



Rationale for estimating genealogical coancestry from molecular markers

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Rationale for estimating genealogical coancestry from molecular markers

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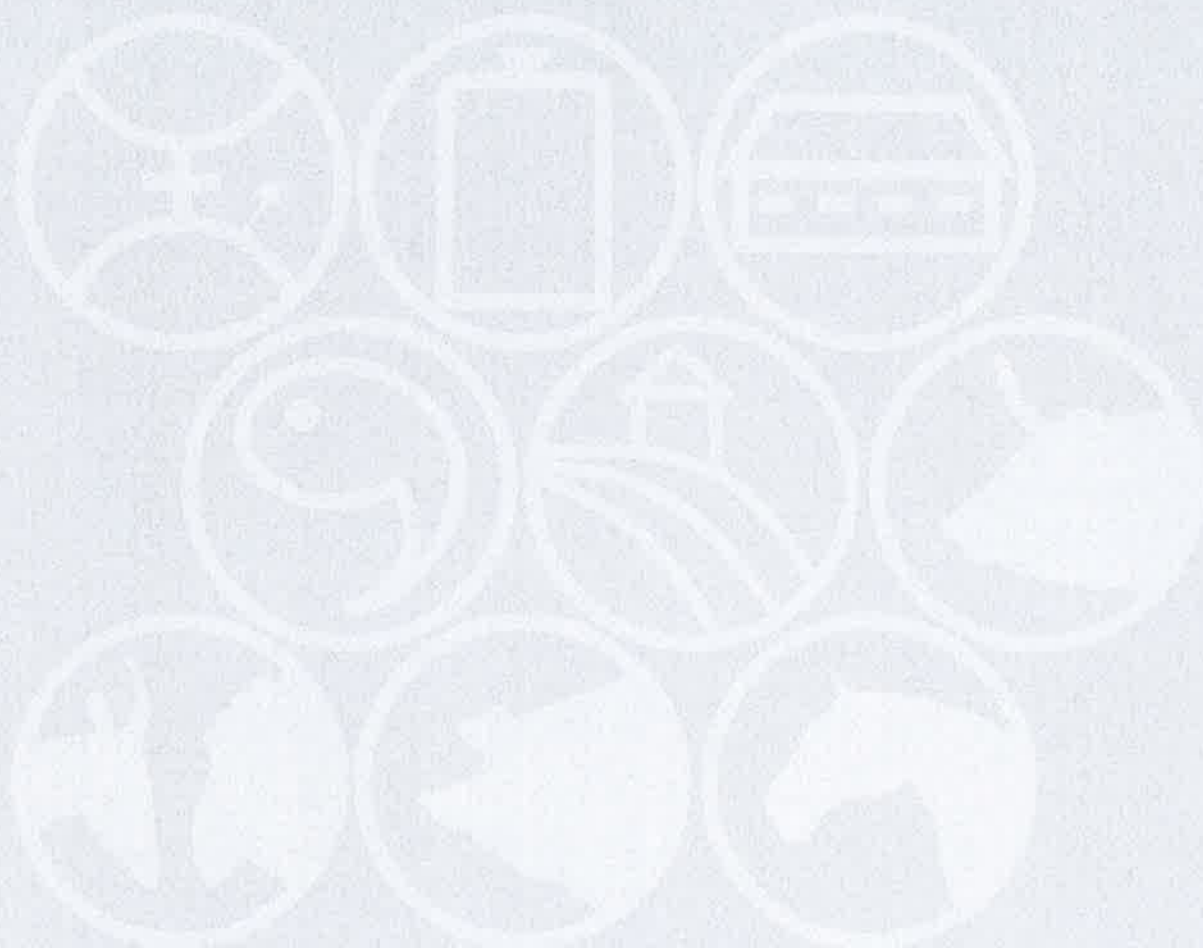
Genetic relatedness or similarity between individuals is a key concept in population, quantitative and conservation genetics. When a genealogy is available, genetic relatedness between individuals is measured by the coancestry coefficient that assumes a founder population where genealogy starts. With molecular markers there are two basic ways of calculating empirically the genetic similarity between individuals: the molecular coancestry and the molecular covariance. Here we derive the expected values of these empirical measures of similarity as a function of the genealogical coancestry if the individuals are linked by genealogical pathways. From these formulas it is easy to derive estimators of genealogical coancestry from molecular data. However, the estimators are severely biased if the distribution of gene frequencies in the founder population is unknown. This is illustrated with some simulation examples. A real data example in dairy cattle is also shown. Estimators of genealogical coancestry from molecular data are easy to derive. If gene frequencies in the founder population are unknown some consequences and alternatives of this limitation are briefly discussed.

Mapping of calving traits in dairy cattle using a genealogy-based mixed model approach

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Among the existing methods for genome-wide association mapping, tree-based association mapping methods show obvious advantages over single marker-based and haplotype-based methods because they incorporate information about the evolutionary history (genealogy) of the genome in the analysis. Local genealogies are genealogies for the longest chromosome region around a marker that do not require recurrent mutation or recombination. We have developed a genealogy-based mixed model (GENMIX) for association mapping for quantitative traits in population with complex pedigree. Using simulated data, we have shown that GENMIX has more power compared to linear mixed model approach in association mapping. We apply the method to map QTL for calving traits in the Danish, Swedish and Finnish Holstein cattle population. The data analyzed included 4,258 AI bulls. Genotypes were obtained with the Illumina BovineSNP50 panel. A total of 38,545 informative, high-quality SNP markers were used for the association analysis. The traits analyzed were calving ease, calf size and stillbirth. Additionally, two combined indices, birth index and calving index, were analyzed. The chromosomal regions harbouring QTL for these calving traits were identified.

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