

THE UNIVERSITY



OF HONG KONG

Department of Mathematics

Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

Single-Nucleotide Polymorphisms, Linkage Disequilibrium and LD Maps Constructed with Constrained Unidimensional Scaling

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on Wednesday, November 23, 2005 at 2:00p.m.
in Room 517, Meng Wah Complex

Abstract

In this talk, I will introduce the study with the Single-Nucleotide Polymorphisms (SNPs). And the linkage disequilibrium (LD) and LD maps are discussed, including their importance in the genomic studies. The final part is the introduction of our formulation with the constrained unidimensional scaling model, where the objects are required to place in a given order on the real line, for the LD maps. Here, quadratic programming procedure is considered to solve this problem. The application to linkage disequilibrium (LD) maps for human genome is presented. We will also give some concluding remarks.

All are welcome
