

# A Haplotyping Algorithm for Non-Recombinant Pedigree Data Containing Missing Members

Doan Dai Duong and Patricia A. Evans

Faculty of Computer Science

University of New Brunswick, Fredericton, NB, Canada

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## Abstract

The development of a computational method for inferring haplotypes from genotypes (haplotyping problem) has received much attention. We propose an  $O(nm^3)$  time algorithm for the haplotyping problem for non-recombination pedigree data containing missing members, which improves on the best prior work by a factor of  $n^2$ . This algorithm uses the Mendelian laws of inheritance to infer all recoverable haplotypes and missing members. This algorithm has also been tested on simulated data and the results show that it can recover most missing members as well as infer haplotypes for all members very quickly.