Symposium on Statistical and Computational Methods for Pharmacogenetic Epidemiology of Cancer

August 11 and 12, 2016
Memorial Sloan Kettering Cancer Center
New York, New York

Meeting Location	**Laurance S. Rockefeller Board Room**
	Rockefeller Research Laboratories
	430 East 67th Street (between 1st Avenue & York Avenue)
	New York, NY 10065

Schedule	Content	Title
Thursday, August 11, 2016		
7:45-8:15am	**Continental Breakfast**	
8:15-8:30am	**Introductory Remarks – Jaya Satagopan**, PhD and **Sanjay Shete**, PhD	
	Welcome – **Sara Olson**, PhD, Memorial Sloan Kettering Cancer Center	
8:30-10:00am	**Session 1: Pharmacogenetic studies of complex disorders**	
	Chair: Jian Wang, PhD, MD Anderson Cancer Center	
	Richard Weinshilboum, MD	**Pharmacogenomics of breast cancer endocrine therapy**
	Mayo Clinic	
	Paul Chapman, MD	**The history of RECIST: How did we get here?**
	Memorial Sloan Kettering	
	Malcolm Pike, PhD	**Modeling the hormonal chemoprevention of ovarian**
	Memorial Sloan Kettering	**cancer - Issues and opportunities**
10:00-10:30am	**Coffee Break**	
10:30-12:00pm	**Session 2: Risk Prediction and Classification**	
	Chair: Phil Gona, PhD, University of Massachusetts Medical School	
	Giovanni Parmigiani, PhD	**Cross-study analysis of prediction algorithms in genomics**
	Harvard T.H. Chan	
	School of Public Health	

	Hyun Min Kang, PhD University of Michigan	**On the explained versus predictable heritability of complex traits**
	Li-Xuan Qin, PhD Memorial Sloan Kettering	**A cautionary note on using cross-validation for molecular classification**
12:00-12:30pm	**Group Photo**	
12:30-2:00pm	**Lunch and Posters**	
2:00-3:30pm	**Session 3: Therapeutic targets (Methods)**	
	Chair: Karla Ballman, PhD, Weill Cornell Medicine	
	Melissa Rotunno, PhD National Cancer Institute	**Identifying novel susceptibility variants cor complex cancers using exome sequencing in families**
	Alison Motsinger-Reif, PhD North Carolina State University	**Methods and applications for dose-response gene mapping**
	Sibo Zhao, PhD candidate New York University confounder	**Causal mediation analysis with unmeasured mediator-outcome**
3:30-4:00pm	**Coffee Break**	
3:30-5:00pm	**Session 4: Electronic records and software packages**	
	Chair: Huann-Sheng Chen, PhD, National Cancer Institute	
	Bhramar Mukherjee, PhD University of Michigan	**Joint analysis of electronic health record data and GWAS data in a health system population: The Michigan Genomics Initiative**
	Jason Moore, PhD University of Pennsylvania	**Automating data science for cancer genomics**
5:00pm	**End of Day 1**	

Friday, August 12, 2016

7:45-8:30am	**Continental Breakfast**	
8:30-10:00am	**Session 5: Therapeutic targets (Applications)**	
	Chair: Marinela Capanu, PhD, Memorial Sloan Kettering Cancer Center	
	Nancy Cox, PhD Vanderbilt University	**TBA**
	Peter Kraft, PhD Harvard T. H. Chan School of Public Health	**A multi-tissue transcriptome-wide association study identifies novel breast cancer susceptibility loci**
	Omar De la Cruz Cabrera, PhD Kent State University	**Characterization of cancer clonal heterogeneity via single cell analysis for treatment selection**
10:00-10:30am	**Coffee Break**	
10:30am-12:00pm	**Session 6: Study Designs**	
	Chair: Mengling Liu, PhD, New York University	
	Christopher Amos, PhD Dartmouth Geisel School of Medicine	**Interactions in smoking behavior - identifying targets and designs for smoking cessation**
	Lorenzo Trippa, PhD Harvard T.H. Chan School of Public Health	**Bioinformatics tools for incorporating biological knowledge into genetic analysis**
	Donald Berry, PhD	**Adaptive biomarker-driven platform clinical trials using**

	MD Anderson Cancer Center	longitudinal models and time trend models of control therapy
12:00-1:30pm	Lunch and Posters	
1:30-2:30pm	Session 7: Gene-treatment interactions	
	Chair: Cody Chiuzan, PhD, Columbia University	
	Alexia Iasonos, PhD	Quantifying treatment benefit in molecular subgroups to assess a predictive biomarker
	Memorial Sloan Kettering	
	Tim Ahles, PhD	Cognitive effects of cancer treatments - Interactions of chemotherapy, genetic factors, and smoking
	Memorial Sloan Kettering	
2:30-3:00pm	Floor Discussion and Closing Remarks	
3:00pm	Departure	

Symposium on Statistical and Computational Methods for Pharmacogenetic Epidemiology of Cancer Poster Session

Name	University/Affiliation	Title of Abstract
Qin, Li-Xuan	Memorial Sloan Kettering Cancer Center	A Cautionary Note on using Cross-validation for Molecular Classification
Govindarajulu, Usha	SUNY Downstate School of Public Health	Evaluating Treatment Effect in Multicenter Trials with Small Centers Using Survival Modeling
Zhao, Sibo	NYU School of Medicine	Causal Mediation Analysis with Unmeasured Mediator-Outcome Confounder
Huang, Yuan	Yale University	Promote Sign Consistency in the Joint Learning of Possibly Heterogeneous Networks
Liu, Zhonghua	Harvard School of Public Health	A Semi-supervised Learning approach to functional annotations for coding and noncoding variants
Urbanowicz, Ryan	University of Pennsylvania	Interpretable modeling of epistatic and heterogeneous associations in epidemiology with rule-based machine learning
Smieszek, Sandra	Case Western Reserve University	Cancer genetic risk and the longevous phenotype in the AMISH
De la Cruz Cabrera, Omar	Kent State University	Characterization of cancer clonal heterogeneity via single cell analysis for treatment selection