

**Beyond HapMap: 3rd Annual International
Community Analysis Meeting**

**The Broad Institute of MIT and Harvard
May 8-10, 2006**

Schedule of Events

Lectures to be held in the Broad Institute Auditorium

Poster Displays - Broad Museum

Monday, May 8

7:30 a.m. – 9:00 a.m.

**Registration and Breakfast
(Breakfast provided in the Broad Museum)**

9 a.m. – 12 noon

Session 1

Introduction and Welcome – David Altshuler

Kelly Frazer

Update on HapMap: Phase I and II

Gil McVean

Update from the HapMap Analysis Group

Refreshment Break - Broad Museum

John Rioux

A high resolution HLA and SNP haplotype map for disease association studies in the extended human MHC

Jonathan Pritchard

A worldwide survey of haplotype variation in the human genome: Comparison to HapMap

Steven McCarroll

A genome-wide map of common human deletion polymorphisms

Manolis Dermitzakis

Interrogating functional variation in the ENCODE regions

12:30 p.m. – 1:30 p.m.

Conference Lunch - Broad Museum

1:30 p.m. – 5:00 p.m.

Session 2

Matthew Stephens

Finding (almost) all the SNPs in resequencing data

Molly Przeworski

How reliable are empirical genome scans for selective sweeps?

Benjamin Voight
A map of recent positive selection in the human genome

Michael Eberle
Linkage disequilibrium analysis reveals signatures of natural selection in the human genome

Refreshment Break - Broad Museum

Vincent Plagnol
Evidence for ancestral structure in human populations

Jim Mullikin
Unbiased inferences about human demographic history from HapMap data

Simon Myers
Sequence motifs for human recombination hotspots

5:30 p.m. – 7:30 p.m.

Poster Reception - Broad Museum

Tuesday, May 9

8:30 a.m. – 9 a.m.

Breakfast - Broad Museum

9 a.m. – 12 noon.

Session 3

Goncalo Abecasis
Efficient design and analysis of genome wide association studies

Nan Laird
Family-based designs in the age of gene-association studies

Stacey Gabriel
New genomic technologies for whole genome genotyping and directed re-sequencing

Refreshment Break - Broad Museum

Alkes Price
Practical solution for population stratification

Anders Albrechtsen
MCMC Based method for modeling higher-order non-linear gene-gene-environment interactions for multifactorial diseases using large-scale data

Mikkel Schierup
Whole genome association mapping by incompatibility

Dana Pe'er
Genetic variation and regulatory networks: Mechanisms and complexity

12:30 p.m. – 1:30 p.m.

Conference Lunch – Broad Museum

1:30 p.m. – 5:00 p.m.

Session 4

Aravinda Chakravarti

QT-interval genetics and the risk of sudden cardiac death

John Todd

More bottlenecks in disease gene discovery

Matt McQueen

Genome-wide association study of body mass index

Jason Cooper

A genome-wide association study of non-synonymous SNPs identifies a type1 diabetes locus at the interferon-induced helicase gene, IFIH1, region on chromosome 2p24.3

Refreshment Break - Broad Museum

Barbara Stranger

Genome-wide associations of gene expression variation in humans

Robert Graham

A common haplotype of interferon regulatory factor 5 (Irf5) bearing two functional non-coding variants is associated with risk to human lupus

Terreia Jones

Using CEPH cell lines to discover genomic variation associated with cancer drug phenotypes: Thiopurine methyltransferase vs. HapMap SNPs

5:30 p.m. – 7:30 p.m.

Reception Sponsored by Novartis Institutes for BioMedical Research

250 Massachusetts Avenue – Cambridge

(about a 5-minute walk from The Broad Institute)

Wednesday, May 10

8:30 a.m. – 9:00 a.m.

Breakfast – Broad Museum

9:00 a.m. – 12 noon

Session 5

Philip Awadala

Genome-wide SNPs and identification of candidate vaccine targets in the Plasmodium falciparum genome

Dyann Wirth

A haplotype map for plasmodium falciparum

Eleazar Eskin
Whole genome association in inbred mouse strains

Refreshment Break - Broad Museum

Evan Eichler
Genome structural variation among the HapMap samples

Christine Seidman
To be announced

Phil Reilly
To be announced

12 noon

Conference Adjourns