statistical Association.

## Education Workshop Course Tutors



**Kaitlin Wade, PhD**

Course organizer  
MRC Integrative Epidemiology Unit



**Carolina Borges, PhD**

MRC Integrative Epidemiology Unit at the  
University of Bristol, Bristol, UK  
Population Health Sciences, Bristol Medical  
School, University of Bristol, Bristol, UK



**Jie Zheng, PhD**

MRC Integrative Epidemiology Unit at the  
University of Bristol, Bristol, UK  
Population Health Sciences, Bristol Medical  
School, University of Bristol, Bristol, UK

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