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Extracting information from genotype data of closely related individuals. Preliminary report.

Extracting information from dense genotype data to discover regions shared between relatives is a powerful technique to discover genes that give predispositions to a given disease. The problem offers different computational and statistical challenges from the modeling of errors of genotype data to the combinatorial analysis of the pedigree describing the relationship among the individuals that have been genotyped. Different algorithms have been developed, some of which are though impractical since their running time grows exponentially in the size of the pedigree of the individuals. A new algorithm, approximate but robust, is described. The idea behind the algorithm is to loose some of the constraints and perform a sort of gradient descent to extract statistical information in a practical way. (Received September 16, 2008)