

DEVELOPMENTS IN UTILIZING PEDIGREES IN GENETIC ANALYSIS WITHIN ASREML

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SUMMARY

This paper outlines some developments in the fitting of genetic models in ASReML. We consider use of genetic groups, partial selfing in open pollinated tree species, the use of a Reduced Animal Model and QTL detection.

Keywords: genetic groups, IBD, QTL, reduced animal model

INTRODUCTION

ASReML (Gilmour *et al.* 2002) is widely used for estimating variance components in genetic models and less widely used for BLUP analysis. The most common genetic model is for the estimation of additive genetic variance in pedigreed populations, possibly including environmental and maternal variances. In this case each individual receives half of its genetic material from each parent and its inbreeding coefficient is half the genetic relationship between its parents. Variations on this theme include maternal grandsire models, partial selfing, inbred populations, use of the reduced animal model (RAM) in the BLUP context and situations where the base animals represent distinct genetic groups. Release 2 of ASReML (Gilmour *et al.* 2005) has improved facility in these areas.

ASReML can handle the more general problem of non-standard relationships in that it allows the user to supply the relationship matrix to be used or its inverse. This is suitable when examining epistatic and dominance effects. Another application is where we desire to identify quantitative trait loci (QTL) for inbred and outbred populations. Several methods are available for backcross and F2 populations derived from inbred populations (Gianola 2003). Most require fitting a sequence of models to examine the likelihood surface. A new mixed model approach for such cases and based on the simultaneous fitting of random marker covariates is available in ASReML (Gilmour 2004a). For outbred populations, we need an identity by descent (IBD) matrix for each marker locus. Such matrices are derived in various ways (outside ASReML, see Seaton *et al.* 2002) and used in a mixed model to detect whether there is evidence for segregating QTL.

The usual relationship matrix is formed recursively (Henderson 1976; Mrode 1998). It is initialized typically by assuming base animals are unrelated. The values for each progeny are given using $\mathbf{a}_p = [(\mathbf{a}_s + \mathbf{a}_d)/2, 1+f_p]$ where \mathbf{a}_s and \mathbf{a}_d are the sire and dam rows of the existing relationship matrix, \mathbf{a}_p is the new row being defined and $f_p = a_{sd}/2$ is the inbreeding coefficient where a_{sd} is the relationship between the parents. It turns out that the inverse of this matrix is sparser than the matrix itself and as easy to form recursively. However, there are some special cases which we now consider.