

# **“Rapid Computation of Allele Sharing in Large, Complex Pedigrees”**

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## **Abstract**

Linkage mapping on large pedigrees is typically more powerful than mapping on smaller pedigrees, given a fixed sample size, yet there are few methods for performing such analyses. Here, I present a single-point method for computing the probability of pairs of alleles being IBD at a locus. The method can use a pedigree of essentially arbitrary size and complexity, unbroken, and all the genotype data at that locus. I will describe the method used for computing this probability as well as a novel algorithm for determining the condensed identity coefficients for pairs of individuals in the pedigree, an essential ingredient in the efficacy of the method. I will also discuss possible applications of the method as well as its use on a complex 3,028 person pedigree comprising 13 generations.