### A COMPUTATIONALLY EFFICIENT TRANSFORMATION OF THE MIXED MODEL EQUATIONS FOR MULTIPLE TRAIT MODELS

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## **INTRODUCTION**

The use of BLUP methods for the evaluation of livestock is now widespread amongst countries and species. Multiple trait animal models are commonly used (e.g. BREEDPLAN, PIGBLUP). These models incorporate all the available information on performance and pedigree and by including the criteria for selection in the analysis can avoid potential biases that may result if they are omitted. (Sorensen and Kennedy, 1984).

Although there are relatively few non-zero elements in the coefficient matrix of the mixed model equations (MME) BLUP methods require large quantities of computing resources: time, random access memory and disk storage. The requirement for resources is proportional to the numbers of animals in the analysis and the square of the number of traits. Until recently there has been little research into development of computationally efficient algorithms for use with multiple trait animal models. Schaeffer and Kennedy (1986) suggest how their method of 'iterating on the data' described for a single trait model can be adapted for use with a multiple trait model. Tier and Graser (1991) describe an implicit representation of the MME which reduces the requirement for memory, disk storage and time. A partial factoring out of some common terms enabled them to achieve a significant reduction in the amount of computations required per iteration. This paper describes a simple transformation to the MME which reduces the demand for resources to an almost linear function of the number of animals and traits.

#### MODELS

Consider the simple model y = XB + Zu + e, where y is a vector of observations, b is a vector of fixed effects, u and e are vectors of breeding values and residuals respectively and X and Z are (known) incidence matrices assigning observations (y) to effects (b, u and e).

The MME for this model are:

X'R <sup>-1</sup> X	X'R <sup>-1</sup> Z	]	Γ	ĥ	]	<b>X</b> ' <b>R</b> <sup>-1</sup> <b>y</b>	]
 Z'R <sup>-1</sup> X	Z'R <sup>-1</sup> Z+A <sup>-1</sup> *G <sup>-1</sup>			^ u	]=	<b>Z</b> ' <b>R</b> <sup>-1</sup> <b>y</b>	

Where  $\mathbf{R}$  is a matrix of (co)variances between residuals, commonly assumed to be (block) diagonal for (multiple) single trait models,  $\mathbf{A}$  is the numerator relationship matrix and  $\mathbf{G}$  is a matrix of (co)variances between traits.

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For single trait models **R** is assumed to be  $I\sigma_e^2$  and **G** is a scalar ( $\sigma_a^2$ ). For multiple trait models with t traits **R** is assumed to be block diagonal and **G** is a square (txt) matrix.

The structure of these equations for multiple trait animal models, in terms of their non-zero elements, is described in detail by Tier and Graser (1991). Each animal with some observations gives rise to a set of square (txt) blocks in each partition. These blocks are identical and in the absence of maternal effects the matrix  $Z'R^{-1}Z$  is block diagonal. Blocks are accumulated in the partition  $X'R^{-1}X$  but remain independent in the partitions  $X'R^{-1}Z$  and  $Z'R^{-1}X$ . Off-diagonal blocks in the partition  $(Z'R^{-1}Z + A^{-1}*G^{-1})$  arise from elements in  $A^{-1}$  which only occur between mates, and between parents and offspring. When repeated and parent-offspring matings are ignored, each animal with both parents known gives rise to 6 off diagonal elements in  $A^{-1}$  and hence 6 off-diagonal blocks in this partition: (sire x dam, dam x sire, sire x animal, dam x animal, animal x dam and animal x sire). When there are N animals one can expect a maximum of  $6Nt^2$  elements in off-diagonal blocks arising from  $A^{-1}*G^{-1}$ , all of which must be mutiplied once per iteration. There are a maximum of  $7Nt^2$  elements in this partition when the diagonal blocks are included. The numbers of traits observed on each animal. Although six elements arise between the animal and its parents a single number can be used to describe them all because the four parent-offspring elements are the same, and the mate-mate element is exactly minus one half the parent-offspring element.

## TRANSFORMATION

Let G = LL' and  $H = I^*L$ ,  $(H' = I^*L' and H^{-1} = I^*L^{-1})$ . A simple transformation to the MME can reduce the diagonal blocks arising from  $A^{-1*}G^{-1}$  from being square to being diagonal, this leads to a corresponding reduction in the amount of multiplication and input required during each iteration, then pre-multiply both sides of the MME by

I	٥٦	and insert	[ I	٦٥	LI	0 ]
lo	Η		Lo	нЈ	lo	<b>H</b> -1 ]

between the terms on the left hand side; viz.

$$\begin{bmatrix} \mathbf{I} & \mathbf{O} \\ \mathbf{O} & \mathbf{H}' \end{bmatrix} \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{A}^{-1} * \mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \mathbf{I} & \mathbf{O} \\ \mathbf{O} & \mathbf{H} \end{bmatrix} \begin{bmatrix} \mathbf{I} & \mathbf{O} \\ \mathbf{O} & \mathbf{H}^{-1} \end{bmatrix} \begin{bmatrix} \mathbf{\hat{b}} \\ \mathbf{\hat{u}} \end{bmatrix}$$
$$= \begin{bmatrix} \mathbf{I} & \mathbf{O} \\ \mathbf{O} & \mathbf{H} \end{bmatrix} \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix}$$

multiply out:

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 $\begin{bmatrix} \mathbf{X}^{\mathbf{R}^{-1}\mathbf{X}} & \mathbf{X}^{\mathbf{R}^{-1}\mathbf{Z}\mathbf{H}} \\ \mathbf{H}^{\mathbf{Z}}^{\mathbf{R}^{-1}\mathbf{X}} & \mathbf{H}^{\mathbf{Z}}^{\mathbf{R}^{-1}\mathbf{Z}\mathbf{H}+\mathbf{A}^{-1}*\mathbf{I}} \end{bmatrix} \begin{bmatrix} \mathbf{\hat{b}} \\ \mathbf{H}^{-1}\mathbf{\hat{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}^{\mathbf{R}^{-1}\mathbf{y}} \\ \mathbf{H}^{\mathbf{Z}}^{\mathbf{R}^{-1}\mathbf{y}} \end{bmatrix}$ 

(Note (B\*C)(D\*E) = BD\*CE, Searle p.265).

As a result of this transformation there is a small increase in the number of elements in the partition  $X'R^{-1}ZH$  but a dramatic decrease in the numbers of elements in the partition  $H'Z'R^{-1}ZH+A^{-1}*I^{-1}$ . The increase in elements in the partition  $X'R^{-1}ZH$  can be minimised by arranging the traits in decreasing frequency of observation.

The dramatic decrease in the numbers of non-zero elements in the partition  $H'Z'R^{-1}ZH+A^{-1}*I$  results from the transformation of the non-zero off-diagonal blocks from being square to being diagonal. Thus there is a reduction of 6Nt(t-1) multiplications per iteration.

#### **ACKNOWLEDGEMENTS**

The authors wish to thank the Meat Research Corporation and Tierzucht Forschung e. V. München for their financial support of this work.

#### REFERENCES

SCHAEFFER, L.R., KENNEDY, B.W. (1986) J. Dairy Sci. 69:575-579. SEARLE, S.R. (1982) Matrix Algebra useful for Statistics. Wiley, New York. SORENSEN, D.A., KENNEDY, B.W. (1984) J. Anim. Sci. 59:1213-1223. TIER, B., GRASER, H.-U. (1991) J. Anim. Breed. Genet. 108:81-88.