ESTIMATING THE DOMINANCE RELATIONSHIP MATRIX USING A SIMULATION APPROACH

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For a given trait, dominance genetic effects result from the joint action of pairs of alleles at a locus. Related individuals may have these pair of alleles in common through shared ancestry, and a dominance relationship matrix (D) that represents the probability that individuals share the same pair of alleles by descent can be constructed. This D matrix can be used in the analysis, together with the additive relationship matrix (A), to further partition total genetic effects. The dominance matrix D can be very difficult to construct using direct methods, and a monte-carlo simulation approach has been implemented to approximate D. This method repeatedly traverses the pedigree, sampling two genes for each individual (one from each parent). The sampled genes of all individuals are examined pair wise and the counts of events contributing to each of 15 identity states accumulated. For inbred individuals, the genes are sampled with replacement f times, where f is the filial generation. A number of relationship matrices, including A and D, can be calculated from these identity states.

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