



1st NHGRI-funded Conference: Haplotype Analysis of Population & Pedigree Data in Association Studies

Wed 5/7/2008

Meeting Room - Heritage 2

<u>Time</u>	<u>Topic</u>	<u>Speaker</u>
08:00 - 08:30 AM	Registration	
08:30 - 08:45 AM	Welcome and Introduction	<i>Kui Zhang, Ph.D. & David B. Allison, Ph.D., UAB</i>
Session I: Haplotype Inference from Unrelated Individuals		
08:45 - 08:50 AM	Overview by Moderator	<i>José R Fernández, Ph.D., UAB</i>
08:50 - 09:25 AM	Statistical methods for large-scale population genotype data and their application to haplotype inference	<i>Matthew Stephens, Ph.D., Chicago University</i>
09:25 - 10:00 AM	Haplotype analysis in the presence of informatively missing genotype data	<i>Nianjun Liu, UAB</i>
10:00 - 10:15 AM	BREAK	
10:15 - 10:50 AM	Bayesian methods for haplotype inference from unrelated individuals	<i>Zhaohui Qin, Ph.D., University of Michigan</i>
10:50 - 11:30 AM	Panel and Discussion moderated by	<i>David B. Allison, Ph.D., UAB</i>
11:30 - 1:30 PM	LUNCH	
Session II: Haplotype-based Association Methods from Unrelated Individuals		
1:30 - 1:35 PM	Overview by Moderator	<i>Rui Feng, Ph.D., UAB</i>
1:35 - 2:10 PM	Likelihood-Based Inferences on Haplotype-Disease Associations, with Applications to Untyped SNPs	<i>Danyu Lin, Ph.D., University of North Carolina at Chapel Hill</i>
2:10 - 2:45 PM	Tree- and forest-based genomewide association analysis	<i>Heping Zhang, Ph.D., Yale University</i>
2:45 - 3:00 PM	BREAK	
3:00 - 3:35 PM	A gene-trait similarity regression for haplotype analysis in genome-wide association studies	<i>Jung-Ying Tzeng, Ph.D., North Carolina State University</i>
3:35 - 4:10 PM	Haplotype sharing for genome-wide case-control association studies	<i>Glen Satten, Ph.D., Center for Disease Control</i>
4:10 - 4:50 PM	Panel and Discussion moderated by	<i>Guimin Gao, UAB</i>
5:30 - 7:00 PM	DINNER	Meeting Room Centennial 1 & 2
7:00 - 9:00 PM	Debate Session: Is the haplotype analysis critical in genome wide association studies?	Con: <i>Derek Gordon, Ph.D., Rutgers University</i> Pro: <i>Daniel Schaid, Ph.D., Mayo Clinic</i> Provocateur: <i>Michael Province, Ph.D., Washington University St. Louis</i>

Conference Website: <http://www.soph.uab.edu/ssg/default.aspx?id=1940>





Thu 5/8/2008

Meeting Room - Heritage 2

<u>Time</u>	<u>Topic</u>	<u>Speaker</u>
Session III: Haplotype Inference for Pedigrees		
08:30 - 08:35 AM	Overview by Moderator	<i>Guimin Gao, Ph.D., UAB</i>
08:35 - 09:10 AM	Challenges for haplotype inference from large pedigrees	<i>Jeffrey O'Connell, Ph.D., University of Maryland</i>
09:10 - 09:45 AM	Computational methods for haplotype inference from general pedigrees	<i>Jing Li, Ph.D., Case Western Reserve University</i>
9:45 - 10:15 AM	BREAK	
10:15 - 10:50 AM	Statistical methods for haplotype inference from general pedigrees	<i>Kui Zhang, Ph.D., University of Alabama at Birmingham</i>
10:50 - 11:30 AM	Panel and Discussion by moderator	<i>Hemant Tiwari, Ph.D., UAB</i>
11:30 - 1:30 PM	LUNCH	
Session IV: Haplotype-based Association Methods		
1:30 - 1:35 PM	Overview by Moderator	<i>Nianjun Liu, Ph.D., UAB</i>
1:35 - 2:10 PM	An incomplete-data quasi-likelihood approach to case-Control haplotype association studies with related individuals	<i>Mary Sara McPeck, Ph.D., The University of Chicago</i>
2:10 - 2:45 PM	The performance of imputation methods for haplotype analysis in large pedigrees	<i>Tasha Fingerlin, Ph.D., University of Colorado at Denver</i>
2:45 - 3:00 PM	BREAK	
3:00 - 3:35 PM	Fast and efficient tests of association for untyped markers in case-control studies	<i>Michael Epstein, Ph.D., Emory University</i>
3:35 - 4:15 PM	Panel and Discussion by moderator	<i>Kui Zhang, Ph.D., UAB</i>
4:15 PM	Adjourn	

Organizing Committee

Drs Kui Zhang (UAB) - David Allison (UAB) - Hemant Tiwari (UAB) - Jung-Ying Tzeng (NC State)

We would like to thank our sponsors for their support:

National Human Genome Research Institute



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