

IMS Mini-Meeting Report

IMS sponsored mini-conference on Comparative Genomics

Hemant K Tiwari and David B. Allison, of the Section on Statistical Genetics, Department of Biostatistics at the University of Alabama, Birmingham, write:

The IMS-sponsored mini-conference on "Statistical Integration of Genetic Information across Data Domains: Biomedical, Agricultural and Comparative Genomics" was held on 2 December, 2002 at University of Alabama at Birmingham. The conference was a great success, according to participants' feedback and evaluations. The participants were from such diverse backgrounds as genetics, pathology, clinical research, biostatistics, agriculture and animal research. We had several participants from Auburn University and from the Centers for Disease Control and Prevention (CDC) in Atlanta. The event was videotaped and will be available on our website as soon as processing is complete (www.soph.uab.edu/Statgenetics/Events/IMS/IMSConf.htm). The event was covered by the local broadcast and print media (e.g., see: www.soph.uab.edu/Statgenetics/Events/IMS/haley-post.htm). Presentation topics included QTL across studies and designs (Dr Chris Haley); Comparative genomics of Diabetes (Dr Philip Wood); Incorporation of gene information for conducting meta-analysis (Dr Carol Etzel); Integrating QTL mapping data across species (Dr David Allison); Mapping epistatic genes for complex traits (Dr Nengjun Yi); and Combined microarray and linkage studies (Dr Grier Page).

Morning session started with the opening remarks given by Dr Philip Wood, Professor of Genetics, University of Alabama, Birmingham. He discussed the genetics of type 2 diabetes mellitus which is on the rise world-wide. He described effective genomic approaches to understand the genetic components and pathogenesis of

type 2 diabetes using murine models.

The keynote speaker, Dr Chris Haley, Head of the Department of Genetics and Biometry at Roslin Institute, Edinburgh, is a leading expert on statistical methods for the detection, mapping and utilization of quantitative trait loci and applications of genomics studies in the area of fatness, meat quality and reproduction in pigs. He addressed the identification of loci controlling variation in complex traits, particularly quantitative trait loci. He pointed out complexities such as parent of origin effects and epistatic interactions, in localizing QTLs in pigs and elaborated on how the lessons learned from livestock research can help in understanding the complex traits in human populations.

Dr Carol J. Etzel, Department of Epidemiology, UT M.D Anderson Cancer Center, Houston, gave a talk on meta-analysis for human linkage analysis. She discussed the challenges in meta-analysis of genetic studies due to publication bias, time-lag bias, different phenotypic measures and among-study heterogeneity.

The afternoon session started with Dr David Allison, Head of the Section on Statistical Genetics, Department of Biostatistics, University of Alabama at Birmingham, giving a presentation on the importance of comparative genomics. He emphasized how empirical Bayes methods can help to localize disease susceptibility loci or traits by using available information about homology between genomes of different species such as human, mouse, pig, rat, drosophilae, etc.

Dr Nengjun Yi, Section on Statistical Genetics, Department of Biostatistics, University of Alabama at Birmingham,

talked about statistical modeling of interaction effects in QTLs using the Bayesian approach. He showed utility and performance of his new method using reversible jump Markov Chain Monte Carlo algorithm to determine the number of QTLs and their significant effects by simulation studies.

The last speaker of the event was Dr Grier Page, Section on Statistical Genetics, Department of Biostatistics, University of Alabama at Birmingham. He discussed how microarray analysis and linkage analysis of genomic regions could be incorporated to identify disease susceptibility genes.

For more conference information, including a list of speakers, the slides of the talks and synchronized video feed, see www.soph.uab.edu/Statgenetics/Events/IMS/IMSConf.htm.

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