

**Third RECOMB Satellite Workshop on
Computational Methods for SNPs and Haplotypes**

University of Southern California January 27-28, 2007
1050 Childs Way, MCB Bldg. Rm. 101, Los Angeles, CA 90089-0273

Agenda

Day-1

Saturday, January 27, 2007

<u>A.M.</u>	8:30-9:00	<i>Continental Breakfast</i>
	9:00-9:10	Introduction
	9:10-9:35	Andrew Clark <i>Association Testing with Phased Haplotypes vs. Unphased Diploypes</i>
	9:35-10:00	Carlos Bustamante <i>Bayesian Inference for Whole Genome Association Studies</i>
	10:00-10:25	Magnus Nordborg <i>Association Mapping in Arabidopsis</i>
	10:25-11:00	<i>Coffee Break</i>
	11:00-11:25	Hua Tang <i>Reconstructing Ancestry Blocks in Admixed Individuals Using High Density Genotype Data</i>
	11:25-11:50	Eran Halperin <i>Leveraging the HapMap Correlation Structure in Association Studies</i>
	11:50-12:15	Russell Schwartz <i>Near-Perfect Phylogenies and the Human Genome</i>
<u>P.M.</u>	12:15-2:00	<i>Lunch on your own</i>
	2:00-2:25	Kenneth Lange <i>Bayesian Gaussian Mixture Models for High Density Genotyping Arrays</i>
	2:25-2:50	Ting Chen <i>Sequence-based Prioritization of Nonsynonymous Single Nucleotide Polymorphisms for Study of Disease Mutations</i>
	2:50-3:15	Paul Marjoram <i>Fast 'Coalescent' Simulation (cont.)</i>

Day-1 (Cont.)
Saturday, January 27, 2007

<u>P.M.</u>	3:15-3:45	<i>Coffee Break</i>
	3:45-4:10	Justin Kennedy <i>Genotype Error Detection using Hidden Markov Models of Haplotype Diversity</i>
	4:10-4:35	Alexander Zelikovsky <i>Design and Validation of Methods Searching for Risk Factors in Genotype Case-Control Studies</i>
	4:35-5:00	Lakshmi K. Matukumalli <i>Simultaneous Prediction of multiple traits using Dense Genome-wide SNP Markers</i>
	5:00	Adjourn for First Day Workshop
	6:00	<u>Conference Dinner</u> for <u>Speakers and Committee Members Only.</u> ** **A USC shuttle service will be available. Pick up location will be outside the main entrance of the MCB bldg. on Parking Lot 6.

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Day-2

Sunday, January 28, 2007

<u>A.M.</u>	8:30-9:00	<i>Breakfast</i>
	9:00-9:25	Dan Gusfield <i>Progress on Combinatorial Haplotyping Algorithms</i>
	9:25-9:50	Weixiong Zhang <i>How Accurate is Pure Parsimony Haplotype Inference?</i>
	9:50-10:15	Steven Orzack <i>Exact and Algorithmic Methods for Haplotype Frequency Inferral: What do they tell us?</i>
	10:15-10:40	Yufeng Wu <i>Algorithms for Association: Mapping of Complex Diseases with Ancestral Recombination Graphs</i>
	10:40-11:00	<i>Coffee Break</i>
	11:00-11:25	Gad Kimmel <i>Evaluating Disease Significance in Genome Wide Association Studies</i>
	11:25-11:50	Vineet Bafna <i>Detecting Structural Variation in Normal Humans and Cancers</i>
	11:50-12:15	Jing Li <i>Prioritize and Select SNPs for Association Studies with Multi-stage Designs</i>
<u>P.M.</u>	12:15-12:40	Charles Kooperberg <i>Identifying Interactions in Genetic Association Studies</i>
	12:50	<u>End of the Workshop</u>
