

RECENT ADVANCES IN GENETIC PARAMETER ESTIMATION

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INTRODUCTION

The Average Information (AI) algorithm for obtaining REML estimates of variance components (Johnson and Thompson, 1995, and Gilmour et al. 1995) has been implemented in programs for the estimation of multivariate genetic parameters developed by Johnson (Johnson and Thompson, 1994) and by Madsen (Madsen et al. 1994).

A feature of this algorithm is that, with efficient implementation, it provides a derivative based update to the solutions in about the same time as is required for an EM algorithm update which is two to three times that taken for a single likelihood evaluation (Gilmour et al. 1995). The poster will provide information on the algorithm and the scope of AIREML programs developed by Gilmour, Johnson and Madsen. Some of the programs will be available for demonstration.

SCOPE OF SOME AIREML PROGRAMS

Gilmour has a univariate general purpose REML program using the AI algorithm. The program accommodates a variety of fixed and random factors including random interactions involving factors and covariates. It allows for direct and maternal genetic effects as well as permanent environment and litter effects. This routine will form the basis for a new REML procedure in the GENSTAT package. The largest model fitted to date involved 66,000 effects. Application on binary data will be demonstrated.

Dave Johnson has developed a suite of programs (AIPRE, AIUNI, AIEQ1 and AIMUL) similar in concept and use to the DFREML programs. The sparse matrix package FSPAK forms the basis of the matrix calculations.

AIPRE reads the data, sets up the equations and determines the order of solution.

AIUNI performs univariate analysis for an individual animal model including correlated direct and maternal effects, a second animal effect and/or an additional uncorrelated random effect.

AIEQ1 performs multivariate analysis for an individual animal model. It uses canonical decomposition so requires equal designs for all traits.

AIMUL performs general multivariate analysis for an individual animal model allowing for missing observations and for trait specific models.

REFERENCES

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