

Simultaneous validation of variance component estimation and BLUP software

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The prediction of breeding values depends on reliable estimation of variance components. With knowledge of variance components the breeding value prediction via mixed-model equations (BLUP) requires the solution of linear systems, only. Variance component estimation, on the other hand, is a more complex task leading to nonlinear minimization problems that have to be solved by iterative numerical algorithms. In order to evaluate the reliability of these algorithms benchmark problems have to be constructed where the exact solution is a priori known. We develop techniques to construct such benchmark problems for mixed models including fixed and random effects, 1-way and 2-way classification, ML and REML predictors. Besides the construction of artificial data that produce the desired variance components we describe a projection method to construct benchmark data from simulated data.

Genetic heterogeneity of environmental variance: estimation of variance components using double hierarchical generalized linear models

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Previous studies have shown that environmental sensitivity (i.e. the capability of an animal to adapt to changes in the environment) may be under genetic control, which is essential to take into account if we wish to breed robust farm animals. Linear mixed models including a genetic effect explaining heterogeneity of the environmental variance have previously been used and parameters estimated using EM and MCMC algorithms. We propose the use of double hierarchical generalized linear models (DHGLM), where the squared residuals are assumed to be gamma distributed and the residual variance is fitted using a generalized linear model (GLM). The algorithm iterates between two sets of mixed model equations (MME), one on the level of observations and one on the level of variances. We show by means of simulations that the variance of the random genetic effects in the model for residual variances can be accurately estimated using DHGLM in a population of 10,000 individuals (10 sires with each 1,000 offspring). For each animal, an observation was generated as the sum of a fixed effect (2 levels), a random genetic effect (u) and a random residual. The residual effect was sampled from $N(0, \phi)$, where $\log(\phi)$ was generated as the sum of a fixed effect (2 levels) and a random genetic effect (g). Both genetic effects (u and g) were negatively correlated and sampled from a multivariate normal distribution. We replicated the simulation 20 times and obtained estimates of variance components using DHGLM. The estimated variance components were empirically unbiased (albeit with quite large SE due to the low number of sires). An advantage of DHGLM is that the calculations are based on MME and sparse matrix techniques developed for other MME-based algorithms are possible to utilize. GLM theory provides model checking tools for DHGLM and the h-likelihood gives model selection criteria.