METHODS OF ACCOUNTING FOR MATERNAL EFFECTS IN THE ESTIMATION AND PREDICTION OF GENETIC PARAMETERS

A thesis presented in partial fulfilment
of the requirements for the degree of
Doctor of Philosophy
at Massey University

Goluhewage Sirimathie Wewala

1984

ABSTRACT

Maximum likelihood techniques for estimating variance components have desirable features. Nevertheless, the use of maximum likelihood methods for estimating variance components from unbalanced data is difficult. Moreover, additional complications arise in the context of maternal effects models. In this thesis, procedures for generating maximum likelihood estimates of variance components in a maternal effects model are derived for the case of unbalanced data. A hierarchical design where by each sire is mated to several dams is used, there being observations on parents and offspring. The special structure of the data together with the assumption that the sires and the dams are unrelated is exploited in order to obtain explicit expressions for the inverse and the determinant of the variance-covariance matrix of the observations, which arises in the likelihood function and the partial derivatives thereof. Algorithms are proposed to generate the likelihood function and its partial derivatives which are required for constrained and unconstrained optimization of the function. As an illustration, the procedures are applied to weaning weight data of sheep and 8-week weights of pigs. The procedures are extended to estimate variance components in a multiple-trait setting.

Provided the relevant genetic variances and covariances are known, best linear unbiased prediction techniques can be used to predict direct and maternal genetic values. Predicting direct and maternal genetic values of all animals is not difficult since this is a special case of a multiple-trait evaluation. However, if the objective is to eliminate the influence of the maternal effect so that selection is for direct genetic merit, predictions are required for the direct genetic values of all animals of interest and the maternal genetic values of just their dams. Although no analysis is carried out using actual data, best linear unbiased prediction equations for predicting direct genetic values of all animals and the maternal genetic values of their dams are derived.

In the process, the rapid method of inverting the relationship matrix is modified to enable the inversion of the variance-covariance matrix of the genetic effects. The requirements that have to be satisfied in order to generate the correct inverse are given.

ACKNOWLEDGEMENTS

The author is especially grateful to Professor R.D. Anderson and Professor A.L. Rae for the invaluable guidance and supervision given to her during this study.

Sincere thanks are due to Dr. R.J. Brook and Professor B.I. Hayman for their advice and encouragement.

Particular thanks are due to Dr. G.A. Wickham for his suggestions in certain aspects of the thesis, Dr. S.J. Byrne for her advice in using the optimization routines and Dr. W.C. Smith and Mr. R. Laird for providing the pig data.

The author appreciates the financial assistance given to her through the Helen E. Akers Scholarship, the Farmers Union Scholarship and G.O. Anstiss Scholarship.

Finally, very special thanks are due to her husband and her parents for their support and encouragement.

TABLE OF CONTENTS

LIST OF TABLES