

Workshop IV: Coancestry, Association, and Population Genomics

Tuesday November 29, 2011

- 8:00–9:00 *Continental Breakfast*
- 9:00–9:05 *Welcome and Opening Remarks*
- 9:05–9:55 **Nick Patterson** (Massachusetts Institute of Technology)
New resources and methods for Human Population Genetics
- 9:55–10:20 *Break*
- 10:20–11:10 **Nilanjan Chatterjee** (National Cancer Institute)
A distribution theory for predictive- R^2 in high-dimensional models and its implications for genome-wide association studies
- 11:10–11:40 *Break*
- 11:40–12:30 **Daniel Geschwind** (University of California, Los Angeles (UCLA))
Genome-wide transcriptome profiling reveals the functional impact of rare de novo and recurrent CNVs in autism: implications for analysis of rare variants in sequence data
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:20 **Chiara Sabatti** (Stanford University)
Rare and common copy number variants in population isolates
- 3:30–4:15 *Break*
- 4:30–6:00 **Carlos Bustamante** (Stanford University)
Public Lecture: Interpreting Personal Genomes: Promises and Potential Pitfalls
- 6:00–7:30 *Poster Session & Reception (Hosted by IPAM)*

Wednesday November 30, 2011

- 8:00–9:00 *Continental Breakfast*
- 9:00–9:50 **Richard Durbin** (Sanger Institute)
Extensions of the PSMC model and more recent population structure
- 9:50–10:20 *Break*
- 10:20–11:10 **Eran Halperin** (Tel Aviv University)
Ancestry inference in individuals of mixed ancestry
- 11:10–11:40 *Break*

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- 11:40–12:30 **Kathryn Roeder** (Carnegie-Mellon University)
Estimating Heritability from Genetically Inferred Relationships: Treelets Probe Genetic Dark Matter
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:20 **Matthew Stephens** (University of Chicago)
Inferring effective relative migration surfaces from geographically-indexed large-scale genetic data
- 3:30–4:00 *Break*
- 4:00–4:50 **Yun Song** (University of California, Berkeley (UC Berkeley))
Efficient inference methods for large-scale population genomics

Thursday December 1, 2011

- 8:00–9:00 *Continental Breakfast*
- 9:00–9:50 **Alkes Price** (Harvard University)
- 9:50–10:20 *Break*
- 10:20–11:10 **Itsik Pe'er** (Columbia University)
Rapid and Powerful Genome-Wide Multi-locus Scan for Synergistic Effects in Case-Control Studies
- 11:10–11:40 *Break*
- 11:40–12:30 **Suzanne Leal** (Baylor College of Medicine)
Estimating Genetic Effects and Quantifying Missing Heritability for Complex Traits Due to Rare Variants
- 12:30–2:30 *Lunch (on your own)*
- 2:30–3:20 **Andrew Clark** (Cornell University)
Consequences of explosive population growth on tracts of Identity-by-Descent
- 3:30–4:00 *Break*
- 4:00–4:50 **Rasmus Nielsen** (University of California, Berkeley (UC Berkeley))
Population genetic analyses of new-generation sequencing data

Friday December 2, 2011

- 8:00–9:00 *Continental Breakfast*
- 9:00–9:50 **Montgomery Slatkin** (University of California, Berkeley (UC Berkeley))
The conditional site frequency spectrum and applications to ancient hominims
- 9:50–10:20 *Break*

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10:20–11:10 **Noah Rosenberg** (Stanford University)
Mathematical models of admixture

11:10–11:40 *Break*

11:40–12:30 **John Novembre** (University of California, Los Angeles (UCLA))
Ancestry inference in the era of population genomics

12:30–2:30 *Lunch (on your own)*

2:30–3:20 **Hongzhe Li** (University of Pennsylvania)
Optimal Sparse Segment Identification with Applications in Copy Number Variation Analysis

3:30–4:00 *Break*

4:00–4:50 **Iuliana Ionita** (Columbia University)
Statistical Methods for High-Throughput Genetic Studies and Applications

