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Estimating Relatedness Using Markov Chain Monte Carlo Techniques.

The degree of genetic relatedness between two individuals can be described using a set of three parameters that indicate the probabilities that, at a random chromosomal location, the pair will share 0, 1, or 2 pairs of genetic variants identical by descent from a common ancestor. The estimation of these parameters has a variety of applications including forensics, human disease mapping and plant/animal breeding. Previous studies have developed relatedness estimators for subpopulations that have diverged from a population for which population allele frequencies are known, but require that the user specify a value that gives the degree of divergence. We developed an estimator that considers the degree of divergence to be an unknown parameter to be jointly estimated with the relatedness parameters. Our goal was to estimate how related two individuals from a common subpopulation are and how far this subpopulation has diverged from an original population. (Received September 16, 2008)