

Program of the Conference on Design and Analysis Issues in Genomic Studies in Population Sciences

Conference Center at Harvard Medical
77 Avenue Louis Pasteur

WESNESDAY, October 10 Element Café

7:00pm-9:30pm Pre-registration, Reception and Poster Session

THURSDAY, October 11 Rotunda Room (3rd Level)

7:30-8:30am Registration & Continental Breakfast

8:30-8:40am Opening Remarks (Barry Bloom, Dean, Harvard School of Public Health)

8:40-9:25am Session I: Plenary

Chair: Louise Ryan, Harvard School of Public Health

Augustine Kong, deCODE Genetics

Title: Recent Gene Discoveries and New Challenges for Statistics

9:25-11:10am Session II: Design and Analysis Issues in Genome-Wide Association Studies

Part A (Presentations)

Chair: Christoph Lange, Harvard School of Public Health

9:25-10:00am Nancy Cox, University of Chicago

Title: Opportunities and Challenges in Analysis of GWA

Studies: Examples from the Trenches

10:00-10:35am Kathryn Roeder, Carnegie Mellon University

Title: On the Use of General Control Samples for Genome-Wide

Association Studies: genetic matching highlights causal variants

10:35-11:10am Jonathan Haines, Vanderbilt University

Title: The Importance of Multiple Study Designs for GWA Studies

11:10-11:35am Break

11:35-12:45pm Part B (Panel Discussions)

Panel Leader: Nan Laird, Harvard School of Public Health

Panelists: Mark Daly, Harvard Medical School

Paul Pharoah, University of Cambridge

Kyle Vogan, Senior Editor, Nature Genetics

12:45-1:45pm Lunch

FRIDAY, October 12

Rotunda Room (3rd Level)

7:30-8:30am

Continental Breakfast

8:30-9:15am

Session IV (Plenary)

Chair: Scott Weiss, Harvard Medical School and Channing Laboratory

Eric Schadt, Rosetta Inpharmatics LLC

*Title: Integrating Multiple Types of Large-Scale Functional Genomics
Data Reconstruct Networks Capable of Predicting Complex
System Behavior: Moving beyond Genomewide Association Studies*

9:15-11:00am

**Session V: Design and Analysis Issues in Using “Omics” Techniques
in Population-Based Studies**

Part A: Presentations

*Chair: Winston Hide, Harvard School of Public Health and South African
National Bioinformatics Institute*

9:15-9:50am

Richard Spielman, University of Pennsylvania

*Title: Genetic Analysis of Variation in Gene Expression Within
and Between Human Populations*

9:50-10:25am

Giovanni Parmigiani, Kimmel Cancer Center, Johns Hopkins University

Title: Statistical Methods for Mutational Analysis of Cancer

10:25-11:00am

John Storey, University of Washington

Title: Characterizing Variation in Human Expression Studies

11:00-11:30am

Break

11:30-12:40pm

Part B: Panel Discussions

*Panel Leader: John Quackenbush, Dana-Farber Cancer Institute and
Harvard School of Public Health*

Panelists: Debashis Ghosh, Pennsylvania State University

Karl Kelsey, Brown University

*Charles Lee, Harvard Medical School and Brigham and
Women's Hospital*

12:40-1:00pm

Break for Lunch Pick Up (Working Lunch)

1:00-1:50pm	Next Generation Genotyping/Sequencing Technology Luncheon Panel <i>Moderator:</i> David Christiani, Harvard School of Public Health Steve Lincoln, Affymetrix Inc Gary Schroth, Illumina Inc
1:50-2:00pm	Break
2:00-2:55pm	Roundtable Discussions (Rotunda and Rooms 214 and 216)
2:55-3:05pm	Break
3:05-3:55pm	Group Assembly
3:55-4:00pm	Closing Remarks

Sponsors: Department of Biostatistics, Harvard School of Public Health,
Department of Biostatistics and Computational Biology, Dana Farber Cancer Institute
National Cancer Institute
National Institute of Blood, Heart and Lung
Affymetrix Inc
Illumina Inc

Funding for this conference was made possible (in part) by a grant from the National Cancer Institute. The views expressed in written conference materials or publications and by the speakers and moderators do not necessarily reflect the official policies of the Department of Health and Human Services; nor does mention by trade names, commercial practices, or organizations imply endorsement the U.S. government.