

Consideration of sire relationships when estimating  
variance components with herd by sire interaction

by

Curtis Paul Van Tassell

A Thesis Submitted to the  
Graduate Faculty in Partial Fulfillment of the  
Requirements for the Degree of  
MASTER OF SCIENCE

Department: Animal Science  
Major: Animal Breeding

Signatures have been redacted for privacy

---

Iowa State University  
Ames, Iowa

1989

## TABLE OF CONTENTS

	<u>Page</u>
INTRODUCTION	1
SECTION 1. DATA SIMULATION AND ESTIMATION OF VARIANCE COMPONENTS USING A HERD BY SIRE INTERACTION MODEL	8
Abstract	8
Introduction	9
Data and Methods	16
Data structures	16
Sire relationships	19
Simulation	20
Variance component estimation	24
Calculation of quadratics	26
Expectations of quadratic forms	28
Variance component estimation models	30
Results and Discussion	31
Sire variance component estimates	31
Interaction models	31
Sire models	33
Interaction variance component estimates	43
Interaction models	43
Residual variance component estimates	50
Interaction models	50
Sire models	55
Heritability estimates	57
Interaction models	57

Sire models	60
Relationship matrices from calving ease data	64
Conclusions	75
Literature Cited	77
SECTION II. COMPUTATIONAL METHODS FOR SIMULATION OF DATA UNDER A HERD BY SIRE INTERACTION MODEL AND ESTIMATION OF VARIANCE COMPONENTS	80
Abstract	80
Introduction	80
Materials and Methods	82
Data simulation	85
Inversion of the coefficient matrix	86
Calculating the expectations of the MIVQUE quadratics	89
Estimation of variance components	92
Conclusions	94
Literature Cited	96
SUMMARY	97
REFERENCES	98
ACKNOWLEDGEMENTS	102
APPENDIX A. FORTRAN SIMULATION PROGRAM	104
APPENDIX B. FORTRAN PARTITIONED INVERSION PROGRAM	116
APPENDIX C. FORTRAN PROGRAM TO CALCULATE EXPECTATIONS OF MIVQUE QUADRATIC FORMS	129
APPENDIX D. FORTRAN PROGRAM TO ESTIMATE MIVQUE VARIANCE COMPONENTS AND CALCULATE SAMPLE MEANS AND VARIANCES OF ESTIMATES	142

## LIST OF TABLES

	<u>Page</u>
Table 1. Simulation parameters and observed values for generating data structures, including proportion of filled subclasses, $P_i$ , mean daughters per filled subclass, $\mu_i$ , the maximum daughters per subclass, $n_i$ , and the total number of observations, $N_i$ .	18
Table 2. Models used to calculate variance component estimates, considering variance structure of sire effects ( $\text{Var}(u_1)$ ) and interaction effects ( $\text{Var}(u_2)$ )	30
Table 3. Average MIVQUE sire variance component estimates for each combination of the three structured relationship matrices (RELATE), data structure (STRUCT), and level of interaction simulated (INTER) in the data for all models (MODEL)	32
Table 4. Ratio of MIVQUE variance estimates for the average sire variance estimate for model 3 to the average estimate for model 5 for combinations of the three structured relationship matrices (RELATE), data structure (STRUCT), and interaction level (INTER)	35
Table 5. Ratio of MIVQUE variance estimates for the average sire variance estimate for model 1 to the average estimate for model 2 for combinations of the three structured relationship matrices (RELATE), data structure (STRUCT), and interaction level (INTER)	36
Table 6. Ratios of differences of average MIVQUE sire variance component estimates when interaction is removed from the variance component model measured as a proportion of the interaction variance estimated using model 5 (5I) for models with relationships ignored for sires (models 1 and 3) $((1S-3S)/5I)$ , and for models with relationships included for sires (models 2 and 5) $((2S-5S)/5I)$ for combinations of the three structured relationships (RELATE), data structures (STRUCT), and interaction levels (INTER)	41

Table 7.	Ratios of mean differences adjusted for interaction level in MIVQUE sire variance component estimates from Table 6 for data structures (STRUCT) with differences measured as a proportion of the model 5 interaction estimate (5I) for models 1 and 3 $((1S-3S)/5I)$ and for models 2 and 5 $((2S-5S)/5I)$ for the three structured relationship matrices (RELATE)	42
Table 8.	Average MIVQUE interaction variance component estimates for each combination of the three structured relationship matrices (RELATE), data structure (STRUCT), and level of interaction simulated (INTER) in the data for all models (MODEL)	44
Table 9.	Ratio of model 3 to model 5 interaction variance estimates for combinations of the three structured relationship matrices (RELATE), data structures (STRUCT), and interaction levels (INTER)	46
Table 10.	Average MIVQUE residual variance component estimates for each combination of the three structured relationship matrices (RELATE), data structure (STRUCT), and level of interaction simulated (INTER) in the data for all models (MODEL)	51
Table 11.	Ratios of differences of average MIVQUE residual variance component estimates when interaction is removed from the variance component model measured as a proportion of the interaction variance estimated using model 5 (5I) for models with relationships ignored for sires (models 1 and 3) $((1S-3S)/5I)$ , and for models with relationships included for sires (models 2 and 5) $((2S-5S)/5I)$ for combinations of the three structured relationships (RELATE), data structures (STRUCT), and interaction levels (INTER)	56

Table 12.	Ratios of mean differences adjusted for interaction level in MIVQUE residual variance component estimates from Table 11 for data structures (STRUCT) with differences measured as a proportion of the model 5 interaction estimate (5I) for models 1 and 3 $((1R-3R)/5I)$ and for models 2 and 5 $((2R-5R)/5I)$ for the structured relationship matrices (RELATE)	58
Table 13.	Average heritability estimates for each combination of the three structured relationship matrices (RELATE), data structure (STRUCT), and level of interaction simulated (INTER) in the data for all models (MODEL)	59
Table 14.	Average MIVQUE sire variance component estimates for each combination of the two relationship matrices selected from the calving ease data (RELATE), data structure (STRUCT), and level of interaction (INTER) simulated in the data for all models (MODEL)	66
Table 15.	Average MIVQUE interaction variance component estimates for each combination of the two relationship matrices selected from the calving ease data (RELATE), data structure (STRUCT), and level on interaction simulated (INTER) in the data for all models (MODEL)	68
Table 16.	Average MIVQUE residual variance component estimates for each combination of the two relationship matrices selected from the calving ease data (RELATE), data structure (STRUCT), and level on interaction simulated (INTER) in the data for all models (MODEL)	71
Table 17.	Average MIVQUE heritability estimates for each combination of the two relationship matrices selected from the calving ease data (RELATE), data structure (STRUCT), and level on interaction simulated (INTER) in the data for all models (MODEL)	73

## LIST OF FIGURES

	<u>Page</u>
Figure 1. Types of interaction: (a) change in variance, (b) change in rank, and (c) change in rank and variance	5
Figure 1. Average sire variance estimates for data with three structured relationship matrices (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	34
Figure 2. Average sire variance estimates for data with three proportions of filled subclasses (STRUCT), the relationship matrix for 4 groups of 5 half-sib sires, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	38
Figure 3. Average sire variance estimates for data with interaction simulated at three levels (INTER), the relationship matrix for 4 groups of 5 half-sib sires, and 25% filled subclasses for 5 variance component estimation models (MODEL)	40
Figure 4. Average interaction variance estimates for data with three structured relationship matrices (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	45
Figure 5. Average interaction variance estimates for data with interaction simulated at three levels (INTER), the relationship matrix for 4 groups of 5 half-sib sires, and 25% filled subclasses for 5 variance component estimation models (MODEL)	48
Figure 6. Average interaction variance estimates for data with three proportions of filled subclasses (STRUCT), the relationship matrix for 4 groups of 5 half-sib sires, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	49

Figure 7.	Average residual variance estimates for data with interaction simulated at three levels (INTER), the relationship matrix for 4 groups of 5 half-sib sires, and 25% filled subclasses for 5 variance component estimation models (MODEL)	52
Figure 8.	Average residual variance estimates for data with three structured relationship matrices (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	53
Figure 9.	Average residual variance estimates for data with three proportions of filled subclasses (STRUCT), the relationship matrix for 4 groups of 5 half-sib sires, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	54
Figure 10.	Average heritability estimates for data with three structured relationship matrices (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for the 5 variance component estimation models (MODEL)	61
Figure 11.	Average heritability estimates for data with interaction simulate at three levels (INTER), the relationship matrix for 4 groups of 5 half-sib sires, and 25% filled subclasses for 5 variance component estimation models (MODEL)	62
Figure 12.	Average heritability estimates for data with three proportions of filled subclasses (STRUCT), the relationship matrix for 4 groups of 5 half-sib sires, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	63



Figure 13.	Average sire variance estimates for data with the structured relationship matrix for 10 pairs of half-sib sires (1) and calving ease relationship matrices (4 and 5) (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	67
Figure 14.	Average interaction variance estimates for data with the structured relationship matrix for 10 pairs of half-sib sires (1) and calving ease relationship matrices (4 and 5) (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	69
Figure 15.	Average residual variance estimates for data with the structured relationship matrix for 10 pairs of half-sib sires (1) and calving ease relationship matrices (4 and 5) (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	72
Figure 16.	Average heritability estimates for data with the structured relationship matrix for 10 pairs of half-sib sires (1) and calving ease relationship matrices (4 and 5) (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)	74
Figure 1.	Algorithm to simulate data for interaction models	87
Figure 2.	Algorithm to calculate inverse for mixed model equations	90
Figure 3.	Algorithm to calculate expectations of MIVQUE quadratic forms	93
Figure 4.	Algorithm to calculate MIVQUE estimates	95

## INTRODUCTION

Statistical models have developed over time to explain particular genetic phenomena. The validity of certain models depends on there being an underlying theory of quantitative genetics which allowed them to predict the outcome of specific matings. Genotype by environment ( $G \times E$ ) interaction has been exploited by plant breeders because it is possible to develop highly inbred lines of plants which can be tested and evaluated based on performance of hybrid offspring in a variety of diverse environments. Yates and Cochran (1934) in an early investigation of  $G \times E$  interaction in plant breeding research suggested using the regression of the production of a particular variety receiving a treatment on the average performance of all varieties under the same environment. The slope of the regression provided a measure of the performance of the genotype over environmental factors. Hardwick and Wood (1934) improved the regression method by regressing performance on an environmental variable rather than the average yield for a treatment, because the method suggested by Yates and Cochran (1934) was biased by errors in estimating environmental levels.

Unfortunately, the development of inbred lines in domestic livestock species has not been practical, so that many selection procedures used by plant breeders have not been available to the animal breeder. Therefore, the

similarity of known relatives must be exploited because large samples of identical genotypes are not available for testing in different environments. Further, the prohibitive cost of animal experiments has to a large degree precluded designed experiments investigating genotype by environment interaction in animals. This forces animal breeders to analyze field data and draw conclusions relating to interactions when the data structure, and in particular the degree of balancedness, is less than ideal. Standard, profitable management practices create environmental covariances in field data that would not normally exist under designed experimental conditions. A model accounting for environmental covariances is statistically equivalent to one including genotype by environment (G×E) interactions when G×E interaction effects are distributed independently (i.e.,  $\text{var}(G \times E) = I\sigma_{G \times E}^2$ ) and uncorrelated with other effects in the model (see Henderson (1985) for details). Thus, many literature estimates of G×E interaction and environmental covariance are statistically equivalent. It should be noted that in many studies environmental covariance is reported as  $c^2$ , which is the environmental covariance measured as a proportion of the total variance.

Falconer (1952) pointed out that if only one trait is considered in two environments, G×E interaction can be treated as a genetic correlation between two traits receiving

two treatments, rather than a single trait exhibiting G×E interaction. Dickerson (1962) expanded this approach to include many environments, and estimated genetic correlations using the intra class correlation among performance of the same genotypes across environments. Dickerson (1962) found that this genetic correlation estimate was equivalent to the average of the product moment correlations between rankings of the same genotype in each pair of environments for all the environments and pointed out that an adjustment was necessary in estimating the correlation if the genetic variance was not the same across environments. Dickerson (1962) suggested estimating the genetic correlation as

$$\hat{r}_g = \hat{\sigma}_G^2 / (\hat{\sigma}_G^2 + \hat{\sigma}_{GE}^2 - \text{Var}(\hat{\sigma}_{G_i})),$$

where  $\hat{r}_g$  is the estimated genetic correlation,  $\hat{\sigma}_G^2$  is the estimated average genetic variance,  $\hat{\sigma}_{GE}^2$  is the estimated G×E interaction variance, and  $\text{VAR}(\hat{\sigma}_{G_i})$  is the variance of the estimates of genetic standard deviation within each environment. If the heterogeneity of genetic variance is ignored (i.e.,  $\text{Var}(\hat{\sigma}_{G_i})$ ), the correlation would be estimated at less than unity using the intra class correlation while the true correlation and the estimate by product moment correlation would be perfect. The erroneous interaction estimated by ignoring heterogeneous genetic variance was referred to as "pseudo interaction." Dickerson (1962) concluded that "in general, the standard analysis of variance

is a satisfactory method to estimate interaction and intra class genetic correlation provided adjustment is made for any important variation between environments in the scale of genetic effects."

Consideration must be given to the type of interaction that may exist in a population. Haldane (1946) proposed classifying interaction into four categories. Bowman (1972) suggested a simplification to only three categories (Figures 1a, 1b, and 1c), based on the presence or absence of rank or variance change. The first type of interaction (Figure 1a), that due to change in variance, is not usually a problem if genotypes are distributed equally across environments. The second and third types of interaction (Figures 1b and 1c), where change in rank occurs, are likely to be a larger problem to breeders. The problems associated with each type of interaction will be explored.

The three general types of interaction (Figure 1) will be examined in order. First, if the  $G \times E$  interaction present is that of change in variance (Figure 1a) there are several alternative techniques to manage the problem. The most general approach would be to stabilize the variances in each environment by modifying the mixed model equations to account for heterogeneous variance (Boldman, 1989).

Next,  $G \times E$  interaction associated with change in rank across environments, with or without change in variance,

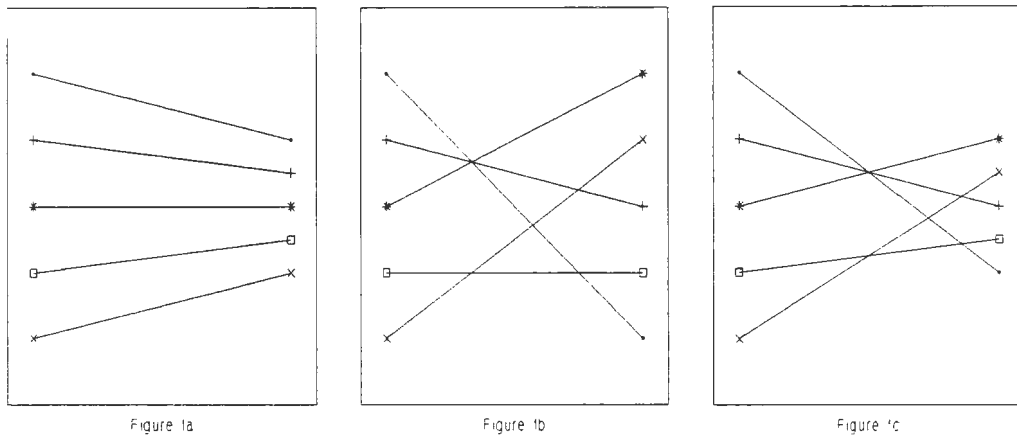


Figure 1. Types of interaction: (a) change in variance, (b) change in rank, and (c) change in rank and variance

(Figure 1b,c) raises several nongenetic questions (Bowman, 1972). First, what percentage of the population is represented by each of the environments? Second, are the conditions likely to continue? Finally, can the environmental difference be reduced to an acceptable level more easily than modifying the breeding program? Additionally, the degree of rank changes are also an important consideration. Answers to these questions may actually allow the breeder to reduce the number of strains required to meet the needs of differing environments to a very few or just one.

In the typical animal evaluation scenario a change in rank across environments suggests that each animal must be

evaluated in each environment. It may be possible to group environments in order to reduce the number of evaluations. For example, Mao and Burnside (1969) found highly significant herd by sire interaction for level of grain feeding in summer. If this interaction was found to be important for the population it may be possible to group herds into several categories of grain feeding and evaluate sires for each group of environments.

Because sire selection is critical to genetic improvement, the implication of G×E interaction on progeny testing is also a concern. If genotype by environment interaction exists breeders need to determine if there is a particular environment under which progeny testing should be performed. It has been argued that sires should be proven in a cross section of environments that are representative of the population in which they would be used. The opposing argument is that sires should be proven in environments where they have the greatest opportunity to demonstrate superiority. Determination of the appropriate progeny testing scheme is then a matter of comparing selection response for the progeny testing schemes. The reader is directed to Bowman (1972) for a complete discussion of the considerations in such a decision.

The purpose of this study was to examine the effects of using a variety of assumptions when designing models for

variance component estimation when herd by sire interaction exists in the data. The assumption of whether it was necessary to include the relationship among sires when estimating sire and interaction variance was examined. Interaction models were compared with sire models ignoring interaction. Simulation was used to allow for the examination of the effects of the degree of relatedness, unbalancedness, and level of interaction on variance component estimates. Computing algorithms and a set of FORTRAN programs are presented for the simulation and estimation phase of the research.



# SECTION 1. DATA SIMULATION AND ESTIMATION OF VARIANCE COMPONENTS USING A HERD BY SIRE INTERACTION MODEL

## Abstract

Effects of sire relationships in sire and herd by sire interaction were examined using simulation and minimum variance quadratic unbiased estimates (MIVQUE) of variance components. Data were simulated for 50 herds and 20 sires for five sire relationship matrices, three degrees of data unbalancedness, and three levels of interaction. A total of 1000 replicates were simulated for each combination of relationship matrix, degree of unbalancedness, and interaction level. The simulation included fixed herds, random sires, herd by sire interaction, and residual effects. Sire variance was held constant at 6.25% of the variance ( $h^2 = .25$ ), interaction variance was simulated at 5%, 15%, and 25% of the total variance, and the remaining variance was simulated as residual variance. Variance structures for sire effects were  $A\sigma_1^2$ , for interaction effects were  $(I \otimes A)\sigma_2^2$ , and for residual effects were  $I\sigma_0^2$ . MIVQUE estimates were calculated for the true (simulation) model as well as for models ignoring relationships for sires and interaction. In addition, estimates were calculated for sire models without interaction. Interaction variance was underestimated when relationships were ignored. Ratios for interaction variance estimates were calculated to compare the model ignoring

relationships to interaction estimates for the true model. The ratios ranged from .75 for the relationship matrix for sires closely related to .99 for the matrix for sires with few genetic ties. Sire variance and heritability estimates increased when variance components were estimated using sire models compared to estimates using interaction models. This overestimation increased with levels of interaction simulated in the data and with the degree of unbalancedness. Estimates of sire variance were as large as 16%, and heritability estimates were as large as .70 using sire models.

### Introduction

The phenotype of an animal is a function of its genotype and environment. The breeder can only observe the phenotype, and therefore, is faced with the problem of basing selection decisions on an estimate of an underlying genetic component that cannot be observed. In addition, selection for quantitative traits deals with, as Falconer (1981) describes, "differences, in so far as they are inherited, depend on genes whose effect are small in relation to the variation arising from other causes." Not only are breeders challenged with the problem of selecting for an unknown quantity, but they also face the problem that genetic differences are often masked or overwhelmed by variation due to other causes. Additional problems arise when the relationship between genotype and environment is not strictly additive, and

genotypes do not behave consistently across treatments, herd levels, or other environmental factors. A nonadditive relationship between genotype and environment is usually referred to as genotype by environment (G×E) interaction.

Several authors have suggested factors that may affect estimates of genotype by environmental interaction. These include (Tong et al., 1977; Norman, 1974; Dickerson, 1962):

- true genotype by environment interaction,
- treating daughters of a sire alike,
- sires used for a short time in a herd so daughters have similar environmental conditions,
- assortative mating,
- failure to remove all herd-year-season effects,
- maternal effects,
- external physical influences, and
- background genotype.

Many researchers have evaluated G×E interaction by estimating the correlation of breeding values of animals based on observations recorded in different environments. The further the correlation deviated from unity the greater the likelihood that G×E interaction was an important consideration.

Robertson et al. (1960) found little evidence for herd by sire interaction when the correlations among breeding value estimates were near unity based on observations at

three levels of herd production. The authors did note that although heritability was relatively constant across herd levels, both genetic and environmental variances increased with herd level. Van Vleck (1963) reported similar results using four herd levels. Van Vleck (1963) noted an increase in heritability in addition to genetic and environmental variances with increasing herd levels.

Bereskin and Lush (1965) reported correlations lower than expected when estimating breeding values for sires when the data were randomly divided into equal halves or based on herd production levels. The authors concluded that the low correlation was due to environmental correlation among daughters of a sire in the same herd.

Sire by region of the United States interactions for milk yield, fat yield, and fat percent were examined by Lytton and Legates (1966). Correlations of sire breeding value estimates for regions approached unity. Sire by region interaction variance was estimated near zero as well. Lytton and Legates (1966) concluded sire by region interaction was not important for the three milk traits. Powell and Dickerson (1977) calculated correlations of breeding value estimates of sires based on data from Canada, Mexico, and the United States. No significant interaction between genotype and country was found, although clear differences were seen for relative genetic levels for each country.

The importance of G×E interaction has also been evaluated by estimating the magnitude of G×E interaction variance. Most of the variance component estimates were computed using Henderson's (1953) Method 1 (HM1) or Method 3 (HM3).

Kelleher et al. (1967) estimated herd-year-season by sire (H×S) variance using HM1 at only 2 percent of the total variance. Lee (1976) used HM1 and HM3 and estimated H×S variance at 0.2 and 2.0 percent of total variance for the two methods, respectively. Lee (1976) found HM1 to be severely biased by nonrandomness of the H×S subclass frequency with respect to sire and herd effects. Mohammed et al. (1982a) estimated herd by sire interaction variance using HM3 at 10 percent of the total variance for milk yield.

Tong et al. (1977) compared parameter estimates using HM1 for two models. The full model included effects for an overall mean, herds, sires, herd by sire interactions, cows, and residual error. The reduced model included all the effects in the full model except herd by sire interaction. The H×S variance accounted for 0.3 to 4.1 percent of the total variance for milk, fat, and protein yield. Heritability estimates increased for all three models when the reduced model was used, and the difference in heritability estimates increased as the proportion of variance due to interaction in the full model increased.

Meyer (1987) used restricted maximum likelihood to estimate environmental correlations ( $C^2$ ) for British Friesian Holsteins. Estimates of  $C^2$  ranged from 2.22% to 3.81% for milk yield, 2.10% to 4.22% for fat yield, and 2.18% to 4.15% for protein yield. Meyer (1987) concluded that environmental correlation was important when considering sire evaluations based on observations in only a few herds.

If G×E interaction is included in a statistical model to account for interaction, the most apparent change is the reduced range of the predictors (Mohammed et al., 1982b). Mohammed et al. (1982b) found that the range in predicted sire transmitting abilities decreased from 813 to 674 kg when herd by sire interaction was included in the model. One of the most useful properties of a model including interaction is that it limits the influence of observations from any single environment on the genotype prediction. The impact of individual herds also has become a concern in animal breeding as there is increasing concern about preferential treatment of animals in a small number of herds. If the effect that a herd can have on an animal's evaluation is limited, then the evaluations may be more accurate. Although the influence of a single environment is limited when G×E interaction is incorporated into an evaluation, this should not greatly affect animals represented in many environments, such as artificial insemination (AI) sires, but may limit the

magnitude of evaluations of non-AI bulls proven in only a few herds. Thus, the animals that are represented in a variety of environments may still have a wide range of predicted genotypes.

The use of G×E interaction to limit bias due to differential management has been discussed by several authors. Meyer (1987) claims that "sire evaluation procedures should account for  $C^2$  effects to minimize bias due to preferential treatment and to avoid overestimates of the accuracy of sire proofs, in particular for limited herd-use sires." Norman (1974) also recommended including herd by sire interaction in the form of a  $C^2$  effect in the herdmate comparison although several studies indicated that true herd by sire interaction was not likely to be a major concern in the dairy population. Norman's (1974) major justification for including an environmental correlation in a national sire evaluation was to limit the impact of a single herd on sire predictions and to attempt to limit the effect of preferential treatment.

Statistical tools available to the animal breeder have improved considerably in the recent past. The methods used in prediction of random factors have improved greatly, such as prediction of breeding values for animals that are candidates for selection. The discovery by Henderson (1976) of a rapid and feasible method to compute the inverse of the

numerator relationship matrix ( $A^{-1}$ ) led to one of the largest single improvements in prediction of breeding values. The use of known covariances among traits to improve accuracy in multiple trait prediction as suggested by Quass and Pollak (1981) improved animal evaluation methods as well. Also, large improvements were being made in techniques for estimating variance components. Henderson (1953) suggested three methods of variance component estimation based on the analysis of variance techniques, however these methods were limited due to both underlying assumptions and the use simple variance structures (e.g., the difficulty in using  $A^{-1}$  or multiple trait models). LaMotte (1973) and Rao (1971a,1971b) independently developed MIVQUE, the minimum variance quadratic unbiased estimation and MINQUE, the minimum norm quadratic unbiased estimation techniques. These two methods are identical in procedure, differing in the derivation of the quadratics and the assumption of normality. MIVQUE provides a more powerful method of estimating variance components allowing for unbiased estimation of variance components under a wider range of models, including the use of  $A^{-1}$  and multiple trait models.

Foulley and Henderson (1989) modified the multiple trait model suggested by Quass and Pollak (1981) to allow for the use of known relationships to predict herd (or herd-year-season) by sire (H×S) interaction effects and, more



importantly, the estimation of the  $H \times S$  variance components. It is computationally more difficult to include these relationships, but it is clearly logical to expect related sires to have correlated genotype by environment interaction effects because the interaction is some function of the genetic component shared by relatives. Foulley and Henderson (1989) found that ignoring sire relationships in estimating variance components will lead to a underestimation of  $G \times E$  interaction variance.

The purpose of this study was to examine the effect of ignoring sire relationships when estimating herd by sire interaction variance components when interaction was present. Simulation was used to examine the effects of a range in interaction levels. A variety of relationship matrices were used to simulate and analyze the data, ranging from relationship matrices for sires having few relationship ties to matrices for sires that were closely related. In addition, several level of unbalancedness were examined to determine the affect on variance estimates.

## Data and Methods

### Data structures

The term data structure is used to describe a distribution of observations that is repeatedly used to simulate data considering a variety of underlying parameters. That is, the data structure defines the incidence of the data

but not the actual observations. For this study three data structures were used, each including 20 sires having daughters in 50 herds. The structures differed in the degree of unbalancedness, but the expected total number of observations was 2000 in all three data structures. This was done by altering the expected percent of filled subclasses,  $P_i$ , and the mean number of observations in each subclass,  $\mu_i$ , for each of the data structures, or simply  $P_i \mu_i = C$ ,  $i=1,2,3$ , where  $C$  is a constant for all three data structures.

The three data structures were randomly generated as follows: generate a random number from a uniform distribution for each herd-sire subclass, if this value was smaller than the expected proportion of filled subclasses,  $P_i$ , then a second random value was drawn from the generator, and this value was then rescaled to represent a value from a discrete uniform distribution with a range of 1 to  $n_i$ , to determine the number of observations for that herd-sire subclass. The value of  $n_i$  was chosen for each data structure so that the average number of daughters per herd sire subclass for subclasses with records was  $\mu_i = \frac{1}{n_i} \sum_{j=1}^{n_i} j = \frac{1+n_i}{2}$ , but  $\mu_i = C/P_i$ , so  $n_i = 2C/P_i - 1$ ,  $i=1,2,3$ . Thus, each data structure had the same total number of observations expected regardless of the degree of unbalancedness. The values used to generate the data structures, and the actual values observed in the data structures are given in Table 1.

Table 1. Simulation parameters and observed values for generating data structures, including proportion of filled subclasses,  $P_i$ , mean daughters per filled subclass,  $\mu_i$ , the maximum daughters per subclass,  $n_i$ , and the total number of observations,  $N_i$

Data Set		$P_i$	$\mu_i$	$n_i$	$N_i$
1	sim <sup>a</sup>	1.00	2.00	3	2000
	obs <sup>b</sup>	1.00	2.02	3	2015
2	sim	0.25	8.00	15	2000
	obs	0.26	7.64	15	1994
3	sim	0.10	20.00	39	2000
	obs	0.12	20.70	39	2401

<sup>a</sup>Parameters used to generate data structure.

<sup>b</sup>Observed from data sets generated.

The pseudo-random continuous standard (i.e., [0,1)) uniform distribution generator used in this study was that described by Wichmann and Hill (1982), and this will produce more than  $10^{13}$  pseudo-random numbers before repeating. A vector of 500 elements was filled with values from the generator, then these values were selected and replaced randomly using a second independent generator of the same type. In this way, the numbers produced by the random number generators were shuffled to insure that no correlation existed among the pseudo-random numbers.

Connectedness of the data set, as described by Searle (1971), was insured by checking the data structure using the algorithm described by Fernando et al. (1983) because disconnectedness may influence variance component estimation

(Schaeffer, 1975). If the data set was disconnected a new data structure was generated and tested for connectedness. This was repeated until a completely connected data structure was generated.

### Sire relationships

Five different sire relationship matrices,  $A_i$ , were used to simulate records for daughters of bulls. The first three relationship structures were for different size half-sib sire groups. Let  $H_n$  be defined as  $\frac{1}{2}I_n + \frac{1}{2}J_n$ , where  $I_n$  is an  $n \times n$  identity matrix and  $J_n$  is an  $n \times n$  matrix with all elements 1. The first relationship matrix was for 10 pairs of half-sib sires, then  $A_1 = I_{10} \otimes H_2$ , where  $\otimes$  denotes the direct or Kronecker product (see Searle, 1982 for discussion of the direct product operator). The second set of relationships was for 4 sets of 5 half-sib sire groups, or  $A_2 = I_4 \otimes H_5$ . The last structured relationship matrix was for 20 half-sib sires, i.e.,  $A_3 = H_{20}$ .

The last two relationship matrices were generated from a data set representative of the current national artificial insemination (AI) dairy sire population. The inverse of Wright's numerator relationship matrix for 334 sires was obtained from the national calving ease evaluation data set (Berger, personal communication, Department of Animal Science, Iowa State University, 1989). This matrix was inverted to obtain the numerator relationship matrix (NRM).

The NRM for the 334 sires contained 13740 (12.32%) nonzero off-diagonal elements averaging 0.14585. The range of nonzero off-diagonal elements was from 0.015625 to 0.5 with 0.125 the most common degree of relatedness. The fourth relationship structure was generated by randomly choosing 20 sires from 100 young sires in the list of 334. None of these 100 sires had sons or grandsons in the data set, and they should be representative of the degree of relatedness among young sires being progeny tested by AI organizations. The fifth relationship structure was created by randomly choosing 20 sires from all of the 334 sires in the data set.

Because Wright's NRM is positive definite (Henderson, 1975), it can be factored using a Cholesky decomposition, so that

$$A_i = L_i L_i', \quad i=1,2,\dots,5, \quad [1]$$

where  $L_i$  is a lower triangular matrix. Each relationship matrix was decomposed using the Cholesky decomposition algorithm described by Burden et al. (1981).

### Simulation

The model used to simulate the data was:

$$y = Xb + Zu + e, \quad [2]$$

where

$y$  is an  $n \times 1$  vector of observations,

$n$  is the number of observations in the data set,

$X$  is an  $n \times h$  incidence matrix for herd effects,

$h$  is the number of herds,

$\mathbf{b}$  is an  $h \times 1$  vector of fixed herd effects,

$\mathbf{Z} = [\mathbf{Z}_1 | \mathbf{Z}_2]$ ,

$\mathbf{Z}_1$  is an  $n \times s$  incidence matrix for sire effects,

$s$  is the number of sires,

$\mathbf{Z}_2$  is an  $n \times r$  incidence matrix for interaction effects,

$r$  is the number of interaction effects,

$\mathbf{u}' = [\mathbf{u}'_1 | \mathbf{u}'_2]$ ,

$\mathbf{u}_1$  is an  $s \times 1$  vector of random sire effects,

$\mathbf{u}_2$  is an  $r \times 1$  vector of random interaction effects, and

$\mathbf{e}$  is an  $n \times 1$  vector of random residual effects.

If we denote the  $i^{\text{th}}$  numerator relationship matrix as  $\mathbf{A}_i$ , then let  $\bar{\mathbf{A}}_i = \mathbf{I}_h \otimes \mathbf{A}_i$ . Then,  $\bar{\mathbf{A}}_i$  describes the correlation of herd by sire interaction effects within herd due to relationships among sires. The following simplifying assumptions for expected values and variance structure for the random variables were used.

$$E \begin{bmatrix} \mathbf{y} \\ \mathbf{u}_1 \\ \mathbf{u}_2 \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{Xb} \\ 0 \\ 0 \\ 0 \end{bmatrix}.$$

$$V \begin{bmatrix} y \\ u_1 \\ u_2 \\ e \end{bmatrix} = \begin{bmatrix} z_1 A Z_1' \sigma_1^2 + z_2 \bar{A} Z_2' \sigma_2^2 + I \sigma_0^2 & z_1 A \sigma_1^2 & z_2 \bar{A} \sigma_2^2 & I \sigma_0^2 \\ A Z_1' \sigma_1^2 & A \sigma_1^2 & 0 & 0 \\ \bar{A} Z_2' \sigma_2^2 & 0 & \bar{A} \sigma_2^2 & 0 \\ I \sigma_0^2 & 0 & 0 & I \sigma_0^2 \end{bmatrix}.$$

In addition, let

$$V = V_0 \sigma_0^2 + V_1 \sigma_1^2 + V_2 \sigma_2^2,$$

$$V_0 = Z_0 G_0 Z_0' = I_n I_n I_n = I_n, \quad [3]$$

$$V_1 = Z_1 G_1 Z_1', \quad G_1 = A, \quad \text{and} \quad [4]$$

$$V_2 = Z_2 G_2 Z_2', \quad G_2 = \bar{A}. \quad [5]$$

Finally,  $\sigma_0^2$ ,  $\sigma_1^2$ , and  $\sigma_2^2$  are the residual, sire, and interaction components of variance, respectively. When sire models were used to analyze the data the residual variance was redefined as the sum of the residual and interaction components used in the simulation.

The mixed model equations (MME) for [2] are

$$\begin{bmatrix} X'X & X'Z_1 & X'Z_2 \\ Z_1'X & Z_1'Z_1 + G_1^{-1}\tilde{\alpha}_1 & Z_1'Z_2 \\ Z_2'X & Z_2'Z_1 & Z_2'Z_2 + G_2^{-1}\tilde{\alpha}_2 \end{bmatrix} \begin{bmatrix} \tilde{b} \\ \tilde{u}_1 \\ \tilde{u}_2 \end{bmatrix} = \begin{bmatrix} X'y \\ Z_1'y \\ Z_2'y \end{bmatrix}, \quad [6]$$

where  $\tilde{\alpha}_i = \tilde{\gamma}_0^2 / \tilde{\gamma}_i^2$ , and  $\tilde{\gamma}_i^2$  is the prior estimate of  $\sigma_i^2$ .

Because the residual variance differed for the sire and interaction models, the ratios of error variance to sire variance were different for sire and interaction models.

Equation [6] can be rewritten as  $\tilde{\tilde{C}}\tilde{s} = W'y$ , where

$W = [X|Z_1|Z_2]$  and

$\tilde{s}' = [\tilde{b}' \ \tilde{u}'_1 \ \tilde{u}'_2]$ . Then  $\tilde{s} = \tilde{\tilde{C}}^{-1}W'y$ .

The tilde ( $\sim$ ) will be used to indicate a value (scalar, vector, or matrix) that is a function of the prior estimates of the variance components. That is, the tilde will be used for variables for which the value may change if the priors change.

The inverse of the coefficient matrix,  $\tilde{\tilde{C}}^{-1}$ , exists because herds are the only fixed effects considered in the model, i.e.,  $\tilde{\tilde{C}}$  is full rank because the mean is included in herd effects.

Data were simulated using three levels of interaction variance, 5, 15, and 25 percent of the total variance. Although the level of interaction variance changed in the data sets, sire and total variance were constant across all simulations. Sire variance accounted for 6.25 percent of the total variance, and the total variance,  $\sigma_T^2 = \sigma_0^2 + \sigma_1^2 + \sigma_2^2$ , was held constant. This resulted in a constant heritability,  $h^2$ , for all the data sets. Heritability was defined as the portion of total variance accounted for by additive genetic variance, or  $4\sigma_1^2/\sigma_T^2$ . Heritability was 0.25 in this study, which is a common estimate for milk yield in dairy cattle.



A total of 1000 replicates were generated for each relationship matrix, data structure, and interaction level combination.

Herd effects were simulated using a normal distribution function random number generator supplied by Meyer (personal communication, University of Edinburg, Edinburg, Scotland, 1989) based on a Kinderman-Ramage procedure described by Kennedy and Gentle (1980). Herd variance,  $\sigma_H^2$ , was 36 percent of the total random effect variance, i.e.  $\sigma_H^2 = 0.36\sigma_T^2$ . The herd effects were independently and identically distributed and uncorrelated with other effects in the model.

Sire effects were simulated by generating a vector of independent standard normal deviates,  $r$ , and computing the vector of sire effects as  $u_1 = L_1 r \sigma_1$ , where  $L_1$  is the decomposition matrix described in [1]. Then  $V(u_1) = L_1 V(r) L_1' = L_1 I L_1' \sigma_1^2 = A_1 \sigma_1^2$ . Herd by sire interaction was simulated using a similar procedure so that  $V(u_2) = \bar{A} \sigma_2^2$ . The right hand sides (RHS) of the mixed model equations and the sum of squared observations,  $y'y$ , were calculated as the data were simulated.

#### Variance component estimation

Minimum variance quadratic unbiased estimation (MIVQUE) was chosen as the method to estimate variance components for several reasons: 1) because MIVQUE does not require iteration, the same calculations used to compute the

expectations of the quadratic forms would not need to be repeated for replicates of the same data structure, model, and prior estimate of the variance components, 2) MIVQUE provides the minimum variance estimate of variance components when using the true model and prior, and both are known in this study because the data were simulated, and 3) MIVQUE is unbiased when the correct model is used, therefore bias due to using an incorrect model may be estimated by comparing the unbiased estimates to those obtained using the incorrect model.

Using the MIVQUE quadratics suggested by Rao (1971a), the class of symmetric matrices  $B$ , such that  $BX = 0$  and  $\text{tr}(BV_i) = p_i$ ,  $i = 0, 1, 2, \dots, k$ , where  $\text{tr}()$  indicates the trace operation, and  $V_i$  are discussed in [3], [4], and [5]. If  $\sigma' = (\sigma_0^2 \ \sigma_1^2 \ \dots \ \sigma_k^2)$ , then  $y'By$  is a class of unbiased translation invariant estimates of  $p'\sigma$ , where

$p' = (p_1 \ p_2 \ \dots \ p_k)$ . The minimum variance estimator of  $p'\sigma$  from that class is  $y'\tilde{B}y$ , where

$$\tilde{B} = \sum_{i=0}^k \lambda_i \tilde{R}V_i\tilde{R},$$

$$\tilde{R} = \tilde{V}^{-1}(I - \tilde{P}_V),$$

$$\tilde{P}_V = X(X'\tilde{V}^{-1}X)^{-1}X'\tilde{V}^{-1},$$

$$\tilde{V} = \sum_{i=0}^k V_i \tilde{\gamma}_i, \text{ and}$$

$\tilde{\gamma}_i$  is the prior estimate of  $\sigma_i^2$ .

The MIVQUE of  $p'\sigma$  is  $\tilde{\lambda}'\tilde{Q}$ , where  $\tilde{\lambda}$  is a solution to

$\tilde{S}\tilde{\lambda} = p$ , and  $\tilde{S}$  is a  $k+1$  by  $k+1$  matrix whose  $i, j^{\text{th}}$  element is  $\text{tr}(\tilde{R}V_i\tilde{R}V_j)$ . More simply,  $\tilde{S}$  is the matrix of the expectations of the quadratic forms

$$\tilde{Q}' = (\tilde{Q}_0 \tilde{Q}_1 \tilde{Q}_2 \dots \tilde{Q}_k), \text{ and}$$

$$\tilde{Q}_i = Y' \tilde{R}V_i \tilde{R}Y. \quad [7]$$

$$\text{Then, } \tilde{S}\tilde{\sigma} = \tilde{Q}, \quad [8]$$

equating the quadratics to their expectations.

Finally,  $\tilde{\sigma} = \tilde{S}^{-1}\tilde{Q}$ .

Calculation of quadratics A simpler form of the Rao (1971a) quadratic forms were computed as described by Schaeffer (1979). The quadratics were reorganized to use the solutions from the MME. Expanding [7],

$$\begin{aligned} \tilde{Q}_i &= Y' [(\tilde{V}^{-1} - \tilde{V}^{-1}X(X'\tilde{V}^{-1}X)^{-1}X'\tilde{V}^{-1})V_i(\tilde{V}^{-1} - \tilde{V}^{-1}X(X'\tilde{V}^{-1}X)^{-1}X'\tilde{V}^{-1})]Y \\ &= (Y - X\tilde{b})'\tilde{V}^{-1}V_i\tilde{V}^{-1}(Y - X\tilde{b}), \text{ where} \end{aligned}$$

$$\tilde{b} = (X'\tilde{V}^{-1}X)^{-1}X'\tilde{V}^{-1}Y,$$

i.e.,  $\tilde{b}$  is a solution to the generalized least squares equations.

Then

$$\begin{aligned} \tilde{Q}_i &= (Y - X\tilde{b})'\tilde{V}^{-1}Z_iG_iZ_i'\tilde{V}^{-1}(Y - X\tilde{b}) \\ &= (Y - X\tilde{b})'\tilde{V}^{-1}Z_iG_i\tilde{\gamma}_i(\tilde{\gamma}_i^{-1}G_i^{-1}\tilde{\gamma}_i^{-1})\tilde{\gamma}_iG_iZ_i'\tilde{V}^{-1}(Y - X\tilde{b}), \text{ and} \end{aligned}$$

because

$$\tilde{u}_i = \tilde{\gamma}_iG_iZ_i'\tilde{V}^{-1}(Y - X\tilde{b}), \text{ (Henderson, 1973),}$$

$$\begin{aligned} \tilde{Q}_i &= \tilde{u}_i'G_i^{-1}\tilde{u}_i\tilde{\gamma}_i^{-2} \\ &= \tilde{u}_i'\tilde{u}_i\tilde{\gamma}_i^{-2} \text{ if } G_i = I. \end{aligned} \quad [9]$$

If we define  $\tilde{\mathbf{u}}_0 = \tilde{\mathbf{e}}$ , the estimated residual effects, then for  $i=0$  the calculation of  $\tilde{Q}_0 = \tilde{\mathbf{e}}'\tilde{\mathbf{e}}$  would require that the residual be calculated for each observation, but using results from the MME [6],

$$\begin{aligned}
\tilde{\mathbf{e}}'\tilde{\mathbf{e}} &= (\mathbf{y} - \mathbf{X}\tilde{\mathbf{b}} - \mathbf{Z}\tilde{\mathbf{u}})'(\mathbf{y} - \mathbf{X}\tilde{\mathbf{b}} - \mathbf{Z}\tilde{\mathbf{u}}) \\
&= \mathbf{y}'\mathbf{y} - 2\tilde{\mathbf{b}}'\mathbf{X}'\mathbf{y} - 2\tilde{\mathbf{u}}'\mathbf{Z}'\mathbf{y} + \tilde{\mathbf{b}}'(\mathbf{X}'\mathbf{X} + \mathbf{X}'\mathbf{Z}\tilde{\mathbf{u}}) \\
&\quad + \tilde{\mathbf{u}}'(\mathbf{Z}'\mathbf{X}\tilde{\mathbf{b}} + \mathbf{Z}'\mathbf{Z}\tilde{\mathbf{u}}) \\
&= \mathbf{y}'\mathbf{y} - 2\tilde{\mathbf{b}}'\mathbf{X}'\mathbf{y} - 2\tilde{\mathbf{u}}'\mathbf{Z}'\mathbf{y} + \tilde{\mathbf{b}}'\mathbf{X}'\mathbf{y} \\
&\quad + \tilde{\mathbf{u}}'_1(\mathbf{Z}'_1\mathbf{X}\tilde{\mathbf{b}} + \mathbf{Z}'_1\mathbf{Z}_1\tilde{\mathbf{u}}_1 + \mathbf{Z}'_1\mathbf{Z}_2\tilde{\mathbf{u}}_2) \\
&\quad + \tilde{\mathbf{u}}'_2(\mathbf{Z}'_2\mathbf{X}\tilde{\mathbf{b}} + \mathbf{Z}'_2\mathbf{Z}_1\tilde{\mathbf{u}}_1 + \mathbf{Z}'_2\mathbf{Z}_2\tilde{\mathbf{u}}_2) \\
\tilde{\mathbf{e}}'\tilde{\mathbf{e}} &= \mathbf{y}'\mathbf{y} - \tilde{\mathbf{b}}'\mathbf{X}'\mathbf{y} - 2\tilde{\mathbf{u}}'_1\mathbf{Z}'_1\mathbf{y} - 2\tilde{\mathbf{u}}'_2\mathbf{Z}'_2\mathbf{y} \\
&\quad + \tilde{\mathbf{u}}'_1(\mathbf{Z}'_1\mathbf{y} - \mathbf{G}_1^{-1}\tilde{\mathbf{u}}_1\tilde{\gamma}_1) \\
&\quad + \tilde{\mathbf{u}}'_2(\mathbf{Z}'_2\mathbf{y} - \mathbf{G}_2^{-1}\tilde{\mathbf{u}}_2\tilde{\gamma}_2) \\
&= \mathbf{y}'\mathbf{y} - \tilde{\mathbf{b}}'\mathbf{X}'\mathbf{y} - \tilde{\mathbf{u}}'_1\mathbf{Z}'_1\mathbf{y} - \tilde{\mathbf{u}}'_2\mathbf{Z}'_2\mathbf{y} - \tilde{\mathbf{u}}'_1\mathbf{G}_1^{-1}\tilde{\mathbf{u}}_1\tilde{\gamma}_1 - \tilde{\mathbf{u}}'_2\mathbf{G}_2^{-1}\tilde{\mathbf{u}}_2\tilde{\gamma}_2 \\
&= \mathbf{y}'\mathbf{y} - \tilde{\mathbf{s}}'\mathbf{W}'\mathbf{y} - \sum_{i=1}^2 \tilde{\mathbf{u}}'_i\mathbf{V}_i^{-1}\tilde{\mathbf{u}}_i\tilde{\gamma}_i.
\end{aligned}$$

Because  $\tilde{\boldsymbol{\sigma}} = \tilde{\mathbf{S}}^{-1}\tilde{\mathbf{Q}}$ , a linear combination of the MIVQUE quadratics defined by  $\mathbf{H}$ , such that  $\mathbf{H}^{-1}$  exists, is also MIVQUE. That is, solving  $\mathbf{H}\tilde{\mathbf{S}}\tilde{\boldsymbol{\sigma}} = \mathbf{H}\tilde{\mathbf{Q}}$  implies

$$\begin{aligned}
\tilde{\boldsymbol{\sigma}} &= (\mathbf{H}\tilde{\mathbf{S}})^{-1}\mathbf{H}\tilde{\mathbf{Q}} \\
&= \tilde{\mathbf{S}}^{-1}\mathbf{H}^{-1}\mathbf{H}\tilde{\mathbf{Q}} \\
&= \tilde{\mathbf{S}}^{-1}\tilde{\mathbf{Q}} \text{ (Henderson, 1984).}
\end{aligned}$$

Thus to simplify calculations, the quadratic form used in place of  $\tilde{\mathbf{e}}'\tilde{\mathbf{e}}$  is

$$Q_0 = \mathbf{y}'\mathbf{y} - \tilde{\mathbf{s}}'\mathbf{W}'\mathbf{y}. \quad [10]$$

Expectations of quadratic forms To calculate the expectations of the quadratic forms, it is useful to partition the nonaugmented coefficient matrix,  $W'W$ , and the inverse of the augmented equations. Let

$$M = \begin{bmatrix} M_0 \\ M_1 \\ M_2 \end{bmatrix} = \begin{bmatrix} X & Z_1 & Z_2 \\ Z_1'X & Z_1'Z_1 & Z_1'Z_2 \\ Z_2'X & Z_2'Z_1 & Z_2'Z_2 \end{bmatrix}, \text{ and}$$

$$\tilde{C}^{-1} = \begin{bmatrix} \tilde{C}^0 \\ \tilde{C}^1 \\ \tilde{C}^2 \end{bmatrix}, \text{ such that } \begin{bmatrix} \tilde{b} \\ \tilde{u}_1 \\ \tilde{u}_2 \end{bmatrix} = \begin{bmatrix} \tilde{C}^0W'y \\ \tilde{C}^1W'y \\ \tilde{C}^2W'y \end{bmatrix}.$$

Then the expectation of [9] for  $i=1,2$ ,  
 $E(\tilde{u}_i'G_i^{-1}\tilde{u}_i) = E(Y'W\tilde{C}^iG_i^{-1}\tilde{C}^iW'y) = E(Y'\tilde{B}_iY)$ , where  
 $\tilde{B}_i = W\tilde{C}^iG_i^{-1}\tilde{C}^iW'$ .

$$\begin{aligned} E(Y'\tilde{B}_iY) &= \text{tr}(\tilde{B}_iV) = \sum_{j=0}^k \text{tr}(\tilde{B}_iV_j)\sigma_j^2 \\ &= \sum_{j=0}^k \text{tr}(\tilde{B}_iZ_jG_jZ_j')\sigma_j^2 \\ &= \sum_{j=0}^k \text{tr}(W\tilde{C}^iG_i^{-1}\tilde{C}^iW'Z_jG_jZ_j')\sigma_j^2 \\ &= \sum_{j=0}^k \text{tr}(\tilde{C}^iG_i^{-1}\tilde{C}^iW'Z_jG_jZ_j'W)\sigma_j^2 \\ &= \sum_{j=0}^k \text{tr}(\tilde{C}^iG_i^{-1}\tilde{C}^iM_j'G_jM_j)\sigma_j^2. \end{aligned}$$

The expectation of [10] is

$$E(Y'y - \tilde{s}'W'y) = E(Y'y) - E(\tilde{s}'W'y). \quad [11]$$

Taking the first half of the expectation of the quadratic form in [11],

$$\begin{aligned}
E(Y'Y) &= \sum_{i=0}^k \text{tr}(V_i) \sigma_i^2 + b'X'Xb \\
&= \sum_{i=0}^k \text{tr}(Z_i G_i Z_i') \sigma_i^2 + b'X'Xb \\
&= \sum_{i=0}^k \text{tr}(G_i Z_i' Z_i) \sigma_i^2 + b'X'Xb.
\end{aligned}$$

This simplifies to

$$E(Y'Y) = \sum_{i=0}^k n \sigma_i^2 + b'X'Xb, \quad [12]$$

if the diagonal elements of  $G_i$  are all 1, because the trace of a product of two matrices is the sum of the products of the diagonal elements if one or both of the matrices is diagonal (Henderson, 1984). All diagonal elements of  $G_i$  are one, if there is no inbreeding among sires, which was the case in this study. The second half of the expectation of the quadratic form in [11] is

$$\begin{aligned}
E(\tilde{s}'W'y) &= E(Y'W\tilde{C}^{-1}W'y) \\
&= E(W\tilde{C}^{-1}W'V) + b'X'W\tilde{C}^{-1}W'Xb \\
&= E\left(\sum_{i=0}^k \text{tr}(W\tilde{C}^{-1}W'Z_i G_i Z_i') \sigma_i^2 + b'X'Xb\right) \\
&= E\left(\sum_{i=0}^k \text{tr}(\tilde{C}^{-1}W'Z_i G_i Z_i'W) \sigma_i^2 + b'X'Xb\right) \\
&= E\left(\sum_{i=0}^k \text{tr}(\tilde{C}^{-1}M_i' G_i M_i) \sigma_i^2 + b'X'Xb\right). \quad [13]
\end{aligned}$$

Combining [11] and [13],

$$\begin{aligned}
E(Y'y - \tilde{s}'W'y) &= \sum_{i=0}^k n \sigma_i^2 + b'X'Xb \\
&\quad - E\left(\sum_{i=0}^k \text{tr}(\tilde{C}^{-1}M_i' G_i M_i) \sigma_i^2 + b'X'Xb\right) \\
&= \sum_{i=0}^k (n - \text{tr}(\tilde{C}^{-1}M_i' G_i M_i)) \sigma_i^2.
\end{aligned}$$

Finally, the variance components are estimated by equating the expectations to the quadratics as described in [8].

Variance component estimation models      Variance

components were calculated for 5 models described in Table 2. The models differ in that the two simplest models (1 and 2) consider only sire and residual variance, while the remaining models include interaction variance. Models 1 and 2 will be referred to as sire models, while models 3, 4, and 5 will be designated as interaction models. Within the sire and interaction model types, the models differ by the way sire relationships were included when estimating sire and interaction variance components.

Table 2. Models used to calculate variance component estimates, considering variance structure of sire effects ( $\text{Var}(\mathbf{u}_1)$ ) and interaction effects ( $\text{Var}(\mathbf{u}_2)$ )

Model	$\text{Var}(\mathbf{u}_1))^a$	$\text{Var}(\mathbf{u}_2))^a$
——— sire models ———		
1	$\mathbf{I}\sigma_1^2$	-
2	$\mathbf{A}\sigma_1^2$	-
——— interaction models ——		
3	$\mathbf{I}\sigma_1^2$	$\mathbf{I}\sigma_2^2$
4	$\mathbf{A}\sigma_1^2$	$\mathbf{I}\sigma_2^2$
5	$\mathbf{A}\sigma_1^2$	$(\mathbf{I}\otimes\mathbf{A})\sigma_2^2$

<sup>a</sup> $\mathbf{I}$  = identity matrix,  
 $\mathbf{A}$  = relationship matrix.

## Results and Discussion

Results are presented for the three structured relationship matrices (i.e., 10 pairs of half-sib sires, 4 sets of 5 half-sib sires, and 20 half-sib sires). Estimates for sire, interaction, and residual variance components are examined to show the effect of underlying assumptions in the analysis model with respect to the relationship matrices. In addition, heritability estimates will be examined. Results for each variance component are discussed for sire and interaction models separately. The effect of sire relationships, data structures, and interaction will be examined for each model type. A brief discussion will follow describing the results found for the relationship matrices taken from the calving ease data.

### Sire variance component estimates

Sire variance estimates averaged over 1000 replicates for each combination of relationship matrix, data structure, and interaction level are in Table 3 for each model. These estimates of sire variance were calculated using the true values of the variance components for the prior estimates in the MIVQUE estimators.

Interaction models Sire variance was underestimated when sire relationships were ignored. This can be verified by comparing estimates for models 3 and 5 for a specific data structure, relationship matrix, and interaction level in



Table 3. Average<sup>a</sup> MIVQUE sire variance component estimates<sup>b</sup> for each combination of the three structured relationship matrices (RELATE), data structure (STRUCT), and level of interaction simulated (INTER) in the data for all models (MODEL)

STRUCT <sup>d</sup>	INTER <sup>e</sup>	RELATE <sup>c</sup>	1					2					3				
		MODEL	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
100%	5%		.06192	.06271	.06130	.06206	.06210	.06085	.06466	.06022	.06391	.06405	.04794	.06392	.04745	.06327	.06327
100%	15%		.06346	.06423	.06161	.06229	.06242	.06135	.06463	.05954	.06251	.06285	.04873	.06498	.04734	.06312	.06311
100%	25%		.06489	.06580	.06170	.06242	.06267	.06230	.06537	.05926	.06182	.06232	.05009	.06678	.04773	.06363	.06362
25%	5%		.06607	.06708	.06078	.06148	.06153	.06454	.06884	.05948	.06287	.06298	.05077	.06764	.04681	.06239	.06237
25%	15%		.07829	.08017	.06206	.06288	.06292	.07622	.08157	.06079	.06371	.06366	.05925	.07889	.04703	.06270	.06272
25%	25%		.08919	.09156	.06227	.06309	.06324	.08618	.09310	.06022	.06316	.06348	.06621	.08813	.04385	.06116	.06117
10%	5%		.08152	.08303	.06174	.06249	.06237	.07975	.08518	.06046	.06344	.06356	.06272	.08297	.04738	.06310	.06316
10%	15%		.12132	.12420	.06209	.06302	.06287	.11512	.12533	.05903	.06208	.06216	.09166	.12031	.04582	.06113	.06109
10%	25%		.16013	.16409	.06242	.06354	.06321	.15313	.16775	.05845	.06172	.06152	.11981	.15668	.04654	.06195	.06196

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>True value for sire variance is .0625.

<sup>c</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>d</sup>Data structure, percentage of herd-sire subclasses filled.

<sup>e</sup>Interaction level simulated, measured as a percent of the total variance.

Table 3. Figure 1 provides a characteristic example of the changes in sire variance for the different models examined by comparing sire variance estimates for the three structured relationship matrices for the intermediate levels of interaction and unbalancedness.

The bias in average sire variance estimates for each relationship matrix by ignoring relationships was nearly constant across levels of interaction and unbalancedness. Table 4 presents the ratio of the average sire variance estimates when relationships were ignored or included for interaction models. The values in Table 4 indicate the average estimate of sire variance when relationships were ignored measured as a portion of that estimate when relationships were accounted for in the variance component model. Clearly, the reduction in sire variance is a function of the relationship matrix across interaction levels and different degrees of data unbalancedness.

Sire variance was unaffected by the level of interaction simulated in the data or the degree of unbalancedness of the data for the interaction models.

Sire models Similar changes in sire variance estimates to those seen for the interaction models were observed when relationships were ignored in the sire models. This can be seen by comparing the average sire variance estimates from models 1 and 2 (Table 3, Figure 1). Table 5 gives the

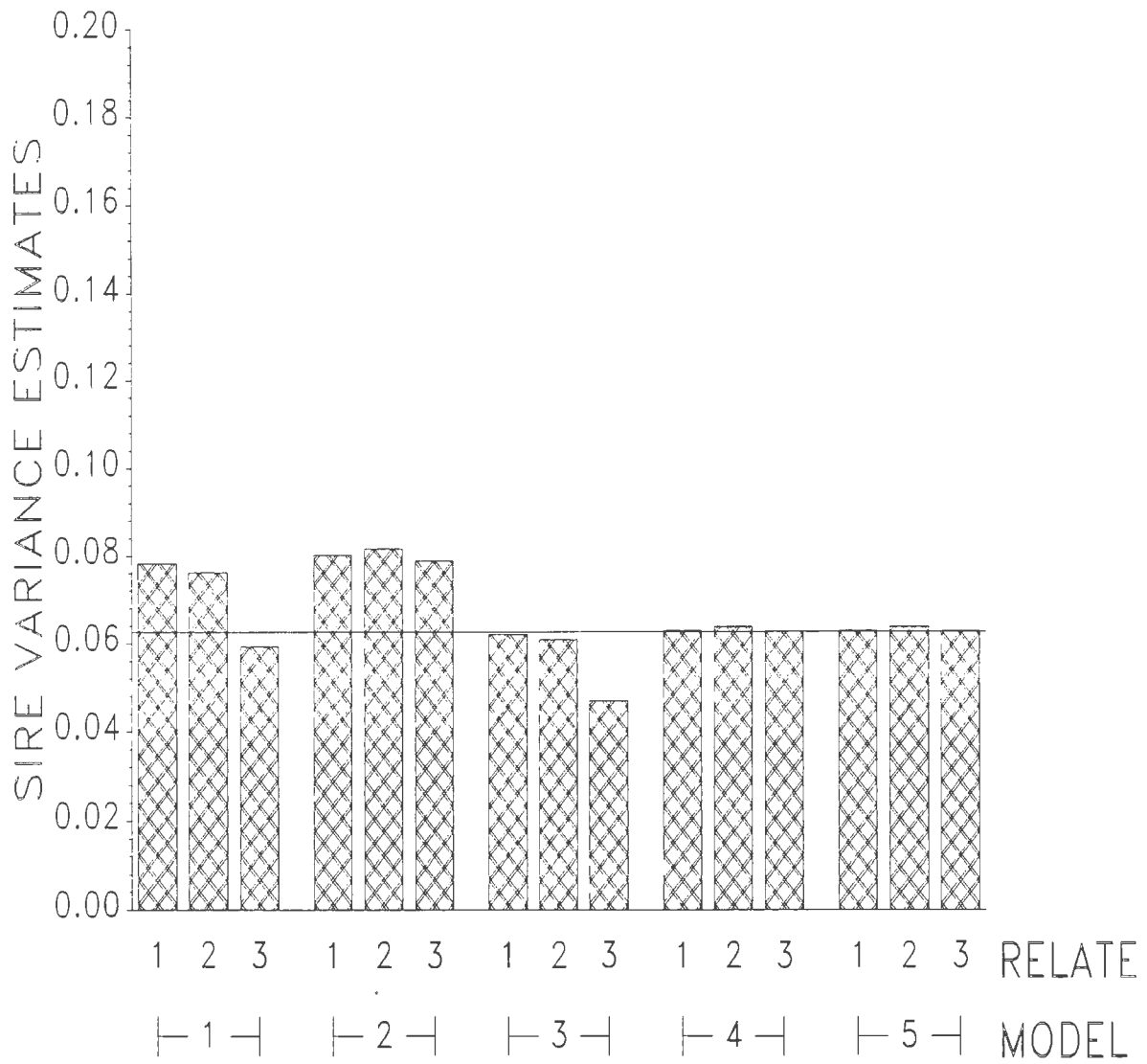


Figure 1. Average sire variance estimates for data with three structured relationship matrices (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

Table 4. Ratio<sup>a</sup> of MIVQUE variance estimates for the average sire variance estimate for model 3 to the average estimate for model 5 for combinations of the three structured relationship matrices (RELATE), data structure (STRUCT), and interaction level (INTER)

STRUCT <sup>c</sup>	INTER <sup>d</sup>	RELATE <sup>b</sup>	1	2	3
100%	5%		.98712	.94020	.74996
100%	15%		.98702	.94733	.75012
100%	25%		.98452	.95090	.75024
25%	5%		.98781	.94443	.75052
25%	15%		.98633	.95492	.74984
25%	25%		.98466	.94865	.71685
10%	5%		.98990	.95123	.75016
10%	15%		.98759	.94965	.75004
10%	25%		.98750	.95010	.75113
MEAN			.98990	.94860	.74654

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>c</sup>Data structure, percentage of herd-sire subclasses filled.

<sup>d</sup>Interaction level simulated, measured as a percent of the total variance.

Table 5. Ratio<sup>a</sup> of MIVQUE variance estimates for the average sire variance estimate for model 1 to the average estimate for model 2 for combinations of the three structured relationship matrices (RELATE), data structure (STRUCT), and interaction level (INTER)

STRUCT <sup>c</sup>	INTER <sup>d</sup>	RELATE <sup>b</sup>	1	2	3
100%	5%		.98740	.94108	.75000
100%	15%		.98801	.94925	.74992
100%	25%		.98617	.95304	.75007
25%	5%		.98494	.93754	.75059
25%	15%		.97655	.93441	.75105
25%	25%		.97412	.92567	.75128
10%	5%		.98181	.93625	.75594
10%	15%		.97681	.91854	.76187
10%	25%		.97587	.91285	.76468
MEAN			.98130	.93429	.75393

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>c</sup>Data structure, percentage of herd-sire subclasses filled.

<sup>d</sup>Interaction level simulated, measured as a percent of the total variance.

average estimates of sire variance when relationships were ignored (model 1) measured as a proportion of the estimate when relationships were included (model 2). The proportionate decreases in sire variance when ignoring relationships are very similar for a given relationship matrix for both sire (Table 4) and interaction models (Table 5).

Average sire variance increased as the level of unbalancedness increased in the data (Figure 2). When the data were nearly balanced (100% filled herd-sire subclasses) the sire variances estimated using sire models were similar to the corresponding estimates obtained with the interaction models. In contrast, when the data were unbalanced, the sire variance estimates were inflated, and this overestimation increased with the level of unbalancedness. The increase in sire variance as unbalancedness increased may be due to increased confounding of sire breeding value predictions and underlying herd by sire interaction effects. Thus, as the number of subclasses with daughters decreased for each sire, the number of different interaction effects under which daughters produced records decreased. This could lead to the underlying interaction effects contributing to the predictions of sire breeding values.

Sire variance estimates and biases also increased as the level of interaction simulated in the data increased

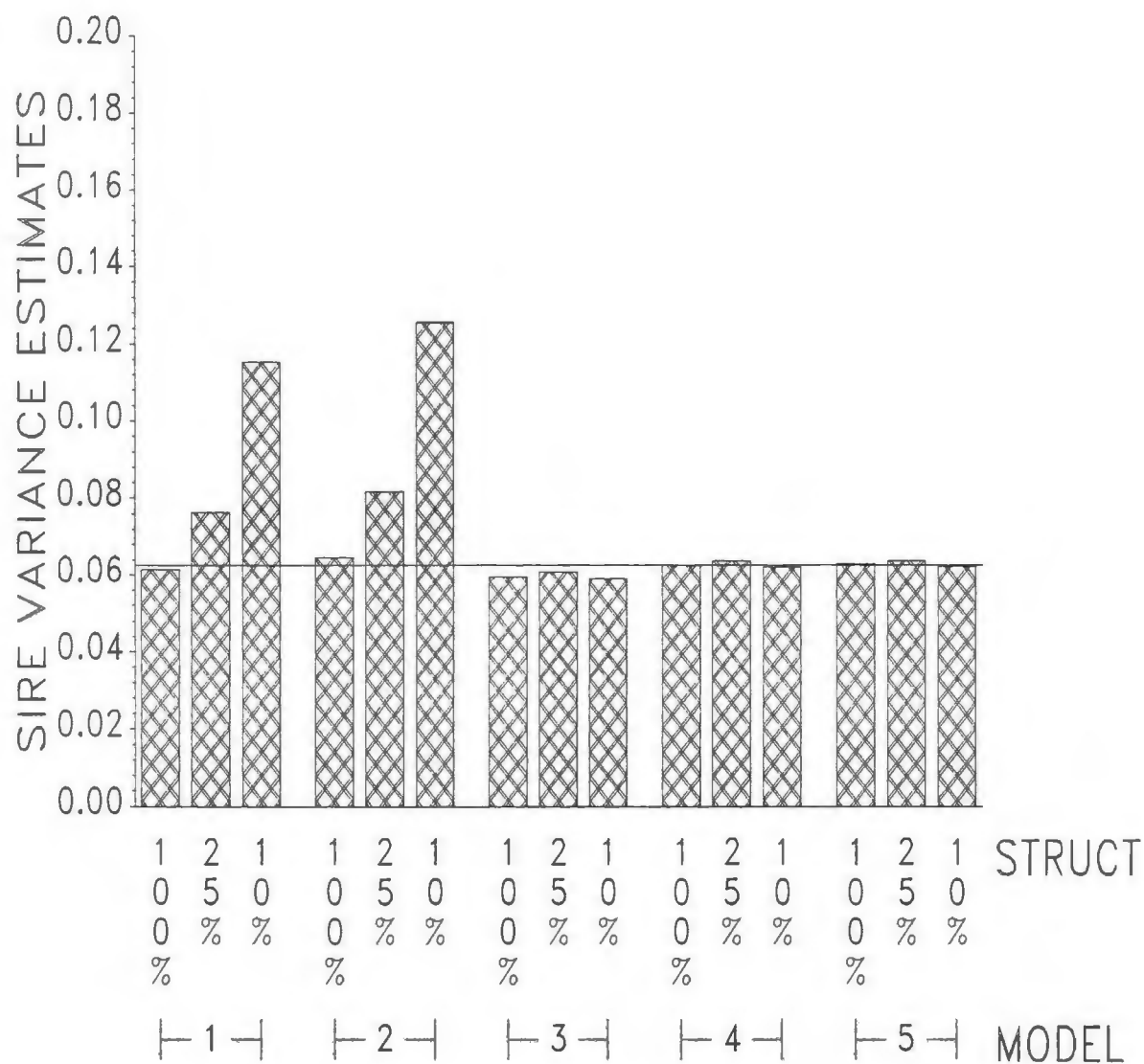


Figure 2. Average sire variance estimates for data with three proportions of filled subclasses (STRUCT), the relationship matrix for 4 groups of 5 half-sib sires, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

(Figure 3). This suggests that if it is assumed that interaction is not important in a population, but is actually present, the sire variance will be overestimated. This would be further compounded by any unbalancedness in the data set.

When comparing sire and interaction models that treated sire relationships alike for estimating sire variance (i.e., models 1 vs. 3 and 2 vs. 5), the sire variance estimated from the sire models was higher than the estimate from the interaction model. That is, the average model 1 estimate of sire variance was greater than the estimate for model 3, and the sire variance estimate from model 2 was greater than the corresponding average for model 5. These differences were measured in proportion to the interaction variance estimate using the true model (model 5) for the same data sets. The proportions presented in Table 6 were similar for each data structure and relationship matrix combination across interaction levels. The similarity of the proportions within a given data structure and relationship matrix combination suggests that the increase in sire variance for each combination was proportional to the level of interaction present in the data. The means were compared by calculating ratios of means for the data structures. These ratios, given in Table 7, were similar for all the relationship matrices. This suggests that the proportionate increase in sire variance when adjusted for the level of interaction in the



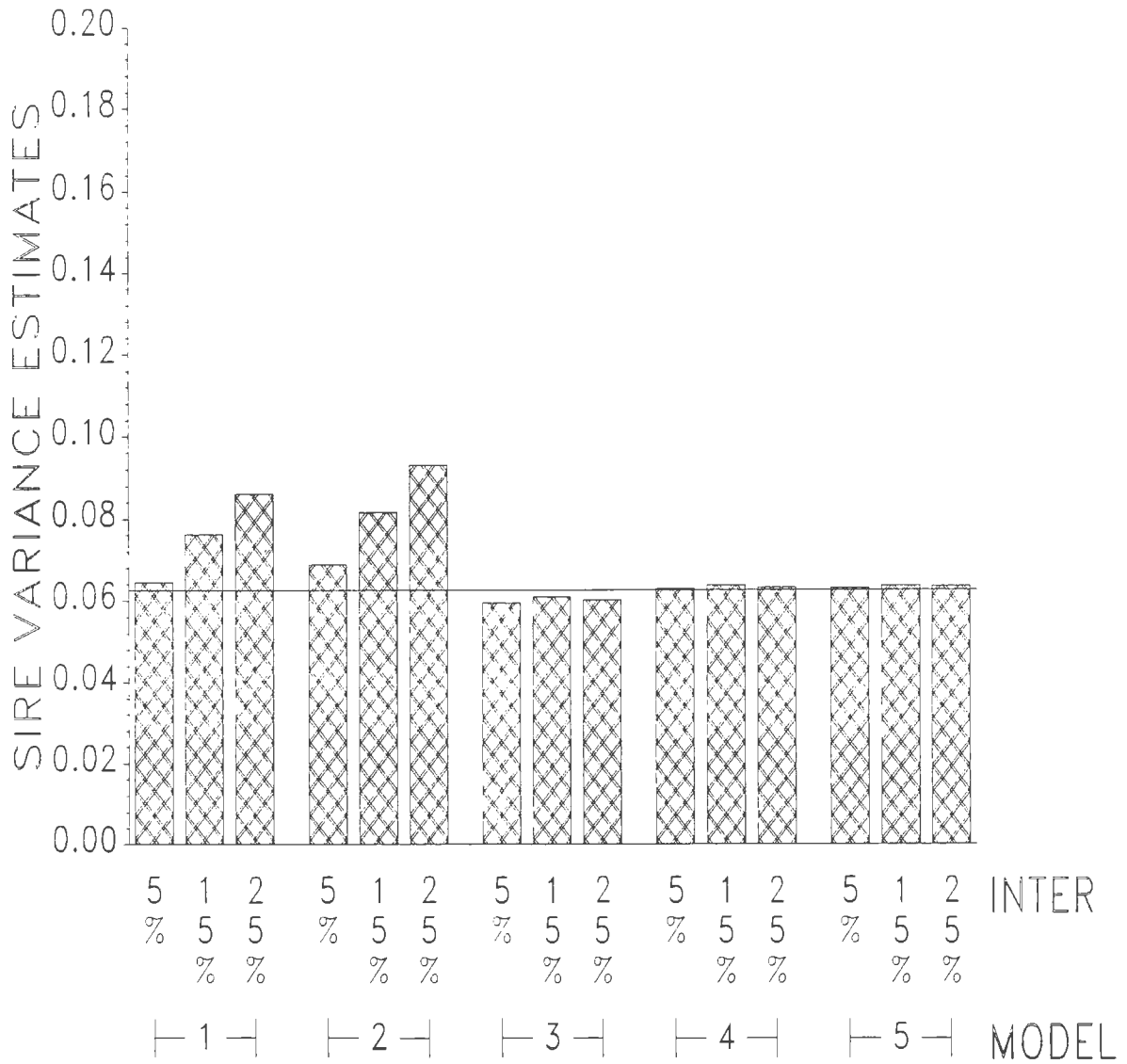


Figure 3. Average sire variance estimates for data with interaction simulated at three levels (INTER), the relationship matrix for 4 groups of 5 half-sib sires, and 25% filled subclasses for 5 variance component estimation models (MODEL)

Table 6. Ratios<sup>a</sup> of differences of average MIVQUE sire variance component estimates when interaction is removed from the variance component model measured as a proportion of the interaction variance estimated using model 5 (5I) for models with relationships ignored for sires (models 1 and 3) ((1S-3S)/5I), and for models with relationships included for sires (models 2 and 5) ((2S-5S)/5I) for combinations of the three structured relationships (RELATE), data structures (STRUCT), and interaction levels (INTER)

STRUCT <sup>c</sup>	INTER <sup>d</sup>	RELATE <sup>b</sup>	1		2		3	
		RATIO	(1S-3S)/5I	(2S-5S)/5I	(1S-3S)/5I	(2S-5S)/5I	(1S-3S)/5I	(2S-5S)/5I
100%	5%		.01244	.01224	.01240	.01200	.00977	.01297
100%	15%		.01225	.01199	.01189	.01169	.00929	.01249
100%	25%		.01266	.01242	.01201	.01205	.00934	.01251
100%	MEAN		.01244	.01222	.01210	.01192	.00947	.01266
25%	5%		.10667	.11192	.10187	.11798	.08034	.10692
25%	15%		.10748	.11424	.10266	.11916	.08186	.10832
25%	25%		.10616	.11168	.10374	.11837	.08986	.10835
25%	MEAN		.10677	.11261	.10276	.11850	.08402	.10786
10%	5%		.39052	.40790	.38472	.43119	.30262	.39081
10%	15%		.39241	.40632	.37373	.42091	.30146	.38945
10%	25%		.39189	.40460	.37798	.42409	.29868	.38612
10%	MEAN		.39161	.40627	.37881	.42540	.30092	.38879

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>c</sup>Data structure, percentage of herd-sire subclasses filled.

<sup>d</sup>Interaction level simulated, measured as a percent of the total variance.

Table 7. Ratios<sup>a</sup> of mean differences adjusted for interaction level in MIVQUE sire variance component estimates from Table 6 for data structures (STRUCT) with differences measured as a proportion of the model 5 interaction estimate (5I) for models 1 and 3 ((1S-3S)/5I) and for models 2 and 5 ((2S-5S)/5I) for the three structured relationship matrices (RELATE)

STRUCT <sup>c</sup>	RELATE <sup>b</sup> RATIO	1 (1S-3S)/5I	2 (2S-5S)/5I	3 (1S-3S)/5I	3 (2S-5S)/5I
100% / 25%		.11663	.10850	.11774	.10055
100% / 10%		.03180	.03007	.03194	.02801
25% / 10%		.27265	.27718	.27126	.27857

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>c</sup>Ratio comparing data structures, percentage of filled herd-sire subclasses.

data was similar for the relationships considered, and these increases were a consistent function of the data structure.

#### Interaction variance component estimates

Average MIVQUE estimates of interaction variance from the interaction models are in Table 8. Variance components are summarized by relationship matrix, data structures, and interaction level. These estimates were calculated using the true values as the prior estimates of the variance components in the MIVQUE estimators.

Interaction models Interaction variance was underestimated if the relationship among sires was ignored in estimating the interaction variance. Similar to the results observed for sire variance estimates, the underestimation of interaction increased with an increasing degree of relatedness among sires. For example, Figure 4 shows the effect of varying levels of sire relationships on interaction for the data sets with data structures having 25% filled subclasses and interaction simulated at 15% of the total variance. The average interaction variance estimate when relationships were ignored measured as a proportion of the estimate when considering relationships are in Table 9. Values in each column of Table 9 are nearly identical for a particular relationship matrix. This suggests that when relationships among sires are ignored in estimating interaction variance that the reduction in the estimated

Table 8. Average<sup>a</sup> MIVQUE interaction variance component estimates<sup>b</sup> for each combination of the three structured relationship matrices (RELATE), data structure (STRUCT), and level of interaction simulated (INTER) in the data for all models (MODEL)

STRUCT <sup>d</sup>	INTER <sup>e</sup>	RELATE <sup>c</sup>								
		MODEL	1	2	3	4	5	3	4	5
100%	5%	.04922	.04922	.04982	.04833	.04833	.05082	.03760	.03761	.05013
100%	15%	.14893	.14892	.15101	.14380	.14378	.15228	.11226	.11225	.14966
100%	25%	.24855	.24854	.25192	.23960	.23960	.25303	.18941	.18941	.25260
25%	5%	.04906	.04907	.04959	.04714	.04719	.04967	.03695	.03694	.04929
25%	15%	.14933	.14937	.15100	.14278	.14275	.15030	.11201	.11202	.14928
25%	25%	.25085	.25086	.25358	.23784	.23778	.25024	.18673	.18673	.24883
10%	5%	.04972	.04971	.05065	.04760	.04758	.05014	.03800	.03803	.05069
10%	15%	.14875	.14857	.15094	.14223	.14211	.15008	.11401	.11399	.15206
10%	25%	.24590	.24542	.24933	.23780	.23727	.25049	.18398	.18402	.24531

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>True value for interaction variance is .05, .15, and .25, for interaction simulated at 5%, 15%, and 25% of the total variance, respectively.

<sup>c</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>d</sup>Data structure, percentage of herd-sire subclasses filled.

<sup>e</sup>Interaction level simulated, measured as a percent of the total variance.

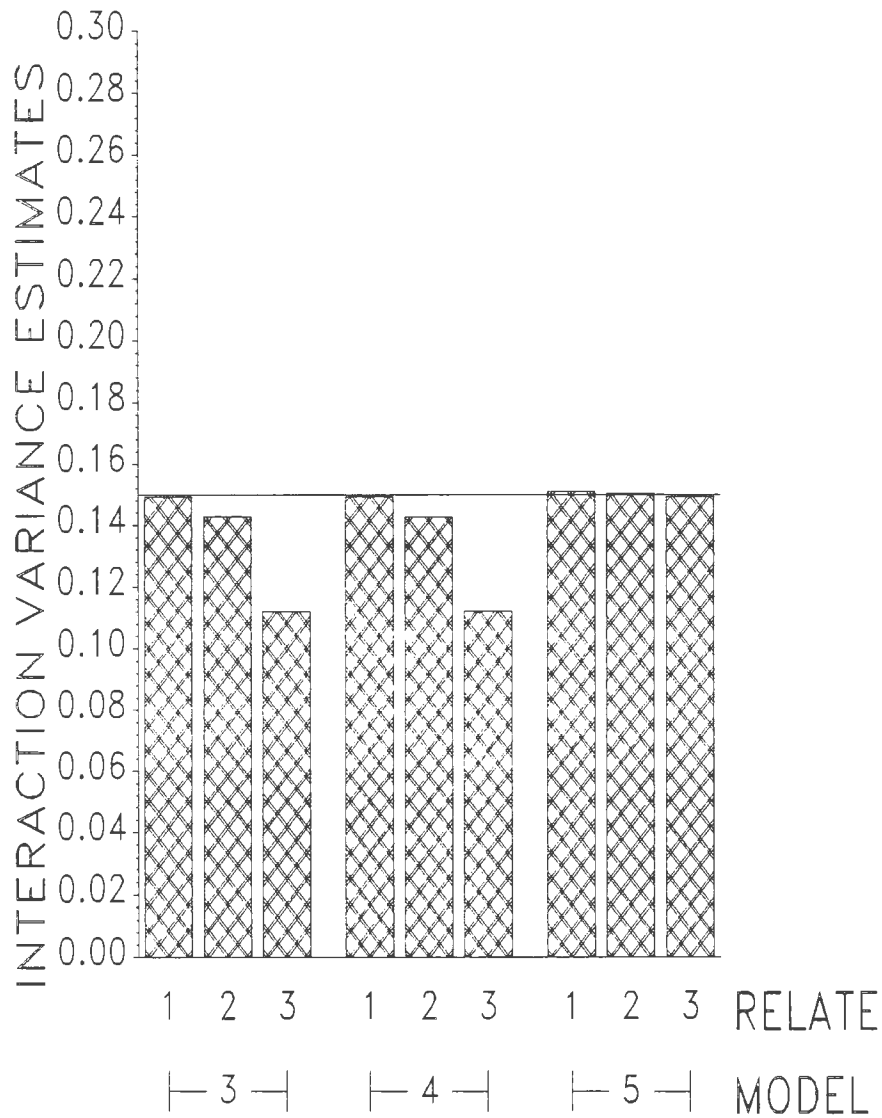


Figure 4. Average interaction variance estimates for data with three structured relationship matrices (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

Table 9. Ratio<sup>a</sup> of model 3 to model 5 interaction variance estimates for combinations of the three structured relationship matrices (RELATE), data structures (STRUCT), and interaction levels (INTER)

STRUCT <sup>b</sup>	INTER <sup>d</sup>	RELATE <sup>b</sup>	1	2	3
100%	5%		.98796	.95100	.75005
100%	15%		.98623	.94431	.75010
100%	25%		.98662	.94692	.74984
25%	5%		.98931	.94906	.74964
25%	15%		.98894	.94997	.75033
25%	25%		.98923	.95045	.75043
10%	5%		.98164	.94934	.74965
10%	15%		.98549	.94769	.74977
10%	25%		.98624	.94934	.74999
MEAN			.98685	.94868	.74998

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>c</sup>Data structure, percentage of herd-sire subclasses filled.

<sup>d</sup>Interaction level simulated, measured as a percent of the total variance.

interaction variance depends on the degree of relatedness among sires and level of interaction in the data. The reduction in interaction variance estimates when ignoring relationships was independent of the data structure. The proportions in Table 9 for interaction variance are very similar to those seen for the sire variance estimates in Tables 4 and 5.

As the level of interaction simulated increased, the average estimates of interaction variance increased. There seemed to be no interaction with levels of relationships or unbalancedness. Figure 5 contains interaction variance estimates for the interaction models for the data sets spanning interaction levels for the intermediate levels of unbalancedness (25% filled subclasses) and relationships (4 groups of 5 half-sib sires). Interaction variance estimated by model 3 was approximately equal to that estimated by model 4 and estimates by both models was less than that for the true model (model 5).

The degree of unbalancedness present in the data did not alter interaction variance estimates. Figure 6 presents average interaction estimates for data including the three levels of unbalancedness and intermediate unbalancedness and sire relationships.



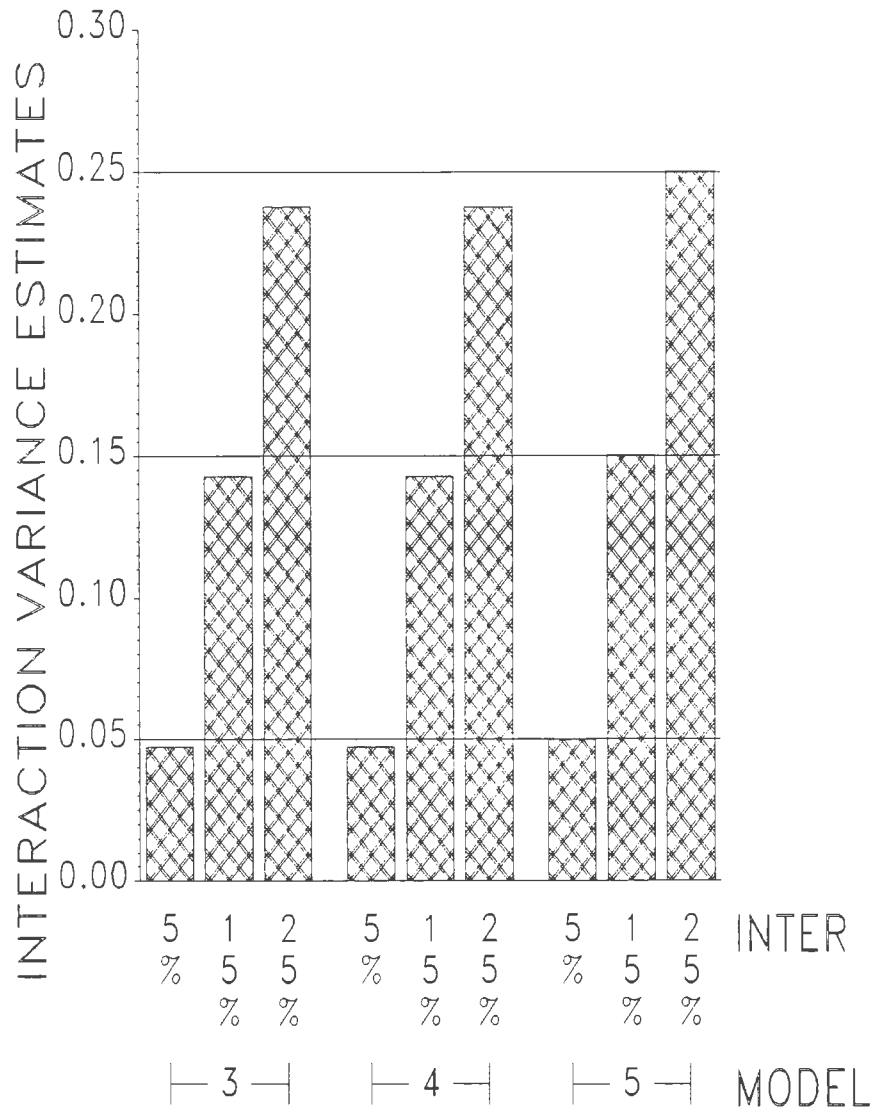


Figure 5. Average interaction variance estimates for data with interaction simulated at three levels (INTER), the relationship matrix for 4 groups of 5 half-sib sires, and 25% filled subclasses for 5 variance component estimation models (MODEL)

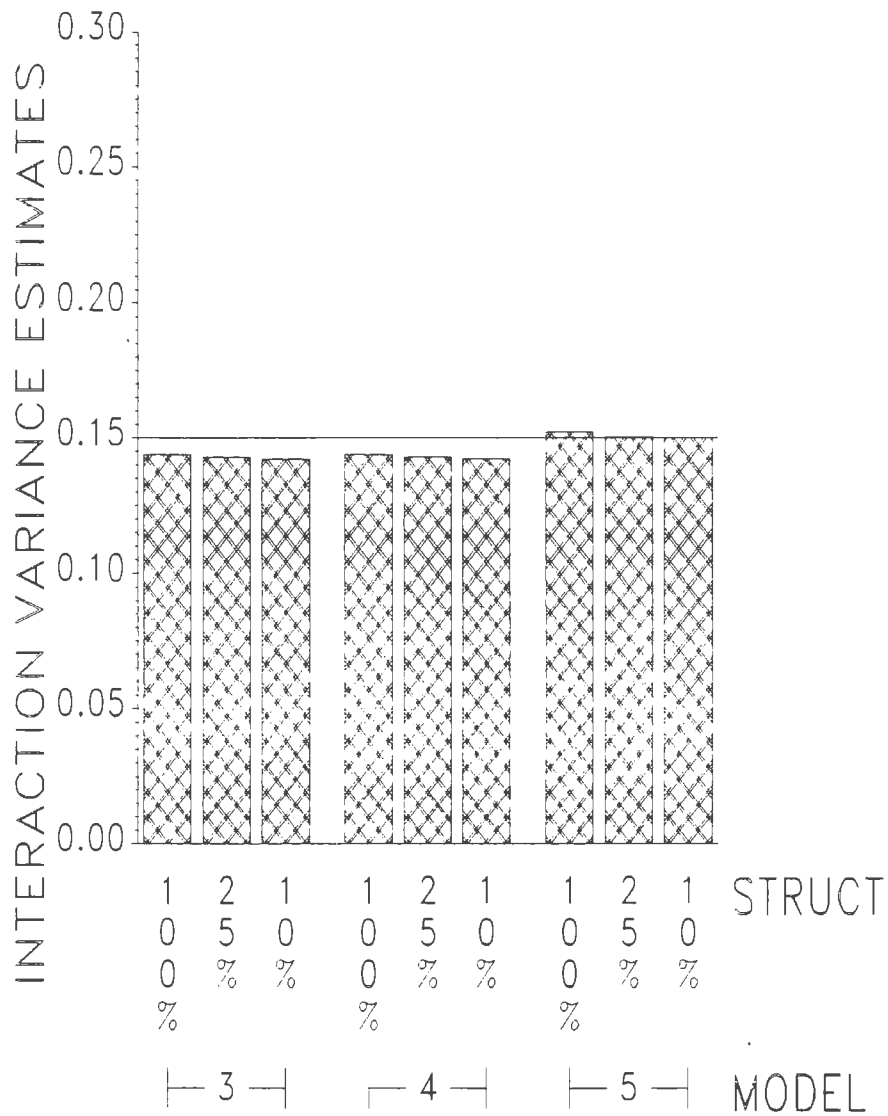


Figure 6. Average interaction variance estimates for data with three proportions of filled subclasses (STRUCT), the relationship matrix for 4 groups of 5 half-sib sires, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

### Residual variance component estimates

Average MIVQUE estimates of residual variance components for combinations of relationship matrices, unbalancedness, and interaction levels are presented in Table 10. These estimates were calculated using the true values as the prior estimates of the variance components in the MIVQUE estimator. Residual variance component estimates were nearly identical within sire and interaction model types.

Interaction models The level of interaction variance affected average residual variance estimates in that the total variance was held constant for all simulations, so that any increase in the level of interaction simulated corresponded to a decrease in the residual variance generated in the data. Figure 7 shows the decrease in residual variance estimates associated with the increasing level of interaction present for the data sets with intermediate unbalancedness and relatedness. The effect of sire relationships are presented in Figure 8, where average residual variances were estimated for data with different relationship matrices, data structures with 25% filled subclasses, and interaction simulated at 15% of the total variance. The degree of sire relationships did not affect average residual variances for interaction models. Similarly, Figure 9 presents average residual variance estimates for data with varying degrees of unbalancedness and

Table 10. Average<sup>a</sup> MIVQUE residual variance component estimates<sup>b</sup> for each combination of the three structured relationship matrices (RELATE), data structure (STRUCT), and level of interaction simulated (INTER) in the data for all models (MODEL)

STRUCT <sup>d</sup>	INTER <sup>e</sup>	RELATE <sup>c</sup>	1					2					3				
		MODEL	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
100%	5%		.93836	.93836	.89130	.89130	.89136	.93690	.93690	.89069	.89069	.89088	.92576	.92576	.88981	.88981	.88982
100%	15%		.93373	.93373	.79133	.79134	.79126	.92710	.92710	.78959	.78959	.78912	.89901	.89901	.79168	.79168	.79169
100%	25%		.92804	.92804	.69035	.69035	.69031	.91819	.91819	.68910	.68909	.68899	.87064	.87065	.68951	.68951	.68948
25%	5%		.92452	.92453	.88985	.88985	.88984	.92460	.92463	.89128	.89128	.89125	.91684	.91685	.89073	.89073	.89072
25%	15%		.89651	.89655	.79113	.79113	.79112	.89269	.89274	.79173	.79174	.79176	.86896	.86897	.78991	.78991	.78992
25%	25%		.86785	.86790	.69024	.69024	.69025	.85739	.85745	.68932	.68933	.68935	.82161	.82163	.68991	.68991	.68994
10%	5%		.90985	.90989	.89202	.89202	.89199	.90697	.90705	.89000	.88998	.89000	.90627	.90632	.89269	.89269	.89268
10%	15%		.84320	.84331	.79014	.79014	.79011	.84206	.84230	.79085	.79085	.79085	.83031	.83046	.78946	.78946	.78945
10%	25%		.77792	.77810	.69033	.69033	.69032	.77454	.77492	.68972	.68972	.68972	.75634	.75658	.69043	.69043	.69044

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>True value for residual variance for interaction models is .8875, .8775, and .8675, for interaction simulated at 5%, 15%, and 25% of the total variance, respectively, and .9375 for all sire models.

<sup>c</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>d</sup>Data structure, percentage of herd-sire subclasses filled.

<sup>e</sup>Interaction level simulated, measured as a percent of the total variance.

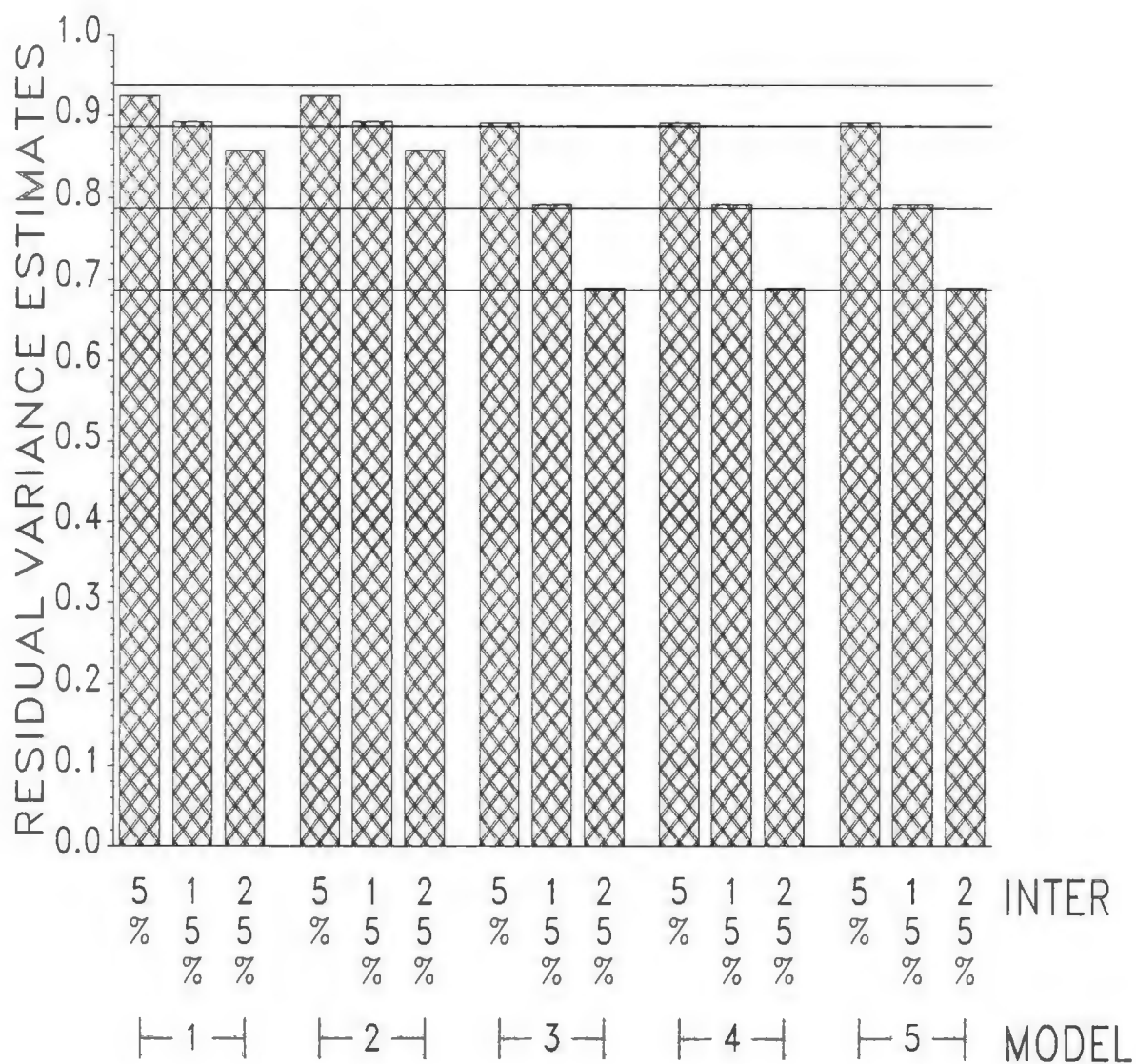


Figure 7. Average residual variance estimates for data with interaction simulated at three levels (INTER), the relationship matrix for 4 groups of 5 half-sib sires, and 25% filled subclasses for 5 variance component estimation models (MODEL)

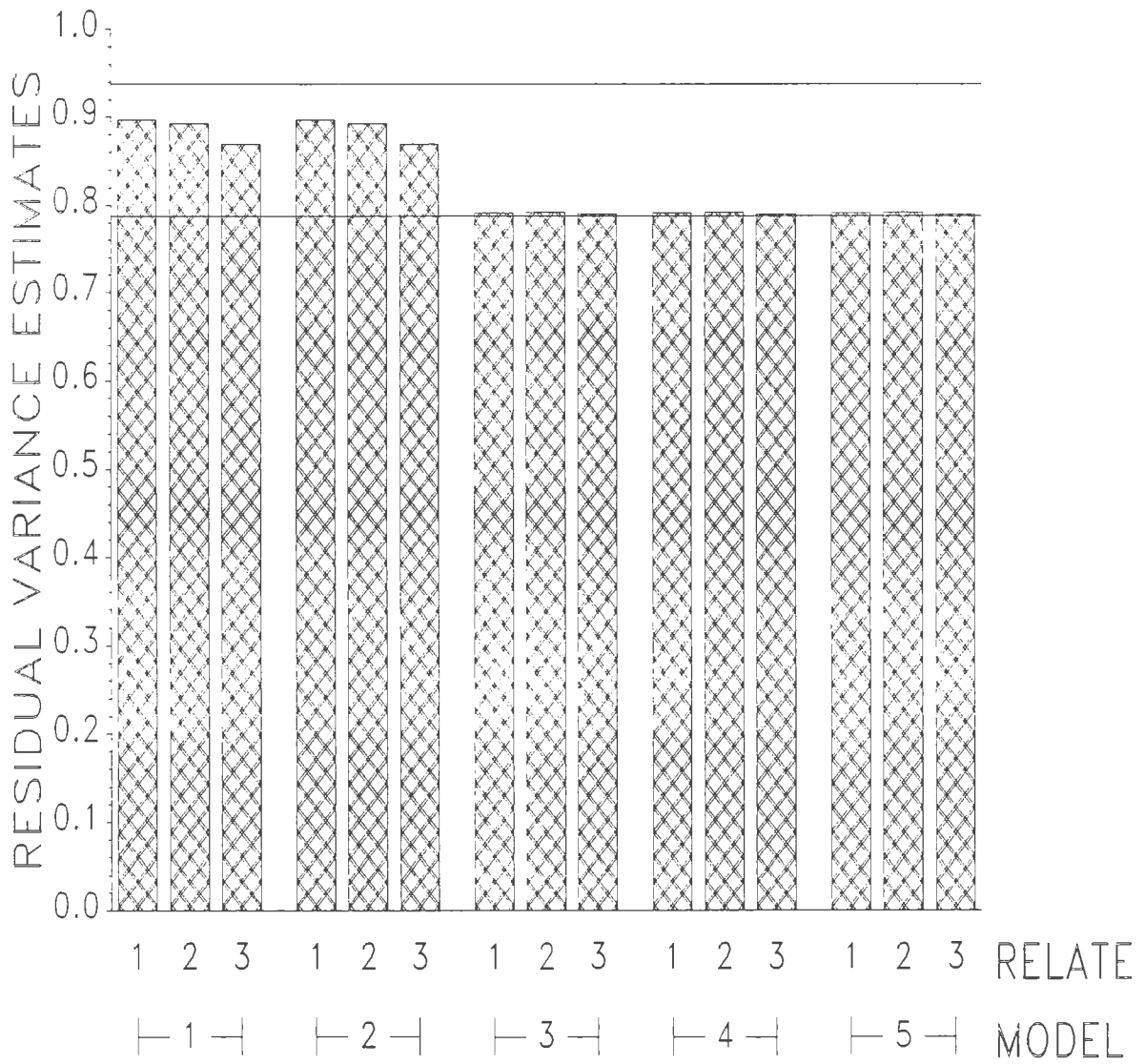


Figure 8. Average residual variance estimates for data with three structured relationship matrices (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

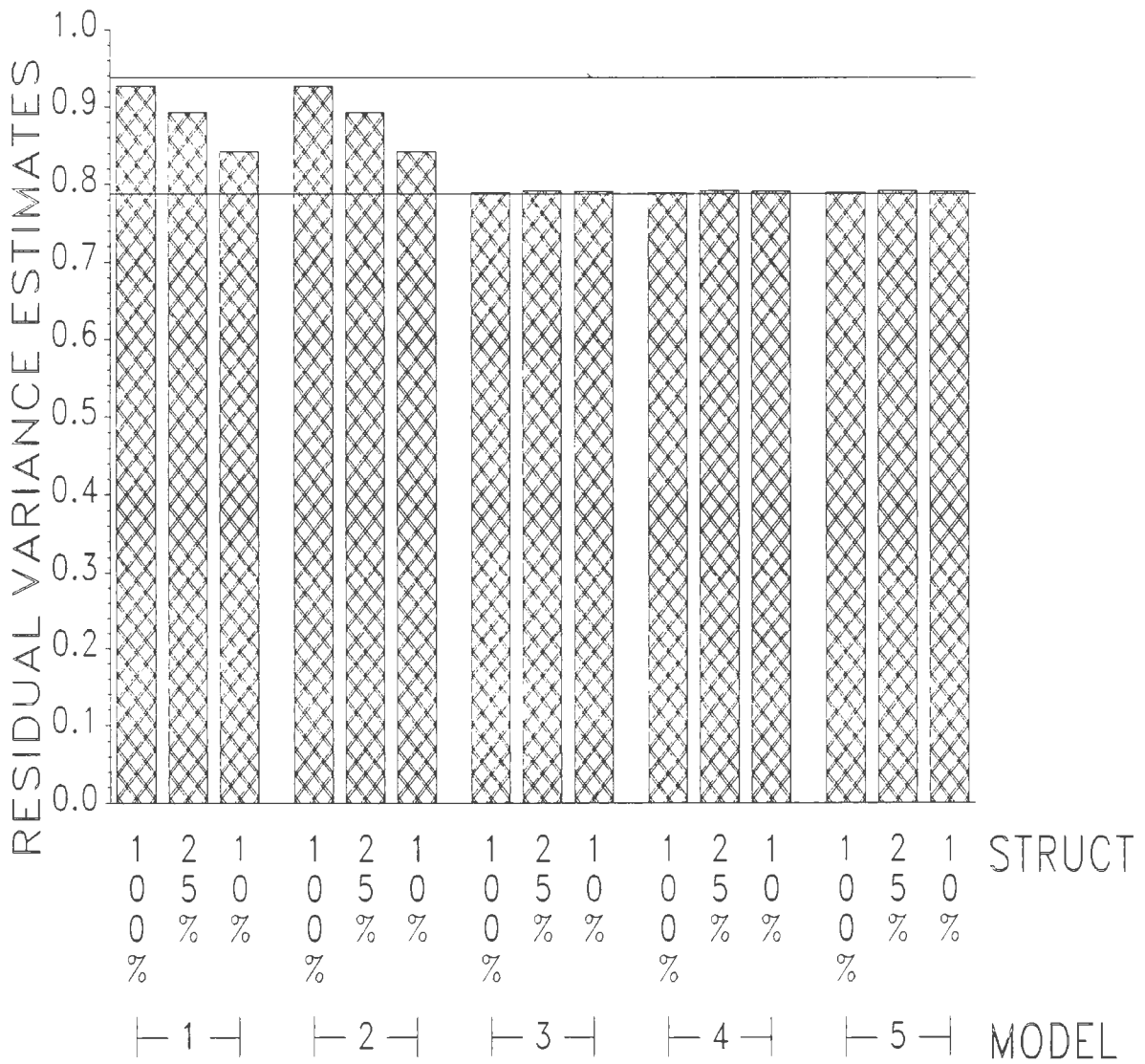


Figure 9. Average residual variance estimates for data with three proportions of filled subclasses (STRUCT), the relationship matrix for 4 groups of 5 half-sib sires, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

medial interaction and sire relationships. Unbalancedness did not affect average residual variance estimates for interaction models.

Sire models Residual variance in the sire models included both the residual and interaction variance from the interaction models (this value is indicated with the highest horizontal line in Figures 7, 8, and 9). In nearly all cases the residual variance was underestimated when components of variance were estimated with a sire model. The degree of underestimation of residual variance increased with increasing levels of interaction (Figure 7), sire relationships (Figure 8), and data unbalancedness (Figure 9).

Comparing residual variance estimates for sire and interaction models, the average estimates for the sire models were always higher for the sire models than the interaction models. Similar to the comparison made for the changes in sire variance estimates, differences in residual variance estimates were calculated for models treating sire relationships alike (i.e., models 1 vs. 3 and 2 vs. 5), and these differences were also measured in proportion to the interaction variance estimate using the true model (model 5) for the same data sets. The proportions presented in Table 11 were similar for each data structure and relationship matrix combination across interaction levels. This is similar to the pattern noted for the sire variance



Table 11. Ratios<sup>a</sup> of differences of average MIVQUE residual variance component estimates when interaction is removed from the variance component model measured as a proportion of the interaction variance estimated using model 5 (5I) for models with relationships ignored for sires (models 1 and 3) ((1S-3S)/5I), and for models with relationships included for sires (models 2 and 5) ((2S-5S)/5I) for combinations of the three structured relationships (RELATE), data structures (STRUCT), and interaction levels (INTER)

STRUCT <sup>c</sup>	INTER <sup>d</sup>	RELATE <sup>b</sup> RATIO	1 (1R-3R)/5I	(2R-5R)/5I	2 (1R-3R)/5I	(2R-5R)/5I	3 (1R-3R)/5I	(2R-5R)/5I
100%	5%		.94460	.94340	.90929	.90555	.71714	.71694
100%	15%		.94298	.94345	.90301	.90609	.71716	.71709
100%	25%		.94351	.94367	.90539	.90582	.71706	.71722
100%	MEAN		.94370	.94351	.90589	.90582	.71712	.71708
25%	5%		.69913	.69954	.67083	.67204	.52972	.53013
25%	15%		.69788	.69821	.67172	.67186	.52954	.52954
25%	25%		.70041	.70057	.67164	.67176	.52928	.52924
25%	MEAN		.69914	.69944	.67140	.67188	.52951	.52964
10%	5%		.35202	.35341	.33845	.34005	.26790	.26909
10%	15%		.35153	.35246	.34122	.34282	.26864	.26970
10%	25%		.35130	.35206	.33862	.34013	.26868	.26962
10%	MEAN		.35162	.35264	.33943	.34100	.26841	.26947

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>c</sup>Data structure, percentage of herd-sire subclasses filled.

<sup>d</sup>Interaction level simulated, measured as a percent of the total variance.

differences. The similarity of the proportions for data structure and relationship matrix combinations suggests that the increase in residual variance for each combination was proportional to the level of interaction present in the data. The means were compared across data structures by calculating ratios of means for the data structures. The ratios, given in Table 12, were similar for all the relationship matrices. This suggests that the proportionate increase in residual variance when adjusted for the level of interaction in the data was similar for the relationships considered, and these increases were a consistent function of the data structure.

#### Heritability estimates

Average estimates of heritability for combinations of relationships, unbalancedness, and interaction levels are presented in Table 13. These estimates were calculated using the true values as the prior estimates of the components for the MIVQUE estimators.

Interaction models Average heritability estimates were usually slightly overestimated when relationships were ignored for interaction variance but included for sire variance estimates (i.e., for model 4). This is probably due to the decrease in total variance corresponding to the underestimate of interaction variance when ignoring relationships. However, when relationships were ignored for sire variance estimates as well (model 3), there was a

Table 12. Ratios<sup>a</sup> of mean differences adjusted for interaction level in MIVQUE residual variance component estimates from Table 11 for data structures (STRUCT) with differences measured as a proportion of the model 5 interaction estimate (5I) for models 1 and 3 ((1R-3R)/5I) and for models 2 and 5 ((2R-5R)/5I) for the structured relationship matrices (RELATE)

STRUCT <sup>c</sup>	RELATE <sup>b</sup> RATIO	1		2		3	
		(1R-3R)/5I	(2R-5R)/5I	(1R-3R)/5I	(2R-5R)/5I	(1R-3R)/5I	(2R-5R)/5I
100% / 25%		1.34980	1.34895	1.34927	1.34818	1.35430	1.35392
100% / 10%		2.68387	2.67553	2.66888	2.65637	2.67174	2.66112
25% / 10%		1.98835	1.98342	1.97801	1.97033	1.97279	1.96549

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>c</sup>Ratio comparing data structures, percentage of herd-sire subclasses filled.

Table 13. Average<sup>a</sup> heritability estimates<sup>b</sup> for each combination of the three structured relationship matrices (RELATE), data structure (STRUCT), and level of interaction simulated (INTER) in the data for all models (MODEL)

STRUCT <sup>d</sup>	INTER <sup>e</sup>	RELATE <sup>c</sup>	1					2					3				
		MODEL	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
100%	5%		.24571	.24879	.24287	.24580	.24580	.24195	.25617	.23906	.25286	.25271	.19570	.25617	.19348	.25330	.25023
100%	15%		.25266	.25558	.24410	.24665	.24664	.24616	.25865	.23776	.24909	.24840	.20425	.26715	.19765	.25864	.24913
100%	25%		.25946	.26294	.24475	.24749	.24763	.25195	.26395	.23784	.24780	.24644	.21617	.28248	.20461	.26760	.25095
25%	5%		.26439	.26818	.24090	.24351	.24357	.25902	.27511	.23659	.24922	.24904	.20840	.27227	.19072	.24958	.24652
25%	15%		.31846	.32550	.24529	.24834	.24808	.31123	.33143	.24120	.25216	.25017	.25335	.32946	.19653	.25688	.24766
25%	25%		.36899	.37782	.24546	.24836	.24841	.36112	.38739	.24067	.25169	.24993	.29570	.38307	.19701	.25754	.24203
10%	5%		.32515	.33070	.24298	.24577	.24510	.31957	.33944	.23909	.25009	.24999	.25657	.33157	.19185	.25054	.24784
10%	15%		.49667	.50682	.24420	.24757	.24652	.47419	.51079	.23347	.24460	.24328	.39306	.49891	.19061	.24862	.23985
10%	25%		.67103	.68483	.24474	.24876	.24683	.64883	.69892	.23137	.24316	.23972	.53933	.67464	.19869	.25736	.24333

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>True value for heritability is .25.

<sup>c</sup>Relationship matrices, 1: 10 pairs of half-sib sire pairs; 2: 5 half-sib sires; 3: 20 half-sib sires.

<sup>d</sup>Data structure, percentage of filled herd-sire subclasses filled.

<sup>e</sup>Interaction level simulated, measured as a percent of the total variance.

noticeable decrease in heritability estimates. This underestimation of heritability increased as the degree of sire relationships increased. Figure 10 presents a characteristic example of the effect of sire relationships on heritability by displaying estimates for data sets for all the structured relationship matrices and the data structure with 25% filled subclasses and interaction simulated at 15% of the total variance. Figure 11 shows heritability estimates for data across the three levels of interaction and the relationship matrix for 4 groups of 5 half-sib sires and the data structure with intermediate (15% filled subclasses) unbalancedness. Interaction level present in the data did not affect average heritability estimates for interaction models. Figure 12 contains average heritability estimates for data with differing levels of unbalancedness with intermediate sire relationships and interaction. Unbalancedness did not affect heritability estimates for the interaction models.

Sire models Heritability estimates using sire models ranged from slightly underestimated to dramatically overestimated (Table 13). Heritability estimates decreased if relationships were ignored using model 1 compared to the estimates including relationships using model 2, and this bias increased with increasing levels of sire relatedness (Figure 10). However, heritability increased with the level

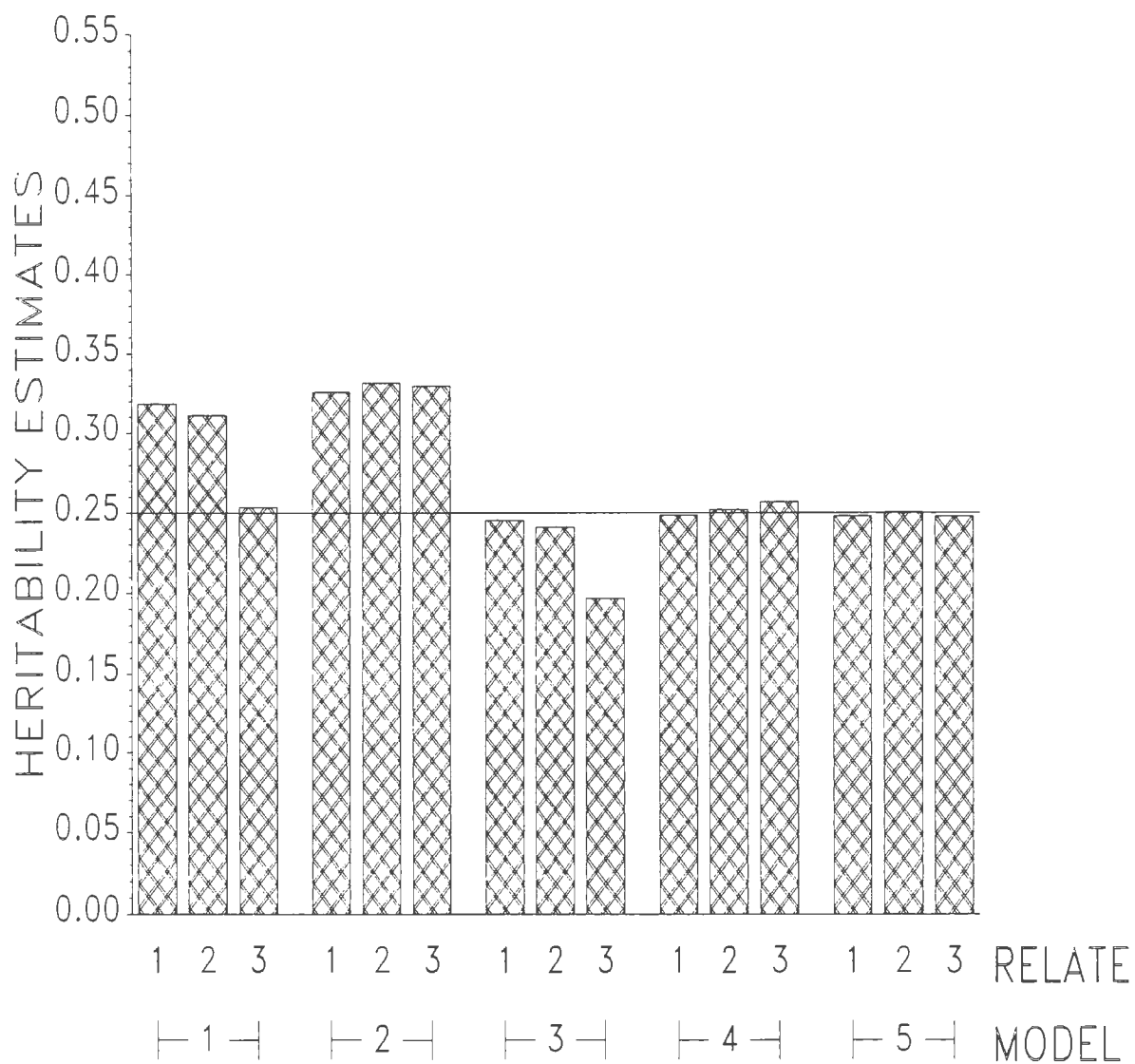


Figure 10. Average heritability estimates for data with three structured relationship matrices (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for the 5 variance component estimation models (MODEL)

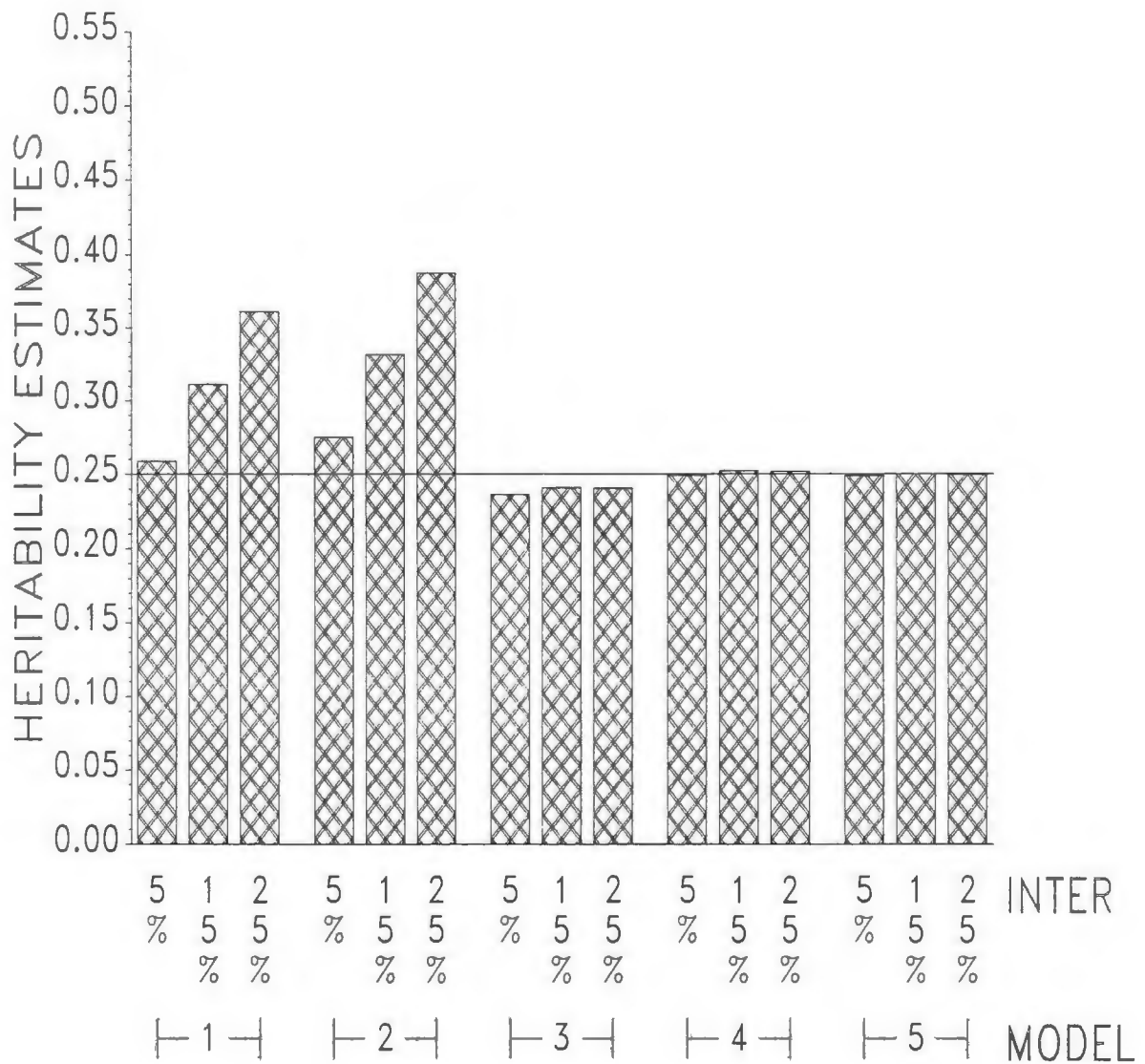


Figure 11. Average heritability estimates for data with interaction simulate at three levels (INTER), the relationship matrix for 4 groups of 5 half-sib sires, and 25% filled subclasses for 5 variance component estimation models (MODEL)

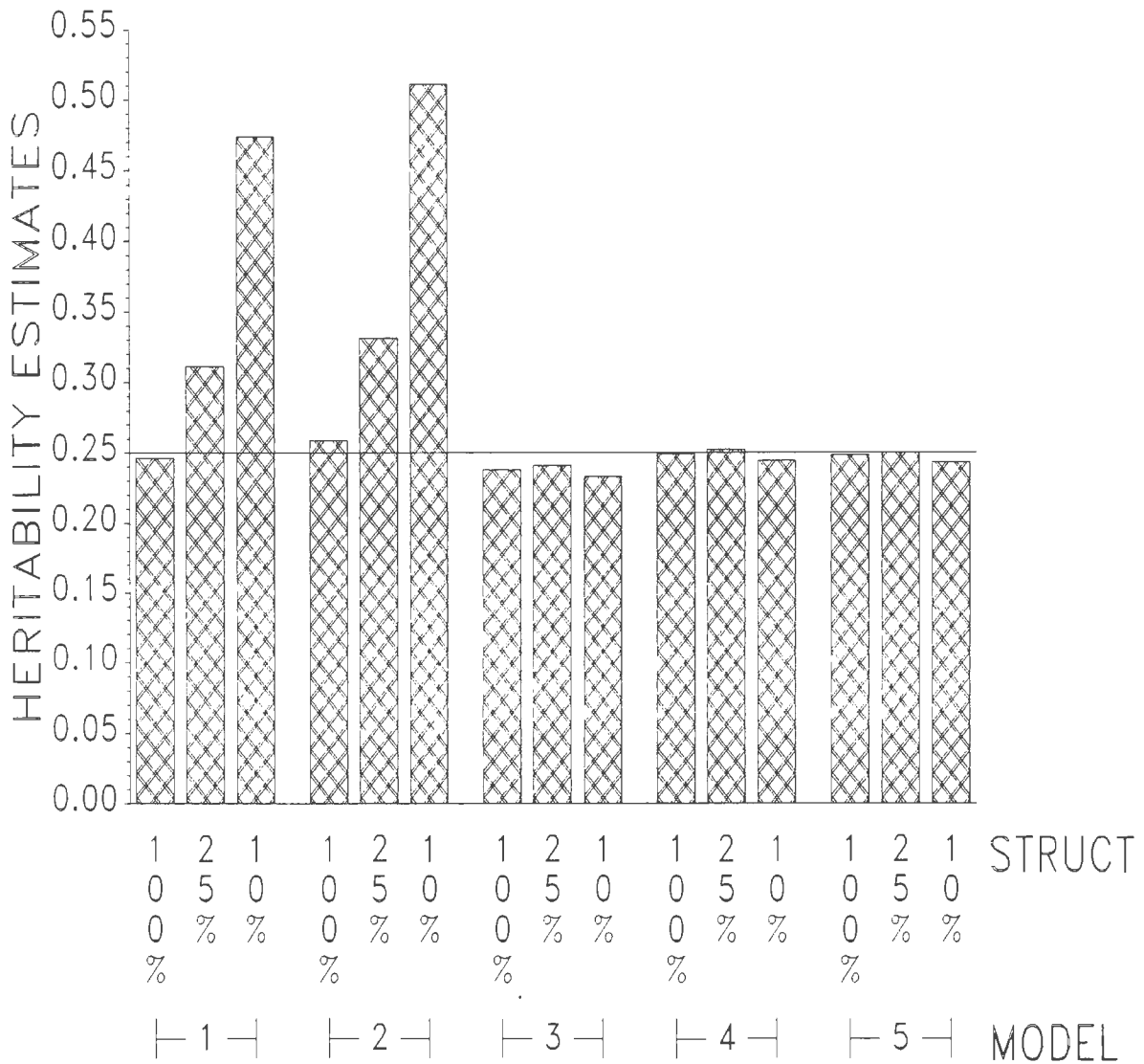


Figure 12. Average heritability estimates for data with three proportions of filled subclasses (STRUCT), the relationship matrix for 4 groups of 5 half-sib sires, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)



of interaction (Figure 11) and the degree of unbalancedness (Figure 12) regardless of whether relationships were included or ignored. The dramatic biases in heritability estimates can be attributed to two major factors: first, any bias in sire estimates is magnified when calculating additive genetic variance based on sire variance estimates (4 times), and second, the biases in sire and residual variance component estimates tended to be in opposite directions, so that often as sire variance estimates increased the total variance estimate decreased. As a result, the heritability often increased drastically when interaction was removed from the model.

#### Relationship matrices from calving ease data

Average variance component and heritability estimates for the relationship matrices selected from the calving ease evaluation data were calculated. These relationship matrices will be referred to as the calving ease (CE) relationship matrices. Relationship matrix 4, that of the young sires, had average nonzero off-diagonals of .099 with 14.74% filled off-diagonal elements. Relationship matrix 5, that for 20 sires without restrictions, had average nonzero off-diagonal elements of .155 with 13.16% of the off-diagonals being nonzero. The most common nonzero off-diagonal element in both relationship matrices 4 and 5 was .0625.

Table 14 contains average sire variance estimates for the relationship structures 4 and 5. Figure 13 graphically presents the effects of the relationships from field data compared to the first structured relationship matrix (10 pairs of half-sib sires) on average sire variance estimates for data with median unbalancedness and interaction level. The ratio of average sire variance estimates for interaction models including or ignoring sire relationships (i.e., for models 3 to 5) was .98535 and .98054 for relationship matrices 4 and 5, respectively. The analogous ratio for sire models (i.e., models 1 to 2) was .98219 and .96977. These ratios were very similar to those seen for matrix 1 for the same comparisons (Table 4, Table 5). In general, ignoring the sire relationships did not have a large effect on sire variance estimates for these data due to the low degree of relatedness among sires.

Table 15 contains average interaction variance component estimates for the CE relationship matrices for combinations of data structure and interaction levels. Figure 14 compares estimates of interaction variance for the structured relationship matrix for 10 pairs of half-sib sires (relationship matrix 1) with estimates for the relationship structures from the calving ease data (relationship matrices 4 and 5) for data simulated using intermediate levels of interaction and unbalancedness. The average ratio of the

Table 14. Average<sup>a</sup> MIVQUE sire variance component estimates<sup>b</sup> for each combination of the two relationship matrices selected from the calving ease data (RELATE), data structure (STRUCT), and level of interaction (INTER) simulated in the data for all models (MODEL)

STRUCT <sup>d</sup>	INTER <sup>e</sup>	RELATE <sup>c</sup>	4					5				
		MODEL	1	2	3	4	5	1	2	3	4	5
100%	5%		.06353	.06449	.06290	.06383	.06386	.06119	.06264	.06058	.06198	.06205
100%	15%		.06421	.06504	.06235	.06310	.06317	.06389	.06548	.06206	.06349	.06369
100%	25%		.06461	.06551	.06154	.06233	.06246	.06517	.06642	.06205	.06307	.06333
25%	5%		.06725	.06836	.06191	.06282	.06285	.06642	.06825	.06118	.06263	.06266
25%	15%		.07702	.07859	.06090	.06184	.06190	.07655	.07891	.06079	.06215	.06223
25%	25%		.09030	.09245	.06355	.06457	.06464	.08928	.09245	.06253	.06402	.06395
10%	5%		.08193	.08333	.06219	.06302	.06310	.08049	.08293	.06115	.06216	.06219
10%	15%		.12033	.12281	.06158	.06234	.06244	.12169	.12692	.06321	.06400	.06393
10%	25%		.16321	.16696	.06233	.06299	.06315	.15848	.16580	.06001	.06076	.06054

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>True value for sire variance is .0625.

<sup>c</sup>Relationship matrices, 4: 20 young sires from the calving ease data; 5: 20 sires of any age from the same data set.

<sup>d</sup>Data structure, percentage of filled herd-sire subclasses filled.

<sup>e</sup>Interaction level simulated, measured as a percent of the total variance.

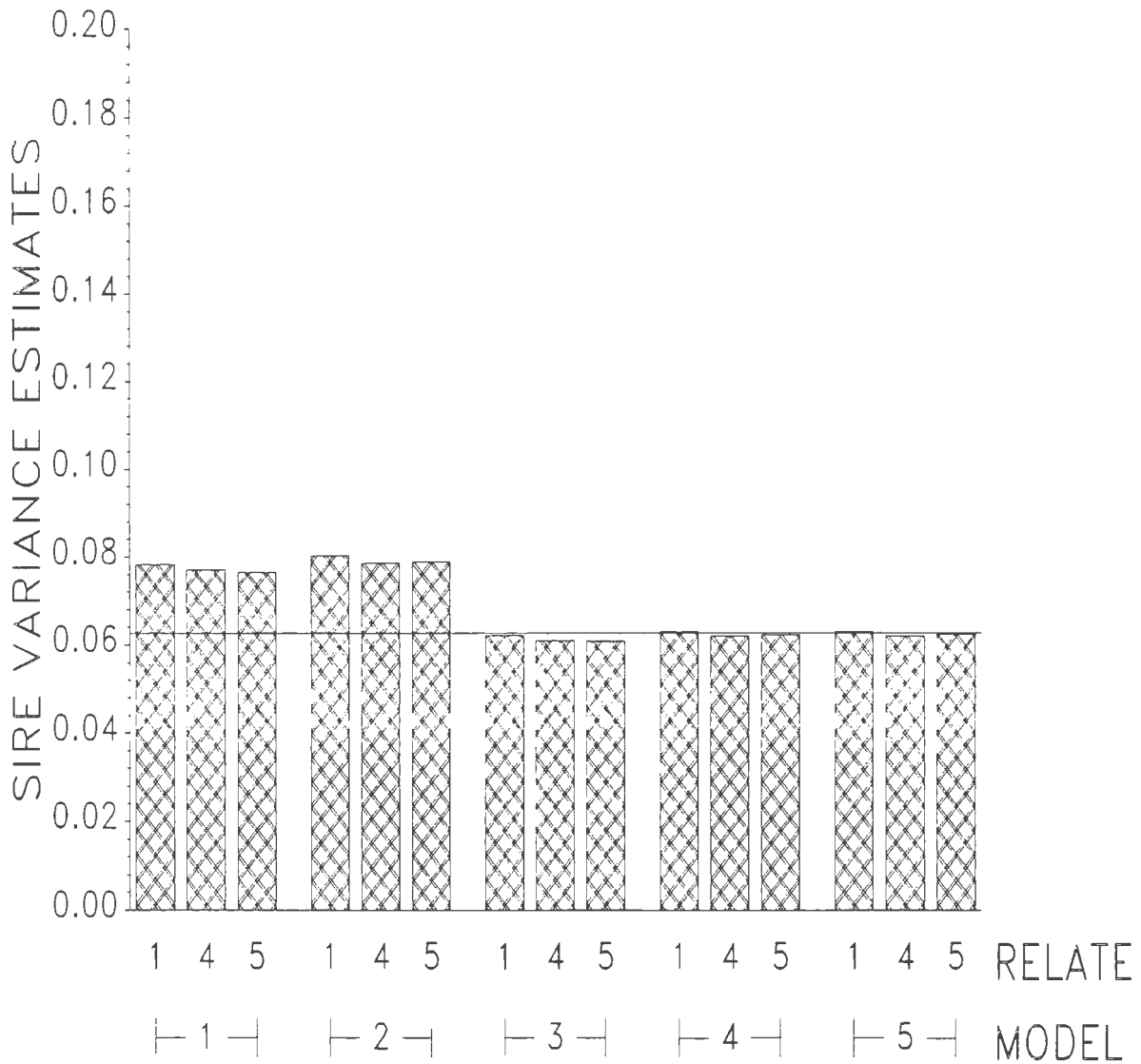


Figure 13. Average sire variance estimates for data with the structured relationship matrix for 10 pairs of half-sib sires (1) and calving ease relationship matrices (4 and 5) (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

Table 15. Average<sup>a</sup> MIVQUE interaction variance component estimates<sup>b</sup> for each combination of the two relationship matrices selected from the calving ease data (RELATE), data structure (STRUCT), and level on interaction simulated (INTER) in the data for all models (MODEL)

STRUCT <sup>d</sup>	INTER <sup>e</sup>	RELATE <sup>c</sup>	4			5		
		MODEL	3	4	5	3	4	5
100%	5%		.04907	.04907	.04981	.04893	.04893	.04971
100%	15%		.14811	.14811	.15038	.14761	.14761	.15114
100%	25%		.24629	.24628	.25014	.24598	.24596	.25153
25%	5%		.04854	.04853	.04926	.04848	.04846	.04992
25%	15%		.14828	.14828	.15059	.14594	.14586	.15020
25%	25%		.24626	.24628	.25017	.24528	.24516	.25233
10%	5%		.04876	.04878	.04941	.04947	.04952	.05031
10%	15%		.14758	.14766	.14968	.14572	.14595	.14826
10%	25%		.24966	.24980	.25319	.24610	.24613	.25009

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>True value for interaction variance is .05, .15, and .25, for interaction simulated at 5%, 15%, and 25% of the total variance, respectively.

<sup>c</sup>Relationship matrices, 4: 20 young sires from the calving ease data; 5: 20 sires of any age from the same data set.

<sup>d</sup>Data structure, percentage of filled herd-sire subclasses filled.

<sup>e</sup>Interaction level simulated, measured as a percent of the total variance.

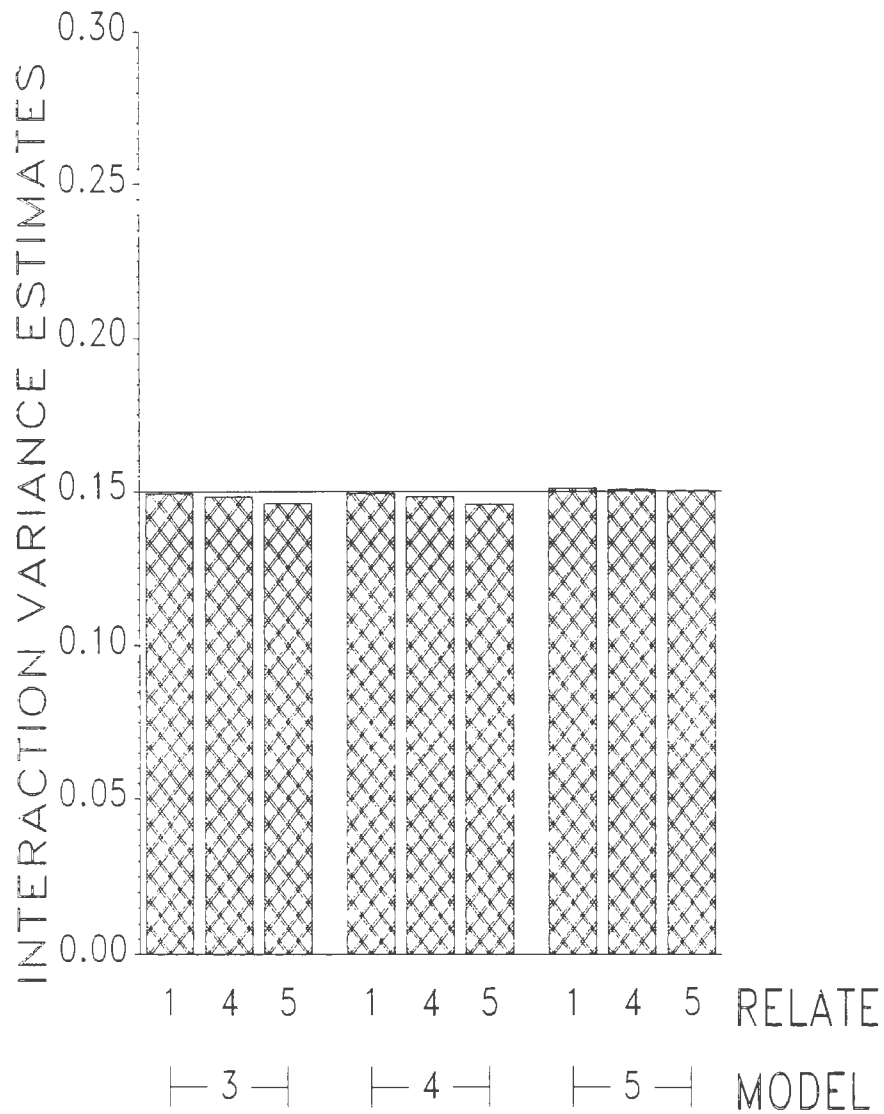


Figure 14. Average interaction variance estimates for data with the structured relationship matrix for 10 pairs of half-sib sires (1) and calving ease relationship matrices (4 and 5) (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

interaction variance estimates for models 3 and 5 were .98533 and .97822 for the young and all sire relationship matrices, respectively. This value is similar to those observed for relationship matrix 1 for the same comparisons (Table 9). Similar to the results seen for sire variance, there was little bias caused by ignoring sire relationships in these data.

Average residual variance component estimates are presented in Table 16. Figure 15 compares estimates of residual variance for the relationship matrix for 10 pairs of half-sib sires (relationship matrix 1) with estimates for the relationship matrices for the calving ease data (relationship matrices 4 and 5) for data simulated with intermediate levels of interaction and unbalancedness. Including or ignoring relationships in the variance component estimation procedure had little effect on estimates of estimates of residual variance. Residual variance estimates were nearly identical for model 3 (ignoring all relationships), model 4 (ignoring relationships for interaction effects), and model 5 (including relationships for sire and interaction effects). Average heritability estimates for the relationships selected from the calving ease data are presented in Table 17. Heritability tended to be overestimated using sire models, while the estimates using interaction models were much less biased. Figure 16 compares heritability estimates for the

Table 16. Average<sup>a</sup> MIVQUE residual variance component estimates<sup>b</sup> for each combination of the two relationship matrices selected from the calving ease data (RELATE), data structure (STRUCT), and level on interaction simulated (INTER) in the data for all models (MODEL)

STRUCT <sup>d</sup>	INTER <sup>e</sup>	RELATE <sup>c</sup>										
		MODEL	1	2	3	4	5	1	2	3	4	5
100%	5%		.93835	.93835	.89144	.89144	.89143	.93889	.93889	.89211	.89211	.89243
100%	15%		.93226	.93226	.79064	.79064	.79059	.93183	.93183	.79071	.79072	.79051
100%	25%		.92691	.92690	.69143	.69144	.69123	.92546	.92546	.69033	.69034	.69034
25%	5%		.92688	.92688	.89259	.79259	.89260	.92510	.92509	.89087	.89087	.89086
25%	15%		.89545	.89547	.79063	.79063	.79064	.89462	.89463	.79169	.79169	.79160
25%	25%		.86492	.86495	.69077	.69077	.69079	.86225	.86227	.68922	.68922	.68918
10%	5%		.90804	.90809	.89061	.89061	.89061	.90816	.90822	.89037	.89036	.89036
10%	15%		.84453	.84466	.79152	.79152	.79151	.84317	.84336	.79104	.79104	.79104
10%	25%		.77943	.77964	.69077	.69077	.69077	.77846	.77878	.69048	.69048	.69048

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>True value for residual variance for interaction models is .8875, .8775, and .8675, for interaction simulated at 5%, 15%, and 25% of the total variance, respectively, and .9375 for all sire models.

<sup>c</sup>Relationship matrices, 4: 20 young sires from the calving ease data; 5: 20 sires of any age from the same data set.

<sup>d</sup>Data structure, percentage of filled herd-sire subclasses filled.

<sup>e</sup>Interaction level simulated, measured as a percent of the total variance.



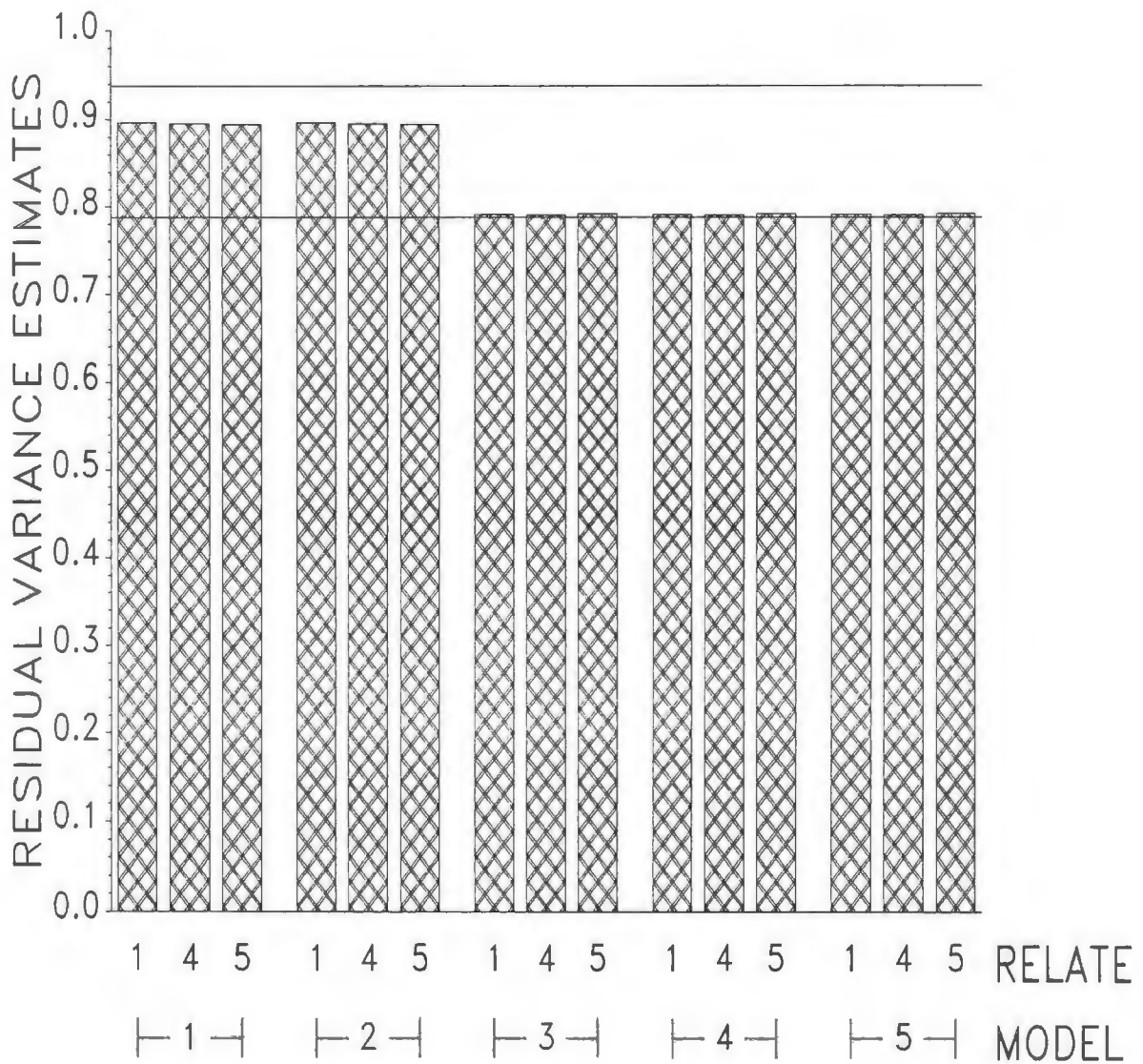


Figure 15. Average residual variance estimates for data with the structured relationship matrix for 10 pairs of half-sib sires (1) and calving ease relationship matrices (4 and 5) (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

Table 17. Average<sup>a</sup> MIVQUE heritability estimates<sup>b</sup> for each combination of the two relationship matrices selected from the calving ease data (RELATE), data structure (STRUCT), and level on interaction simulated (INTER) in the data for all models (MODEL)

STRUCT <sup>d</sup>	INTER <sup>e</sup>	RELATE <sup>c</sup> MODEL	4					5				
			1	2	3	4	5	1	2	3	4	5
100%	5%		.25193	.25550	.24905	.25251	.25245	.24293	.24834	.24013	.24533	.24533
100%	15%		.25578	.25888	.24717	.24999	.24971	.25464	.26048	.24615	.25139	.25133
100%	25%		.25889	.26230	.24465	.24761	.24720	.26089	.26565	.24639	.25027	.24987
25%	5%		.26837	.27245	.24475	.24810	.24803	.26576	.27258	.24247	.24787	.24761
25%	15%		.31413	.32001	.24130	.24477	.24444	.31236	.32126	.24105	.24613	.24544
25%	25%		.37451	.38241	.25129	.25500	.25427	.37116	.38314	.24776	.25327	.25133
10%	5%		.32762	.33266	.24542	.24843	.24857	.32202	.33095	.24116	.24486	.24478
10%	15%		.49155	.50030	.24161	.24433	.24431	.49755	.51583	.24858	.25136	.25062
10%	25%		.68072	.69326	.24294	.24520	.24503	.66447	.68910	.23561	.23827	.23669

<sup>a</sup>Average of 1000 replicates.

<sup>b</sup>True value for heritability is .25.

<sup>c</sup>Relationship matrices, 4: 20 young sires from the calving ease data; 5: 20 sires of any age from the same data set.

<sup>d</sup>Data structure, percentage of filled herd-sire subclasses filled.

<sup>e</sup>Interaction level simulated, measured as a percent of the total variance.

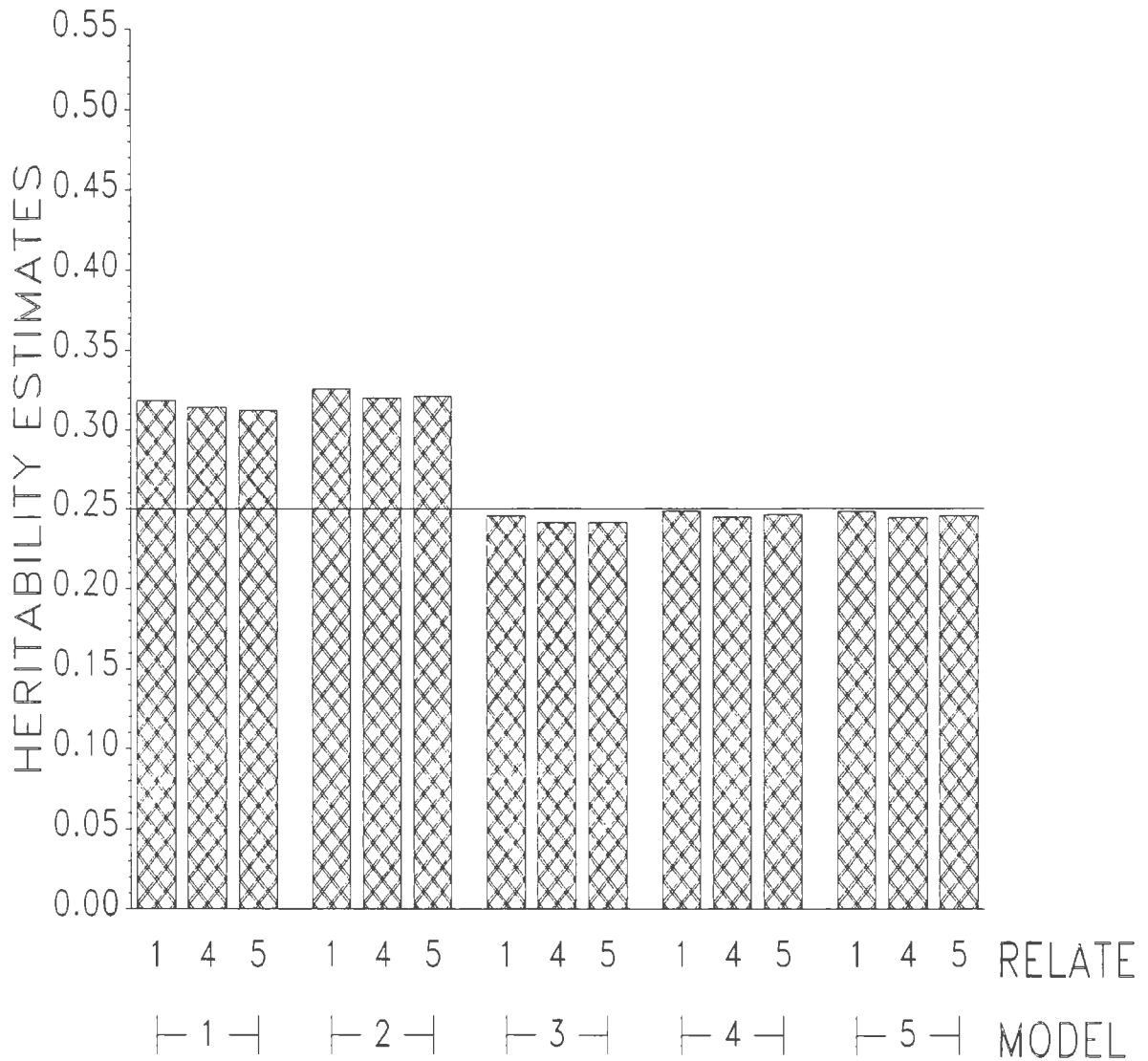


Figure 16. Average heritability estimates for data with the structured relationship matrix for 10 pairs of half-sib sires (1) and calving ease relationship matrices (4 and 5) (RELATE), 25% filled subclasses, and interaction simulated at 15% of the total variance for 5 variance component estimation models (MODEL)

structured relationship matrix for 10 pairs of half-sib sires (relationship matrix 1) with estimates for the relationship structures for the calving ease data (relationship matrices 4 and 5). As one would expect from results for the variance component estimates, there were only minor biases in heritability estimates caused by ignoring sire relationships.

### Conclusions

Estimation of interaction variance in a population was extended to include the relationship matrix among sires as part of the variance component estimation procedure. By ignoring relationships, the interaction variance tends to be underestimated because herd by sire effects are correlated within herds. The average bias in estimated interaction variance increased as sires were more related. Sire variance was overestimated in sire models, and the bias depended on the level of unbalancedness in the data. If the data were severely unbalanced the sire variance was often extremely biased. The bias in sire variance was compounded by increasing levels of interaction in the data. Residual variance was also underestimated when variance components were estimated using sire models. Bias increased with levels of sire relatedness, unbalancedness, and interaction. Although interaction was underestimated when relationships were ignored, the degree of bias was relatively small for the relationship matrices thought to be representative of the AI

population. This suggests that relationships may be ignored with little effect when sires are not closely related and interaction is not extremely high. However, even with relatively low levels of interaction there were substantial biases in heritability estimates when interaction was removed from the model. This indicates that interaction should be included in the variance component model, even if the data are moderately unbalanced and interaction is present at low levels. This is the case even if relationships must be ignored for the interaction effects.

This study was a starting point in exploring the effects of relationships in estimating herd by sire interaction variance. There are many questions unanswered by the results of this study. For example, it is of interest to know the generality of the conclusions for different variance component estimation methods. This is an important question because restricted maximum likelihood methods are becoming the standard method used for estimating variance components in animal breeding data. It is unclear how selection would affect the variance component estimates. Finally, it would be interesting to know the properties of variance component estimates in the presence of environmental correlations within herds (i.e.,  $c^2$ ) and herd by sire interaction effect. Clearly, this study provided a good foundation to investigate other problems, but many questions remain to be resolved.

## Literature Cited

- Bereskin, B. and J. L. Lush. 1965. Genetic and environmental factors in dairy sire evaluation. III. Influence of environmental and other extraneous correlations among daughters. J. Dairy Sci. 48:356-360.
- Burden, R. L., J. D. Faires, and A. C. Reynolds. 1981. Numerical Analysis. 2nd Edition. Prindle, Weber, and Schmidt, Boston, Massachusetts.
- Dickerson, G. E. 1962. Implications of genetic - environmental interaction in animal breeding. Anim. Prod. 4:47-63.
- Falconer, D. S. 1952. The problem of environment and selection. Am. Nat. 86:293.
- Falconer, D. S. 1981. Introduction to quantitative genetics. Longman, Inc., New York, New York.
- Fernando, R. L., D. Gianola, and M. Grossman. 1983. Identifying all connected subsets in a two-way classification without interaction. J. Dairy Sci. 66:1399-1402.
- Foulley, J. L. and C. R. Henderson. 1989. A simple model to deal with sire by treatment interactions when sires are related. J. Dairy Sci. 72:167-172.
- Henderson, C. R. 1953. Estimation of variance and covariance components. Biometrics 9:226-252.
- Henderson, C. R. 1973. Sire evaluation and genetic trends. pp 10-41 in Proceedings of the Animal Breeding and Genetics Symposium in Honor of Dr. Jay L. Lush. ASAS and ADSA, Champaign, Illinois.
- Henderson, C. R. 1975. A rapid method for computing the inverse of a relationship matrix. J. Dairy Sci. 58:1727-1730.
- Henderson, C. R. 1976. A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. Biometrics 32:69-83.
- Henderson, C. R. 1984. Applications of Linear Models in Animal Breeding. University of Guelph, Guelph, Ontario.

- Kelleher, D. J., A. E. Freeman, and J. L. Lush. 1967. Importance of bull x herd-year-season interaction in milk production. J. Dairy Sci. 50:1703-1707.
- Kennedy, W. J. and J. E. Gentle. 1980. Statistical Computing. Marcel Dekker, Inc., New York, New York.
- LaMotte, L. R. 1973. Quadratic estimation of variance components. Biometrics 29:311-330.
- Lee, A. J. 1976. Estimation of variance components in large herd-by-sire designs with interactions. J. Dairy Sci. 59:2138-2145.
- Lytton, V. H. and J. E. Legates. 1966. Sire by region interaction for production traits in dairy cattle. J. Dairy Sci. 49:874-878.
- Meyer, K. 1987. Estimates of variances due to sire x herd interactions and environmental covariances between paternal half-sibs for first lactation dairy production. Livest. Prod. Sci. 17:95-115.
- Mohammed, W. A., A. J. Lee, and M. Grossman. 1982a. Interactions of sires with feeding and management factors in Illinois Holstein cows. J. Dairy Sci. 65:625-631.
- Mohammed, W. A., A. J. Lee, and M. Grossman. 1982b. Genotype - environment interaction in sire evaluation. J. Dairy Sci. 65:857-860.
- Norman, H. D. 1974. Factors that should be considered in a national sire summary model. J. Dairy Sci. 57:955-962.
- Powell, R. L. and F. N. Dickinson. 1977. Progeny tests of sires in the United States and in Mexico. J. Dairy Sci. 60:1768-1772.
- Quass, R. L. and E. J. Pollak. 1981. Mixed model methodology for farm and ranch beef testing programs. J. Anim. Sci. 51:1277-1287.
- Rao, C. R. 1971a. Estimation of variance and covariance components - MINQUE theory. J. Multivariate Anal. 1:257-275.
- Rao, C. R. 1971b. Minimum variance quadratic unbiased estimation of variance components. J. Multivariate Anal. 1:445-456.

- Robertson, A., L. K. O'Connor, and J. Edwards. 1960. Progeny testing dairy bulls at different management levels. Anim. Prod. 2:141-152.
- Schaeffer, L. R. 1975. Disconnectedness and variance component estimation. Biometrics 31:969-977.
- Schaeffer, L. R. 1979. Notes on linear model theory and Henderson's mixed model techniques. Mimeograph notes. Animal and Poultry Sciences Department, University of Guelph, Guelph, Ontario.
- Searle, S. R. 1971. Linear models. John Wiley and Sons, New York, New York.
- Searle, S. R. 1982. Matrix algebra useful for statistics. John Wiley and Sons, New York, New York.
- Tong, A. K., B. W. Kennedy, and J. E. Moxley. 1977. Sire by herd interaction for milk yield and composition traits. Can. J. Anim. Sci. 57:383-388.
- Van Vleck, L. D. 1963. Genotype and environment in sire evaluation. J. Dairy Sci. 46:983-987.
- Wichmann, B. A. and I. D. Hill. 1982. Algorithm AS 183. An efficient and portable pseudo-random number generator. Appl. Statist. 26:118-121



## SECTION II. COMPUTATIONAL METHODS FOR SIMULATION OF DATA UNDER A HERD BY SIRE INTERACTION MODEL AND ESTIMATION OF VARIANCE COMPONENTS

### Abstract

Computing algorithms are presented for simulation of data to study variance component estimation for a herd by sire interaction model. Computing procedures are also introduced for calculating minimum variance quadratic unbiased estimates (MIVQUE) of variance components. These procedures are well suited to a simulation study where data structures and relationship matrices are identical for many replications.

### Introduction

Simulation provides a powerful tool for animal breeders to test and characterize statistical methods used in animal evaluation, variance component estimation, and other problems. One use of simulation is to generate data sets with known parameters and evaluate the ability of a statistical method to estimate or predict those underlying values under a variety of conditions. Some methods are more appropriate for use in simulation than others. Specifically, noniterative methods are best suited for simulation studies where replicated data are considered. By using a noniterative method, one can simulate a number of replicates without needing to build and invert the coefficient matrix for each replicate. The coefficient matrix would be defined

by the incidence of data relative to the effects in a model, such as herds, sires, dams, and litters, along with the variance structure of any random effects in the model and the prior estimates of the variance components associated with those effects. For each model and set of prior estimates of variance components, only one inverse is calculated for replicates that are simulated using a particular data structure and relationship matrix. The right hand sides will change with each set of new observations.

Noniterative methods were applied in the simulation study of Van Tassell (1989) to investigate the effects of sire relationships, data unbalancedness, and level of herd by sire interaction on variance component estimation. The methods considered in the study were those of the direct solution to Henderson's (1973) mixed model equations (MMEs) and to Rao's (1971) Minimum Variance Quadratic Unbiased Estimation (MIVQUE) technique. The purpose of this article is to give algorithms and computational procedures for simulating data with a correlated structure due to relationships among sires, inversion using partitioned matrices, expectation of MIVQUE quadratic forms, and estimation of variance components for sire and interaction models.

### Materials and Methods

The simulation and MIVQUE programs were written in FORTRAN and run under the IBM VS-FORTRAN compiler on a National Advanced Systems 9160 (NAS 9160). In addition, many of the programs were run using the vector and array syntax translator (VAST) system (Pacific Sierra Research Corp., 1988) to utilize the vector processing facility available on the NAS 9160.

The model used to simulate the data and estimate the variance components was,

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}, \quad [1]$$

where

$\mathbf{y}$  is an  $n \times 1$  vector of observations,

$n$  is the number of observations in the data set,

$\mathbf{X}$  is an  $n \times h$  incidence matrix for herd effects,

$h$  is the number of herds,

$\mathbf{b}$  is an  $h \times 1$  vector of fixed herd effects,

$\mathbf{Z} = [\mathbf{Z}_1 | \mathbf{Z}_2]$ ,

$\mathbf{Z}_1$  is an  $n \times s$  incidence matrix for sire effects,

$s$  is the number of sires,

$\mathbf{Z}_2$  is an  $n \times r$  incidence matrix for interaction effects,

$r$  is the number of interaction effects,

$\mathbf{u}' = [\mathbf{u}'_1 | \mathbf{u}'_2]$ ,

$\mathbf{u}_1$  is an  $s \times 1$  vector of random sire effects,

$u_2$  is an  $r \times 1$  vector of random interaction effects, and  $e$  is an  $n \times 1$  vector of random residual effects.

If we denote the numerator relationship matrix as  $A$ , then let  $\bar{A} = I_h \otimes A$ . Then,  $\bar{A}$  describes the correlation of herd by sire interaction effects within herd due to relationships among sires. The following simplifying assumptions for expected values and variance structure for the random variables were used.

$$E \begin{bmatrix} y \\ u_1 \\ u_2 \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \end{bmatrix}.$$

$$V \begin{bmatrix} y \\ u_1 \\ u_2 \\ e \end{bmatrix} = \begin{bmatrix} Z_1 A Z_1' \sigma_1^2 + Z_2 \bar{A} Z_2' \sigma_2^2 + I \sigma_0^2 & Z_1 A \sigma_1^2 & Z_2 \bar{A} \sigma_2^2 & I \sigma_0^2 \\ A Z_1' \sigma_1^2 & A \sigma_1^2 & 0 & 0 \\ \bar{A} Z_2' \sigma_2^2 & 0 & \bar{A} \sigma_2^2 & 0 \\ I \sigma_0^2 & 0 & 0 & I \sigma_0^2 \end{bmatrix}.$$

In addition, let

$$\begin{aligned} V &= V_0 \sigma_0^2 + V_1 \sigma_1^2 + V_2 \sigma_2^2, \\ V_0 &= Z_0 G_0 Z_0' = I_n I_n I_n = I_n, \\ V_1 &= Z_1 G_1 Z_1', \quad G_1 = A, \quad \text{and} \\ V_2 &= Z_2 G_2 Z_2', \quad G_2 = \bar{A}. \end{aligned}$$

Finally,  $\sigma_0^2$ ,  $\sigma_1^2$ , and  $\sigma_2^2$  are the residual, sire, and interaction components of variance, respectively.

Then, the mixed model equations (MMEs) for [1] are

$$\begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z}_1 & \mathbf{X}'\mathbf{Z}_2 \\ \mathbf{Z}_1'\mathbf{X} & \mathbf{Z}_1'\mathbf{Z}_1 + \mathbf{G}_1^{-1}\tilde{\alpha}_1 & \mathbf{Z}_1'\mathbf{Z}_2 \\ \mathbf{Z}_2'\mathbf{X} & \mathbf{Z}_2'\mathbf{Z}_1 & \mathbf{Z}_2'\mathbf{Z}_2 + \mathbf{G}_2^{-1}\tilde{\alpha}_2 \end{bmatrix} \begin{bmatrix} \tilde{\mathbf{b}} \\ \tilde{\mathbf{u}}_1 \\ \tilde{\mathbf{u}}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}_1'\mathbf{y} \\ \mathbf{Z}_2'\mathbf{y} \end{bmatrix}, [2]$$

where  $\mathbf{G}_1 = \mathbf{A}$  or  $\mathbf{I}$ , and  $\mathbf{G}_2 = \bar{\mathbf{A}}$  or  $\mathbf{I}$  (the definition for both depending on the variance component estimation model used),  $\tilde{\alpha}_i = \tilde{\gamma}_0^2 / \tilde{\gamma}_i^2$ , and  $\tilde{\gamma}_i^2$  are the prior estimates of  $\sigma_i^2$ . The residual, sire, and interaction variances are,  $\sigma_0^2$ ,  $\sigma_1^2$ , and  $\sigma_2^2$  respectively. Equation [2] can be rewritten as  $\tilde{\mathbf{C}}\tilde{\mathbf{s}} = \mathbf{W}'\mathbf{y}$ , where  $\mathbf{W} = [\mathbf{X}|\mathbf{Z}_1|\mathbf{Z}_2]$  and  $\tilde{\mathbf{s}}' = [\tilde{\mathbf{b}}' \ \tilde{\mathbf{u}}_1' \ \tilde{\mathbf{u}}_2']$ . Then  $\tilde{\mathbf{s}} = \tilde{\mathbf{C}}^{-1}\mathbf{W}'\mathbf{y}$ .

The tilde (~) was used to indicate a value (scalar, vector or matrix) that was a function of the prior estimates of the variance components (i.e., a variable for which the value may change if the priors change). To simplify notation in defining the quadratic forms and calculating the expectations, the following notation was used,

$$\mathbf{M} = \begin{bmatrix} \mathbf{M}_0 \\ \mathbf{M}_1 \\ \mathbf{M}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X} & \mathbf{Z}_1 & \mathbf{Z}_2 \\ \mathbf{Z}_1'\mathbf{X} & \mathbf{Z}_1'\mathbf{Z}_1 & \mathbf{Z}_1'\mathbf{Z}_2 \\ \mathbf{Z}_2'\mathbf{X} & \mathbf{Z}_2'\mathbf{Z}_1 & \mathbf{Z}_2'\mathbf{Z}_2 \end{bmatrix}, \text{ and}$$

$$\tilde{\mathbf{C}}^{-1} = \begin{bmatrix} \tilde{\mathbf{C}}^0 \\ \tilde{\mathbf{C}}^1 \\ \tilde{\mathbf{C}}^2 \end{bmatrix}, \text{ such that } \begin{bmatrix} \tilde{\mathbf{b}} \\ \tilde{\mathbf{u}}_1 \\ \tilde{\mathbf{u}}_2 \end{bmatrix} = \begin{bmatrix} \tilde{\mathbf{C}}^0\mathbf{W}'\mathbf{y} \\ \tilde{\mathbf{C}}^1\mathbf{W}'\mathbf{y} \\ \tilde{\mathbf{C}}^2\mathbf{W}'\mathbf{y} \end{bmatrix}.$$

### Data simulation

Since  $A$  is positive definite,  $A$  can be factored as  $A = LL'$  using a Cholesky decomposition (Burden et al., 1981) where  $L$  is a lower triangular matrix (Henderson, 1975). Correlated sire effects and herd by sire effects were simulated using the decomposition matrix  $L$ , generating a vector of correlated sire effects by calculating  $u_1 = Lr\sigma_1$ , where  $r$  is a vector of standard normal deviates and  $\sigma_1$  is the sire standard deviation. The variance of the sire effects was then  $\text{Var}(u_1) = L\text{Var}(r)L'\sigma_1^2 = LL'\sigma_1^2 = A\sigma_1^2$ . Similarly, the herd by sire effects were generated as  $u_2 = (I \otimes L)r\sigma_2$ , where  $I$  is an identity matrix with dimension equal to the number of herds in the simulation and  $\sigma_2$  is the herd by sire standard deviation. Then,  $\text{Var}(u_2) = (I \otimes L)(I \otimes L)'\sigma_2^2 = (I \otimes A)\sigma_2^2$ . The herd and residual effects were simulated using normal distributions with  $\sigma_h$  and  $\sigma_0$  as the respective standard deviations.

The MIVQUE quadratic forms described by Van Tassell (1989) were used, and these quadratics require the sum of the squared observations ( $y'y$ ) and the solutions to the mixed model equations (MME). The simulation program calculated the right hand sides (RHS) of the MME and  $y'y$  for each replicate. This is more efficient and requires less file space than generating and storing each observation.

The algorithm used to simulate the data is described in Figure 1 and the FORTRAN simulation program is included in Appendix A.

### Inversion of the coefficient matrix

The advantage to using MIVQUE is that it is a noniterative procedure, and that the quadratic forms can be expressed in terms of the solutions to the mixed model equations. Therefore, because solutions to the MME are required for each replicate of the data, a direct solution using the inverse of the coefficient matrix is the most efficient tool for calculating the solutions. Using a simple sire model, direct inversion of the coefficient matrix is feasible in most cases. However, when herd by sire interaction effects are considered, the coefficient matrix increases in dimension dramatically. The block diagonal nature of the herd by sire interaction portion enables one to use a partitioned matrix inversion method which is more efficient than a direct inversion approach. If we define the coefficient matrix as

$$\tilde{\mathbf{C}} = \begin{bmatrix} \tilde{\mathbf{Q}} & \mathbf{R} \\ \mathbf{R}' & \tilde{\mathbf{S}} \end{bmatrix},$$

where  $\tilde{\mathbf{Q}}$  is the leading diagonal submatrix corresponding to herd and sire effects, or

---

```

Read relationship matrix.
1 Read variance components parameters from files.
  Simulate herd, sire, and herd by sire effects.
     $b = r_1 \sigma_h$ 

     $u_1 = Lr_2 \sigma_s$ 

     $u_2 = (I \otimes L)r_3 \sigma_i$ 

2 Read herd, sire, and number of daughters from data
  structure file.

  Do for number of daughters.
    Error =  $r \sigma_e$ .

    Sum  $e^2 = \text{sum } e^2 + \text{error}^2$ .

    Obs =  $b(\text{herd}) + u_1(\text{sire}) + u_2(\text{herd}, \text{sire}) + \text{error}$ .

    Sum  $\text{obs}^2 = \text{sum } \text{obs}^2 + \text{obs}^2$ .

    Add obs to RHS portion for sire, herd, and
      interaction.
    (next daughter)
  Go to 2 until data structure file completed.
  Save RHS, sum  $\text{obs}^2$ , herd, sire, and interaction effects
    and sum  $e^2$  to a file.
  Go to 1 until all parameters used.

```

---

Figure 1. Algorithm to simulate data for interaction models



$$\tilde{Q} = \begin{bmatrix} X'X & 0 \\ 0 & Z_1'Z_1 + G_1^{-1}\tilde{\alpha}_1 \end{bmatrix}.$$

The matrix  $R$  describes the incidence of herd and sire effects in relation to the interaction effects,

$$R = \begin{bmatrix} X'Z_2 \\ Z_1'Z_2 \end{bmatrix},$$

and  $\tilde{S}$  is the submatrix corresponding to the interaction effects,

$$\tilde{S} = [Z_2'Z_2 + G_2^{-1}\tilde{\alpha}_2],$$

Then,

$$\tilde{C}^{-1} = \begin{bmatrix} \tilde{F} & \tilde{G} \\ \tilde{G}' & \tilde{H} \end{bmatrix},$$

where,

$$\tilde{F} = \tilde{P}^{-1},$$

$$\tilde{G} = -\tilde{P}^{-1}R\tilde{S}^{-1},$$

$$\tilde{H} = \tilde{S}^{-1} + \tilde{S}^{-1}R'\tilde{P}^{-1}R\tilde{S}^{-1}, \text{ and}$$

$$\tilde{P} = \tilde{Q} - R\tilde{S}^{-1}R'.$$

This particular form of partitioned inversion is useful because  $\tilde{S}$  is a block diagonal matrix, with blocks of order equal to the number of sires, so  $\tilde{S}^{-1}$  can be calculated as the inverse of each of the submatrices. As a result, the largest

matrix that is inverted is  $\tilde{P}$ , which is equal in dimension to the number of herds and sires combined.

Significant memory savings can be achieved by storing  $\tilde{S}$  (and  $\tilde{S}^{-1}$ ) as three dimensional arrays, where the first two dimensions correspond to the number of sires, and the third dimension corresponds to the number of herds. Then, in the two dimensional array for each herd the relationship matrix scaled by the variance ratio and incidence of daughters were stored. In this way, only the nonzero blocks are stored, rather than the fully stored block diagonal matrix. Further memory savings can be made by using the space allocated for the inverse of the coefficient matrix as workspace for intermediate results during the inversion. The inversion procedure is outlined in Figure 2 and the FORTRAN partitioned inversion program is included in Appendix B.

#### Calculating the expectations of the MIVQUE quadratics

The expectations of the quadratic forms were derived by Van Tassell (1989). Two general forms of the expectations are

$$E(\tilde{u}_i' G_i \tilde{u}_i) = \sum_{j=0}^k \text{tr}(\tilde{C}^i' G_i \tilde{C}^i W' Z_j G_j Z_j' W) \sigma_j^2$$

$$= \sum_{j=0}^k \text{tr}(\tilde{C}^i' G_i \tilde{C}^i M_j' G_j M_j) \sigma_j^2, \text{ and}$$

$$E(y'y - \tilde{s}' W' y) = \sum_{i=0}^k (N - \text{tr}(\tilde{C}^{-1} M_i' G_i M_i)) \sigma_i^2, \text{ and } \tilde{C}^i, M_i, G_i,$$

and  $W$  have been defined previously.

---

```

Read relationship inverse.
1 Read list of parameters including variances and
  models used to generate an inverse.
  If sire model
  then.
    Initialize coefficient matrix with variance ratio times
    the relationship matrix using the partition Q.
2 Read herd, sire, and number of daughters from data
  structure file.
  Add the number of daughters to the following for each
  record read:
    herd diagonal,
    sire diagonal,
    herd by sire off-diagonals.
  Go to 2 unless end of file reached.
  Invert Q.
else.
  Initialize coefficient matrix with sire variance ratio
  times relationship matrix to herd and sire partition,
  Q, and interaction ratio times the block diagonal
  matrix of relationship matrices to the interaction
  partition, S.
3 Read herd, sire, and the number of daughters from
  the data structure file.
  Add the number of daughters to the following for
  each record read:
    herd diagonal (in Q),
    sire diagonal (in Q),
    interaction diagonal (in S),
    herd by sire off-diagonals (in Q),
    herd by interaction off diagonals (in R),
    sire by interaction off diagonals (in R).
  Go to 3 unless end of file is reached.
  Invert the partitioned matrix.
     $H = S^{-1}$ .
     $F = Q$ .
     $G^* = (R * S^{-1})'$ .
     $F = (E - F * R')^{-1}$ .
     $G = -E * (F)'$ .
     $G^* = G'$ .
  End if.
  Write inverse and parameters used to a file.
  Go to 1 if not the end of the parameter list.

```

---

Figure 2. Algorithm to calculate inverse for mixed model equations

If one defines the following matrices:

$$\tilde{D}_i = \tilde{C}^i{}' G_i^{-1} \tilde{C}^i, \quad i = 1, 2,$$

$$\tilde{D}_3 = \tilde{C},$$

$$E_i = M_i' G_i M_i, \quad i = 1, 2, \text{ and}$$

$$E_3 = W' W,$$

then the matrix of the expectation of the quadratics,  $\tilde{K}$ , is

$$\tilde{K} = \begin{bmatrix} \text{tr}(\tilde{D}_1 E_1) & \text{tr}(\tilde{D}_1 E_2) & \text{tr}(\tilde{D}_1 E_3) \\ \text{tr}(\tilde{D}_2 E_1) & \text{tr}(\tilde{D}_2 E_2) & \text{tr}(\tilde{D}_2 E_3) \\ N - \text{tr}(\tilde{D}_3 E_1) & N - \text{tr}(\tilde{D}_3 E_2) & N - \text{tr}(\tilde{D}_3 E_3) \end{bmatrix},$$

where  $N$  is the total number of daughters and  $\text{tr}()$  denotes the trace operation.

The expectations simplify for a sire model by defining the following matrices:

$$\tilde{D}_1 = \tilde{C}^1{}' G_1^{-1} \tilde{C}^1,$$

$$\tilde{D}_2 = \tilde{C},$$

$$E_1 = M_1' G_1 M_1,$$

$$E_2 = W' W, \text{ and}$$

$$\tilde{K} = \begin{bmatrix} \text{tr}(\tilde{D}_1 E_1) & \text{tr}(\tilde{D}_1 E_2) \\ N - \text{tr}(\tilde{D}_2 E_1) & N - \text{tr}(\tilde{D}_2 E_2) \end{bmatrix}.$$

Because  $\tilde{D}_i$  and  $E_i$  for  $i=1,2,3$ , are symmetric the trace was calculated as a sum of the inner products of the rows or columns of the matrix products rather than calculating the

row by column product as suggested by matrix multiplication. When programming with FORTRAN, calculating inner products of columns is preferable, because these values are stored sequentially in memory (using the IBM VS-FORTRAN compiler). This process reduce time spent paging through memory to find the elements, as they will be accessed sequentially if the product is carried out column-wise. Operating sequentially in a matrix or vector becomes critical when vectorization is desired or matrix sizes increase.

The calculation of the  $\tilde{D}$  and  $E$  matrices was also improved by exploiting the block diagonal nature of  $G_2^{-1}$  and  $G_2$  for herd by sire interaction. Further improvements could be made in the FORTRAN programs included in Appendix C by exploiting the symmetry of the  $W'W$ ,  $\tilde{C}$ , and the  $G^i$  matrices when computing the  $\tilde{D}$  and  $E$  matrices.

The general algorithm used to calculate the expectations of the MIVQUE quadratic forms is given in Figure 3 and the FORTRAN program is included in Appendix C.

#### Estimation of variance components

Variance components are estimated by completing several steps. Solutions to the mixed model equations are computed by multiplying the inverse of the coefficient matrix (calculated in the partitioned inversion program) by the vector of right hand sides generated in the simulation program.

---

```

Read relationship matrix and inverse.
1 Read list of parameters including variances and
  models used to generate an inverse.
  If sire model
  then.
    Set up  $W'W$  from the data structure file.
    Calculate  $M_1'G_1M_1$  ( $E_1$ ) and write to an external file.

    Write  $W'W$  ( $E_2$ ) to an external file.
    Read  $C$  ( $D_2$ ) from file created by inversion program.

    Calculate  $\tilde{C}_1'G_1^{-1}\tilde{C}_1$  ( $D_1$ ) and write to an external file.
    Do for the number of equations in the MME (herds+sires):
      Read column  $k$  of  $D_1$  ( $d_1^k$ ),  $D_2$  ( $d_2^k$ ),
         $E_1$  ( $e_1^k$ ),  $E_2$  ( $d_1^k$ ).
      Calculate inner products for columns, i.e.,
         $d_i^k \cdot e_j^k$ ,  $i, j = 1, 2$ , and add to  $i, j$  element of  $F$ .
      (next column)
       $F_{i2} = N - F_{i2}$ ,  $i=1, 2$ .
    else.
      Set up  $W'W$  from the data structure file.
      Calculate  $M_1'G_1M_1$  ( $E_1$ ) and write to an external file.

      Calculate  $M_2'G_2M_2$  ( $E_2$ ) and write to an external file.

      Write  $W'W$  ( $E_3$ ) to an external file.
      Read  $C$  ( $D_3$ ) from file created by inversion program.

      Calculate  $\tilde{C}_1'G_1^{-1}\tilde{C}_1$  ( $D_1$ ) and write to an external file.

      Calculate  $\tilde{C}_2'G_2^{-1}\tilde{C}_2$  ( $D_2$ ) and write to an external file.
      Do for the number of equations in the MME:
        read column  $k$  of  $D_1$  ( $d_1^k$ ),  $D_2$  ( $d_2^k$ ),  $D_3$  ( $d_3^k$ ),
           $E_1$  ( $e_1^k$ ),  $E_2$  ( $d_1^k$ ),  $E_3$  ( $e_3^k$ ),
        calculate inner products for columns, i.e.,
           $d_i^k \cdot e_j^k$ ,  $i, j = 1, 2, 3$ , and add to  $i, j$  element of  $F$ .
        (next column)
         $F_{i3} = N - F_{i3}$ ,  $i=1, 2, 3$ .
      End if.
      Write parameters and expectation matrix.
      Go to 1 if not the end of the parameter list.

```

---

Figure 3. Algorithm to calculate expectations of MIVQUE quadratic forms

Then calculate the following quadratics for the interaction models:

$$\tilde{Q}_1 = \tilde{u}'_1 G_1^{-1} \tilde{u}_1,$$

$$\tilde{Q}_2 = \tilde{u}'_2 G_2^{-1} \tilde{u}_2, \text{ and}$$

$$\tilde{Q}_3 = y'y - \tilde{b}'x'y - \tilde{u}'_1 z'_1 y - \tilde{u}'_2 z'_2 y,$$

where  $\tilde{b}, \tilde{u}_1$ , and  $\tilde{u}_2$  are the mixed model solutions for herds, sires, and interaction, respectively, and  $G_1^{-1}$  and  $G_2^{-1}$  are as defined in [2].

The following quadratics were calculated for sire models:

$$\tilde{Q}_1 = \tilde{u}'_1 G_1^{-1} \tilde{u}_1,$$

$$\tilde{Q}_2 = y'y - \tilde{b}'x'y - \tilde{u}'_1 z'_1 y.$$

The expectations of the quadratics calculated in the expectation step are equated to the quadratics and solved by inversion to obtain the variance component estimates.

The estimation algorithm is described in Figure 4 and the FORTRAN program is included in Appendix D.

### Conclusions

These algorithms provide a basis to develop software well suited to simulation studies by optimizing known properties of the matrices such as symmetry and sparsity. The procedures outlined can be modified for different models using the same general approach. The FORTRAN programs developed in this project are available for use.

---

```

Read relationship matrix and inverse.

1 Read list of parameters including variances and
  models used to generate an inverse.

Read inverse of coefficient matrix.
Read matrix of expectations of quadratic forms.
Invert expectation matrix.

Do for the number of replicates:
  Read RHS.
  Solve mixed model equations.
  If sire model
  then.
    Calculate sire model quadratics
       $Q_1 = \tilde{u}'_1 G_1^{-1} \tilde{u}_1,$ 
       $Q_2 = y'y - \tilde{b}'x'y - \tilde{u}'_1 z'_1 y.$ 
      Estimate variance components and write to a file.
    else.
      Calculate interaction model quadratics
         $Q_1 = \tilde{u}'_1 G_1^{-1} \tilde{u}_1,$ 
         $Q_2 = \tilde{u}'_2 G_2^{-1} \tilde{u}_2,$  and
         $Q_3 = y'y - \tilde{b}'x'y - \tilde{u}'_1 z'_1 y - \tilde{u}'_2 z'_2 y,$ 
        Estimate variance components and write to a file.
      (next replicate)
  End if.
Go to 1 if not the end of the parameter list.

```

---

Figure 4. Algorithm to calculate MIVQUE estimates



## Literature Cited

- Burden, R. L., J. D. Faires, and A. C. Reynolds. 1981. Numerical Analysis. 2nd Edition. Prindle, Weber, and Schmidt, Boston, Massachusetts.
- Henderson, C. R. 1973. Sire evaluation and genetic trends. pp 10-41 in Proceedings of the Animal Breeding and Genetics Symposium in Honor of Dr. Jay L. Lush. ASAS and ADSA, Champaign, Illinois.
- Henderson, C. R. 1975. A rapid method for computing the inverse of a relation matrix. J. Dairy Sci. 58:1727-1730.
- Pacific Sierra Research Corp. 1988. VAST user's guide - NAS 91X0 and XL VPF options. Document number ES05-001-00. Pacific Sierra Research Corporation, Los Angeles, California.
- Rao, C. R. 1971. Estimation of variance and covariance components - MINQUE theory. J. Multivariate Anal. 1:257-275.
- Van Tassell, C.P. 1989. Consideration of sire relationships when estimating variance components with herd by sire interaction. Unpublished M.S. Thesis. Iowa State University, Ames, Iowa.

### SUMMARY

This thesis examines the effect of including the relationship among sires in the procedure for estimating variance components for herd by sire interaction models. The first section of the thesis provided the theoretical basis for simulation of data and variance component estimation. Simulation methods were described allowing for the generation of correlated sire and interaction effects shared by common relatives. The MIVQUE quadratic forms described by Rao (1971a) were presented and these quadratic forms were rearranged to a more computable form. The expectation of the quadratic forms were also described for sire and interaction models. Finally, the results from the analysis of simulated data were presented using sire and interaction models for data simulated using different levels of sire relatedness, unbalancedness, and interaction.

Computational algorithms were presented in the second section of the thesis. The algorithms described were used in developing a set of FORTRAN programs based on the theoretical results presented in the first section. The algorithms attempt to maximize efficiency by exploiting known properties of matrices and to utilize vector facilities available on the NAS 9160.

## REFERENCES

- Bereskin, B. and J. L. Lush. 1965. Genetic and environmental factors in dairy sire evaluation. III. Influence of environmental and other extraneous correlations among daughters. J. Dairy Sci. 48:356-360.
- Boldman, K. G. 1989. Heterogeneity of variances by herd production level and its effect on dairy cow and sire evaluation. Unpublished Ph.D. dissertation. Iowa State University, Ames, Iowa.
- Bowman, J. C. 1972. Genotype x environment interactions. Ann. Genet. Sel. Anim. 4:117-123.
- Burden, R. L., J. D. Faires, and A. C. Reynolds. 1981. Numerical Analysis. 2nd Edition. Prindle, Weber, and Schmidt, Boston, Massachusetts.
- Dickerson, G. E. 1962. Implications of genetic - environmental interaction in animal breeding. Anim. Prod. 4:47-63.
- Falconer, D. S. 1952. The problem of environment and selection. Am. Nat. 86:293.
- Falconer, D. S. 1981. Introduction to quantitative genetics. Longman, Inc., New York, New York.
- Fernando, R. L., D. Gianola, and M. Grossman. 1983. Identifying all connected subsets in a two-way classification without interaction. J. Dairy Sci. 66:1399-1402.
- Foulley, J. L. and C. R. Henderson. 1989. A simple model to deal with sire by treatment interactions when sires are related. J. Dairy Sci. 72:167-172.
- Haldane, J. B. S. 1946. The interaction of nature and nurture. Ann. Eugen. (Lond.) 13:197-205.
- Hardwick, R. C. and J. T. Wood. 1934. Regression methods for studying genotype-environment interactions. Heredity, Lond. 28:209-222.
- Henderson, C. R. 1953. Estimation of variance and covariance components. Biometrics 9:226-252.

- Henderson, C. R. 1973. Sire evaluation and genetic trends. pp 10-41 in Proceedings of the Animal Breeding and Genetics Symposium in Honor of Dr. Jay L. Lush. ASAS and ADSA, Champaign, Illinois.
- Henderson, C. R. 1975. A rapid method for computing the inverse of a relationship matrix. J. Dairy Sci. 58:1727-1730.
- Henderson, C. R. 1976. A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. Biometrics 32:69-83.
- Henderson, C. R. 1984. Applications of Linear Models in Animal Breeding. University of Guelph, Guelph, Ontario.
- Henderson, C. R. 1985. Equivalent linear models to reduce computations. J. Dairy Sci. 68:2267-2277.
- Kelleher, D. J., A. E. Freeman, and J. L. Lush. 1967. Importance of bull x herd-year-season interaction in milk production. J. Dairy Sci. 50:1703-1707.
- Kennedy, W. J. and J. E. Gentle. 1980. Statistical Computing. Marcel Dekker, Inc., New York, New York.
- LaMotte, L. R. 1973. Quadratic estimation of variance components. Biometrics 29:311-330.
- Lee, A. J. 1976. Estimation of variance components in large herd-by-sire designs with interactions. J. Dairy Sci. 59:2138-2145.
- Lytton, V. H. and J. E. Legates. 1966. Sire by region interaction for production traits in dairy cattle. J. Dairy Sci. 49:874-878.
- Mao, I. L. and E. B. Burnside. 1969. Sire by herd environment interaction for milk production. J. Dairy Sci. 52:1055-1062.
- Meyer, K. 1987. Estimates of variances due to sire x herd interactions and environmental covariances between paternal half-sibs for first lactation dairy production. Livest. Prod. Sci. 17:95-115.
- Mohammed, W. A., A. J. Lee, and M. Grossman. 1982a. Interactions of sires with feeding and management factors in Illinois Holstein cows. J. Dairy Sci. 65:625-631.

- Mohammed, W. A., A. J. Lee, and M. Grossman. 1982b. Genotype - environment interaction in sire evaluation. J. Dairy Sci. 65:857-860.
- Norman, H. D. 1974. Factors that should be considered in a national sire summary model. J. Dairy Sci. 57:955-962.
- Pacific Sierra Research Corporation. 1988. VAST user's guide - NAS 91X0 and XL VPF options. Document number ES05-001-00. Pacific Sierra Research Corporation, Los Angeles, California.
- Powell, R. L. and F. N. Dickinson. 1977. Progeny tests of sires in the United States and in Mexico. J. Dairy Sci. 60:1768-1772.
- Quass, R. L. and E. J. Pollak. 1981. Mixed model methodology for farm and ranch beef testing programs. J. Anim. Sci. 51:1277-1287.
- Rao, C. R. 1971a. Estimation of variance and covariance components - MINQUE theory. J. Multivariate Anal. 1:257-275.
- Rao, C. R. 1971b. Minimum variance quadratic unbiased estimation of variance components. J. Multivariate Anal. 1:445-456.
- Robertson, A., L. K. O'Connor, and J. Edwards. 1960. Progeny testing dairy bulls at different management levels. Anim. Prod. 2:141-152.
- Schaeffer, L. R. 1975. Disconnectedness and variance component estimation. Biometrics 31:969-977.
- Schaeffer, L. R. 1979. Notes on linear model theory and Henderson's mixed model techniques. Mimeograph notes. Animal and Poultry Sciences Department, University of Guelph, Guelph, Ontario.
- Searle, S. R. 1971. Linear models. John Wiley and Sons, New York, New York.
- Searle, S. R. 1982. Matrix algebra useful for statistics. John Wiley and Sons, New York, New York.
- Tong, A. K., B. W. Kennedy, and J. E. Moxley. 1977. Sire by herd interaction for milk yield and composition traits. Can. J. Anim. Sci. 57:383-388.

Van Vleck, L. D. 1963. Genotype and environment in sire evaluation. J. Dairy Sci. 46:983-987.

Wichmann, B. A. and I. D. Hill. 1982. Algorithm AS 183. An efficient and portable pseudo-random number generator. Appl. Statist. 26:118-121.

Yates, F. and W. G. Cochran. 1934. The analysis of groups of experiments. J. Agric. Sci. 28:556-580.

## ACKNOWLEDGEMENTS

This project would not have been possible without the support and assistance of many people.

Financial support for this project was provided by the National Association of Animal Breeders.

I would like to thank the members of my committee including Drs. D. A. Harville, A. E. Freeman, and M. F. Rothschild for providing helpful suggestions during the study and for making many useful comments for revising this thesis. I am especially grateful to Dr. P. J. Berger for serving as my major professor during my stay at Iowa State. He encouraged me to investigate herd by sire interaction and gave me the freedom to develop the idea into a thesis project.

I would like to thank Dr. C. R. Henderson for suggesting the idea of considering relationships in interaction and for encouraging me to continue to study this problem. His death was a great loss to the animal breeding community. I would like to thank Dr. L. R. Schaeffer for suggesting the use of the Cholesky decomposition to simulate the correlation structure for related sires. Also, I would like to thank Dr. J. A. Hoekstra for extensive help in solving computational problems.

I appreciate the support and atmosphere provided by my fellow graduate students. I am especially grateful for the

assistance and friendship of Dr. Keith Boldman and Hiroshi Takahashi who patiently answered endless questions and added immeasurably to my education at Iowa State. I am also thankful for the friendship of all the animal breeding group, especially my officemates Mark Boggess and Chris Skaggs, who have each been all that anyone could ever hope for in friends.

I would also like to thank Brenda and Stephanie who have been the two best friends a person could ever hope to have. They have always been there when I needed them most. Finally, and most of all, I would like to thank my family for their support. The time spent with Stephen, Jill, Jesse, and Becky has always been very special. I cannot thank my parents enough for their love and support. I never could have made it without their help. Thanks Mom and Dad - I love you both very much.



## APPENDIX A. FORTRAN SIMULATION PROGRAM

```

C =====
C PROGRAM SIMULATE
C =====
C
C LAST REVISED: 7/20/89
C *****
C PURPOSE AND STRATEGY: TO SIMULATE A DATA SET FOR ANALYSIS OF
C HERD-SIRE INTERACTION WITH VARYING LEVELS OF VARIANCES. THE
C MODEL USED TO SIMULATE THE DATA IS:
C 
$$Y_{ijk} = H_i + S_j + (HS)_{ij} + E_{ijk} \quad \text{IN SCALAR FORM}$$

C 
$$Y = XB + Z1U1 + Z2U2 + E \quad \text{IN MATRIX FORM}$$

C 
$$V(Y) = Z1*V(U1)*Z1' + Z2*V(U2)*Z2'$$

C WHERE:
C X IS A MODEL MATRIX OF FIXED EFFECTS (HERDS IN THIS CASE)
C B IS A VECTOR OF FIXED (HERD) EFFECTS
C Z1 IS A MODEL MATRIX FOR SIRE EFFECTS
C U1 IS A RANDOM VECTOR OF SIRE EFFECTS WITH  $V(U1) = A * V_s$ 
C WHERE  $V_s$  IS THE SIRE VARIANCE
C Z2 IS A MODEL MATRIX OF INTERACTION EFFECTS
C U2 IS A RANDOM VECTOR OF HERD-SIRE INTERACTION EFFECTS WITH
C  $VAR(U2) = I @ A * V_i$ , WHERE @ IS THE DIRECT PRODUCT
C OPERATOR, AND  $V_i$  IS THE INTERACTION VARIANCE
C E IS A RANDOM RESIDUAL WITH  $V(E) = I * V_r$ 
C
C HERD EFFECTS ARE SIMULATED USING A UNIFORM DISTRIBUTION OVER
C THE RANGE OF VALUES SUPPLIED IN THE INPUT. THE RANDOM
C EFFECTS ARE SIMULATED BY FIRST SIMULATING A VECTOR OF
C INDEPENDENT RANDOM NORMAL DEVIATES, WHICH IS PREMULIPLIED
C BY L, THE LOWER TRIANGULAR DECOMPOSITION OF A, SUCH THAT
C  $A = LL'$ . THE VECTOR OF DEVIATES THEN HAS A DISTRIBUTION
C  $V(U) = L * I * L' = LL' = A$ .
C
C THE DATA STRUCTURE CREATED BY CRDATA IS THEN READ, AND FOR ANY
C SUBCLASS WITH DAUGHTERS OBSERVATIONS ARE GENERATED AND ADDED
C TO THE RHS'S OF THE MIXED MODEL EQUATIONS. SUM OF SQUARED
C RESIDUALS AND OBSERVATIONS IS ALSO CALCULATED. AFTER THE
C DATA STRUCTURE FILE HAS BEEN COMPLETELY READ AND ALL
C OBSERVATIONS SIMULATED, THE RHS, SUMS OF SQUARES, AND THE
C TRUE SIRE, AND HERD-SIRE VALUES ARE WRITTEN OUT.
C
C NORMAL RANDOM NUMBER GENERATOR SUBROUTINE WAS WRITTEN BY
C KARIN MEYER
C *****
C
C PARAMETER (NH=50,NS=20,NR=1000)
C PARAMETER (IVECL=500)
C
C DIMENSION RHS(NH+NS+NH*NS),HRND(NH),SRND(NS),HSRND(NS,NH),

```

```

+          A(NS,NS),L(NS,NS),WORK(NS),RNVEC(IVECL),SEEDV(6),
+          OSEEDV(6)

REAL*8     RHS,HRND,SRND,HSRND,A,L,WORK,HVAR,HSD,GVAR,SVAR,SSD,
+          HSVAR,HSSD,ERRVAR,ERRSD,ALPHAS,ALPHAI,SIRAT,DPZERO,ERR,
+          PHENO,EPE,YPY,DNTOT,DATTOT,UNIFRM,DNSND,RNVEC,DDD

```

```

REAL*4     RHVAR,RGVAR,RHSVAR

```

```

INTEGER*4  LOW,DATA,PARM,SIM,TVAL,PRMOUT,SEED,OBS,NOREPS,NOHERD,
+          NOSIRE,NOHXS,NOEQN,HERD,SIRE,N,SIREQN,HSEQN,IEQN,
+          IC,NDAU,REP,NREL,NDSTR,NN,SEEDV,OSEEDV,VECSET

```

```

NOREPS    = NR
NOHERD    = NH
NOSIRE    = NS
NOHXS     = NH * NS
NOEQN     = NOHXS + NH + NS
DPZERO    = 0.0D0

```

```

C *****
C ***** SET UP I/O UNITS *****
C *****
C
C FILE    I/O  F/V  COMMENTS
C -----
C LOW      I    V    RELATIONSHIP MATRIX #; LOWER TRIANGULAR MATRIX
C              FROM THE CHOLESKY DECOMPOSITION OF THE
C              RELATIONSHIP MATRIX.
C DATA    I    V    THE DATA STRUCTURE TO SIMULATE CREATED IN CRDATA.
C              FILE FORMAT: DAT.STR. #, # OBS;
C              NO. SUBCLASSES*{HERD,SIRE,N,SIREQN,HSEQN,IEQN}
C PARM      I    F    PARM FILE WITH HERD MIN, MAX, GENETIC AND HXS VAR
C SIM       0    V    RHS OUTPUT FILE WITH FORMAT:
C              #PARMS*{DAT.STR.#,SVAR,IVAR,EVAR,RELAT.#,NOREPS;
C              NOREPS*[RHS,Y'Y,E'E,#OBS]}
C TVAL      0    V    OUTPUT FILE WITH UNDERLYING VALUES FOR HERD,
C              SIRE, AND HXS WITH FILE FORMAT:
C              #PARMS*{DAT.STR.#,SVAR,IVAR,EVAR,RELAT.#,NOREPS;
C              NOREPS*[HERDS,SIRES,INTERACTION EFFECTS]}
C PRMOUT    0    F    PARM FILE WITH MODELS AND VARIANCE RATIOS
C OBS       0    F    FILE THAT SAS PROC VARCOMP WILL READ FOR TESTING
C              MIVQUE. FILE FORMAT: NOBS*{PARM#,SIRE,HERD,OBS}
C SEED      I/O  F    READ RANDOM NUMBER GENERATOR SEED AT BEGINNING OF
C              RUN AND REWINDS AND WRITES STARTING SEED AT END
C -----

```

```

LOW       = 10
DATA      = 11
PARM      = 12

```

```

SIM      = 13
TVAL     = 14
PRMOUT   = 15
OBS      = 16
SEED     = 17

NN = 0
READ (SEED,*) SEEDV
READ (LOW) NREL
READ (LOW) L
1 READ (PARM,*,END=100) RHVAR,RGVAR,RHSVAR

      NN = NN + 1
      VECSET = 0
      HVAR = DBLE(RHVAR)
      HSD = DSQRT(HVAR)
      GVAR = DBLE(RGVAR)
      SVAR = 0.25D0*GVAR
      SSD = DSQRT(SVAR)
      HSVAR = DBLE(RHSVAR)
      HSSD = DSQRT(HSVAR)
      ERRVAR= 1.0D0 - SVAR - HSVAR
      ERRSD = DSQRT(ERRVAR)
      ALPHAS= ERRVAR/SVAR
      ALPHAI= ERRVAR/HSVAR
      SIRAT = (ERRVAR+HSVAR)/SVAR

C *****
C ***** WRITE PARM CARD FOR EACH MODEL WITH TRUE ALPHAS *****
C ***** WRITE PARAMETERS AND NUMBER OF REPS AT BEGINNING *****
C ***** OF DATA SETS *****
C ***** PRINT PARAMETERS USED IN EACH SET OF REPS *****
C *****
      DO 200 IC = 1,5
        IF (IC.LE.2) THEN
          WRITE(PRMOUT,*) IC,SIRAT,DPZERO
        ELSE
          WRITE(PRMOUT,*) IC,ALPHAS,ALPHAI
        END IF
200 CONTINUE
      REWIND DATA
      READ (DATA) NDSTR,DATTOT

      WRITE (SIM) NDSTR,SVAR,HSVAR,ERRVAR,NREL,NOREPS
      WRITE (TVAL) NDSTR,SVAR,HSVAR,ERRVAR,NREL,NOREPS

C *** PRINT PARAMETERS USED ***
      WRITE(6,205) HVAR,SVAR,HSVAR,ERRVAR,ALPHAS,ALPHAI,
+      NREL,NDSTR,SEEDV

```

```

205     FORMAT ('1PARAMETERS USED IN THIS RUN',//,' HERD VAR   ',
+    F15.7,/,', SIRE VAR   ',F15.7,/,
+    ' HD X SR VAR',F15.7,/,', ERROR VAR   ',F15.7,//,', ALPHAS ',
+    F18.7,/,', ALPHAI ',F18.7,//,', RELATIONSHIP MATRIX #',I2,/,
+    ' DATA STRUCTURE #',I2,//,', SEEDS USED ',6(I6,1X))

C      ***** SET UP THE UNIFORM NUMBER GENERATOR *****
      DDD = UNIFRM(VECSET,RNVEC,SEEDV)

C      *****
C      ***      SIMULATE THE DATA      NOREPS = NUMBER OF REPLICATES      ***
C      *****

      DO 300 REP = 1,NOREPS
        REWIND DATA
        READ(DATA) NDSTR,DATTOT
        CALL SVCPCDP (0.0D0,RHS(1),1,NOEQN)
        YPY  = 0.0D0
        EPE  = 0.0D0
        DNTOT = 0.0D0
        CALL NORMAL (HRND,VECSET,SEEDV,RNVEC,NOSIRE)
        DO 400 IC = 1,NOHERD
          HRND(IC) = HRND(IC)*HSD
400      CONTINUE
        CALL NORMAL (SRND,VECSET,SEEDV,RNVEC,NOSIRE)
        CALL NORMAL (HSRND,VECSET,SEEDV,RNVEC,NOHXS)
        CALL LAC    (L,SRND,WORK,SSD,NOSIRE,1)
        CALL LAC    (L,HSRND,WORK,HSSD,NOSIRE,NOHERD)

        WRITE(TVAL) HRND,SRND,HSRND

2      READ(DATA,END=500) HERD,SIRE,N,SIREQN,HSEQN,IEQN

C      ***** BUILD RIGHT HAND SIDES *****

      DO 600 NDAU = 1,N
        ERR  = ERRSD*DNSND(VECSET,SEEDV,RNVEC)
        PHENO = HRND(HERD) + SRND(SIRE) +
+          HSRND(SIRE,HERD) + ERR
        YPY  = YPY + PHENO**2
        EPE  = EPE + ERR**2
        DNTOT = DNTOT + 1.0D0
        RHS(HERD) = RHS(HERD) + PHENO
        RHS(SIREQN) = RHS(SIREQN) + PHENO
        RHS(HSEQN) = RHS(HSEQN) + PHENO
        IF (REP.EQ.1) WRITE(OBS) NN,HERD,SIRE,PHENO
600      CONTINUE

C      *** READ NEXT HERD-SIRE COMBINATION ***

```

```

        GO TO 2
500      CONTINUE
        IF (DATTOT.NE.DNTOT) THEN
          WRITE(6,505)
505      +      FORMAT('OBSERVATION TOTALS FOR SIMUL AND CRDATA ',
          +      'DO NOT MATCH - PROGRAM HALTED')
          STOP 'OBSERVATION TOTALS MISMATCH'
        END IF
        WRITE (SIM) RHS,YPY,EPE,DNTOT

C      *** NEXT REPLICATE ***
300      CONTINUE

C      *** END OF DATA SET - READ NEXT SET OF PARAMETERS ***
      GO TO 1
100      CONTINUE

C      *** END OF SIMULATION SAVE SEED TO FILE FOR NEXT RUN ***
      REWIND SEED
      WRITE (SEED,*) SEEDV

      STOP
      END

C      =====
C      SUBROUTINE LAC (L,A,TEMP,CONST,N1,N2)
C      =====
C
C      LAST REVISED: 4/17/89
C      *****
C
C      SUBROUTINE TO PERFORM A MATRIX MULTIPLICATION OF L * A * CONST
C
C      WHERE:
C      L IS AN LOWER TRIANGULAR N1 x N1 MATRIX
C      A IS N1 x N2 MATRIX
C      TEMP IS A WORK VECTOR THAT MUST BE DIMENSIONED A LEAST N1 LONG
C      CONST IS A CONSTANT - USED TO SCALE THE MATRIX PRODUCT
C      N1 AND N2 ARE THE DIMENSIONS OF L AND A
C
C      *****

      PARAMETER (NH=50,NS=20,NR=1000)
      DIMENSION L(NS,NS),A(NS,N2),TEMP(NS)

      REAL*8      L,A,TEMP,CONST,ACC

      INTEGER*4  N1,N2,IC,JC,KC

```

```

C   *** MODIFICATION TO ALLOW SUBROUTINE CALLS THE SAME WHILE ***
C   *** IMPROVING VECTORIZING ***
C   IF (NS.NE.N1) THEN
C       WRITE (6,5)
5       FORMAT ('1PROGRAM HALTED SINCE MAIN PROGRAM AND SUBROUTINE ',
+           'LAC PARAMETERS DO NOT MATCH')
C       STOP 'LAC PARAMETERS INCORRECT'
C   END IF

C   DO 100 JC = 1,N2
C       DO 200 IC = 1,N1
C           ACC = 0.0D0
C           DO 300 KC = 1,IC
C               ACC = ACC + L(IC,KC)*A(KC,JC)
300           CONTINUE
C           TEMP(IC) = ACC*CONST
200           CONTINUE
C           DO 400 IC = 1,N1
C               A(IC,JC) = TEMP(IC)
400           CONTINUE
100       CONTINUE

C   RETURN
C   END

C   =====
C   DOUBLE PRECISION FUNCTION UNI(ISEED1,ISEED2,ISEED3)
C   =====
C
C   LAST REVISED: 7/19/89
C   *****
C
C   SUBROUTINE TO GENERATE RANDOM VALUES FROM A CONTINUOUS UNIFORM
C   (0,1) DISTRIBUTION USING THE ALGORITHM DESCRIBED BY
C   B.A. WICHMANN AND I.D. HILL, 1982 AN EFFICIENT AND PORTABLE
C   PSEUDO-RANDOM NUMBER GENERATOR (ALGORITHM AS 183), APPLIED
C   STATISTICS 31(2):188-190
C
C   SUBROUTINES NEEDED: NONE
C
C   *****
C
C   REAL*8 DMOD1,DMOD2,DMOD3
C   INTEGER*4 ALPHA1,ALPHA2,ALPHA3,MODUL1,MODUL2,MODUL3,
+       ISEED1,ISEED2,ISEED3
C
C   DATA ALPHA1/171/,ALPHA2/172/,ALPHA3/170/
C   DATA MODUL1/30269/,MODUL2/30307/,MODUL3/30327/
C   DATA DMOD1/30269.D0/,DMOD2/30307.D0/,DMOD3/30327.D0/

```

```

ISEED1 = MOD(IDINT(ALPHA1*DFLOAT(ISEED1)),MODUL1)
ISEED2 = MOD(IDINT(ALPHA2*DFLOAT(ISEED2)),MODUL2)
ISEED3 = MOD(IDINT(ALPHA3*DFLOAT(ISEED3)),MODUL3)

UNI = DMOD((DFLOAT(ISEED1)/DMOD1 + DFLOAT(ISEED2)/DMOD2 +
+          DFLOAT(ISEED3)/DMOD3),1.0D0)

RETURN
END

C =====
C DOUBLE PRECISION FUNCTION UNIFORM (VECSET,RNVEC,SEEDV)
C =====
C
C LAST REVISED: 7/19/89
C *****
C
C SUBROUTINE TO GENERATE RANDOM VALUES FROM A
C   CONTINUOUS UNIFORM (0,1) DISTRIBUTION
C
C NOTE:
C   SIX INTEGER SEEDS ARE USED TO USED AS SEEDS FOR TWO INDEPENDENT
C   UNIFORM NUMBER GENERATORS
C   THE FIRST GENERATOR IS USED TO GENERATE UNIFORM VALUES
C   THE SECOND GENERATOR IS USED TO RANDOMLY SHUFFLE THE VALUES
C   GENERATED BY THE FIRST GENERATOR TO ELEMIMATE ANY POSSIBLE
C   PATTERNS IN THE RANDOM NUMBER GENERATORS
C
C SUBROUTINES NEEDED: UNI
C
C *****

INCLUDE (RNCARD)
DIMENSION RNVEC(IVECL),SEEDV(6)
REAL*8 RNVEC,UNI
INTEGER*4 VECSET,SEEDV,ELEM

IF (VECSET.NE.0) THEN
  ELEM = 1 + IDINT(IVECL*UNI(SEEDV(1),SEEDV(2),SEEDV(3)))
  IF (ELEM.EQ.IVECL+1) ELEM=IVECL
  UNIFORM = RNVEC(ELEM)
  RNVEC(ELEM) = UNI(SEEDV(4),SEEDV(5),SEEDV(6))
ELSE
  DO 100 ELEM = 1,IVECL
    RNVEC(ELEM) = UNI(SEEDV(4),SEEDV(5),SEEDV(6))
100  CONTINUE
  VECSET=1
  UNIFORM = 0.0D0
END IF

```



RETURN  
END

C=====

DOUBLE PRECISION FUNCTION FKINRA(T)

C=====

C PURPOSE : EVALUATE DENSITY IN DISTRIBUTDDD

IMPLICIT DOUBLE PRECISION (A-H,O-Z)

DATA A/2.216035867166471/, C/0.180025191068563/

PIFAC=1.DO/DSQRT(8.DO\*DATAN(1.DO))

XX=PIFAC\*DEXP(T\*T\*0.5DO)

FKINRA=XX-C\*(A-DABS(T))

RETURN

END

C=====

SUBROUTINE NORMAL(SNDVEC,VECSET,SEED,RNVEC,N)

C=====

C PURPOSE : SAMPLE N PSEUDO-RANDOM NUMBERS FROM A STANDARDISED NORMA  
C DISTRIBUTION WITH MEAN 0 AND VARIANCE 1

C STRATEGY : THE NORMAL DISTRIBUTION IS APPROXIMATED BY A MIXTURE OF  
C DISTRIBUTIONS, NAMELY A CENTRAL AND A TAIL REGION.  
C THE DENSITY FOR THE CENTRE IS DECOMPOSED INTO A TRIANGUL  
C DENSITY AND 3 NEARLY LINEAR DENSITIES.

C THIS PROCEDURE IS DUE TO KINDERMANN AND RAMAGE (1976) :  
C COMPUTER GENERATION OF NORMAL RANDOM VARIABLES. J.A.S.A  
C 71 , 893-896.

C PROGRAM IS WRITTEN AFTER DESCRIPTION OF THEIR ALGORITHM  
C IN 'STATISTICAL COMPUTING' BY W.J.KENNEDY & J.E. GENTLE,  
C MARCEL DEKKER, NEW YORK, 1980, PAGE 205-207.

C KM 1/8  
C-----

PARAMETER (IVECL=500)

IMPLICIT DOUBLE PRECISION (A-H,O-Z)

DIMENSION SNDVEC(N),RNVEC(IVECL),SEED(6)

REAL\*8 RNVEC

INTEGER\*4 SEED,VECSET

DATA A1 / 0.884070402298758/,

\* A2 / 0.973310954173898/,

\* A3 / 0.986655477086949/,

```

* A4 / 0.958720824790463/,
* A5 / 0.755591531667601/,
* A6 / 0.911312780288703 /,
* A7 / 0.872834976671790 /,
* A8 / 0.805577924423817 /,
* F1 / 1.13113163544180 /,
* F51 / 0.630834801921960 /,
* F52 / 0.034240503750111 /,
* F71 / 0.479727404222441 /,
* F72 / 1.105473661022070 /,
* F73 / 0.049264496373128 /,
* F81 / 0.595507138015940 /,
* F82 / 0.5955071380015940 /,
* G1 / 2.216035867166471 /,
* G2 / 0.180025191068563 /

G1SQ=G1*G1

DO 100 II=1,N

U1=UNIFORM(VECSET,RNVEC,SEED)

IF(U1.LT.A1)THEN
    U2=UNIFORM(VECSET,RNVEC,SEED)
    SNDVEC(II)=G1*(F1*U1+U2-1.D0)
C    PRINT *,II,'TRIANGLE',SNDVEC(II)

ELSE IF(U1.GE.A2)THEN
C    TAIL REGION
    10    U2=UNIFORM(VECSET,RNVEC,SEED)
        U3=UNIFORM(VECSET,RNVEC,SEED)
        IF(U2*U2.GE.G1SQ/(G1SQ-2.D0*DLOG(U3)))GO TO 10
        IF(U1.LT.A3)THEN
            SNDVEC(II)=DSQRT(G1SQ-2.D0*DLOG(U3))
        ELSE
            SNDVEC(II)=-DSQRT(G1SQ-2.D0*DLOG(U3))
        END IF

C    PRINT *,II,'TAIL',SNDVEC(II)
ELSE IF(U1.GE.A4)THEN
    50    U2=UNIFORM(VECSET,RNVEC,SEED)
        U3=UNIFORM(VECSET,RNVEC,SEED)
        T=G1-(F51*DMIN1(U2,U3))
        IF(DMAX1(U2,U3).LE.A5)GO TO 59
        IF(F52*DABS(U2-U3).GT.FKINRA(T))GO TO 50
    59    IF(U2.LT.U3)THEN
            SNDVEC(II)=T
        ELSE
            SNDVEC(II)=-T
        END IF

```

```

C      PRINT *,II,'LINEAR THREE',SNDVEC(II)
      ELSE IF(U1.GE.A6)THEN
70      U2=UNIFORM(VECSET,RNVEC,SEED)
        U3=UNIFORM(VECSET,RNVEC,SEED)
        T=F71+(F72*DMIN1(U2,U3))
        IF(DMAX1(U2,U3).LE.A7)GO TO 79
        IF(F73*DABS(U2-U3).GT.FKINRA(T))GO TO 70
79      IF(U2.LT.U3)THEN
          SNDVEC(II)=T
        ELSE
          SNDVEC(II)=-T
        END IF

C      PRINT *,'LIN ONE',II,SNDVEC(II)
      ELSE
80      U2=UNIFORM(VECSET,RNVEC,SEED)
        U3=UNIFORM(VECSET,RNVEC,SEED)
        IF(DMAX1(U2,U3).GT.A8)GO TO 80
        T=F81-(F82*DMIN1(U2,U3))
        IF(U2.LT.U3)THEN
          SNDVEC(II)=T
        ELSE
          SNDVEC(II)=-T
        END IF
C      PRINT *,II,'LIN ONE',SNDVEC(II)

      END IF

100  CONTINUE

      RETURN
      END

C      =====
C      DOUBLE PRECISION FUNCTION DNSND(VECSET,SEED,RNVEC)
C      =====
C
C      LAST REVISED: 7/19/89
C      *****
C      FUNCTION TO GENERATE SINGLE RANDOM NORMAL DEVIATE WITH MEAN 0
C      AND VARIANCE 1
C
C      SUBROUTINE NEEDED: NORMAL
C      *****

      PARAMETER (IVECL=500)
      DIMENSION RNVEC(IVECL),SNDVEC(1),SEED(6)

      REAL*8 RNVEC,SNDVEC

```

```
INTEGER*4 SEED,VECSET  
CALL NORMAL (SNDVEC,VECSET,SEED,RNVEC,1)  
DNSND = SNDVEC(1)  
RETURN  
END
```

## APPENDIX B. FORTRAN PARTITIONED INVERSION PROGRAM

@PROCESS DC(MAT)

```

C =====
C PROGRAM INVERT
C =====
C
C LAST REVISED: 4/30/89
C *****
C PURPOSE AND STRATEGY:
C   PROGRAM TO INVERT COEFFICIENT MATRIX - USING PARTITIONED
C   MATRIX RESULTS SINCE H*S PORTION OF EQUATIONS ARE BLOCK DIAG
C *****
C COMMON /MAT/ C,Q,R,S
C PARAMETER (NH=50,NS=20,NR=1000)
C
C DIMENSION C(NH*NS+NH+NS,NH*NS+NH+NS),Q(NH+NS,NH+NS),
+ R(NH+NS,NH*NS),S(NS,NS,NH),A(NS,NS),AINV(NS,NS)
C
C REAL*8 C,Q,R,S,A,AINV,ALPHAS,ALPHAI,COLL,DNTOT,DPN,ONEG,
+ DPONE
C
C INTEGER*4 NOSIRE,NOHERD,NHPS,NHSI,NOEQN,INPUT,PARM,RLT,
+ INVRS,HERD,SIRE,N,SIREQN,HSEQN,IEQN,MODEL,BEGIN,IDEN1,IDEN2,
+ RELNUM,NADD,IC,JC,KC,LC,IAC,JAC,KAC,LAC,NDSTR
C
C CALL SPINIT
C
C NOSIRE = NS
C NOHERD = NH
C NHPS   = NH + NS
C NHSI   = NH * NS
C NOEQN  = NHPS + NHSI
C ONEG   = -1.0D0
C DPONE  = 1.0D0
C
C *****
C ***** SET UP UNIT DEFINITIONS FOR I/O UNITS *****
C *****
C
C UNIT  I/O  F/V  COMMENT
C -----
C INPUT  I    V   DATA STRUCTURE FILE FROM CRDATA. FILE FORMAT:
C                   DAT.STR.#,NO OBS;
C                   NO. SUBCLASSES*{HERD,SIRE,N,SIREQN,HSEQN,IEQN}
C PARM    I    F   PARAMETER LIST INCLUDES MODEL SWITCH, VARIANCE
C                   RATIOS FOR SIRE AND INTERACTION VARIANCE
C RLT     I    V   RELATIONSHIP FILE WITH RELATIONSHIP NUMBER;
C                   A; AND A INVERSE
C INVRS   O    V   OUTPUT FILE WITH FORMAT
C                   MODEL,DAT.STR.#,NO OBS,REL.#,ALPHAS,ALPHAI;

```

```

C                                     INVERSE OF COEFFICIENT MATRIX
C
C *****
C
C INPUT = 10
C PARM  = 11
C RLT   = 14
C INVRS = 15
C
C *****
C READ THE RELATIONSHIP NUMBER, RELATIONSHIP MATRIX, AND INVERSE
C FROM THE RELATIONSHIP FILE. IF THERE IS NO RELATIONSHIP MATRIX
C PRESENT SET RELNUM=0, A=I, AINV=I
C *****
C
C READ (RLT,END=20) RELNUM
C   READ (RLT) A
C   READ (RLT) AINV
C   GO TO 40
20 CONTINUE
C   RELNUM = 0
C   CALL SVCPDP(0.0D0,A(1,1),1,NOSIRE**2)
C   CALL SVCPDP(0.0D0,AINV(1,1),1,NOSIRE**2)
C   DO 30 IC = 1,NOSIRE
C     A(IC,IC) = DPONE
C     AINV(IC,IC) = DPONE
30 CONTINUE
40 CONTINUE
C
C *****
C READ PARAMETERS FROM PARAMETER FILE
C   MODEL IS SWITCH FOR USING SIRE RELATIONSHIPS IN ESTIMATING
SIRE
C   VARIANCE
C   ALPHAS IS THE PRIOR ESTIMATE FOR THE ERROR TO SIRE VARIANCE
RATIOS
C   ALPHAI IS THE PRIOR ESTIMATE FOR THE ERROR TO HXS VARIANCE
C
C MODEL SWITCH AND VARIANCE STRUCTURE USED:
C
C   MODEL      VAR(S)      VAR(HXS)      IDEN1      IDEN2
C   =====
C   1           I          N.A.           1          N.A.
C   2           A          N.A.           0          N.A.
C   3           I          I             1          1
C   4           A          I             0          1
C   5           A          I X A          0          0
C   =====

```

```

C *****
1 READ (PARM,*,END=2200) MODEL,ALPHAS,ALPHAI
C *** RESET VARIABLES ***
  CALL SVCPPDP(0.0D0,Q(1,1),1,NHPS**2)
  CALL SVCPPDP(0.0D0,R(1,1),1,NHPS*NHSI)
  CALL SVCPPDP(0.0D0,S(1,1,1),1,NOSIRE**2*NOHERD)
  CALL SVCPPDP(0.0D0,C(1,1),1,NOEQN**2)

C *****
C ADD VARIANCE RATIO TIMES A-1 TO W'W IF RELATIONSHIPS ARE USED
C OR THE RATIO IS ADDED TO THE SIRE AND INTERACTION DIAGONAL
C IF RELATIONSHIPS ARE IGNORED, AND GET THE INVERSE
C *****

C *** ADD VARIANCE RATIO TO SIRE EQUATIONS ***

  BEGIN = NOHERD + 1
  IF ((MODEL.EQ.1).OR.(MODEL.EQ.3)) THEN
C *** ADD SIRE VARIANCE RATIO TO SIRE DIAGONALS ONLY ***
    IDEN1 = 1
    DO 500 IC = BEGIN,NHPS
      Q(IC,IC) = ALPHAS
500 CONTINUE
  ELSE
C *** ADD SIRE VARIANCE RATIO TIMES INVERSE OF ***
C *** RELATIONSHIP MATRIX TO SIRE EQUATIONS ***
    IDEN1 = 0
    DO 600 IC = BEGIN,NHPS
      IAC = IC - NOHERD
      DO 600 JC = BEGIN,NHPS
        JAC = JC - NOHERD
        Q(JC,IC) = AINV(JAC,IAC)*ALPHAS
600 CONTINUE
  END IF

C *** ADD VARIANCE RATIO TO INTERACTION EQUATIONS ***

  IF ((MODEL.EQ.3).OR.(MODEL.EQ.4)) THEN
C *** ADD INTERACTION VARIANCE RATIO TO DIAGONALS ONLY ***
    IDEN2 = 1
    DO 700 IC = 1,NOHERD
      DO 700 JC = 1,NOSIRE
        S(JC,JC,IC) = ALPHAI
700 CONTINUE
  ELSE IF (MODEL.EQ.5) THEN
C *** ADD INTERACTION VARIANCE RATION TIMES INVERSE OF ***
C *** (I X A) TO INTERACTION EQUATIONS ***
    IDEN2 = 0

```



```

      DO 800 IC = 1,NOHERD
        DO 800 JC = 1,NOSIRE
          DO 800 KC = 1,NOSIRE
            S(KC,JC,IC) = AINV(KC,JC)*ALPHAI
800      CONTINUE
      END IF

C      *****
C      ***** BUILD THE W'W MATRIX *****
C      *****

      REWIND INPUT
      READ (INPUT) NDSTR,DNTOT
      IF (MODEL.LE.2) THEN
2        READ (INPUT,END=100) HERD,SIRE,N,SIREQN,HSEQN,IEQN
          DPN = DFLOAT(N)
          Q(HERD,HERD) = Q(HERD,HERD) + DPN
          Q(HERD,SIREQN) = DPN
          Q(SIREQN,HERD) = DPN
          Q(SIREQN,SIREQN) = Q(SIREQN,SIREQN) + DPN
          GO TO 2
        ELSE
3        READ (INPUT,END=100) HERD,SIRE,N,SIREQN,HSEQN,IEQN
          DPN = DFLOAT(N)
          Q(HERD,HERD) = Q(HERD,HERD) + DPN
          Q(HERD,SIREQN) = DPN
          Q(SIREQN,HERD) = DPN
          Q(SIREQN,SIREQN) = Q(SIREQN,SIREQN) + DPN
          R(HERD,IEQN) = DPN
          R(SIREQN,IEQN) = DPN
          S(SIRE,SIRE,HERD) = S(SIRE,SIRE,HERD) + DPN
          GO TO 3
        END IF
100      CONTINUE

C      *****
C      *****
C      *** INVERT THE COEFICIENT MATRIX ***
C      *****
C      USING PARTITIONED MATRIX RESULTS,
C      *****
C      
$$X = \begin{array}{c|c} Q & R \\ \hline R' & S \end{array}$$

C      *****
C      THEN IF  $INV(X) = C$ 
C      *****
C      
$$C = \begin{array}{c|c} E & F \\ \hline F' & G \end{array}$$

C      *****

```

```

C
C      WHERE,
C
C      E = INV(P)
C
C      F = -INV(P)*R*INV(S)
C
C      G = INV(S) + INV(S)*R'*INV(P)*R*INV(S)
C
C      P = Q - R*INV(S)*R'
C
C      STRATEGY:
C
C      1) SET UP Q,R,S
C      2) CALCULATE INV(S)
C      3) E <= Q
C      4) F' <= (R*INV(S))'
C      5) E <= INV(E - F*R')
C      6) F <= - E*(F')'
C      7) G <= DIAG(INV(S))
C      8) G <= G - F'*F
C      9) F' <= (F)'
C
C      *****
C
C      IF (MODEL.LE.2) THEN
C          CALL INVRT(Q,NHPS,NHPS)
C          WRITE(INVRS) MODEL,NDSTR,DNTOT,RELNUM,ALPHAS,ALPHAI
C          CALL MATRIX(Q,NHPS,NHPS,NHPS,INVRS,0)
C          WRITE (6,1005) MODEL,NDSTR,RELNUM,ALPHAS
1005      FORMAT (' INVERSE GENERATED FOR:',/, ' MODEL ',I2,/,
+              ' DATA STRUCTURE ',I2,/, ' RELATIONSHIP MATRIX ',I2,/,
+              ' SIRE VARIANCE RATIO ',F20.10,///)
C      ELSE
C
C      *****
C      ***** INVERT S *****
C      *****
C          IF (MODEL.LT.5) THEN
C              DO 1020 IC = 1,NOHERD
C                  DO 1020 JC = 1,NOSIRE
C                      S(JC,JC,IC) = 1.0D0/S(JC,JC,IC)
1020      CONTINUE
C          ELSE
C              DO 1050 IC = 1,NOHERD
C                  CALL INVRT(S(1,1,IC),NOSIRE,NOSIRE)
1050      CONTINUE
C          END IF
C
C      *****

```

```

C ***** COPY Q TO E *****
C *****
      DO 1100 JC = 1,NHPS
        DO 1100 IC = 1,NHPS
          C(IC,JC) = Q(IC,JC)
1100      CONTINUE

C *****
C ***** CALCULATE (R*INV(S))' AND STORE IN F' *****
C *****
      DO 1200 IC = 1,NOHERD
        NADD = (IC - 1)*NOSIRE
        DO 1200 JC = 1,NOSIRE
          JAC = NHPS + NADD + JC
          DO 1200 KC = 1,NHPS
            COLL = 0.0D0
            DO 1300 LC = 1,NOSIRE
              LAC = LC + NADD
              COLL = COLL + R(KC,LAC)*S(LC,JC,IC)
1300          CONTINUE
            C(JAC,KC) = COLL
1200      CONTINUE

C *****
C ***** CALCULATE E *****
C *****
      SINCE E=Q AND F'=(R*INV(S))' FROM PRIOR STEPS
C *****
      THEN E = INV(E - (F')'*R')
      = INV(Q - R*INV(S)*R')
C *****
      DO 1400 IC = 1,NHPS
        DO 1400 JC = 1,NHPS
          COLL = 0.0D0
          DO 1500 KC = 1,NHPSI
            KAC = NHPS + KC
            COLL = COLL + C(KAC,IC)*R(JC,KC)
1500          CONTINUE
          C(JC,IC) = C(JC,IC) - COLL
1400      CONTINUE

C *****
C ***** CALCULATE FINAL VALUE FOR E *****
C *****
      INVERT E = P = Q - R*INV(S)*R'
C *****
      CALL INVRT(C,NOEQN,NHPS)

C *****
C ***** CALCULATE FINAL VALUE FOR F *****

```

```

C
C      SINCE  $E=INV(P)$  AND  $F'=(R*INV(S))'$  FROM PREVIOUS STEPS
C       $F <= -1*E*(F')' = -INV(P)*R*INV(S) = F$ 
C      *****
      DO 1600 IC = 1,NHPSI
        IAC = NHPS + IC
        DO 1600 JC = 1,NHPS
          COLL = 0.0D0
          DO 1700 KC = 1,NHPS
            COLL = COLL + C(IAC,KC)*C(KC,JC)
1700          CONTINUE
          C(JC,IAC) = ONEG*COLL
1600        CONTINUE

C      *****
C      ***** COPY BLOCKS FROM INV(S) TO G *****
C      *****
      DO 1800 IC = 1,NOHERD
        NADD = NHPS + (IC-1)*NOSIRE
        DO 1800 JC = 1,NOSIRE
          JAC = JC + NADD
          DO 1800 KC = 1,NOSIRE
            KAC = KC + NADD
            C(KAC,JAC) = S(KC,JC,IC)
1800          CONTINUE

C      *****
C      CALCULATE FINAL G
C
C      SINCE  $G=INV(S)$ ,  $F' = INV(S)*R'$ , AND  $F=-INV(P)*R*INV(S)$ 
C      FROM PRIOR STEPS, THEN,
C
C       $G <= G - (F')*F = INV(S) + INV(S)*R'*INV(P)*R*INV(S) = G$ 
C      *****
      BEGIN = NHPS + 1
      DO 1900 IC = BEGIN,NOEQN
        DO 1900 JC = BEGIN,NOEQN
          COLL = 0.0D0
          DO 2000 KC = 1,NHPS
            COLL = COLL + C(IC,KC)*C(KC,JC)
2000          CONTINUE
          C(IC,JC) = C(IC,JC) - COLL
1900        CONTINUE

C      *****
C      ***** COPY F TO F' *****
C      *****
      DO 2100 IC = BEGIN,NOEQN
        DO 2100 JC = 1,NHPS
          C(IC,JC) = C(JC,IC)

```

2100 CONTINUE

```

C *****
C ***** OUTPUT THE INVERSE *****
C *****
      WRITE(INVRS) MODEL,NDSTR,DNTOT,RELNUM,ALPHAS,ALPHAI
      CALL MATRIX(C,NOEQN,NOEQN,NOEQN,INVRS,0)
      WRITE (6,2105) MODEL,NDSTR,RELNUM,ALPHAS,ALPHAI
2105  FORMAT (' INVERSE GENERATED FOR:',/, ' MODEL ',I2,/,
+         ' DATA STRUCTURE ',I2,/, ' RELATIONSHIP MATRIX ',I2,/,
+         ' SIRE VARIANCE RATIO ',F20.10,/, ' INTERACTION',
+         ' VARIANCE RATIO ',F20.10)
      END IF
C  *** READ NEXT SET OF PARAMETERS ***
      GO TO 1

```

2200 CONTINUE  
STOP  
END

```

C =====
C SUBROUTINE COLI (X,N,NUNIT)
C =====

```

```

C LAST REVISED: 4/18/89
C *****
C SUBROUTINE TO INPUT A VECTOR OF LENGTH N OR THE I COLUMN OF
C MATRIX X IF THE FIRST VARIABLE IN THE CALL IS X(1,I). THE VECTOR
C IS READ FROM UNIT NUNIT.
C *****

```

DIMENSION X(N)

REAL\*8 X  
INTEGER\*4 N,NUNIT

READ(NUNIT) X

RETURN  
END

```

C =====
C SUBROUTINE COLO (X,N,NUNIT)
C =====

```

```

C LAST REVISED: 4/21/89
C *****
C SUBROUTINE TO OUTPUT A VECTOR OF LENGTH N OR THE I COLUMN OF
C MATRIX X IF THE FIRST VARIABLE IN THE CALL IS X(1,I). THE VECTOR
C IS WRITTEN FROM UNIT NUNIT.
C *****

```

```

DIMENSION X(N)

REAL*8 X
INTEGER*4 N,NUNIT

WRITE(NUNIT) X

RETURN
END

C =====
C SUBROUTINE MATRIX (X,N,IR,IC,NUNIT,IO)
C =====
C
C LAST REVISED: 4/30/89
C *****
C SUBROUTINE TO INPUT OR OUTPUT A DOUBLE PRECISION R BY C MATRIX X
C A ROW AT A TIME TO UNIT NUMBER NUNIT.
C
C FORMAT OF SUBROUTINE CALL IS:
C     CALL MATRIX(X,N,IR,IC,NUNIT,IO),
C
C WHERE:
C     X      IS THE MATRIX TO INPUT OR OUTPUT
C     N      IS THE LEADING DIMENSION OF X AS DECLARED IN THE
C             CALLING PROGRAM
C     IR     IS THE NUMBER OF ROWS TO I/O
C     IC     IS THE NUMBER OF COLUMNS TO I/O
C             NOTE: SUBROUTINE OUTPUTS LEADING BLOCK OF MATRIX ONLY
C     NUNIT  IS THE FORTRAN UNIT NUMBER TO READ OR READ
C     IO     IS AN INPUT OR OUTPUT SWITCH  SUBROUTINE
C             READS  IF IO=1
C             WRITES IF IO=0
C
C *****
C
DIMENSION X(N,IC)

REAL*8 X
INTEGER*4 N,IR,IC,NUNIT,IO

IF (IO.EQ.1) THEN
    DO 100 I = 1,IC
        CALL COLI (X(1,I),IR,NUNIT)
100    CONTINUE
ELSEIF (IO.EQ.0) THEN
    DO 200 I = 1,IC
        CALL COLO (X(1,I),IR,NUNIT)
200    CONTINUE

```

```

ELSE
  WRITE(6,*) 'READ OR WRITE NOT SPECIFIED FOR SUBROUTINE MATRIX'
  STOP
END IF

```

```

RETURN
END

```

```

C=====
C      SUBROUTINE INVRT( A, IA, N)
C=====

```

```

C      PURPOSE : INVERT A NON-SYMMETRIC MATRIX OF ORDER N
C                MATRIX MUST BE NON-SINGULAR (PROGRAM STOPS IF SINGULARIT
C                ENCOUNTERED), BUT CAN BE NON-POSITIVE DEFINITE

```

```

C      STRATEGY : USE GAUSS-JORDAN ALGORITHM
C                  (WITH PARTIAL PIVOTING)
C                  TIME REQUIRED IS PROPORTIONAL TO THE CUBIC POWER OF THE
C                  OF THE MATRIX.
C                  PROGRAMMED AFTER STOER,J. AND BULIRSCH,R. : INTRODUCTIO
C                  NUMERICAL ANALYSIS. SPRINGER VERLAG 1980, PP. 169-172.

```

```

C                  THE ORIGINAL MATRIX IS STORED WITHIN THE ROUTINE AND MU
C                  WITH ITS INVERSE, THE PRODUCT IS CHECKED FOR DEVIATIONS
C                  THE IDENTITY MATRIX

```

```

C      PARAMETERS :
C      - A : MATRIX TO BE INVERTED, DOUBLE PRECISION, DECLARED W
C            ROW DIMENSION IA AND COLUMN DIMENSION AT LEAST N IN
C            CALLING PROGRAM;
C            OVERWRITTEN WITH INVERSE
C      - IA : ROW DIMENSION OF A (AS DECLARED)
C      - N : ORDER OF THE MATRIX TO BE INVERTED, MUST BE STORED
C            FIRST N ROWS AND COLUMNS OF A

```

```

C      ERROR STOPS : - MATRIX SINGULAR
C                    - PROGRAM DIMENSIONS EXCEEDED

```

```

C      ROUTINES REQUIRED : NONE

```

```

C
C
C-----KM 12/

```

```

IMPLICIT DOUBLE PRECISION (A-H,O-Z)
PARAMETER (NH=50,NS=20,NR=1000)
DIMENSION A(IA,N),B(NH+NS,NH+NS),VEC(NH+NS),IFLAG(NH+NS)

```

```

MORDER = NS + NH

```

```

      IF(N.GT.MORDER)STOP 'ROUTINE INVERT : PROGRAM DIMENSIONS EXCEEDED'
C     MINIMUM VALUE TO BE DISTINGUISHED FROM 0.D0
      ZERO=1.D-12

      DIAG=0.D0
      OFF=0.D0
      DO 1 I=1,N
1      IFLAG(I)=I
C     STORE MATRIX PRIOR TO INVERSION
      DO 22 I=1,N
      DO 22 J=1,N
22     B(J,I)=A(J,I)

      DO 2 I=1,N

C     FIND MAXIMUM ELEMENT IN THE COLUMN (START AT I-TH EL. ONLY)
      XX=DABS(A(I,I))
      IMAX=I
      DO 3 J=I+1,N
      ZZ=DABS(A(J,I))
      IF(ZZ.GT.XX)THEN
      XX=ZZ
      IMAX=J
      END IF
3     CONTINUE

C     CHECK FOR SINGULARITY
      IF(XX.LT.ZERO) STOP 'SUBROUTINE INVERT : MATRIX IS SINGULAR'

C     INTERCHANGE ROW I AND ROW WITH MAX. ELEMENT IN THE COLUMN
      IF(IMAX.GT.I)THEN
      DO 4 K=1,N
      SAVE=A(I,K)
      A(I,K)=A(IMAX,K)
      A(IMAX,K)=SAVE
4     CONTINUE
      ISAVE=IFLAG(I)
      IFLAG(I)=IFLAG(IMAX)
      IFLAG(IMAX)=ISAVE
      END IF

C     TRANSFORM THE MATRIX
      SAVE=1.D0/A(I,I)
      DO 5 J=1,N
5     A(J,I)=A(J,I)*SAVE
      A(I,I)=SAVE
      DO 6 K=1,N
      IF(K.EQ.I)GO TO 6
      DO 7 J=1,N

```



```

      IF(J.NE.I)A(J,K)=A(J,K)-A(J,I)*A(I,K)
7      CONTINUE
      A(I,K)=-A(I,K)*SAVE
6      CONTINUE

2      CONTINUE

C      INTERCHANGE COLUMNS (ANALOGOUS TO PREVIOUS ROW CHANGES )
      DO 8 I=1,N
      DO 9 K=1,N
      J=IFLAG(K)
9      VEC(J)=A(I,K)
      DO 10 K=1,N
10     A(I,K)=VEC(K)
8      CONTINUE

C      MULTIPLY MATRIX WITH ITS INVERSE, CHECK ELEMENTS
      DO 33 I=1,N
      DO 33 J=1,N
      XX=0.DO
      DO 34 K=1,N
34     XX=XX+A(K,J)*B(I,K)
      IF(I.EQ.J)THEN
C      IF(DABS(XX-1.DO).GT.ZERO)PRINT *,I,XX
      DIAG=DIAG+XX
      ELSE
C      IF(DABS(XX).GT.ZERO)PRINT *,I,J,XX
      OFF=OFF+XX
      END IF
33     CONTINUE
C      XX=DIAG/N
C      PRINT *, 'DIAGONAL : SUM =',DIAG,'      AVERAGE =',XX
C      XX=OFF/(N*(N-1))
C      PRINT *, 'OFF-DIAG : SUM =',OFF,'      AVERAGE =',XX

      RETURN
      END

```

APPENDIX C.    FORTRAN PROGRAM TO CALCULATE EXPECTATIONS OF  
MIVQUE QUADRATIC FORMS

```
@PROCESS DC(BIGMAT)
```

```
C =====
C PROGRAM EXPECT
C =====
```

```
C
C
C LAST REVISED: 4/30/89
C *****
```

```
C PURPOSE AND STRATEGY: TO CALCULATE THE EXPECTATIONS OF QUADRATICS
C FOR MIVQUE VARIANCE COMPONENT ESTIMATION FOR ONE OF FIVE MODELS
C AND GIVEN VARIANCE RATIOS. THE PARAMETERS ARE READ FROM A FILE,
C SO MORE THAN ONE EXPECTATION MAY BE CALCULATED IN A SINGLE RUN
C AND THE EXPECTATIONS WILL BE WRITTEN TO DISK CONSECUTIVELY.
C THE EXPECTATIONS CALCULATED MUST ALL BE FOR THE SAME DATA
C STRUCTURE AND RELATIONSHIP MATRIX. THE EXPECTATIONS ARE
C CALCULATED USING THE METHOD DESCRIBED BY L.R. SCHAEFFER. 1979.
C NOTES ON LINEAR MODEL THEORY AND HENDERSON'S MIXED MODEL
C TECHNIQUES. 266-276; 298-305. THE METHOD ALLOWS CALCULATION
C OF THE EXPECTATIONS BY USING TRACES OF PRODUCTS OF THE
C COEFFICIENT MATRIX FROM THE MIXED MODEL EQUATIONS AND THE
C INVERSE.
```

```
C IT IS IMPORTANT TO NOTE THAT ALL MATRICES ARE FULL STORED IN THIS
C PROGRAM DESPITE THE FACT THAT ALMOST ALL ARE SYMMETRIC. THERE
C ARE TWO REASONS FOR THIS: 1) TO ALLOW OPTIMUM VECTORIZATION OF
C SINCE THE NAS 9160 HAS A VECTOR PROCESSOR TO MAXIMIZE
C EFFICIENCY OF CERTAIN VECTOR OPERATIONS, AND 2) IN USING THE
C EXPANDED MEMORY AVAILABLE IN THE EXPANDED ARCHITECTURE OF
C IT IS EXTREMELY IMPORTANT TO CONFINE MATRIX OPERATIONS WITHIN
C ONE COLUMN AT A TIME, AND THIS IS DIFFICULT USING HALF STORED
C MATRICES.
```

```
C *****
```

```
COMMON /BIGMAT/ MAT,WORK,RES,TR,AM,AMINV
```

```
PARAMETER (NH=50,NS=20,NR=1000)
```

```
DIMENSION MAT(NH+NS+NH*NS,NH+NS+NH*NS),WORK(NH+NS+NH*NS),
+ RES(NH+NS+NH*NS),K(3,3),A(NS,NS),AINV(NS,NS),TR(NH+NS+NH*NS,6),
+ AM(NH*NS,NH*NS),AMINV(NH*NS,NH*NS)
```

```
REAL*8 MAT,WORK,RES,K,A,AINV,TR,ALPHAS,ALPHAI,DNTOT,DPN,
+ DPONE,DATTOT,AM,AMINV
```

```
INTEGER*4 NOHERD,NOSIRE,NOHXS,NDIM,NHPS,NOEQN,OLDINT,INT,
+ INPUT,RLT,EXP,C,CADD,CVICS,CVICI,WZVZWS,WZVZWI,WPW,HERD,SIRE,N,
+ SIREQN,HSEQN,IEQN,NVC,NDSTR,RELNUM,MODEL,IC,JC,IDEN1,IDEN2,
+ INVSTR,INVREL
```

```
CALL SPINIT
```

NOHERD = NH  
 NOSIRE = NS  
 NOHXS = NH \* NS  
 NDIM = NH + NS + NH\*NS  
 NHPS = NOHERD+NOSIRE

OLDINT = 0  
 DPONE = 1.0D0

```

C *****
C *****          SET UP UNIT DEFINITIONS FOR I/O UNITS          *****
C *****
C
C FILE   I/O  V/F  COMMENT
C -----
C INPUT   I    V   DATA STRUCTURE FILE FROM CRDATA. FILE FORMAT:
C                   DAT.STR#,NUMBER OF RECORDS;
C                   NHS{HERD,SIRE,NDAUS,SIREQN,HSEQN,IEQN}
C RLT      I    V   RELATIONSHIP FILE WITH FORMAT:
C                   REL#;A, A INVERSE.
C EXP      O    V   OUTPUT FILE FOR EXPECTATIONS OF QUADRATICS WITH
C                   FILE FORMAT:
C                   NPARM*{MODEL,DAT.STR.#,NO OBS,REL.#,
C                   ALPHAS,ALPHAI;EXPECT}
C C         I    V   INPUT FILE CONTAINING THE INVERSE OF THE
C                   COEFFICIENT MATRIX WITH FILE FORMAT:
C                   NPARM*{MODEL,DAT.STR.#,NO OBS,REL.#,
C                   ALPHAS,ALPHAI;INVERSE}
C CVICS    I/O   V   Cs'VsINVCs SCRATCH FILE
C CVICI    I/O   V   Ci'ViINVCi SCRATCH FILE
C WPW      I/O   V   W'W SCRATCH FILE
C WZVZWS   I/O   V   W'ZsVsZs'W SCRATCH FILE
C WZVZWI   I/O   V   W'ZiViZi'W SCRATCH FILE
C -----
  
```

INPUT = 10  
 RLT = 11  
 EXP = 12  
 C = 23

```

C *****
C READ THE RELATIONSHIP NUMBER, RELATIONSHIP MATRIX, AND INVERSE
C FROM THE RELATIONSHIP FILE. IF THERE IS NO RELATIONSHIP MATRIX
C PRESENT SET RELNUM=0, A=I, AINV=I
C *****
  
```

READ (RLT,END=20) RELNUM  
 READ (RLT) A  
 READ (RLT) AINV

```

      GO TO 40
20    CONTINUE
      RELNUM = 0
      CALL SVCPPD(0.0D0,A(1,1),1,NOSIRE**2)
      CALL SVCPPD(0.0D0,AINV(1,1),1,NOSIRE**2)
      DO 30 IC = 1,NOSIRE
        A(IC,IC) = DPONE
        AINV(IC,IC) = DPONE
30    CONTINUE
40    CONTINUE

C      *****
C      READ PARAMETERS FROM PARAMETER FILE
C      MODEL IS SWITCH FOR USING SIRE RELATIONSHIPS IN ESTIMATING
SIRE  VARIANCE
C      ALPHAS IS THE PRIOR ESTIMATE FOR THE ERROR TO SIRE VARIANCE
RATIOS ALPHAI IS THE PRIOR ESTIMATE FOR THE ERROR TO HXS VARIANCE
C
C      RELATION SWITCH AND VARIANCE STRUCTURE USED:
C
C      MODEL      VAR(S)      VAR(HXS)      IDEN1      IDEN2
C      =====
C      1          I          N.A.          1          N.A.
C      2          A          N.A.          0          N.A.
C      3          I          I            1          1
C      4          A          I            0          1
C      5          A          I X A        0          0
C      =====
C      *****

C      *****
C      READ PARAMETERS FROM FRONT OF INVERSE FILE AND CHECK VALUE OF
C      MODEL AND SET NVC, INT, NOEQN, IDEN1, IDEN2, AND I/O UNITS BASED
C      ON THE MODEL TO BE USED
C      *****
1    READ (C,END=1300) MODEL,INVSTR,DNTOT,INVREL,ALPHAS,ALPHAI
      CALL SVCPPD(0.0D0,MAT(1,1),1,NDIM**2)
      CALL SVCPPD(0.0D0,K(1,1),1,9)
      REWIND INPUT
      DO 150 JC = 21,26
        IF (JC.NE.23) REWIND JC
150   CONTINUE
      READ (INPUT) NDSTR,DATTOT

      IF ((RELNUM.NE.INVREL).OR.(NDSTR.NE.INVSTR).OR.

```

```

+      (DATTOT.NE.DNTOT)) THEN
+      WRITE (*,*) RELNUM,INVREL,NDSTR,INVSTR,DATTOT,DNTOT
+      WRITE(6,5)
5      FORMAT('1EXPECTATION HALTED - PROBLEM WITH INVERSE ',
+            'PARAMETERS MATCHING WITH RELATIONSHIP FILE ',
+            'OR DATA STRUCTURE FILE')
+      STOP 'INVERSE PARAMETER MISMATCH'
END IF

IF (MODEL.LE.2) THEN
C      *** MODELS 1 AND 2 ***
      NVC      = 2
      INT      = 1
      CADD     = 21
      CVICS    = 22
      WZVZWS   = 24
      WPW      = 25
      NOEQN    = NOHERD + NOSIRE
      IF (MODEL.EQ.1) THEN
C          *** MODEL 1 ***
          IDEN1 = 1
      ELSEIF (MODEL.EQ.2) THEN
C          *** MODEL 2 ***
          IDEN1 = 0
      END IF
ELSE
C      *** MODELS 3, 4, AND 5 ***
      NVC      = 3
      INT      = 2
      CADD     = 20
      CVICS    = 21
      CVICI    = 22
      WZVZWS   = 24
      WZVZWI   = 25
      WPW      = 26
      NOEQN    = NOHERD + NOSIRE + NOHERD*NOSIRE
      IF (MODEL.EQ.3) THEN
C          *** MODEL 3 ***
          IDEN1 = 1
          IDEN2 = 1
      ELSEIF (MODEL.EQ.4) THEN
C          *** MODEL 4 ***
          IDEN1 = 0
          IDEN2 = 1
      ELSEIF (MODEL.EQ.5) THEN
C          *** MODEL 5 ***
          IDEN1 = 0
          IDEN2 = 0
      ELSE
          WRITE(6,105)

```

```

105          FORMAT('1INVALID VALUE FOR MODEL - PROGRAM HALTED')
          STOP 'INVALID VALUE FOR MODEL'
        END IF
      END IF

C *****
C *****      BUILD THE W'W MATRIX      *****
C *****

      IF (MODEL.LE.2) THEN
2        READ (INPUT,END=100) HERD,SIRE,N,SIREQN,HSEQN,IEQN
          DPN = DFLOAT(N)
          MAT(HERD,HERD)      = MAT(HERD,HERD) + DPN
          MAT(HERD,SIREQN)    = DPN
          MAT(SIREQN,HERD)    = DPN
          MAT(SIREQN,SIREQN) = MAT(SIREQN,SIREQN) + DPN
          GO TO 2
      ELSE
3        READ (INPUT,END=100) HERD,SIRE,N,SIREQN,HSEQN,IEQN
          DPN = DFLOAT(N)
          MAT(HERD,HERD)      = MAT(HERD,HERD) + DPN
          MAT(HERD,SIREQN)    = DPN
          MAT(SIREQN,HERD)    = DPN
          MAT(HERD,HSEQN)     = DPN
          MAT(HSEQN,HERD)     = DPN
          MAT(SIREQN,SIREQN) = MAT(SIREQN,SIREQN) + DPN
          MAT(SIREQN,HSEQN)   = DPN
          MAT(HSEQN,SIREQN)   = DPN
          MAT(HSEQN,HSEQN)    = DPN
          GO TO 3
      END IF
100    CONTINUE
      CALL MATRIX (MAT,NDIM,NOEQN,NOEQN,WPW,0)

C *****
C CALCULATE THE PRODUCTS NECESSARY FOR CALCULATING THE TRACES
C TO DETERMINE THE EXPECTATIONS OF THE QUADRATICS CONSIDERING
C RELATIONSHIPS
C
C THE QUADRATICS ARE:
C
C      Q1 = Us' VsINV Us
C      Q2 = Ui' ViINV Ui
C      Q3 = Y'Y - B'X'Y - U'Z'Y
C          = E'E + (Us' VsINV Us)*ALPHAS + (Ui' ViINV Ui)*ALPHAI
C
C THE EXPECTATIONS ARE
C
C      E(Q1) = TR{Cs'VsINVCsW'ZsVsZs'W} VAR(S)
C              + TR{Cs'VsINVCsW'ZiViZi'W} VAR(HXS)

```

```

C          + TR{Cs'VsINVCsW'W}          VAR(E)
C
C          E(Q2) = TR{Ci'ViINVCiW'ZsVsZs'W} VAR(S)
C          + TR{Ci'ViINVCiW'ZiViZi'W} VAR(HXS)
C          + TR{Ci'ViINVCiW'W}          VAR(E)
C
C          E(Q2) = N - TR{CW'ZsVsZs'W} VAR(S)
C          + N - TR{CW'ZiViZi'W} VAR(HXS)
C          + N - TR{CW'W}          VAR(E)
C
C          WHERE Vs = A
C          Vi = BLOCK DIAGONAL OF A'S
C
C          *****
C
C          *** CALCULATE W'ZsAZs'W ***
C          CALL XPAX (MAT,NOEQN,A,1, IDEN1,WORK,NOHERD,RES,WZVZWS)
C
C          IF (MODEL.GE.3) THEN
C              *** CALCULATE W'ZiAZi'W ***
C              CALL XPAX (MAT,NOEQN,A,NOHERD, IDEN2,WORK,NHPS,RES,WZVZWI)
C          END IF
C
C          *** READ INVERSE OF COEFFICIENT MATRIX ***
C          CALL MATRIX(MAT,NDIM,NOEQN,NOEQN,C,1)
C
C          *** CALCULATE Cs'AinvCs ***
C          CALL XPAX (MAT,NOEQN,AINV,1, IDEN1,WORK,NOHERD,RES,CVICS)
C
C          IF (MODEL.GE.3) THEN
C              *** CALCULATE Ci'AinvCi ***
C              CALL XPAX (MAT,NOEQN,AINV,NOHERD, IDEN2,WORK,NHPS,RES,CVICI)
C          END IF
C
C          *** RESET FILES TO START OF MATRICES ***
C          DO 850 JC = 21,26
C              IF (JC.NE.23) REWIND JC
850      CONTINUE
C
C          *****
C          CALCULATE TRACES
C          *****
C
C          COPY CALCULATED MATRIX PRODUCTS TO A TEMPORARY MATRIX TO CALCULATE
C          TRACES OF PRODUCTS OF THOSE CALCULATE TO FORM THE EXPECTATIONS
C
C          FOR MODELS 1 AND 2 THE COLUMNS USED FOR TEMPORARY VECTOR STORAGE
C          ARE:
C          1 <= CsAinvCs
C          2 <= C

```



```

C      3 <= W'ZsAZs'W
C      4 <= W'W
C
C      FOR MODELS 3, 4, AND 5 THE COLUMNS USED ARE:
C      1 <= CsAinvCs
C      2 <= CiAinvCi
C      3 <= C
C      4 <= W'ZsAZs'W
C      5 <= W'ZiAZi'W
C      6 <= W'W
C
C      *****
C
C      IF (MODEL.LE.2) THEN
C      *** MODELS WITH SIRE ONLY ***
C      *** CALCULATE TRACES OF MATRIX PRODUCTS FOR QUADRATICS ***
      K(2,1) = DNTOT
      K(2,2) = DNTOT
      DO 900 IC = 1,NOEQN
        CALL COLI (TR(1,1),NOEQN,22)
        DO 1000 JC = 1,NOEQN
          TR(JC,2) = MAT(JC,IC)
1000      CONTINUE
          CALL COLI (TR(1,3),NOEQN,24)
          CALL COLI (TR(1,4),NOEQN,25)
          DO 900 JC = 1,NOEQN
            K(1,1) = K(1,1) + TR(JC,1)*TR(JC,3)
            K(1,2) = K(1,2) + TR(JC,1)*TR(JC,4)
            K(2,1) = K(2,1) - TR(JC,2)*TR(JC,3)
            K(2,2) = K(2,2) - TR(JC,2)*TR(JC,4)
900      CONTINUE
          DO 950 IC = 1,3
            K(3,IC) = 0.0D0
            K(IC,3) = 0.0D0
950      CONTINUE
          WRITE(6,1004) MODEL,RELNUM,ALPHAS
1004      FORMAT('1 EXPECTATIONS OF MODEL',I2,
+             ' AND RELATIONSHIP MATRIX ',I2,/,
+             ' WITH SIRE VARIANCE RATIO = ',F20.10,/)
          WRITE(6,1005) K(1,1),K(1,2),K(2,1),K(2,2)
1005      FORMAT(1X,'E(Q1) = ',D15.6,' VAR(S)',/,
+             1X,'E(Q1) = ',D15.6,' VAR(E)',/,
+             1X,'E(Q2) = ',D15.6,' VAR(S)',/,
+             1X,'E(Q2) = ',D15.6,' VAR(E)')
      ELSE
C      *** MODEL INCLUDES INTERACTION ***
C      *** CALCULATE TRACES OF MATRIX PRODUCTS FOR QUADRATICS ***
      K(3,1) = DNTOT
      K(3,2) = DNTOT
      K(3,3) = DNTOT

```

```

DO 1100 IC = 1,NOEQN
  CALL COLI (TR(1,1),NOEQN,21)
  CALL COLI (TR(1,2),NOEQN,22)
  DO 1200 JC = 1,NOEQN
    TR(JC,3) = MAT(JC,IC)
1200    CONTINUE
    CALL COLI (TR(1,4),NOEQN,24)
    CALL COLI (TR(1,5),NOEQN,25)
    CALL COLI (TR(1,6),NOEQN,26)
    DO 1100 JC = 1,NOEQN
      K(1,1) = K(1,1) + TR(JC,1)*TR(JC,4)
      K(1,2) = K(1,2) + TR(JC,1)*TR(JC,5)
      K(1,3) = K(1,3) + TR(JC,1)*TR(JC,6)
      K(2,1) = K(2,1) + TR(JC,2)*TR(JC,4)
      K(2,2) = K(2,2) + TR(JC,2)*TR(JC,5)
      K(2,3) = K(2,3) + TR(JC,2)*TR(JC,6)
      K(3,1) = K(3,1) - TR(JC,3)*TR(JC,4)
      K(3,2) = K(3,2) - TR(JC,3)*TR(JC,5)
      K(3,3) = K(3,3) - TR(JC,3)*TR(JC,6)
1100    CONTINUE
    WRITE(6,1104) MODEL,RELNUM,ALPHAS,ALPHAI
1104    FORMAT('1 EXPECTATIONS OF MODEL',I2,
      +      ' AND RELATIONSHIP MATRIX ',I2,/,
      +      ' WITH SIRE VARIANCE RATIO          = ',F20.10,/,
      +      ' AND WITH INTERACTION VARIANCE RATIO = ',F20.10,/)
    WRITE(6,1105) (K(1,I),I=1,3),(K(2,I),I=1,3),(K(3,I),I=1,3)
1105    FORMAT(1X,'E(Q1) = ',D15.6,' VAR(S)',/,
      +      1X,'E(Q1) = ',D15.6,' VAR(I)',/,
      +      1X,'E(Q1) = ',D15.6,' VAR(E)',/,
      +      1X,'E(Q2) = ',D15.6,' VAR(S)',/,
      +      1X,'E(Q2) = ',D15.6,' VAR(I)',/,
      +      1X,'E(Q2) = ',D15.6,' VAR(E)',/,
      +      1X,'E(Q3) = ',D15.6,' VAR(S)',/,
      +      1X,'E(Q3) = ',D15.6,' VAR(I)',/,
      +      1X,'E(Q3) = ',D15.6,' VAR(E)')
    END IF

    WRITE(EXP) MODEL,NDSTR,DNTOT,RELNUM,ALPHAS,ALPHAI
    WRITE(EXP) K

    OLDINT = INT
C    *** READ MORE PARAMETERS ***
    GO TO 1

1300 CONTINUE

    STOP
    END
C =====
    SUBROUTINE COLI (X,N,NUNIT)

```

```

C =====
C
C LAST REVISED: 4/18/89
C *****
C SUBROUTINE TO INPUT A VECTOR OF LENGTH N OR THE I COLUMN OF
C MATRIX X IF THE FIRST VARIABLE IN THE CALL IS X(1,I). THE VECTOR
C IS READ FROM UNIT NUNIT.
C *****
C
C DIMENSION X(N)
C
C REAL*8 X
C INTEGER*4 N,NUNIT
C
C READ(NUNIT) X
C
C RETURN
C END
C
C =====
C SUBROUTINE COLO (X,N,NUNIT)
C =====
C
C LAST REVISED: 4/21/89
C *****
C SUBROUTINE TO OUTPUT A VECTOR OF LENGTH N OR THE I COLUMN OF
C MATRIX X IF THE FIRST VARIABLE IN THE CALL IS X(1,I). THE VECTOR
C IS WRITTEN FROM UNIT NUNIT.
C *****
C
C DIMENSION X(N)
C
C REAL*8 X
C INTEGER*4 N,NUNIT
C
C WRITE(NUNIT) X
C
C RETURN
C END
C
C =====
C SUBROUTINE MATRIX (X,N,IR,IC,NUNIT,IO)
C =====
C
C LAST REVISED: 4/20/89
C *****
C SUBROUTINE TO INPUT OR OUTPUT A DOUBLE PRECISION R BY C MATRIX X
C A ROW AT A TIME TO UNIT NUMBER NUNIT.
C
C FORMAT OF SUBROUTINE CALL IS:

```

```

C      CALL MATRIX(X,N,IR,IC,NUNIT,IO),
C
C      WHERE:
C          X      IS THE MATRIX TO INPUT OR OUTPUT
C          N      IS THE LEADING DIMENSION OF X AS DECLARED IN THE
C                  CALLING PROGRAM
C          IR      IS THE NUMBER OF ROWS TO I/O
C          IC      IS THE NUMBER OF COLUMNS TO I/O
C                  NOTE: SUBROUTINE OUTPUTS LEADING BLOCK OF MATRIX ONLY
C          NUNIT   IS THE FORTRAN UNIT NUMBER TO READ OR READ
C          IO      IS AN INPUT OR OUTPUT SWITCH  SUBROUTINE
C                  READS  IF IO=1
C                  WRITES IF IO=0
C
C      *****
C
C      DIMENSION X(N,IC)
C
C      REAL*8      X
C      INTEGER*4  N,IR,IC,NUNIT,IO
C
C      IF (IO.EQ.1) THEN
C          DO 100 I = 1,IC
C              CALL COLI (X(1,I),IR,NUNIT)
100      CONTINUE
C      ELSEIF (IO.EQ.0) THEN
C          DO 200 I = 1,IC
C              CALL COLO (X(1,I),IR,NUNIT)
200      CONTINUE
C      ELSE
C          WRITE(6,*) 'READ OR WRITE NOT SPECIFIED FOR SUBROUTINE MATRIX'
C          STOP
C      END IF
C
C      RETURN
C      END
C
C      =====
C      SUBROUTINE XPAX (X,DIM,A,BLK,IDEN,COLL,ST,RES,NUNIT)
C      =====
C
C      LAST REVISED: 4/26/89
C      *****
C      SUBROUTINE TO MULTIPLY PRE- AND POST- MULTIPLY A SYMMETRIC
C      MATRIX A BY  X' AND X RESPECTIVELY, WHERE X IS ALSO SYMMETRIC.
C
C      THE MATRIX  A CAN BE A BLOCK DIAGONAL MATRIX WHERE ALL THE
C      BLOCKS ARE IDENTICAL, AND IN THAT CASE, ONLY ONE BLOCK
C      NEEDS TO BE INCLUDED IN THE SUBROUTINE CALL ALONG WITH THE
C      NUMBER OF BLOCKS.  THE RESULTING PRODUCT IS RETURNED AND BOTH

```

C X AND A ARE LEFT INTACT. TWO WORK VECTORS MUST ALSO BE  
 C INCLUDED IN THE CALL. IF A IS BLOCK DIAGONAL, THEN THE FIRST  
 C VECTOR MUST BE AS LONG AS THE DIMENSION OF EACH BLOCK TIMES  
 C THE NUMBER OF BLOCKS. THE SECOND WORK VECTOR MUST BE AT LEAST  
 C AS LONG AS THE M, THE DIMENSION OF X.

C THE FORMAT OF THE SUBROUTINE CALL IS:

C CALL XPAX (X,DIM,A,BLK,IDEN,COLL,ST,RES,NUNIT)

C WHERE:

C X IS A SYMMETRIC M\*M MATRIX  
 C DIM IS THE DIMENSION OF X USED IN THE CALLING PROGRAM  
 C NOTE: REGARDLESS OF THE DIMENSION OF X USED (DIM)  
 C X MUST BE DIMENSIONED WITH LEADING DIMENSION OF M  
 C A IS A SYMMETRIC N\*N MATRIX  
 C BLK IS THE NUMBER OF BLOCKS IF A IS BLOCK DIAGONAL  
 C IDEN IS A SWITCH TO DETERMINE IF A IS AN IDENTITY, IF  
 C IDEN=0 A IS NOT AN IDENTITY MATRIX, IF IDEN=1  
 C A IS AN IDENTITY MATRIX AND  $X'AX = X'X$   
 C COLL IS A DOUBLE PRECISION WORK VECTOR OF LENGTH AT  
 C LEAST LENGTH BLK\*N  
 C ST IS THE STARTING ROW IN X TO USE IF  $M > N$ , MUST BE  
 C INCLUDED EVEN IF  $ST=0$ . NOTE: THIS VARIABLE SHOULD  
 C BE ONE LESS THAN THE STARTING ROW OR COLUMN,  
 C E.G. IF THE ELEMENTS OF X TO BE USED FOR THE QUADRATIC  
 C START IN ROW(COLUMN) 100 THEN USE  $ST=99$  IN THE CALL  
 C RES IS THE SECOND DOUBLE PRECISION WORK VECTOR OF  
 C LENGTH AT LEAST M  
 C NUNIT IS THE UNIT TO WRITE THE RESULTING MATRIX TO  
 C A COLUMN AT A TIME

C \*\*\*\*\*

PARAMETER (NH=50,NS=20,NR=1000)  
 DIMENSION X(NH+NS+NH\*NS,NH+NS+NH\*NS),A(NS,NS),COLL(NH+NS+NH\*NS),  
 + RES(NH+NS+NH\*NS)  
 INTEGER\*4 DIM,BLK,IDEN,ST,N,M,IC,JC,KC,LC,TOT,  
 + XADD,XIND,VADD,VIND,NUNIT  
 REAL\*8 X,A,COLL,RES,COLL1

N = NS  
 M = NH+NS+NH\*NS  
 TOT = N\*BLK

IF (IDEN.EQ.0) THEN  
 DO 100 IC = 1,DIM  
 DO 200 JC = 1,BLK  
 VADD = (JC-1)\*N  
 XADD = VADD + ST

```

DO 200 KC = 1,N
  COLL1 = 0.0D0
  VIND = VADD + KC
  DO 300 LC = 1,N
    XIND = XADD + LC
    COLL1 = COLL1 + X(XIND,IC)*A(LC,KC)
300    CONTINUE
    COLL(VIND) = COLL1
200  CONTINUE
  DO 400 JC = 1,DIM
    COLL1 = 0.0D0
    DO 500 KC = 1,TOT
      XIND = ST + KC
      COLL1 = COLL1 + COLL(KC)*X(XIND,JC)
500    CONTINUE
    RES(JC) = COLL1
400  CONTINUE
    CALL COLO(RES,DIM,NUNIT)
100  CONTINUE
ELSE
  DO 600 IC = 1,DIM
    DO 700 JC = 1,DIM
      COLL1 = 0.0D0
      DO 800 KC = 1,TOT
        XIND = ST + KC
        COLL1 = COLL1 + X(XIND,IC)*X(XIND,JC)
800    CONTINUE
      RES(JC) = COLL1
700  CONTINUE
      CALL COLO(RES,DIM,NUNIT)
600  CONTINUE
END IF

RETURN
END

```

APPENDIX D.   FORTRAN PROGRAM TO ESTIMATE MIVQUE VARIANCE  
                  COMPONENTS AND CALCULATE SAMPLE MEANS AND  
                  VARIANCES OF ESTIMATES

```

@PROCESS DC(BIGMAT)
C =====
C PROGRAM ESTIMATE
C =====
C
C LAST REVISED: 5/7/89
C *****
C PURPOSE AND STRATEGY:
C CALCULATE MIVQUE VARIANCE COMPONENT ESTIMATES USING
C EXPECTATIONS CALCULATED IN THE EXPECT PROGRAM. SOLUTIONS TO
C THE MIXED MODEL EQUATIONS ARE CALCULATED USING THE INVERSE
C PREVIOUSLY CALCULATED IN THE INVERT PROGRAM AND THE RHS'S
C COMPUTED IN THE SIMUL PROGRAM. QUADRATICS ARE CALCULATED AS
C WEIGHTED QUADRATICS OF THOSE SOLUTIONS. THE SOLUTIONS ARE
C THEN WRITTEN TO DISK. THE MIVQUE ALGORITHM IS BASED ON THE
C METHOD DESCRIBED BY L.R. SCHAEFFER. 1979. NOTES ON LINEAR
C MODEL THEORY AND HENDERSON'S MIXED MODEL TECHNIQUES. 266-276;
C 298-305. THE METHOD ALLOWS CALCULATION OF THE EXPECTATIONS BY
C USING TRACES OF PRODUCTS OF THE COEFFICIENT MATRIX FROM THE
C MIXED MODEL EQUATIONS AND THE INVERSE, AND CALCULATION OF THE
C QUADRATICS WITH Y'Y AND THE SOLUTIONS TO THE MME'S.
C *****

COMMON /BIGMAT/ C,RHS,SOL,TSOL

PARAMETER (NH=50,NS=20,NR=1000)

DIMENSION C(NH+NS+NH*NS,NH+NS+NH*NS),RHS(NH+NS+NH*NS),
+ SOL(NH+NS+NH*NS),TSOL(NH+NS+NH*NS),AINV(NS,NS),
+ SUM(7,15),K(3,3),QUAD(3,2),EST(5,3),IWORK(3),
+ TITLE(15)

INTEGER*4 INPUT,EXP,INV,RLT,ESTIM,TVAL,SOLOUT,REP,NADD,IC,JC,KC,
+ JAC,NBYTE,IWORK,MODEL,NOHERD,NOSIRE,NOHPS,NOEQN,NVC,
+ EMOD,IDEN1,IDEN2,RELNUM,ERLNUM,NDIM,INVREL,SIMREL,
+ SIMREP,TVREL,TVREP,MEANS,NDSTR,TVSTR,IDSTR,EDSTR

REAL*8 C,RHS,SOL,TSOL,AINV,SUM,K,QUAD,EST,ALPHAS,ALPHAI,YPAY,
+ YPY,EPE,DNTOT,COLL,EALPHS,EALPHI,SIMVS,SIMVI,SIMVE,
+ TVVS,TVVI,TVVE,DREP,INOBS,ENOBS,TVALS,TVALI

CHARACTER*25 TITLE

DATA TITLE /'ESTIMATED SIRE VARIANCE ',
+ 'ESTIMATED INTERACTION VAR','ESTIMATED RESIDUAL VAR ',
+ 'ESTIMATED TOTAL VARIANCE ','ESTIMATED HERITABILITY ',
+ 'TRUE' SIRE VARIANCE ','TRUE' INTERACTION VAR ',
+ 'TRUE' RESIDUAL VARIANCE ','TRUE' TOTAL VARIANCE ',
+ 'TRUE' HERITABILITY ','SIRE VARIANCE DIFFERENCE ',
+ 'INTERACTION VAR DIFF ','RESIDUAL VARIANCE DIFF ',

```



+ 'TOTAL VARIANCE DIFF           ', 'HERITABILITY DIFFERENCE   '/

CALL SPINIT

NOHERD = NH

NOSIRE = NS

NOHPS = NH + NS

NDIM = NS + NH + NS\*NH

```

C *****
C *****          SET UP UNIT DEFINITIONS FOR I/O UNITS          *****
C *****
C
C FILE   I/O   F/V   COMMENTS
C -----
C INPUT   I     V    RHS OUTPUT FILE WITH FORMAT:
C                #PARMS*{DAT.STR.#,SVAR,IVAR,EVAR,RELAT.#,NOREPS;
C                NOREPS*[RHS,Y'Y,E'E,#OBS]}
C EXP     I     V    OUTPUT FILE FOR EXPECTATIONS OF QUADRATICS WITH
C                FILE FORMAT:
C                NPARM*{MODEL,DAT.STR.#,NO OBS,REL.#,
C                ALPHAS,ALPHAI;EXPECT}
C                NOTE: EXPECTATION MATRIX IS ALWAYS WRITTEN AND
C                READ AS 3X3 MATRIX EVEN IF ONLY 2 V.C.S
C INV     I     V    INPUT FILE CONTAINING THE INVERSE OF THE
C                COEFFICIENT MATRIX WITH FILE FORMAT:
C                NPARM*{MODEL,DAT.STR.#,NO OBS,REL.#,
C                ALPHAS,ALPHAI;INVERSE}
C RLT     I     V    RELATIONSHIP FILE WITH FORMAT:
C                REL#;A, A INVERSE.
C ESTIM   0     V    OUTPUT FILE OF V.C. ESTIMATES WITH REP NUMBERS
C TVAL    I     V    FILE WITH UNDERLYING VALUES FOR HERD, SIRE, AND
C                HXS WITH FILE FORMAT:
C                #PARMS*{DAT.STR.#,SVAR,IVAR,EVAR,RELAT.#,NOREPS;
C                NOREPS*[HERDS,SIRES,INTERACTION EFFECTS]}
C SOLOUT  0     V    OUTPUT FILE USED IN TEST RUNS FOR SOLUTIONS
C                TO MME'S. FILE FORMAT:#RUNS*{DAT.STR.#,
C                RELAT.#,MODEL,SVAR,IVAR,EVAR,,ALPHAS,ALPHAI,
C                NOREPS; NOREPS*[SOLTION]}
C MEANS   0     V    OUTPUT FILE OF MEANS AND VARIANCES OF V.C. EST
C -----

```

INPUT = 10

EXP = 12

INV = 13

RLT = 14

ESTIM = 15

TVAL = 16

SOLOUT = 17

MEANS = 18

```

C *****
C READ THE RELATIONSHIP NUMBER, RELATIONSHIP MATRIX, AND INVERSE
C FROM THE RELATIONSHIP FILE. IF THERE IS NO RELATIONSHIP MATRIX
C PRESENT SET RELNUM=0, A=I, AINV=I
C *****

      READ (RLT,END=20) RELNUM
      READ (RLT) AINV
      READ (RLT) AINV
      GO TO 40
20  CONTINUE
      RELNUM = 0
      CALL SVCPDP (0.0D0,AINV(1,1),1,NOSIRE**2)
      DO 30 IC = 1,NOSIRE
        AINV(IC,IC) = 1.0D0
30  CONTINUE
40  CONTINUE

C *****
C READ PARAMETERS FROM HEAD OF INVERSE FILE
C   MODEL IS SWITCH FOR USING SIRE RELATIONSHIPS IN ESTIMATING
C   SIRE VARIANCE
C   ALPHAS IS THE PRIOR ESTIMATE FOR THE ERROR TO SIRE
C   VARIANCE RATIOS
C   ALPHAI IS THE PRIOR ESTIMATE FOR THE ERROR TO HXS VARIANCE
C
C MODEL SWITCH AND VARIANCE STRUCTURE USED:
C
C   MODEL      VAR(S)      VAR(HXS)      IDEN1      IDEN2
C   =====
C   1           I          N.A.          1          N.A.
C   2           A          N.A.          0          N.A.
C   3           I          I            1          1
C   4           A          I            0          1
C   5           A          I X A         0          0
C   =====
C *****

1  READ (INV,END=1100) MODEL,IDSTR,INOBS,INVREL,ALPHAS,ALPHAI
C
C   WRITE(99,*) MODEL,IDSTR,INVREL,ALPHAS,ALPHAI
C
C   IF (INVREL.NE.RELNUM) THEN
C     WRITE(6,11)
11  FORMAT('RELATIONSHIP NUMBERS FOR RELATIONSHIP FILE ',
+        'AND INVERSE DO NOT MATCH - PROGRAM HALTED ')
      STOP 'RELATIONSHIP NUMBER MISMATCH'
      END IF

```

```

GO TO (110,120,130,140,150), MODEL
WRITE(6,105)
105  FORMAT('INVALID VALUE FOR MODEL - PROGRAM HALTED')
STOP 'INVALID VALUE FOR MODEL'
110  CONTINUE
C    *** MODEL 1 ***
      NVC = 2
      NOEQN = NOHPS
      IDEN1 = 1
      GO TO 160
120  CONTINUE
C    *** MODEL 2 ***
      NVC = 2
      NOEQN = NOHPS
      IDEN1 = 0
      GO TO 160
130  CONTINUE
C    *** MODEL 3 ***
      NVC = 3
      NOEQN = NDIM
      IDEN1 = 1
      IDEN2 = 1
      GO TO 160
140  CONTINUE
C    *** MODEL 4 ***
      NVC = 3
      NOEQN = NDIM
      IDEN1 = 0
      IDEN2 = 1
      GO TO 160
150  CONTINUE
C    *** MODEL 5 ***
      NVC = 3
      NOEQN = NDIM
      IDEN1 = 0
      IDEN2 = 0
160  CONTINUE

C    ***** READ IN INVERSE OF COEFFICIENT MATRIX *****
CALL SVCPDP (0.0D0,C(1,1),1,NDIM**2)
CALL MATRIX (C,NDIM,NOEQN,NOEQN,INV,1)

C    *** READ PARAMETERS FROM EXPECTATION FILE AND MAKE SURE ***
C    *** THEY MATCH THE ONES READ FROM THE INVERSE FILE *****
READ(EXP) EMOD,EDSTR,ENOBS,ERLNUM,EALPHS,EALPHI
IF ((MODEL.NE.EMOD).OR.(IDSTR.NE.EDSTR).OR.(INOBS.NE.ENOBS).
+   OR.(INVREL.NE.ERLNUM).OR.(ALPHAS.NE.EALPHS).OR.
+   (ALPHAI.NE.EALPHI).OR.(RELNUM.NE.ERLNUM)) THEN
WRITE(6,*) MODEL,EMOD,IDSTR,EDSTR,INOBS,ENOBS,INVREL,

```

```

+           ERLNUM,ALPHAS,EALPHS,ALPHAI,EALPHI,RELNUM,ERLNUM
+       WRITE(6,165)
165      FORMAT('1PROGRAM STOPPED - PARAMETERS FROM INVERSE AND ',
+           'EXPECTION FILES DO NOT MATCH')
+       STOP 'PARAMATERS FROM EXP AND INV DO NOT MATCH'
END IF

C       ***** READ THE MATRIX OF EXPECTATIONS AND INVERT *****
      READ(EXP) K
      CALL INVRT (K,3,NVC)

C       *** REWIND DATA FILES TO THE BEGINNING ***
      REWIND INPUT
      REWIND TVAL

2       READ (INPUT,END=1200) NDSTR,SIMVS,SIMVI,SIMVE,SIMREL,SIMREP
      READ (TVAL) TVSTR,TVVS,TVVI,TVVE,TVREL,TVREP
      IF ((NDSTR.NE.TVSTR).OR.(SIMVS.NE.TVVS).OR.(SIMVI.NE.TVVI)
+       .OR.(SIMVE.NE.TVVE).OR.(SIMREL.NE.TVREL).OR.
+       (SIMREP.NE.TVREP)) THEN
+       WRITE(6,*) NDSTR,TVSTR,SIMVS,TVVS,SIMVI,TVVI,SIMVE,TVVE,
+       SIMREL,TVREL
+       WRITE(6,175)
175      FORMAT('1PROGRAM STOPPED - PARAMETERS FROM SIMULATION ',
+       'AND TRUE VALUE FILES DO NOT MATCH')
+       STOP 'PARAMATERS FROM RHS AND TVAL FILES DO NOT MATCH'
END IF

      IF ((IDSTR.NE.NDSTR).OR.(INVREL.NE.SIMREL)) THEN
+       WRITE(6,*) IDSTR,NDSTR,INVREL,SIMREL
+       WRITE(6,185)
185      FORMAT('1PROGRAM STOPPED - PARAMETERS FROM INVERSE ',
+       'AND SIMULATION FILES DO NOT MATCH')
+       STOP 'PARM FROM INVERSE AND SIMULATION DO NOT MATCH'
END IF

C       WRITE (SOLOUT) NDSTR,SIMREL,MODEL,TVVS,TVVI,TVVE,
C       +       ALPHAS,ALPHAI,SIMREP

      TVALS = TVVE/TVVS
      TVALI = TVVE/TVVI
      CALL SVCDPD (0.0D0,SUM(1,1),1,105)
      DO 170 IC = 1,15
+       SUM(5,IC) = 1.0D6
+       SUM(6,IC) = -1.0D6
170      CONTINUE

      IF (MODEL.LE.2) THEN
+       WRITE (6,5) MODEL,SIMREL,NDSTR,INOOBS,ALPHAS,TVALS,TVALI,
+       SIMVS,SIMVI,SIMVE

```

```

5      FORMAT('1MIVQUE VARIANCE COMPONENT ESTIMATES FOR MODEL',
+        I2,' RELATIONSHIP MATRIX ',I2,' DATA STRUCTURE ',I2,
+        ' AND ',F6.0,' OBSERVATIONS/REP',//,' SIRE VARIANCE ',
+        'RATIO USED FOR EXPECTATIONS',F15.8,/, ' SIMULATED ',
+        'VARIANCE RATIOS: SIRE ',F15.8,', INTERACTION ',F15.8,
+        /, ' SIMULATED ', 'VARIANCES: SIRE ',F15.8,
+        ', INTERACTION ',F15.8,', AND ERROR ',F15.8,/,16X,
+        'ESTIMATED',11X,'ESTIMATED',11X,'ESTIMATED',12X,
+        '""TRUE""',14X,'""TRUE""',13X,'""TRUE""',/,4X,'REP',
+        7X,'SIRE ', 'VARIANCE',5X,'RESIDUAL VARIANCE',5X,
+        'HERITABILITY',7X,'SIRE VARIANCE      RESIDUAL ',
+        'VARIANCE      HERITABILITY',/,1X,124('='))
      ELSE
        WRITE (6,10) MODEL,SIMREL,NDSTR,INOOBS,ALPHAS,ALPHAI,
+          TVALS,TVALI,SIMVS,SIMVI,SIMVE
10     FORMAT('1MIVQUE VARIANCE COMPONENT ESTIMATES FOR MODEL',
+       I2,' RELATIONSHIP MATRIX ',I2,' DATA STRUCTURE ',I2,
+       ' AND ',F6.0,' OBSERVATIONS/REP',//,' VARIANCE ',
+       'RATIO USED FOR EXPECTATIONS: SIRE ',F15.8,', INTER',
+       'ACTION ',F15.8,/, ' SIMULATED VARIANCE RATIOS: SIRE ',
+       F15.8,', INTERACTION ',F15.8,/, ' SIMULATED VARIANCES',
+       ': SIRE ',F15.8,', INTERACTION ',F15.8,', AND ERROR ',
+       F15.8,/, ' ESTIMATED      ESTIMATED      ',
+       'ESTIMATED      ESTIMATED      ""TRUE"" ',
+       '""TRUE""      ""TRUE""      ""TRUE""',/,
+       ' REP      SIRE VAR      INTERACTION VAR      RESIDUAL ',
+       'VAR      HERITABILITY      SIRE VAR      INTERACTION ',
+       'VAR      RESIDUAL VAR      HERITABILITY',/,1X,132('='))
      END IF

C      *****
C      ***** READ THE RIGHT HAND SIDES AND TRUE SOLUTIONS *****
C      *****

      DO 300 REP = 1,SIMREP
        CALL SVCPPD (0.0D0,QUAD(1,1),1,6)
        CALL SVCPPD (0.0D0,EST(1,1),1,15)
        READ (INPUT) RHS,YPY,EPE,DNTOT
        READ (TVAL) TSOL

C      *** CALCULATE SOLUTIONS ***
      DO 400 IC = 1,NOEQN
        COLL = 0.0D0
        DO 500 JC = 1,NOEQN
          COLL = COLL + C(JC,IC)*RHS(JC)
500        CONTINUE
        SOL(IC) = COLL
400        CONTINUE

C      CALL COLO (SOL,NOEQN,SOLOUT)

```

```

C *****
C CALCULATE QUADRATICS
C
C FOR MODELS 1 AND 2
C   QUAD(1,1) IS  $U_s * A_{inv} * U_s$  WHERE  $U_s$  IS THE ESTIMATED SIRE VALUE
C   QUAD(1,2) IS  $U_s * A_{inv} * U_s$  WHERE  $U_s$  IS THE TRUE SIRE VALUE
C   QUAD(2,1) IS THE RESIDUAL  $Y'Y - U_s' * Z_s' * Y$ 
C   QUAD(2,2) IS THE RESIDUAL  $E'E$  WHERE  $E$  IS THE TRUE ERROR
C
C FOR MODELS 3, 4, AND 5
C   QUAD(1,1) IS  $U_s * A_{inv} * U_s$  WHERE  $U_s$  IS THE ESTIMATED SIRE VALUE
C   QUAD(1,2) IS  $U_s * A_{inv} * U_s$  WHERE  $U_s$  IS THE TRUE SIRE VALUE
C   QUAD(2,1) IS  $U_i * A_{inv} * U_i$  WHERE  $U_i$  IS THE EST INTERACTION VALUE
C   QUAD(2,2) IS  $U_i * A_{inv} * U_i$  WHERE  $U_i$  IS THE TRUE INTERACTION VALUE
C   QUAD(3,1) IS THE RESIDUAL  $Y'Y - U_s' * Z_s' * Y - U_i' * Z_i' * Y$ 
C   QUAD(3,2) IS THE RESIDUAL  $E'E$  WHERE  $E$  IS THE TRUE ERROR
C *****

      QUAD(1,1) = YPAY(SOL,AINV,IDEN1,1,NOHERD)
      QUAD(1,2) = YPAY(TSOL,AINV,IDEN1,1,NOHERD)

      IF (MODEL.LE.2) THEN
        COLL = 0.0D0
        DO 600 IC = 1,NOEQN
          COLL = COLL + SOL(IC)*RHS(IC)
600      CONTINUE
        QUAD(2,1) = YPY - COLL
        QUAD(2,2) = EPE
      ELSE
        QUAD(2,1) = YPAY(SOL,AINV,IDEN2,NOHERD,NOHPS)
        QUAD(2,2) = YPAY(TSOL,AINV,IDEN2,NOHERD,NOHPS)
        COLL = 0.0D0
        DO 800 IC = 1,NOEQN
          COLL = COLL + SOL(IC)*RHS(IC)
800      CONTINUE
        QUAD(3,1) = YPY - COLL
        QUAD(3,2) = EPE
      END IF

C   *** CALCULATE MIVQUE V.C. ESTIMATES ***
      DO 900 IC = 1,NVC
        COLL = 0.0D0
        DO 1000 KC = 1,NVC
          COLL = COLL + K(IC,KC)*QUAD(KC,1)
1000      CONTINUE
        EST(IC,1) = COLL
900      CONTINUE

```

```

C      *** CALCULATE LAMOTTE'S "IDEAL ESTIMATES" ***
      EST(1,2) = QUAD(1,2)/DFLOAT(NOSIRE)
      IF (MODEL.LE.2) THEN
        EST(2,2) = QUAD(2,2)/DNTOT
      ELSE
        EST(2,2) = QUAD(2,2)/DFLOAT(NOHERD*NOSIRE)
        EST(3,2) = QUAD(3,2)/DNTOT
      END IF

      EST(4,1) = EST(1,1) + EST(2,1) + EST(3,1)
      EST(4,2) = EST(1,2) + EST(2,2) + EST(3,2)
      EST(5,1) = 4.0D0*EST(1,1)/EST(4,1)
      EST(5,2) = 4.0D0*EST(1,2)/EST(4,2)

      DO 950 IC = 1,5
        EST(IC,3) = EST(IC,1) - EST(IC,2)
950    CONTINUE

      DO 1300 IC = 1,3
        NADD = (IC - 1)*5
        DO 1300 JC = 1,5
          JAC = NADD + JC
          SUM(2,JAC) = SUM(2,JAC) + EST(JC,IC)
          SUM(3,JAC) = SUM(3,JAC) + EST(JC,IC)**2
          IF (EST(JC,IC).LT.SUM(5,JAC)) SUM(5,JAC) = EST(JC,IC)
          IF (EST(JC,IC).GT.SUM(6,JAC)) SUM(6,JAC) = EST(JC,IC)
1300    CONTINUE

      CALL COLO (EST,10,ESTIM)

      IF (REP.LE.30) THEN
        IF (MODEL.LE.2) THEN
          WRITE(6,405) REP,EST(1,1),EST(2,1),EST(5,1),
+             EST(1,2),EST(2,2),EST(5,2)
405      FORMAT(1X,I6,2(F20.12,F22.12,F17.12))
        ELSE
          WRITE(6,505) REP,EST(1,1),EST(2,1),EST(3,1),
+             EST(5,1),EST(1,2),EST(2,2),EST(3,2),EST(5,2)
505      FORMAT(1X,I4,2(F12.8,F20.8,F15.8,F17.8))
        END IF
      END IF

      C      WRITE (99,289) QUAD
      289    FORMAT(1X,6F20.10)
      300    CONTINUE

      DREP = DFLOAT(SIMREP)
      IF (MODEL.LE.2) THEN
        DO 1350 IC = 1,3
          NADD = (IC - 1)*5
          DO 1350 JC = 1,7

```

```

                                SUM(JC,NADD+3) = SUM(JC,NADD+2)
1350      CONTINUE
      END IF

      DO 1400 IC = 1,15
        SUM(1,IC) = DREP
        SUM(4,IC) =
+          (SUM(3,IC)-(SUM(2,IC)**2/DREP))/(DREP-1)
        SUM(2,IC) = SUM(2,IC)/DREP
        SUM(3,IC) = DSQRT(SUM(4,IC))
        SUM(7,IC) = DSQRT(SUM(4,IC)/DREP)
1400      CONTINUE

      IF (MODEL.LE.2) THEN
        WRITE (6,1405) MODEL,SIMREL,NDSTR,DNTOT,ALPHAS,TVALS,
+          TVALI,SIMVS,SIMVI,SIMVE
1405      FORMAT('1MIVQUE ESTIMATE SUMMARY FOR MODEL',I2,
+        ' RELATIONSHIP MATRIX ',I2,', AND DATA STRUCTURE ',
+        I2,' WITH ',F5.0,' OBSERVATIONS/REP',/, ' SIRE VAR',
+        ' IANCE RATIO USED TO CALCULATE EXPECTATIONS ',F15.8,/,
+        ' SIMULATED VARIANCE RATIOS: SIRE ',F15.8,
+        ', INTERACTION ',F15.8,/, ' SIMULATED VARIANCES: ',
+        ' SIRE ',F15.8,', INTERACTION ',F15.8,', AND ERROR ',
+        F15.8,/)
      ELSE
        WRITE (6,1410) MODEL,SIMREL,NDSTR,DNTOT,ALPHAS,ALPHAI,
+          TVALS,TVALI,SIMVS,SIMVI,SIMVE
1410      FORMAT('1MIVQUE ESTIMATE SUMMARY FOR MODEL',I2,
+        ' RELATIONSHIP MATRIX ',I2,', AND DATA STRUCTURE ',
+        I2,' WITH ',F5.0,' OBSERVATIONS/REP',/, ' VARIANCE',
+        ' RATIOS USED TO CALCULATE EXPECTATIONS: SIRE ',F15.8,
+        ' INTERACTION ',F15.8,/, ' SIMULATED VARIANCE ',
+        ' RATIOS: SIRE ',F15.8,', INTERACTION ',F15.8,/,
+        ' SIMULATED VARIANCES: SIRE ',F15.8,', INTERACTION ',
+        F15.8,', AND ERROR ',F15.8,/)
      END IF

      WRITE(6,1415)
1415      FORMAT(59X,'STANDARD',/,9X,'PARAMETER',11X,'REPS',16X,
+        'MEAN',6X,'DEVIATION',12X,'VARIANCE',8X,'MINIMUM',
+        8X,'MAXIMUM',9X,'S.E.M.',/,1X,132('='))

      DO 1500 IC = 1,15
        IF ((MODEL.GT.2).OR.
+          ((IC.NE.2).AND.(IC.NE.7).AND.(IC.NE.12))) THEN
          CALL CHVOUT (TITLE(IC),SUM(1,IC),6)
          CALL CHVOUT (TITLE(IC),SUM(1,IC),MEANS)
        END IF
1500      CONTINUE

```



```

C      *** READ NEXT DATA SET PARAMETERS ***
C      GO TO 2
1200   CONTINUE

C      *** READ NEXT INVERSE ***
C      GO TO 1
1100   CONTINUE

      STOP
      END

C      =====
C      SUBROUTINE CHVOUT (TITLE,VEC,NUNIT)
C      =====
C
C      LAST REVISED: 4/23/89
C      *****
C      SUBROUTINE TO PRINT A CHARACTER STRING AND A VECTOR OF LENGTH 7
C      USING THE FORMAT FOR THE SUMMARY TABLE IN THE MAIN PROGRAM
C      *****

      DIMENSION VEC(7)

      REAL*8 VEC
      CHARACTER*25 TITLE
      INTEGER*4 NUNIT

      WRITE (NUNIT,5) TITLE,VEC
5      FORMAT (1X,A25,F7.0,F20.15,F15.10,F20.15,3F15.10)

      RETURN
      END

C      =====
C      SUBROUTINE COLI (X,N,NUNIT)
C      =====
C
C      LAST REVISED: 4/18/89
C      *****
C      SUBROUTINE TO INPUT A VECTOR OF LENGTH N OR THE I COLUMN OF
C      MATRIX X IF THE FIRST VARIABLE IN THE CALL IS X(1,I). THE VECTOR
C      IS READ FROM UNIT NUNIT.
C      *****

      DIMENSION X(N)

      REAL*8 X
      INTEGER*4 N,NUNIT

      READ(NUNIT) X

```

```

RETURN
END

```

```

C =====
C SUBROUTINE COLO (X,N,NUNIT)
C =====
C
C LAST REVISED: 4/21/89
C *****
C SUBROUTINE TO OUTPUT A VECTOR OF LENGTH N OR THE I COLUMN OF
C MATRIX X IF THE FIRST VARIABLE IN THE CALL IS X(1,I). THE VECTOR
C IS WRITTEN FROM UNIT NUNIT.
C *****

```

```

    DIMENSION X(N)

```

```

    REAL*8 X
    INTEGER*4 N,NUNIT

```

```

    WRITE(NUNIT) X

```

```

RETURN
END

```

```

C =====
C SUBROUTINE MATRIX (X,N,IR,IC,NUNIT,IO)
C =====

```

```

C LAST REVISED: 4/20/89
C *****
C SUBROUTINE TO INPUT OR OUTPUT A DOUBLE PRECISION R BY C MATRIX X
C A ROW AT A TIME TO UNIT NUMBER NUNIT.

```

```

C FORMAT OF SUBROUTINE CALL IS:
C     CALL MATRIX(X,N,IR,IC,NUNIT,IO),

```

```

C WHERE:

```

```

C     X      IS THE MATRIX TO INPUT OR OUTPUT
C     N      IS THE LEADING DIMENSION OF X AS DECLARED IN THE
C             CALLING PROGRAM
C     IR     IS THE NUMBER OF ROWS TO I/O
C     IC     IS THE NUMBER OF COLUMNS TO I/O
C             NOTE: SUBROUTINE OUTPUTS LEADING BLOCK OF MATRIX ONLY
C     NUNIT  IS THE FORTRAN UNIT NUMBER TO READ OR READ
C     IO     IS AN INPUT OR OUTPUT SWITCH  SUBROUTINE
C             READS  IF IO=1
C             WRITES IF IO=0

```

```

C *****

```

```

DIMENSION X(N,IC)

REAL*8      X
INTEGER*4   N,IR,IC,NUNIT,IO

IF (IO.EQ.1) THEN
  DO 100 I = 1,IC
    CALL COLI (X(1,I),IR,NUNIT)
100  CONTINUE
ELSEIF(IO.EQ.0) THEN
  DO 200 I = 1,IC
    CALL COLO (X(1,I),IR,NUNIT)
200  CONTINUE
ELSE
  WRITE(6,*) 'READ OR WRITE NOT SPECIFIED FOR SUBROUTINE MATRIX'
  STOP
END IF

RETURN
END

C=====
C      SUBROUTINE INVRT( A, IA, N)
C=====

C      PURPOSE : INVERT A NON-SYMMETRIC MATRIX OF ORDER N
C                MATRIX MUST BE NON-SINGULAR (PROGRAM STOPS IF SINGULARIT
C                ENCOUNTERED), BUT CAN BE NON-POSITIVE DEFINITE

C      STRATEGY : USE GAUSS-JORDAN ALGORITHM
C                (WITH PARTIAL PIVOTING)
C                TIME REQUIRED IS PROPORTIONAL TO THE CUBIC POWER OF THE
C                OF THE MATRIX.
C                PROGRAMMED AFTER STOER,J. AND BULIRSCH,R. : INTRODUCTIO
C                NUMERICAL ANALYSIS. SPRINGER VERLAG 1980, PP. 169-172.

C                THE ORIGINAL MATRIX IS STORED WITHIN THE ROUTINE AND MU
C                WITH ITS INVERSE, THE PRODUCT IS CHECKED FOR DEVIATIONS
C                THE IDENTITY MATRIX

C      PARAMETERS :
C      - A : MATRIX TO BE INVERTED, DOUBLE PRECISION, DECLARED W
C            ROW DIMENSION IA AND COLUMN DIMENSION AT LEAST N IN
C            CALLING PROGRAM;
C            OVERWRITTEN WITH INVERSE
C      - IA : ROW DIMENSION OF A (AS DECLARED)
C      - N : ORDER OF THE MATRIX TO BE INVERTED, MUST BE STORED
C            FIRST N ROWS AND COLUMNS OF A

```

```

C      ERROR STOPS : - MATRIX SINGULAR
C                      - PROGRAM DIMENSIONS EXCEEDED

```

```

C      ROUTINES REQUIRED : NONE

```

```

C
C-----KM 12/

```

```

CVD$R NOVECTOR

```

```

      IMPLICIT DOUBLE PRECISION (A-H,O-Z)
      DIMENSION A(3,3),B(3,3),VEC(3),IFLAG(3)

```

```

      IF (IA.NE.3) STOP 'DIMENSIONS INCORRECT FOR INVERSE'

```

```

      MTRAIT=3
      IF(N.GT.MTRAIT)STOP 'ROUTINE INVERT : PROGRAM DIMENSIONS EXCEEDED'

```

```

C      MINIMUM VALUE TO BE DISTINGUISHED FROM 0.D0
      ZERO=1.D-12

```

```

      DIAG=0.D0

```

```

      OFF=0.D0

```

```

      DO 1 I=1,N

```

```

1      IFLAG(I)=I
C      STORE MATRIX PRIOR TO INVERSION

```

```

      DO 22 I=1,N

```

```

      DO 22 J=1,N

```

```

22     B(J,I)=A(J,I)

```

```

      DO 2 I=1,N

```

```

C      FIND MAXIMUM ELEMENT IN THE COLUMN (START AT I-TH EL. ONLY)

```

```

      XX=DABS(A(I,I))

```

```

      IMAX=I

```

```

      DO 3 J=I+1,N

```

```

      ZZ=DABS(A(J,I))

```

```

      IF(ZZ.GT.XX)THEN

```

```

      XX=ZZ

```

```

      IMAX=J

```

```

      END IF

```

```

3      CONTINUE

```

```

C      CHECK FOR SINGULARITY

```

```

      IF(XX.LT.ZERO)STOP 'SUBROUTINE INVERT : MATRIX IS SINGULAR'

```

```

C      INTERCHANGE ROW I AND ROW WITH MAX. ELEMENT IN THE COLUMN

```

```

      IF(IMAX.GT.I)THEN

```

```

      DO 4 K=1,N

```

```

        SAVE=A(I,K)
        A(I,K)=A(IMAX,K)
        A(IMAX,K)=SAVE
4      CONTINUE
        ISAVE=IFLAG(I)
        IFLAG(I)=IFLAG(IMAX)
        IFLAG(IMAX)=ISAVE
        END IF

C      TRANSFORM THE MATRIX
        SAVE=1.DO/A(I,I)
        DO 5 J=1,N
5      A(J,I)=A(J,I)*SAVE
        A(I,I)=SAVE
        DO 6 K=1,N
        IF(K.EQ.I)GO TO 6
        DO 7 J=1,N
        IF(J.NE.I)A(J,K)=A(J,K)-A(J,I)*A(I,K)
7      CONTINUE
        A(I,K)=-A(I,K)*SAVE
6      CONTINUE

2      CONTINUE

C      INTERCHANGE COLUMNS (ANALOGOUS TO PREVIOUS ROW CHANGES )
        DO 8 I=1,N
        DO 9 K=1,N
        J=IFLAG(K)
9      VEC(J)=A(I,K)
        DO 10 K=1,N
10     A(I,K)=VEC(K)
8      CONTINUE

C      MULTIPLY MATRIX WITH ITS INVERSE, CHECK ELEMENTS
        DO 33 I=1,N
        DO 33 J=1,N
        XX=0.DO
        DO 34 K=1,N
34     XX=XX+A(K,J)*B(I,K)
        IF(I.EQ.J)THEN
C      IF(DABS(XX-1.DO).GT.ZERO)PRINT *,I,XX
        DIAG=DIAG+XX
        ELSE
C      IF(DABS(XX).GT.ZERO)PRINT *,I,J,XX
        OFF=OFF+XX
        END IF
33    CONTINUE
C      XX=DIAG/N
C      PRINT *, 'DIAGONAL : SUM =',DIAG,'      AVERAGE =',XX
C      XX=OFF/(N*(N-1))

```

```

C      PRINT *, 'OFF-DIAG : SUM =', OFF, '      AVERAGE =', XX
C
C      RETURN
C      END
C
C      =====
C      DOUBLE PRECISION FUNCTION YPAY(Y,A,SW,BLK,ST)
C      =====
C
C      LAST REVISED: 4/19/89
C      *****
C
C      FUNCTION USED TO CALCULATE WEIGHTED QUADRATICS OF THE FORM  $Y'A*Y$ 
C
C      IF A IS A BLOCK DIAGONAL WITH ALL BLOCKS THE SAME, ONLY ONE BLOCK
C      NEEDS TO BE INCLUDED IN THE SUBROUTINE CALL ALONG WITH THE NUMBER
C      OF BLOCKS. THE QUADRATIC IS RETURNED IN THE FUNCTION, AND ALL OF
C      THE MATRICES ARE LEFT INTACT.
C
C      THE FORMAT OF THE FUNCTION CALL IS:
C
C      CALL YPAY(Y,A,SW,BLK,ST)
C
C      WHERE:
C      Y IS THE VECTOR OF OBSERVATIONS FOR THE QUADRATIC
C      A IS THE WEIGHTING MATRIX OF THE QUADRATIC
C      SW IS AN IDENTITY SWITCH
C      IF SW = 0, A IS NOT AN IDENTITY MATRIX AND THE QUADRATIC
C      IS A WEIGHTED SUM OF SQUARES, BUT
C      IF SW = 1, A = I, AND THE QUADRATIC IS SIMPLY THE SUM OF
C      SQUARES FOR Y.
C      NOTE: EVEN IF SW=1 THE NUMBER OF BLOCKS OF A MUST BE
C      INCLUDED SINCE THE SUM OF SQUARES IS CALCULATED
C      FOR N*BLK OBSERVATIONS
C      BLK IS THE NUMBER OF BLOCKS OF IDENTICAL A'S IN THE QUADRATIC
C      ST IS THE VARIABLE TO DETERMINE THE STARTING ELEMENT IN Y.
C      THIS VALUE SHOULD BE ONE LESS THAN THE ACTUAL STARTING
C      LOCATION. E.G. IF THE SOLUTIONS FOR THE TRAIT OF INTEREST
C      START AT THE 100TH LOCATION USE ST=99 IN THE FUNCTION CALL
C
C      *****
C
C      PARAMETER (NH=50,NS=20,NR=1000)
C
C      DIMENSION A(NS,NS),Y(*)
C
C      INTEGER*4 BLK,ST,SW,TOT,NADD,STRT,STOP,YJC,YKC,IC,JC,KC
C      REAL*8 Y,A,COLL1,COLL2
C
C      TOT = BLK*NS

```

```

YPAY = 0.000

IF (SW.EQ.0) THEN
  DO 100 IC = 1,BLK
    NADD = ST + (IC-1)*NS
    COLL1 = 0.000
    DO 200 JC = 1,NS
      YJC = NADD + JC
      COLL2 = 0.000
      DO 300 KC = 1,NS
        YKC = NADD + KC
        COLL2 = COLL2 + Y(YKC)*A(KC,JC)
300      CONTINUE
      COLL1 = COLL1 + COLL2*Y(YJC)
200    CONTINUE
    YPAY = YPAY + COLL1
100  CONTINUE
ELSE
  STRT = ST + 1
  STOP = ST + TOT
  COLL1 = 0.000
  DO 400 IC = STRT,STOP
    COLL1 = COLL1 + Y(IC)**2
400  CONTINUE
  YPAY = COLL1
END IF

RETURN
END

```