Computing procedures for genetic evaluation including phenotypic, full pedigree and genomic information.

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Currently the genomic evaluations use multiple step procedures, which are prone to biases and errors. A single step procedure may be applicable when genomic predictions can be obtained by modifying the numerator relationship matrix A to H=A+Δ, where Δ includes deviations from original relationships. To avoid computing inv(H), mixed model equations due to the additive effect, say [Z'X Z'Z+ k inv(H)] can be expressed in an alternate Henderson form as [H Z'X H Z'Z+ Ik]. The modified equations have a nonsymmetric left-hand side where H may be poorly conditioned numerically. When those equations are solved by the conjugate gradient techniques, the only computations involving H are in the form of Aq or Δq, where q is a vector; the product Aq can be calculated efficiently in linear time using Colleau's indirect algorithm. Several alternative H are possible. One is to substitute the relationships of genotyped animals with the genomic relationship matrix. Another one is derived by conditioning the genetic value of ungenotyped animals on the genetic value of genotyped animals. Comparisons involved the regular equations and the modified equations with simulated Δ. Solutions were obtained by the Preconditioned Conjugate Gradient, which only works with symmetric matrices, and by Bi-Conjugate Gradient Stabilized, which works with nonsymmetric matrices. The convergence rate associated with the nonsymmetric solver was slightly better than that with the symmetric solver for the original equations, although the time per round was twice as high. The convergence rate associated with the modified equations was similar to that with the regular one for the nonsymmetric solver. When computation of terms with Δ can be done efficiently, it may be possible to modify the existing evaluation to incorporate the genomic information at approximately double the cost of the original evaluation.

How to combine pedigree and marker information into a single estimator for the calculation of relationships?

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Relationship coefficients are particularly useful to improve genetic management of endangered populations. These coefficients are traditionally based on pedigree data. In case of incomplete or missing pedigree, they are replaced by coefficients calculated from molecular data when this information is available. However, genotyping a complete population for a sufficient number of markers can be impossible. The main objective of this study was therefore to develop a new method to estimate relationship by combining molecular with pedigree data. It will be useful for specific situations, where neither pedigree nor molecular data are complete. In a companion paper, the compatible coefficients were determined. In this study, based on simulations of pedigree and marker data, the method to combine the selected coefficients was determined. Various parameters were taken into account in the model: number and quality of the marker (e.g. marker informativeness), mutation rate, quality of the pedigree (e.g. generation-equivalents), ... The combined estimator has several advantages. Especially, negative relationship values obtained in literature with molecular-based estimators in case of small inbred populations can be avoided. In conclusion, if this combined estimator was originally developed for the management of an endangered horse population, it should also be a promising alternative to traditionally used estimators, e.g. for the management of small and/or rare breeds; especially in case of inbred populations, with both incomplete pedigree and partial molecular information.

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