THE UNIVERSITY　　　　**OF HONG KONG**

Department of Mathematics

Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

CLUSTAG & WCLUSTAG:
Hierarchical Clustering and Graph Algorithms for Tag-SNP Selection

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on Thursday, November 9, 2006 at 2:30p.m.
in Room 309, Run Run Shaw Building, HKU

Abstract

More than six million single nucleotide polymorphisms (SNPs) in the human genome have been genotyped by the HapMap project by the end of July 2006. Although only a proportion of these SNPs are functional, all can be considered as candidate markers for indirect association studies to detect disease-related genetic variants. The complete screening of a gene or a chromosomal region is nevertheless an expensive undertaking for association studies. A key strategy for improving the efficiency of association studies is to select a subset of informative SNPs, called tag SNPs, for analysis. In this talk, our works CLUSTAG and WCLUSTAG on this subject will be described.

All are welcome