

THE UNIVERSITY



OF HONG KONG

Department of Mathematics

## Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

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### A Recursive Method for Solving Haplotype Frequencies in Multiple Loci Linkage Analysis

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on Wednesday, January 25, 2006 at 2:30p.m.  
in Room 517, Meng Wah Complex

#### Abstract

Multiple loci analysis has become popular with the advanced development in biological experiments. A lot of studies have been focused on the biological and the statistical properties of such multiple loci analysis. In this talk, we study one of the important computational problems: solving the probabilities of haplotype classes from a large linear system  $Ax = b$  derived from the recombination events in multiple loci analysis. Since the size of the recombination matrix  $A$  increases exponentially with respect to the number of loci, fast solvers are required to deal with a large number of loci in the analysis. By exploiting the nice structure of the matrix  $A$ , we develop an efficient recursive algorithm for solving such structured linear systems. In particular, the complexity of the proposed algorithm is of  $O(m \log m)$  operations and the memory requirement is of  $O(m)$  locations where  $m$  is the size of the matrix  $A$ . Numerical examples are given to demonstrate the effectiveness of our efficient solver.

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*All are welcome*

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