INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY
22ND ANNUAL CONFERENCE
CHICAGO, ILLNOIS, USA SEPTEMBER 15-17, 2013
PROGRAM

Sunday, September 15	Registration opens 10:00am	
	Educational Workshop 1:00-5:00pm	
6:00pm	Welcome Reception	
7:30pm	Young Investigators Mixer	
Monday, September 16		**Accepted #**
	7:00-8:30 Breakfast	**Abstract**
8:30 – 10:00 Session 1 Presidential address, best paper in Genetic Epidemiology, and Population Diversity	8:30-9:00 Andreas Ziegler; presidential address	
	9:00-9:15 **Best paper in Genetic Epidemiology** TBA	
	9:15-9:30 Qunyuan Zhang. SMART-scan (Selection of Models for the Analysis of Risk-factor Trees): Leveraging biological knowledge to mine large sets of risk factors with application to microbiome data	1
	9:30-9:45 Kelly Benke Polygenic Risk Score Associations may be improved with simple procedures	2
	9:45-10:00 Ronnie Sebro. Geographic genetic diversity in the United States and implications for genomewide association studies	3
10:00 – 10:30 Coffee break		
10:30-12:00 Session 2 Neel and Williams awards	**Williams:** 11:15-11:30 Jessica Dennis Investigating genetic and epigenetic variation in the chromosome 2q region linked to tissue factor pathway inhibitor plasma l	4
	Williams: 11:30-11:45 Miaoyan Wang Optimal Selection of Individuals for Genotyping in Genetic Association Studies with Related Individuals	5
	Williams: 11:45-12:00 Jae Hoon Sul Effectively identifying eQTLs from multiple tissues by combining mixed model and meta-analytic approaches	6
	Neel: 10:30-10:45. Andrew Jaffe Accounting for cellular heterogeneity is critical in epigenome-wide association studies	7

	Neel: 10:45-11:00 Jennifer Below Reconstructing Pedigrees from Estimates of Genomic Sharing in Admixed Populations	8
	Neel: 11:00-11:15 Charles Yin Kiu Cheung Design matters! A statistical framework to guide sequencing choices in pedigrees	9
12:00 – 1:15 Lunch	**Lunch ON YOUR OWN**	
12:00-1:00	**Committee Meetings tba**	
1:15 – 2:15 Session 3: Genomic annotation and its uses	**1:15 – 1:45 Invited speaker #1. Alviz Brazma, ENCODE** Using high throughput sequencing and other functional assays to study how genome works and some of the lessons learned	
	1:45–2:00 ~~Heather Wheeler~~ Hae Kyung Im Poly-Omic Prediction of Complex Traits – OmicKriging	10
	2:00-2:15 Jianzhong Ma Genome-wide scan of inversions predisposing to secondary rearrangements using case-parent trio data	11
2:15 – 3:45 Poster session with coffee	**POSTER SESSION** – (ODD NUMBER ABSTRACTS PRESENTED)	
3:45 – 4:45 Session 4: Families and sequence data	**3:45-4:00. Special contributed Talk. Adrienne Cupples** Sequence Data in Family Studies: the Framingham Heart Study	12
	4:00-4:15 Wei Gao Sequence Kernel Association Test in Family Samples with Repeated Phenotype Measurements or Multiple Traits	13
	4:15-4:30 Alexandre Bureau Sharing of rare variants by affected relatives: building evidence for causal variants based on exact sharing probabilities	14
	4:30-4:45 Paul Marjoram Design of Sequence-based Follow-up to GWAS	15
4:45 – 5:30 Business meeting		
5:45pm – 9:30pm	Transport for BANQUET – CRYSTAL GARDENS @ Chicago Navy Pier	

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Tuesday, September 17		
	7:00-8:30 Breakfast	
8:30-10:00 Session 5: Genetic epidemiology, Pharmacogenomics, and Methylation	**8:30-9:00 Invited speaker #2. Nadeem Sarwar** The contemporary role of genetic epidemiology in drug discovery and development	
	9:00-9:15 Younghee Lee Variants Affecting Exon Skipping in Very Important Pharmacogenes	16
	9:15-9:30 Richard Howey Imputation without doing imputation: a new method for the detection of non-genotyped causal variants	17
	9:30-9:45 Changshuai Wei Detecting genetic heterogeneity in complex diseases with a weighted U statistic	18
	9:15-9:30 Stacey Winham Functional data analysis of blood-based DNA methylation profiles and ovarian cancer risk	19
10:00-10:30 Coffee break		
10:30-12:00 Session 6. Data Integration	**10:30-11:00 Invited speaker #3. Stephen Montgomery** The impact of rare variation on gene expression in families	
	11:00-11:15 Christian Darabos Inferring Human Phenotype Networks from Pathway-based Analysis	20
	11:15-11:30 ~~Melissa Gymrek~~ Yaniv Erlich Microsatellite Polymorphisms Create an Abundant Source of Expression Variability	21
	11:30-11:45 Yijuan Hu Meta-Analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics	22
	11:45-12:00 Jin J.J.Z Zhou Integrating Multiple Correlated Phenotypes for Genetic Association Analysis Through Heritability	23
12:00 – 1:15 Lunch	**Lunch ON YOUR OWN**	
12:00-1:00pm	**Committee Meetings tba**	
1:15 – 2:45 Poster session 2 (with coffee)	**POSTER SESSION** – (EVEN NUMBERED ABSTRACTS PRESENTED)	

2:45– 4:15 Session 7. Prospective studies and study design	**2:45-3:15 Invited speaker #4. Teri Manolio** New Models for Large Prospective Studies involving Genomics	
	3:15-3:30 Nicholas Timpson Association of plasma uric acid with ischemic heart disease and blood pressure: Mendelian randomization analysis of two large cohorts	24
	3:30-3:45 Saunak Sen (on behalf of Parichoy Choughury) Enhancing case-control genetic studies using sample surveys	25
	3:45-4:00 Glen Satten Testing Association without Calling Genotypes Allows for Systematic Differences in Read Depth between Cases and Controls	26
	4:00-4:15 John Wallace Population Stratification Detection and Correction in Rare Variant Collapsing Methods Using Principal Component Analysis	27
	4:15-5:00 **Final Comments**	