

HSPH Mini-Course on Computational Tools and Statistical Methods for SNPs

Course Organizers: Drs. Tianhua Niu and Peter Kraft
Sponsored by: HSPH Bioinformatics Core

Syllabus

Sites in the DNA sequences where two homologous chromosomes differ at a single DNA base are called single nucleotide polymorphisms (SNPs). The human genome contains at least 10 million SNPs, making them the most abundant genetic “lampposts” for pinpointing causal variants underlying human diseases. With the releases of the high-density Phase I and Phase II Human HapMaps, along with the fast-pacing advancements of the state-of-the-art ultra-high-throughput genotyping technologies such as the Affymetrix 500K SNP arrays, daunting statistical and computational challenges have been posed regarding how to intelligently extract maximal information from the vast amount of data generated in both family- and non-family based genetic studies. The objective of this mini-course is to bring together distinguished, world-class speakers on SNPs to share their valuable insights, expertise, as well as cutting-edge results. In particular, emphases are given for the following five key topics: (1) SNP-Related Experimental Designs and Computational Tools, (2) Tagging SNPs and Haplotypes; (3) SNP-based Whole Genome Linkage Studies, (4) Human HapMap and Whole Genome Association Studies, and (5) SNP Applications in Copy Number Analysis and Loss-Of-Heterozygosity. This mini-course will not only offer an in-depth coverage of the contemporary tools and methods used for SNP analysis, but also will provide a vibrant forum in discussing how to best utilize these avant-garde approaches to improve the experimental designs based on SNPs and to attain the most optimal statistical power in genetic linkage/association studies.

Mini Course Schedule (May 5, 2006 – June 2, 2006)

Location: HSPH Kresge Building, Room G2

Friday, May 5, 2006

1:30PM-3:00PM

Lecture 1. Contemporary Computational Tools and SNP Databases
SPEAKER: Isaac Kohane (Children's Hospital)

3:15PM-4:45PM

Lecture 2. Issues in Large-Scale SNP-based Experimental Designs
SPEAKER: Tianhua Niu (BWH/HSPH)

Friday, May 12, 2006

1:30PM-3:00PM

Lecture 3. "SNP Browser" program (ABI)
SPEAKER: Chris Read (ABI)

Friday, May 19, 2006

1:30PM-3:00PM

Lecture 4. Tagging SNP Selection Methods for Genetic Studies
SPEAKER: Mark Daly (MGH/Broad Institute)

3:15PM-4:45PM

Lecture 5. Efficiency and Power Comparisons for SNP-based vs. Haplotype-based Analytic Strategies
SPEAKER: Paul de Bakker (MGH/Broad Institute)

Friday, May 26, 2006* [*Location: Kresge LL-6]

1:30PM-3:00PM

Lecture 6. Whole-Genome Admixture Scan
SPEAKER: David Reich (HMS)

3:15PM-4:45PM

Lecture 7. Analysis of Copy Number Analysis and Loss-Of-Heterozygosity Using Affymetrix SNP Arrays
SPEAKER: Cheng Li (DFCI)

Friday, June 2, 2006

1:30PM-3:00PM

Lecture 8. Whole Genome Association Studies in Case-Control Setting
SPEAKER: Peter Kraft (HSPH)

3:15PM-4:45PM

Lecture 9. Whole Genome Association Studies in Family-based Setting
SPEAKER: Christoph Lange (Channing/HSPH)