

ADVANCES IN STATISTICAL METHODS FOR CANCER GENETIC EPIDEMIOLOGY

August 22 and 23, 2013
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

Thursday, August 22, 2013

8:15-8:30am **Introductory Remarks** – Jaya Satagopan, PhD and Sanjay Shete, PhD
Welcome – Colin B. Begg, PhD

8:30-10:00am **Session 1: Analysis of pathways using -omics data**
Chair: Sanjib Basu, PhD, Northern Illinois University

Daniel J. Schaid, PhD
Mayo Clinic

Incorporating gene network information into the analysis of
genomewide association studies

Xihong Lin, PhD
Harvard University

Joint analysis of SNP and gene expression data in genetic
association studies of complex diseases

Yen-Tsung Huang, MD, ScD
Brown University

Integrative modeling of multi-platform genomic data

10:00-10:30am **Coffee Break**

10:30-11:30am **Session 2: Sampling designs**
Chair: Phil Gona, PhD, University of Massachusetts Medical School

Lu Chen, PhD candidate
University of Pennsylvania

Semiparametric maximum likelihood estimation with two-phase
stratified case-control sampling

Xiaoyu Song, PhD candidate
Columbia University

A new estimating equation approach for secondary trait analyses
in genetic case-control studies

11:30am-12:00pm **Group Photo**

12:00-1:30pm **Lunch and Posters**

1:30-3:00pm **Session 3: Statistical analysis of sequencing data**
Chair: Kimberly McAllister, PhD, National Institute of Environmental Health Sciences

Duncan C. Thomas, PhD
University of Southern California

Two-phase and family-based designs for sequencing studies

Marinela Capanu, PhD
Memorial Sloan-Kettering Cancer Center

Multiple testing methods for analyzing rare genetic variants

Iuliana Ionita-Laza, PhD
Columbia University

Cluster detection approaches to identify disease genes in CNVs
implicated in psychiatric disorders: applications to whole-exome
sequencing studies on autism and schizophrenia

3:00-3:30pm

Coffee Break

3:30-5:00pm

Session 4: Analysis of high throughput data in cancer genetic epidemiology

Chair: Michael D. Swartz, PhD, University of Texas School of Public Health

Xi Kathy Zhou, PhD
Weill Cornell Medical College

A Bayesian model averaging approach for observational high-throughput data

Sihai Zhao, PhD
University of Pennsylvania

More powerful genetic association testing via a new statistical framework for integrative genomics

Carolyn M. Hutter, PhD
National Cancer Institute

An overview of NCI Epidemiology and Genomics Research Program's resources and activities for analyses of large-scale genetic epidemiology studies of cancer

Dinner (on your own)

8:30-10:00am

Session 5: Gene-environment interactions and risk modeling

Chair: Ruth Ottman, PhD, Columbia University

Iryna Lobach, PhD
University of California -
San Francisco

Case-control studies of gene-environment interactions with error
in measurement of environmental factors

Danielle Braun, PhD candidate
Harvard University

Nonparametric adjustment for measurement error in time to
event data

Rajesh Talluri, PhD
MD Anderson Cancer Center

Risk prediction and estimation of the effect of various
psychological and cultural factors on smoking experimentation
in Mexican American youth

10:00-10:30am

Coffee Break

10:30am-12:00pm

Session 6: Statistical and computational software packages

Chair: Samprit Banerjee, PhD, Weill Cornell Medical College

Annette Molinaro, PhD
University of California –
San Francisco

partDSA: Theory, Software and Application

Marylyn Ritchie, PhD
Penn State University

Bioinformatics tools for incorporating biological knowledge into
genetic analysis

Jason H. Moore, PhD
Dartmouth College

Multifactor dimensionality reduction software for detecting
gene-gene and gene-environment interactions

12:00-1:30pm

Lunch and Posters

1:30-2:30pm

Session 7: Modeling tumor signatures

Chair: Jasmin Divers, PhD, Wake Forest University

Giovanni Parmigiani, PhD
Dana Farber Cancer Center

Statistical modeling of somatic mutation data

Colin B. Begg, PhD
Memorial Sloan-Kettering Cancer Center

Strategies for investigating etiologic heterogeneity

2:30-3:00pm

Coffee Break

3:00-3:15pm

Discussion (5 minutes)

Robert C. Elston, PhD, Case Western Reserve University

Floor Discussion (10 minutes)

3:15pm

Departure

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- Department of Biostatistics, MD Anderson Cancer Center
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**Advances in Statistical Methods for Cancer Genetic Epidemiology
Poster Session**

Number	Name	University/Affiliation	Title of Abstract
1.	Braun, Danielle	Harvard School of Public Health	Nonparametric Adjustment for Measurement Error in Time to Event Data
2.	Talluri, Rajesh	MD Anderson Cancer Center	Risk Prediction and Estimation of the Effect of Various Psychological and Cultural Factors on Smoking Experimentation in Mexican American Youth
3.	Wang, Xuefeng	Harvard School of Public Health	Predicting Serum IgE Level and Blood Counts from Genome-wide Methylation Profile
4.	Song, Xiaoyu	Columbia University	A New Estimating Equation Approach for Secondary Trait Analyses in Genetic Case-Control Studies
5.	Zhao, Sihai	University of Pennsylvania	More Powerful Genetic Association Testing Via a New Statistical Framework for Integrative Genomics
6.	Huang, Yen-Tsung	Brown University	Integrative Modeling of Multi-platform Genomic Data
7.	Lu, Tao	University at Albany	Identifying Human Breast Cell Dynamic Regulatory Network with Group Sparse ODE Model
8.	Lu, Tao	University at Albany	Nonparametric Mixed-effects ODE Models for Gene Regulatory Network Analysis in Prostate Cancer Patients
9.	Cheng, Xin	New York University	Identification of Homogeneous and Heterogeneous Covariate Structure in Pooled Cohort Studies
10.	Zhou, Xi Kathy	Weill Cornell Medical College	A Bayesian Model Averaging Approach for Observational High-Throughput Data
11.	Zhang, Hui	St. Jude Children's Research Hospital	Generalized ANOVA for Concurrently Modeling Mean and Variance for Repeated NGS Measures
12.	Wu, Han	Purdue University	De-convolution of RNA-Seq Reads, and Transcripts Expression Level Quantification