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Using a bull's pedigree in mixed model sire evaluation

by

Gregory Lane Rindsig

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INTRODUCTION

In the past half century, dairy sire evaluation has evolved from a subjective "art" to a highly sophisticated science with complex statistical formulation and requiring advanced computer technology. The equal parent index formed the basis for the daughter dam comparison used by the United States Department of Agriculture (USDA) from 1946 to 1962 to evaluate dairy sires. Then to better account for within herd environmental effects, the herdmate comparison was used. The validity of the herdmate comparison rested on the appropriateness of several assumptions. One being that the herdmates of a bull's daughters were a random sample from the population and another was that the average genetic merit of future herdmates was equal to that of daughter's first herdmates. While these assumptions may have been nearly appropriate initially, they are no longer valid.

Failure of these assumptions became very obvious to the industry. Predicted differences on bulls in A.I. tended to decline in time because later daughters of the bull tended to be compared to a different and superior generation of herdmates. It was also difficult to identify superior young sires because their daughters were competing with those of highly proven older bulls. Thus, improved methods of evaluating dairy bulls was required.

Currently, there are two methods of dairy sire evaluation being widely used. The modified contemporary comparison (MCC) method was introduced in November of 1974 by the USDA to replace the old herdmate comparison. A second method is a linear model approach which has been used in the Northeast region of the United States since 1970. This method uses a mixed model having statistical properties of best linear unbiased prediction (BLUP). Both methods propose to account for proven weaknesses in previously used procedures; however, in somewhat different ways. Development of the MCC was due to doubts that the mixed model would be technologically possible in the near future for nationwide sire evaluation. Research has continued, however, on the linear models procedures in the anticipation that they may eventually be used nationwide.

The desirability of using the BLUP procedure is that its statistical properties are well defined. They are minimum variance of prediction errors, linearity, and unbiasedness. These properties are true if the model accurately describes the data. A feature of the mixed model is that a fixed grouping effect is included so that sire effects are regressed to an appropriate mean. This group mean becomes part of a sire's estimated transmitting ability and is $\hat{S} = \hat{g}_k + \hat{s}_{jk}$. Since it is desired that bulls within a group be as genetically alike as possible, some way of determining this must be made prior to their progeny test. In this study, several grouping strategies are compared empirically. An alternative to grouping is also considered.

REVIEW OF LITERATURE

Background

Some of the early literature speculates as to when the first progeny testing was practiced. These first tests were by some historically well-known farmer breeders of pre-1900. Edwards (1932) points out that Bakewell and Cruikshank are known to have hired out bulls to their neighbors and then brought them back into their own herds if they did well. The progeny test was probably very subjective and simply based on a visit to the neighbor's farm to look at the progeny.

Bonnier (1936), in a review of sire indexes, indicates that Sederholm was the first to attempt a progeny test of a somewhat more objective method. He was able to demonstrate that different sires had very different effects on fat percentages of their daughters. These comparisons were based on daughter-dam differences which became very popular and remained so for a number of years.

The popular view which evolved in the early 1900's was that of "blending inheritance". In other words, the progeny would be an average of the sire and dam. Algebraically, this is:

$$P = \frac{S + D}{2}$$

where P = progeny average, S = sire breeding worth or index, and D = dam average. Solving this equation for the unknown S, an index is derived which, with various modifications, was used for many years. The index is:

$$S = 2P - D.$$

This was referred to as an equal parent or intermediate index.

Yapp (1924) was among several researchers to suggest this index, commenting that "the necessity for the use of this equation is the stimulating, or suppressing influence of the dam". Yapp realized the need to correct for certain factors giving special attention to percent fat and age. Yet, environmental factors that have major effects on production such as herds, years, season, etc., were not accounted for. Regression for imperfect heritability was not done.

Several reviews of progeny testing methods were made in the early thirties. Edwards (1932) discussed the importance of evaluating dairy sires. Lush (1933) also reviewed progeny testing methods. In discussing the equal parent index, he cites its advantages over daughter average is that it removes the errors (except the effects of random environment on the dam's records) arising from differences in the production of the cows to which each bull was bred. Lush also lists the following weaknesses.

1. Easily faked (select poor dam records)
2. If herd environment of dams is different from that of daughters and if corrections are not entirely accurate, the effects are put down as effects of the sire's genotype
3. Does not use information where dam was not used

Lush points out that most of these indexes were basically of the form:

Sire Index = Daughter Average + k(Daughter Average - Dam Average).

When k equals 0 the sire index simply becomes the daughter average. When k equals 1, the aforementioned is the equal parent index. Several researchers proposed indexes where k was between 0 and 1. Norton's index was:

Sire index = Daughter Average + 1/3(Daughter Average - Dam Average)
+ 2/3(Daughter Average - Breed Average)

where 1/3 accounts for the average amount of regression toward the mean. Lush also refers to a study by Turner which indicates that k should equal 3/17.

Goodale (Prentice, 1935) developed the Mount Hope Index based on some crossbreeding experiments. It was his belief that there was a partial dominance for high milk yield and recessiveness for fat percentage. The index was different for milk and fat and also different when daughters were below or above average.

(a) Daughters exceed dams

Milk = Daughter Average + 0.1429(Daughter Average - Dam Average)

Fat = Daughter Average + 1.5(Daughter Average - Dam Average)

(b) Dams exceed daughters

Milk = Daughter Average - 2.333(Dam Average - Daughter Average)

Fat = Daughter Average - 0.677(Dam Average - Daughter Average)

In the 40's and 50's the USDA used a daughter dam comparison to evaluate bulls. By the mid-fifties, the need for a new and better method was apparent; thus, in 1962 the USDA instituted the use of the herdmate comparison. The weaknesses pointed out by Lush of an equal parent type index had become obvious. Bulls with good natural service proofs seldom did well when later used in A.I. Either breeders were giving preferential treatment to daughter or dam records or a positive environmental trend existed. To some extent both may have been true.

The main feature of the herdmate comparison was that herd, year, and season effects were mostly removed. Daughter records of a particular bull were deviated from the average of paternally unrelated cows freshening in a moving five month period centered on the daughter's freshening date. Initially, the USDA index was called a Predicted Average (PA). It was:

$$\text{PA} = \text{Breed Average} + \frac{n}{n + 12} \times (\text{Adjusted Daughter Average} - \text{Breed Average})$$

where n was a number of daughters.

A slight modification was made in 1965 (ARS, 1965). The Breed Average mean was dropped so that sire indexes were given as plus or minus and were now referred to as Predicted Difference (PD). The regression factor was changed from $\frac{n}{n + 12}$ to $\frac{n}{n + 20}$.

In 1967, additional changes were made to the herdmate comparison (Plowman and McDaniel, 1968). Computational adjustments for number of herds, distribution of daughters across herds, number of herdmates, and records per daughter were made. Adjustment for herds was made because within a herd a bull's progeny was not compared to a random sample of bulls in the population but only to bulls recently used in that herd. This was reflected in genetic differences between herds. Also, progeny in a single herd, because of their environmental proximity to each other, performed more similar than their genetic relationship would indicate. Thus, an environmental correlation was included for daughters in one herd. The formula for computing the Predicted Difference was as follows:

$$PD = \frac{\Sigma w_i h^2}{4 + (\Sigma w_i - 1)h^2 + \frac{4\Sigma n_i(n_i - 1)}{N} C^2} \times [(\overline{D} - \overline{HM}) + 0.1 \times (\overline{HM} - \text{Breed Season Average})]$$

where

w_i = weight given to each cow according to the number of records she has completed,

N = total number progeny of a bull,

n_i = number of progeny in the ith herd ($N = n_i$ if all progeny are in one herd),

h^2 = heritability of milk yield from paternal half-sib estimates in nationwide populations,

C^2 = residual correlations among half-sibs in the same herd after they are expressed as deviations from herdmates,

$\overline{D}$ = daughter average,

$\overline{HM}$ = adjusted herdmate average.

The usefulness of the herdmate comparison rested on the validity of several assumptions (Lentz _et al_., 1969). They are:

1. All herd-year seasons are random samples from a single static population.
2. A.I. sires are a random sample from a single, static population.
3. The A.I. daughters are distributed at random among herd-year-seasons.
4. Cows are culled at random.
5. All records are adjusted for age without bias.

While more or less reasonable in the beginning, these assumptions soon lost their validity. This resulted in severe biases in sire evaluations. However, these biases would not have arisen were it not for the ability to select genetically superior sires using Predicted Difference. The resulting problems have thus been "bred out of success". These will be documented in the next two sections.

Genetic trend

An essential assumption of the old herdmate comparison method of sire evaluation is that bulls evaluated over a period of time are compared in a static population. Ironically, should this assumption be valid, it would mean that no genetic improvement was being made. However, proof of the existence of genetic trend is fairly extensive in recent literature.

Verde et al. (1972) used first lactation records from 4779 Holstein, Jersey, and Guernsey paternal half-sisters to estimate genetic trend in Florida. Estimates were made by least squares with herd, year, season, age (linear), and length of record (linear and quadratic), with sire included in the model or deleted. Year constants gave genetic trend estimates of: Holstein, 33 kg milk, -0.7 kg fat, and -0.034 fat percent; Jerseys, 22 kg milk, 1.3 kg fat, and 0.008 kg fat percent; Guernseys, 92 kg milk, 2.8 kg fat, and -0.048 fat percent.

Genetic change in fat corrected milk (FCM) was studied using 11,993 lactation records of 3900 Jersey cows in 12 herds in California by Arave et al. (1964). The genetic change for individual herds ranged from -51 ± 52 to 145 ± 21 lb FCM per year with an average annual genetic change for all herds of 74 lb FCM.

Burnside and Legates (1967) estimated genetic trend using 34,380 first lactation Holstein records from 1953 to 1961. Overall annual trend was estimated from all records. Environmental trend was estimated by analyzing full sisters and paternal half sisters. Comparison of the environmental and total annual trend was used to determine genetic trend. The genetic trend estimates were 45 and 55 kg milk and 0.018 and 0.016 fat percent using full sisters and paternal half sisters, respectively. Harville and Henderson (1967) estimated intraherd genetic trend of 47 ± 17 kg of milk and 1.5 ± 0.6 kg fat per year. Work by Hargrove and Legates (1971) showed annual genetic trend for milk of 53 kg in Holsteins and 25 kg in Jerseys.

Deb *et al*. (1974) used lactation records of Jersey cows to estimate genetic trend in Pennsylvania. The average genetic increase was 18 kg for milk but zero for fat; however, the genetic trend was not significant. Using first lactation Holstein records from Midwest Breeders Cooperative progeny test herds, Powell and Freeman's (1974) best estimate of annual intraherd genetic trend was 82 kg of milk and 1.5 kg of fat.

Genetic merit of herdmates

Another essential assumption of the herdmate comparison is that the average breeding value of herdmates is zero. If this assumption fails to hold, the herdmate deviations are biased. This bias may be quite large. If a bull's daughters are compared to herdmates of higher than average genetic merit, the deviation is smaller than it should be. The resulting predicted difference is thus biased downward. If the average breeding value of herdmates was less than zero, the bias is upward.

Recent investigations have indicated a significant bias due to the genetic level of herdmates. Keown (1974) compared several mixed model methods of sire evaluation using data from the USDA for A.I. bulls summarized in September, 1972. The model used was that employed in the Northeastern A.I. Sire Comparison (NEAISC). It was a mixed model with fixed effects of herd-year-seasons and groups, and random sire effects using only first lactations. Three methods were compared, the first two of which ignored the off-diagonals of the sire coefficients, thus not accounting for the genetic merit of herdmates. Method 3 did consider the off-diagonal sire coefficient elements thus genetic merit of herdmates was accounted for. In comparing evaluations of bulls, the greatest differences occurred between methods not accounting for genetic merit of herdmates with Method 3 which did account for herdmate merit. These differences were even greater than evaluations based on different group definitions.

Norman et al. (1972) examined the effect that average genetic value of the herdmate's sires had on daughter deviation from herdmate average. Using data from the five major dairy breeds, he computed regressions of daughter yield, A.I. herdmate average and daughter deviation from A.I. herdmate average on average predicted difference for milk of herdmate's sires. The first two regressions were positive while the third was negative and not significantly different from minus one. Regressions were similar when computed on average predicted difference for contemporary sires. The authors concluded that, due to the magnitude of the regressions, correcting the daughter herdmate deviation with the average PD of herdmate's sires should remove most of this bias.

In his dissertation, Powell (1972) examined several sire evaluation methods. Various modifications of predicted difference were compared with least squares and mixed models. The correlation between predicted difference not accounting for genetic merit of herdmates with a mixed model (considered optimum) was 0.931 for milk. Using least squares but ignoring the off diagonals of the coefficients matrix resulted in a correlation of 0.95, an increase of 0.02.

Modified contemporary comparison

The USDA-DHIA Modified Contemporary Comparison (MCC) was developed by USDA to replace the old herdmate comparison method of sire evaluations. It is a revised herdmate comparison which statistically adjusts for genetic trend, genetic merit of herdmates, and cow selection in lieu of assuming they do not exist. The first USDA Sire Summary computed was available in November of 1974.

Dickinson *et al.* (1974) has explained the features of the MCC. Improvements in accurately weighting daughter and herdmate information were described. Correction for cow selection was accomplished by deviating first lactation records from first lactation contemporaries. The non-contemporary herdmate average is still included but counts as only one additional contemporary.

Correcting for the genetic merit of contemporaries is done by replacing

[Daughter Average - Average Herdmate Average] + 0.1 x
[Adjusted Herdmate Average - Breed Season Average]

by

Daughter Average - Modified Contemporary Average +
Average Genetic Merit of Contemporary's Sires

This is the mean modified contemporary deviation ($\overline{\text{MCD}}$). The old herdmate comparison method made an average correction for genetic level of the herd whereas the MCC attempts to correct for each individual contemporary sire. In other words, herds are now considered fixed where before they were random. The assumption now is that herdmates are random with respect to their sires rather than to all herdmates.

The adjustment for herdmate's sires must be done iteratively because initial values are biased. On the second pass, the adjustment for herdmate's sires used $\overline{\text{MCD}}$'s computed on the initial round. This continues until differences between iterations are small.

Another feature of the MCC is including pedigree information in a bull's index. Bulls are assigned to pedigree groups based on the following index:

Index = ½ sire's PD + ¼ MGS's PD.

where

½ and ¼ are additive relationships between a bull and his sire and maternal grandsire, respectively,

MGS is maternal grandsire.

These groups were in 50 lb increments except for the extremes where larger classes were required because of fewer bulls. Bulls with only sire PD, only MGS PD, and natural service sires are grouped in a similar manner but separately. If no pedigree information is available, bulls are put into a zero pedigree group. Group averages are then determined by the actual average modified contemporary deviation of daughters of all bulls assigned to each pedigree group.

The final form of a sire index is:

PD74 = Group Average + Repeatability x
(Contemporary Deviation - Group Average)

When repeatability is low, the group average determines a large part of a bull's estimated transmitting ability. However, when repeatability is very high, the group average has virtually no influence.

<u>Best linear unbiased prediction (BLUP)</u>

Henderson (1973) lists four classes of prediction relative to the information available. They are:

1. Best Prediction (BP)
    (a) The form of the joint distribution of records and of the genetic values to be predicted is known.
    (b) Numerical values of the parameters of the distribution are known.
2. Best Linear Prediction (BLP)
    (a) The form of the joint distribution of records and of the genetic values to be predicted is <u>not</u> known or certain parameters are not known.
    (b) Means of genetic values and records and variances and covariances of genetic values and records are known or

well estimated. (In other words, first and second moments are known).

3. Best Linear Unbiased Prediction (BLUP)
   (a) Same as 2a
   (b) Means are unknown but variances and covariances are known (or well estimated).
4. Unnamed
   (a) Same as 2a
   (b) Means, variances, and covariances are unknown but are estimated from the data.

A choice of which class of selection is used rests on knowledge of the joint distribution of records and genetic values to be predicted and knowledge of first and second moments. In dairy cattle, means are not known. Some of these are year, season, and means of new groups because no prior information exists for them. Variances of random effects, such as sires, are not known but are well estimated from volumes of DHI data. Thus, the class of prediction to be considered is BLUP.

Henderson (1973) shows that BLUP is a combination of selection index and generalized least squares. The predictor of w is

$$\hat{w} = P\hat{\beta} + b'(Y-X\hat{\beta})$$

where

$\hat{w}$ is a column vector of predicted genetic values (Bulls' estimated transmitting ability),

P is some linear form of the fixed effects,

$\hat{\beta}$ is same solution to $X'V^{-1}X\hat{\beta} = X'V^{-1}Y$, Y is a column vector of daughter records,

V is the variance covariance matrix Y,

X is a known vector,

b´ is a vector of solutions to regular selection index equations.

Computations are such that $E(\hat{w} - w)^2$ are minimum subject to $\hat{w}$ being unbiased. Henderson (1974) points out two additional properties of BLUP when the distribution is normal.

(1) The prediction is the maximum likelihood estimator, the generalized least squares estimator, and the best linear unbiased estimator of the conditional mean of $\hat{w}$ given the records, y.

(2) If the mean of w is a null vector, of all linear unbiased predictors, BLUP maximizes the probability of a correct ranking of the elements of w.

He also cautions that some predictors may have smaller mean square error of prediction; however, they are biased.

Since solution to obtain BLUP in this form requires the inversion of V, this procedure is impractical for very large sets of data. An alternative method of obtaining solutions, but having BLUP properties was required in sire evaluation.

Henderson (1949) described a mixed model with animal breeding application. Henderson (1963) showed the equivalence of using the mixed model to the combined selection index and generalized least squares method having BLUP properties already mentioned. The mixed model method is also referred to as the Direct Comparison method.

The mixed model can be written:

$$Y = X\beta + Zu + e$$

where

Y is a $n \times 1$ vector of observations,

X is a known fixed matrix, $n \times m$,

β is an unknown fixed vector, $m \times 1$,

Z is a known fixed matrix, $n \times p$,

u is a non-observable random vector with $E(u) = \emptyset$ and $V(u) = G\sigma_e^2$, u is $p \times 1$ and G is $p \times p$,

e is a non-observable random vector with $E(e) = \emptyset$ and $V(e) = R\sigma_e^2$.

The variance of y is:

$$\begin{aligned} V(Y) &= V(X\beta + Zu + e) \\ &= V(X\beta) + V(Zu) + V(e) \\ &= ZV(u)Z' + V(e) \\ &= ZGZ'\sigma_e^2 + R\sigma_e^2 \\ &= (ZGZ' + R)\sigma_e^2 \end{aligned}$$

Assuming G and R are known and u and e are independent, the modified normal equations for obtaining BLUP estimates of β and u are:

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'R^{-1}Y \\ Z'R^{-1}Y \end{bmatrix}$$

The assumption that R = I is often made so that the mixed model can be rewritten:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + RG^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'Y \end{bmatrix}$$

where

$$G^{-1}_{p \times p} = \begin{bmatrix} \sigma_e^2/\sigma_u^2 & 0 & \\ 0 & \sigma_e^2/\sigma_u^2 & \\ & & \ddots \end{bmatrix}$$

Groups

The use of a fixed group effect to account for genetic trend was first introduced by Henderson in 1966 (Henderson, 1973). Two factors have generally been used to determine groups, time and stud affiliation. Bulls born in similar time periods are considered drawn from the same population. If genetic trend is as much as research has indicated, then the population of bulls to pick from in 1975 is very different than it was in 1965. The additional classification by stud is done to further refine the population from which a group of bulls is selected. It is useful because different studs apply varying intensities of selection. This is due in a large part to different goals of selection. Some studs put more emphasis on type relative to production for example. In the Northeast, where mixed model sire evaluations have been routinely computed since 1970, grouping is by stud year (Henderson, 1973).

Several research efforts have been published which compared alternative grouping strategies. Keown (1974) compared three methods of grouping including year in which sires entered service, stud year, and region-year. These comparisons were among Holstein sires which had greater than 1000 first lactation daughters. It was surprising that these sire estimates changed by as much as 60 kg even though they were based on a large number of daughters.

Powell and Freeman (1974) used 6724 first lactation records from 187 Midwest Breeders Cooperative progeny test herds to compare the effect of different group definitions. Ninety sires were assigned to six groups in three different ways. The first definition was by bull's registration number with two grade sires being grouped separately. The two other grouping methods were such that definition three deviated more in time from definition one than did definition two. Sires were also evaluated ignoring groups. Evaluations by definitions two and three and without grouping were compared by rank correlations to evaluations by definition one. Correlations were .997, .973, and .968 for milk and .985, .985, and .976 for fat based on evaluations by definitions two, three and no grouping, respectively. They also computed average absolute differences and average squared differences between the standard and definitions two, three, and no grouping. These were 33, 40, and 43 kg and 3837, 4872, and 5851 kg^2, respectively. They concluded that any grouping tried was preferable to ignoring groups. As an alternative a covariate based on registration number was substituted for groups in the model and gave rank correlation with definition one of .991 and .994 for milk and fat.

Two grouping procedures were compared by Schaeffer _et al_. (1975) using 176,380 Ontario Holstein two-year-olds that freshened from 1958 to 1972. They were year in which first daughter records appeared in the data and A.I. stud ownership by years of first daughter record appearance. They detected no significant difference in group estimates by stud; however, year differences within stud were significant. Overall year differences were not steadily increasing. Their conclusions were that year groupings are essential to account for genetic trend in their data but that stud differences in Ontario were not large enough to cause concern. It was also shown that the grouping procedures that they used had little effect on sire estimates of 20 or more progeny.

If a population of sires to be evaluated is related, estimates of sire merit by BLUP should be more accurate if the additive relationship among sires is taken into account (Henderson, 1973). Kennedy and Moxley (1975) compared mixed model sire evaluations with groups and with the relationship matrix as an alternative to grouping. Fifty-two Holstein A.I. sires having a total of 3288 first lactation milk records were used to compare sire estimates and their error variance of prediction. Eight sires were unrelated to any other in the study. Grouping was by time of entry into service. Rank correlations between methods were .879, .892, .912, .913, and .933 for milk, fat, protein, and fat and protein percent. Differences as large as 100 kg of milk occurred for some sires with few daughters. Prediction error variances were smaller for estimates of sire merit using the relationship method by an average of 18% for milk and 11% for the composition traits. Their study indicated that the relationship method tended to reduce prediction error most for sires with few daughters. This is because using relationships increases the number of possible comparisons among sires. They conclude that the relationship method should be considered as an alternative to grouping. However, in their study, groups were made up of a few sires which caused prediction errors to be larger than necessary in a large population of sires.

Everett et al. (1975) combined the use of the relationship matrix and grouping for sires of the five dairy breeds. Only Holsteins had both sire and maternal grandsire information. Grouping was by sire's date of birth. Comparison of three types of means was made (see Table 1). Group solutions are the direct result of iteration where a constant addition to the sire diagonal was made. No groups are the means of $\hat{s}$ put into identical groups but after iterating solutions. Group Averages are the sum of $\hat{g}_i + \hat{s}_{ij}$ and are different from group solutions because $\hat{s}_{i.}$ is not zero when relationships are considered. According to the authors, if the relationship matrix contributed little or genetic trend was zero, the group averages and group solutions would be nearly equal. Average sire solutions by no grouping were intermediate between group solutions and group averages suggesting that grouping is still desirable (see Table 1).

The possibility of using a pedigree index as a more refined method of assigning sires to groups having predictable genetic differences has been proposed (Powell and Freeman, 1974; Keown, 1974; and Schaeffer et al., 1975). Norman (1974) pointed out that grouping by pedigree could be more effective than grouping by stud-year if there are differences in the quality of bulls purchased each year by individual studs. Another advantage to pedigree grouping would be that fewer groups would be required thus group constants would be better estimated. A third advantage of pedigree grouping would be that breeders would be encouraged to sample bulls with outstanding pedigrees because their estimated transmitting ability would be influenced a great deal by the group mean especially when

Table 1. Holstein group solutions and sire averages for milk

Group	Years	Group solution	No groups	Group average	No of sires
1	44-53	-115	-11	-78	231
2	54-55	- 29	46	6	172
3	56-57	- 21	63	30	161
4	58-59	- 74	64	16	142
5	60-61	-144	115	51	153
6	62-63	-127	145	76	195
7	64-65	29	168	377	291
8	66-67	262	464	620	219
9	68-70	220	573	734	191
10			7	2	622

evaluated on few daughters.

The basis for pedigree grouping is the ability to predict the performance of individuals based on the performance of their parents or simply that the traits of interest are heritable. Lush (1931) pointed out that a complete pedigree is about as accurate as four to six progeny assuming a relatively constant environment during progeny testing. Probably the most extensive study of the relationship of pedigree index and son's proof was by Butcher (1973). He reported good agreement of observed and expected correlations between various pedigree estimates and son performance. Three groups of pedigree records of Holsteins were formed based on son's information. They were:

(1) Sons that entered A.I. at less than 37 months of age

(2) Sons that entered A.I. at more than 37 months of age or non-A.I. sons with multi-herd proofs

(3) Non-A.I. sons with single herd proofs

The data used was as complete as it ever would be. The observed and expected correlations are given in Table 2. Correlations were generally as large as expected. It is interesting that even the third record of the dam was about as predictive as son's proof as was the dam's first record. Pedigree selection was 67% as accurate as theoretically possible and 77% of the accuracy reasonable to obtain. Butcher concluded that pedigree indexes were very useful in predicting a son's breeding value.

Son-parent regressions were computed by Vinson and Freeman (1972) from performance data supplied by seven major A.I. studs. The data used was that available at the time a selection decision was made by stud personnel. For milk yield, regressions were .40, .43, and .43 for son-sire, son-dam, and son-midparent where .87, .30, and .48 were expected. These same regressions for fat yield were .41, .39, and .34. The sire-son regressions were much less than expected; however, possible biases caused by genetic trend, female culling, differences in genetic merit of herdmates may have existed. Correlations for milk yield were .20, .11, and .22 for son-sire, son-dam, and son-midparent, respectively. Correlations for fat yield were .19, .11, and .17.

Dickinson _et_ _al_. (1969) computed sire-son correlations and regressions for Ayrshires, Guernseys, Holsteins, Jerseys, and Brown Swiss. Correlations between predicted difference for milk were .22, .25, .28, .33, and .14 for the five breeds, respectively, and .23, .28, .26, .28, and .16 for fat PD. Regressions were slightly less.

More recently, McDaniel and Bell (1975) reported a study of Holstein bulls to determine whether combining pedigree and progeny information would increase the accuracy of sire summaries. Their results confirmed this especially when bulls had a limited number of daughters. Regressions of A.I. PD milk on a pedigree index identical to that used by USDA in PD74 were .46 and .38.

Table 2. Observed and expected correlations in predicting son's breeding value from various breeding value estimates on ancestors

Ancestors used	Son group 1	Son group 2	Son Group 3
Sire	.43 (.38)[a]	.24 (.31)	.24 (.21)
Dam (first record)	.21 (.17)	.19 (.15)	.17 (.10)
Dam (second record)	.16 (.17)	.16 (.15)	.12 (.10)
Dam (third record)	.16 (.17)	.20 (.15)	.13 (.10)
Dam (Avg. first two records)	.21 (.20)	.20 (.17)	.17 (.12)
Dam (Avg. first three records)	.22 (.21)	.23 (.18)	.17 (.13)
Maternal grandsire	.24 (.18)	.13 (.14)	.12 (.09)
Dam index	.26 (.25)	.23 (.21)	.19 (.14)
Pedigree index	.47 (.45)	.34 (.37)	.30 (.25)

[a] Expected correlations are in parentheses.

The work reviewed has shown that pedigree selection has been fairly effective. This, in spite of the fact that pedigrees and son's proofs were based on herdmate comparisons having all the biases which made new sire evaluation methods necessary. The nature of these biases would tend to make pedigrees less predictive than theoretically possible. Thus, if new and better methods of sire evaluations are used which eliminate the biases of the herdmate comparison, the accuracy of pedigree selection may approach what is theoretically possible.

Powell et al. (1975) has reported the relationship between Pedigree Index (PI), Group Average (GA), and mean Modified Contemporary Deviation ($\overline{\text{MCD}}$) based on sire evaluation by MCC. Data were for Holstein, Guernsey, Jersey, Brown Swiss, Ayrshire and Milking Shorthorn. Regressions of $\overline{\text{MCD}}$ on PI and GA on PI centered around 1.0 although estimates for Jerseys tended to be larger possibly due to a higher heritability in Jerseys. Correlations of $\overline{\text{MCD}}$ and PI ranged from .16 to .40. The high correlation of .40 was for Holsteins where the PI was based on A.I. sire and maternal grandsire information. The correlations between GA and PI were nearly 1.0 except for Brown Swiss which were .83 and .82. By dividing bulls evaluated into quartiles by PI, Powell found that the probability of a bull being plus on daughter performance was about twice as great in the top compared to the bottom quartile. For example, in A.I. Holsteins the percent plus on $\overline{\text{MCD}}$ was 78 in the top quartile and 39 in the bottom quartile.

The upper limit of the accuracy of pedigree selection is $\sqrt{.5} = .71$ assuming the trait is completely determined by additive genes and the most perfect averaging of ancestors is used in a random bred population. Freeman (1976) points out that the attainable accuracy of pedigree selection for special matings is about .58 when the accuracy of sire estimates are 0.9 and dams are estimated with an accuracy of .75. Future sire evaluations by either mixed model or MCC would benefit by the use of unbiased pedigree information. This is extremely promising considering that old and biased methods were at least moderately effective in predicting son's proofs.

DATA DESCRIPTION

These data were obtained from the Iowa State Records Processing Center with the following restrictions:

First lactation
Holstein
Registered sire
Official DHI
Records begun between May, 1967 and May, 1974
From Iowa, Missouri, and Kansas

In addition, records were excluded according to the following criteria established by the USDA:

Those coded as complete but less than 180 days in length
Those coded as incomplete but less than 15 days in length
Those estimated for two or more consecutive test periods
Those initiated by abortion

There were 110,112 records meeting these criteria. All records were 2X, 305 day, mature equivalent (ME). Milk and fat records were converted to kilograms (kg) for analysis. From this initial data set, sires with 40 or more daughters were chosen. Three generation pedigrees on these 450 bulls were provided by the Holstein Friesian Association of America (HFAA). There were 208 bulls whose pedigrees included the following information:

Sire's PD or MCC
Dam's USDA Cow Index
Maternal Grandsire's PD or MCC

The initial data set consisting of 110,112 first lactation records was then reduced to 29,579 records of 208 bulls. Since breaking down environmental subclasses to herd-year-seasons would have reduced the average number of daughters per subclass to less than three, environmental subclasses were defined as herd-years instead of herd-year-seasons. Age adjustment was by factors which also standardize to an average month of freshening (Norman et al., 1974). Consequently, most of the variation in lactation records due to season of calving was eliminated. Records in herd-years within which there was no direct comparison of at least one sire were deleted because they would not contribute to the evaluation of any sire. This is known as statistical disconnectedness. Seven sires no longer had any daughters in the data set leaving 23,544 daughters of 201 sires in 3871 herd-years. This data set was used to obtain sire estimates using the maximum information available meeting the specified criteria. Progeny evaluated were restricted to daughters of the 201 tested sires having the required pedigree information.

Determining groups

Several grouping strategies were compared in this study. The goal was that progeny deviations of sires would be regressed to some subpopulation mean which would be more desirable than regressing to an overall mean. Among those factors which can be considered as criteria for grouping are birth year of sire, pedigree index of sire, dam, and maternal grandsire or stud affiliation. Two pedigree indexes were computed to use as criteria for grouping. They were computed in the following way:

$$\text{Index 1} = u_1(\text{Sire's PD}) + u_2(\text{Maternal Grandsire's PD})$$

where

PD is the most recent USDA-DHI sire evaluation as of November, 1974;

u_1 is the additive relationship between a tested sire and his sire, $u_1 = \frac{1}{2}$;

u_2 is the additive relationship between a tested sire and his maternal grandsire, $u_2 = \frac{1}{4}$.

$$\text{Index 2} = u_1(\text{Sire's PD}) + u_3(\text{CI})$$

where

u_1 and PD are as previously defined;

u_3 is the additive relationship between a tested sire and his dam, $u_3 = \frac{1}{2}$.

CI is the USDA-DHIA cow index computed as follows:

$$CI = w_1\overline{X}_1 + w_2PD$$

where

w_1 and w_2 are selection index weights given to information on the cow and her sire's PD, respectively,

$\overline{X}$ is the cow's mean deviation from modified contemporaries adjusted for merit of herdmate's sire,

PD is the most recent USDA-DHIA sire evaluation as of November, 1974.

The pedigrees of the 201 sires evaluated are listed in Table 3 along with indexes 1 and 2 for both milk and fat. YR stands for year of birth and ST stands for stud code. Table 4 lists simple statistics for the pedigree of the sires tested. A wide range of values were prevalent for all types of pedigrees. The mean CI was 110 kg while the mean PD for sires

Table 3. Pedigrees of bulls evaluated

Bull Code	Bull Number	Sire Number	MGS Number	YR	ST	Index 1 Milk	Index 1 Fat	Index 2 Milk	Index 2 Fat
1	1190953	901195	819476	52	2	43	6	87	6
2	1233487	1013415	1013415	53	4	71	2	180	5
3	1261857	1080016	1156771	54	7	53	6	194	10
4	1268290	886182	1070426	55	4	-106	-1	-70	0
5	1268294	1181068	1104276	55	8	73	5	33	2
6	1279190	1001768	1055021	54	2	-74	0	-134	-3
7	1281874	1013415	1089423	56	4	79	2	118	2
8	1284716	1191720	1024453	56	9	8	4	92	6
9	1287090	1189870	934577	56	6	98	8	18	5
10	1289574	1233487	1024596	56	5	-206	0	-94	4
11	1302712	915940	963902	57	2	-52	0	-45	0
12	1304384	1244845	1172396	57	6	29	0	48	1
13	1305460	1152252	1005816	57	2	-178	-5	-151	-7
14	1315612	1079736	915940	57	8	-5	4	109	6
15	1318021	959466	1033578	57	2	60	7	112	12
16	1323989	1226862	1233487	57	9	-114	-1	-127	-2
17	1324688	1208003	1065220	57	7	86	5	24	2
18	1331709	1262613	1126392	58	7	-98	-1	-148	-4
19	1338728	1293580	1002828	58	9	-156	0	-39	5
20	1343798	1038118	1087035	58	3	-73	9	-15	14
21	1343995	1126392	1074603	58	2	-108	0	-71	0
22	1347112	1250992	915940	59	6	-215	-4	-174	-5
23	1347940	1104074	934577	59	9	76	7	115	9
24	1349691	1244845	1172396	58	9	29	0	48	1
25	1352927	1106455	886182	59	4	-84	0	-67	-1
26	1355784	1013415	1130632	59	9	44	1	62	0
27	1357215	1303198	877660	58	7	12	2	76	2
28	1362410	1259074	1095002	59	8	-177	-2	-76	0
29	1365058	1305460	1190953	59	6	-47	-2	-70	-6
30	1365141	1292880	999669	59	6	-183	-1	-204	-3
31	1365218	1192713	908810	59	7	96	6	199	8
32	1367055	1243697	1014754	59	4	-118	1	-102	0
33	1367353	1113350	1196645	59	9	-9	0	-27	0
34	1367925	915940	999262	59	7	-73	0	-36	0
35	1370173	1303180	1195461	59	6	53	5	27	4
36	1371216	1013415	915940	59	6	-4	0	-40	-1
37	1372052	1275412	1061147	59	6	-13	5	-88	0
38	1375151	1152252	981361	60	7	-219	-5	-169	-4
39	1377052	1057739	833253	60	3	-34	5	-44	4
40	1377954	1181068	1099477	59	7	81	6	209	8
41	1382363	1138451	1013415	60	0	-64	0	-194	-6
42	1382580	1196645	1138451	60	9	-59	-1	-103	-3

Table 3. (Continued)

Bull Code	Bull Number	Sire Number	MGS Number	YR	ST	Index 1 Milk	Index 1 Fat	Index 2 Milk	Index 2 Fat
43	1386406	8218036	1081976	59	2	20	2	131	4
44	1388586	1283917	1150470	60	7	72	0	-99	-7
45	1388721	1205185	1138451	60	7	-72	1	-139	-1
46	1390505	1106455	886162	60	4	-84	0	-67	-1
47	1391447	1189870	1099477	60	3	98	8	15	5
48	1392858	1243697	1027992	60	1	-104	0	-65	1
49	1394348	933122	975138	60	7	33	1	4	0
50	1394655	1138441	1024453	61	6	272	5	265	2
51	1396740	1261857	1156771	60	7	121	13	213	14
52	1396885	1344345	1195201	60	8	68	-1	64	-4
53	1399171	1283917	1150470	61	8	72	0	-36	-5
54	1399380	1196645	1244845	60	6	28	0	140	2
55	1399607	1327405	879145	60	7	-64	0	104	2
56	1399824	1189870	1104074	60	9	123	9	228	11
57	1402761	1378594	1244845	60	2	-229	2	-177	0
58	1404814	1233487	1024596	59	6	-206	0	-94	4
59	1405530	1038509	1226862	60	4	105	3	171	2
60	1406938	1376029	1226862	61	0	-6	0	-59	-1
61	1408640	1376785	1071565	61	8	179	9	233	11
62	1410387	1113350	1035164	61	2	68	2	119	2
63	1410733	1085978	929962	61	7	160	7	125	5
64	1412021	1271122	1196645	61	0	-171	-2	-229	-5
65	1414231	1305460	925394	61	7	-119	-4	-51	-2
66	1415015	1196645	1013415	61	6	8	0	-10	-1
67	1416227	1288610	1237057	62	7	11	-1	120	0
68	1417192	1065220	929962	61	7	75	3	190	5
69	1417208	1199324	1024453	61	8	269	10	353	13
70	1417390	1189870	1252985	62	8	-33	1	38	2
71	1418050	1189870	826653	62	2	51	7	70	5
72	1418927	1189870	866178	62	9	60	6	50	6
73	1419005	1189870	1303198	61	6	107	8	179	8
74	1420015	1305460	1230640	61	2	-68	-4	-28	-3
75	1420487	1189870	934577	61	8	98	8	63	5
76	1421258	1181068	1113350	61	0	71	4	22	2
77	1423320	1189870	1171453	62	2	149	7	231	10
78	1423733	1305460	1091409	62	2	-77	-4	37	0
79	1423926	1189870	852063	62	9	111	8	156	7
80	1424245	1189870	1007680	62	2	28	5	16	3
81	1426597	1092490	1010936	62	7	123	3	119	0
82	1427381	1383926	1292927	62	8	103	7	220	11
83	1428145	1288610	1196645	62	8	-44	-2	-36	-3
84	1428649	1138451	1154156	61	8	-173	-2	-63	-1

Table 3. (Continued)

Bull Code	Bull Number	Sire Number	MGS Number	YR	ST	Index 1		Index 2	
						Milk	Fat	Milk	Fat
85	1428809	1189870	1265694	61	6	180	7	261	8
86	1429640	1382768	1024453	62	7	-222	-6	-110	-3
87	1430145	1492073	8218036	62	7	19	0	104	1
88	1431678	1169870	1080990	62	8	120	9	179	10
89	1431977	1315612	1225191	62	0	-68	1	17	3
90	1432733	1189870	1221490	62	7	49	6	15	5
91	1432960	1371548	1275636	62	0	-12	1	10	0
92	1433269	1237057	1243697	62	6	49	1	124	1
93	1433567	1437235	8229512	62	2	-13	4	55	5
94	1433785	1181029	1000390	62	7	72	8	157	10
95	1435690	1342896	1329790	61	8	43	5	316	14
96	1435884	1368257	915940	62	2	-160	-5	-221	-9
97	1438016	1239242	1297472	62	7	20	4	15	3
98	1438533	1305460	925394	62	7	-119	-4	-51	-2
99	1442117	1341149	1303502	63	7	42	0	281	5
100	1443161	1189679	860768	62	0	180	5	247	6
101	1444368	1013415	8160321	62	9	10	1	91	2
102	1444974	1350414	1188192	62	0	-197	-5	-198	-7
103	1445718	6248207	1046466	63	2	-149	1	-44	7
104	1445725	1244845	1038509	63	8	157	3	160	3
105	1447141	1189870	1024856	62	9	100	10	170	12
106	1447395	1237057	1189870	63	8	142	5	163	4
107	1447414	1085978	929962	63	7	160	7	184	6
108	1447666	1368263	1167530	63	2	-102	-1	34	4
109	1448297	8218036	915940	63	6	-50	0	83	3
110	1448475	1305460	963902	63	2	-19	-3	107	-1
111	1452345	1223243	919383	63	7	245	10	138	5
112	1452497	1080108	929716	63	8	-373	-6	-524	-13
113	1453732	1378594	1244845	64	0	-229	2	-113	4
114	1454800	1071565	1189870	63	8	183	8	247	14
115	1455276	1263538	1226862	62	0	-105	0	14	0
116	1455965	1329588	1024453	64	8	142	5	337	12
117	1457846	1347065	1171453	63	6	112	2	195	4
118	1458169	1237057	1123184	63	6	113	3	53	0
119	1459513	1410237	1144239	64	2	-97	0	-19	3
120	1461530	1085978	955619	64	7	199	9	265	10
121	1461578	842876	1024453	64	7	222	7	329	10
122	1461984	1237057	956081	64	0	135	3	278	6
123	1462168	1378594	1196645	63	3	-281	1	-274	0
124	1463035	1237057	1138451	64	0	53	0	96	0
125	1463216	1242221	1046466	64	2	300	12	406	18
126	1463314	1243399	1268290	64	9	-259	-4	-229	-4

Table 3. (Continued)

Bull Code	Bull Number	Sire Number	MGS Number	YR	ST	Index 1 Milk	Index 1 Fat	Index 2 Milk	Index 2 Fat
127	1464902	1427381	1283917	64	8	379	16	373	14
128	1464967	1323989	1289574	64	6	32	2	114	4
129	1466179	1271810	1329249	64	9	79	0	70	0
130	1466180	1419755	1013415	64	0	159	5	154	3
131	1466757	1406271	1040291	64	9	156	10	181	10
132	1468034	8264804	1024453	64	8	-393	-3	-397	0
133	1468276	1271810	1210507	64	4	280	5	352	7
134	1468738	1440501	1364341	64	0	212	6	256	5
135	1468880	1397517	1148993	64	6	-111	0	17	3
136	1469019	1378594	1124915	64	2	-391	0	-375	0
137	1470014	1252985	1292927	64	8	-264	-9	-147	-5
138	1471171	1189870	1056882	64	8	84	7	142	8
139	1471473	1098656	1013415	64	9	-134	-1	-157	-3
140	1471824	1244845	1144239	64	0	77	0	210	4
141	1472098	1492073	8160321	60	2	-18	0	99	4
142	1473709	1210507	1024453	64	4	293	5	336	7
143	1474265	1376402	1261357	64	0	-220	1	-112	1
144	1474780	1410117	1234506	64	6	101	4	331	13
145	1474835	1252985	1288605	64	0	-266	-10	-98	-4
146	1476170	8271846	1283309	64	2	-157	-5	-28	0
147	1476235	1237666	1015951	64	0	-135	0	-294	-3
148	1477381	1189870	1239242	64	7	115	8	192	8
149	1478014	1189870	1205185	64	2	75	7	197	14
150	1478618	1282720	1251811	64	0	-210	-4	-52	-3
151	1479824	1223243	1189870	65	4	235	10	265	11
152	1480896	1395116	1271810	65	0	85	2	169	5
153	1480902	1271810	1395116	64	0	155	4	182	3
154	1481973	1243697	1232296	65	3	0	5	-55	4
155	1481989	1459996	1024453	65	8	-111	-2	-115	0
156	1482274	1378594	1189870	65	7	-229	5	-119	9
157	1483048	1406271	1150470	65	0	112	8	231	10
158	1483494	1381027	1195221	65	0	-131	0	-116	-1
159	1483720	1450228	1189870	65	9	290	11	335	9
160	1483844	1014925	1113350	65	3	-89	0	24	3
161	1489812	1282185	1234506	65	4	70	1	300	11
162	1489981	1410984	1157986	65	8	-69	2	87	9
163	1490427	1352968	1199324	65	0	-1	6	121	10
164	1492486	1210507	1244845	65	4	305	5	347	4
165	1492600	1410984	8236666	65	0	-63	3	-29	3
166	1495772	1422258	1189870	65	0	8	4	75	6
167	1496635	1378594	1271810	65	0	128	5	106	3
168	1496636	1378594	1271810	65	4	-199	3	-134	4

Table 3. (Continued)

Bull Code	Bull Number	Sire Number	MGS Number	YR	ST	Index 1		Index 2	
						Milk	Fat	Milk	Fat
169	1500395	1277619	1038509	66	4	74	0	159	2
170	1500404	1381027	1113350	66	9	-90	0	24	5
171	1502035	1347065	1378594	66	0	-84	2	46	4
172	1505354	1315612	1225191	66	0	-57	1	-9	1
173	1507983	1189870	8218036	66	2	90	6	93	5
174	1509612	1378594	1126534	66	2	-182	8	-41	13
175	1512625	1459996	1050848	66	8	-150	-4	-56	-4
176	1513417	1339836	1383004	66	2	-5	3	53	5
177	1513667	1381027	1271810	67	0	-14	1	21	1
178	1514126	1410117	1210078	66	6	-27	3	72	6
179	1514953	1459996	1113350	66	2	-143	-3	-183	-5
180	1516215	1492073	8212300	66	8	-155	-1	78	3
181	1517948	1210507	1347065	67	8	288	4	320	5
182	1517981	1210507	1271810	66	4	336	5	391	6
183	1519406	1459996	1286091	66	0	-161	-4	-74	-5
184	1519514	1098656	1161385	66	0	-162	-2	-179	-5
185	1519754	1378594	1404456	67	0	-369	0	-204	3
186	1523437	1459996	1292880	67	0	-189	-4	-123	-3
187	1526107	1331709	1283917	66	0	139	1	185	1
188	1527567	1492073	8203807	67	2	36	2	184	8
189	1528129	1436907	1268134	66	0	-83	0	-32	0
190	1529142	1402113	1128307	67	0	-184	-3	-59	0
191	1530457	1369144	1261357	67	0	-282	-5	-113	-1
192	1535235	1271810	1196645	66	9	141	3	25	-1
193	1536957	1507983	1242221	68	2	1	0	58	0
194	1537984	1381027	1130632	67	0	-92	0	-74	0
195	1538732	1355784	1244845	67	4	315	5	352	9
196	1541451	1347940	1189870	66	0	317	15	438	17
197	1543753	1239242	1189870	68	7	96	6	294	10
198	1547948	1410387	1242221	68	2	66	0	138	0
199	1549100	1237057	1189870	68	8	142	5	205	10
200	1550180	1271810	1189870	68	4	194	6	263	9
201	1552390	1347940	1210507	68	4	403	13	529	20

Table 4. Means, standard deviations, and ranges for pedigrees of 201 bulls evaluated

			Mean	Standard deviation	Low	High
Sire	PD milk		0	277	-851	655
	PD fat		- 0.4	8.9	- 23.2	30.0
	Repeatability		92	17	28	99
Dam	CI milk		110	189	-417	668
	CI fat		5.9	7.4	- 13.2	26.8
	Average number of records		6.7	2.5	1	13
	Average number of records indexed		4.7	2.6	1	10
	Repeatability		40	4.6	23	44
Maternal grandsire	PD milk		13	218	-700	655
	PD fat		0.5	7.0	- 23.2	22.7
	Repeatability		86	21.6	20	99
	Index 1	milk	3	154	-394	403
		fat	- 0.1	4.8	- 13.4	14.0
	Index 2	milk	55	169	-525	529
		fat	2.8	5.8	- 14.1	19.8

and maternal grandsires was zero and 13 kg, respectively, for milk. Means for fat were 5.9, -0.4, and 0.5 for CI, sire's PD and maternal grandsire's PD. In the selection of bulls, more emphasis was placed on the quality of the dam than the sire.

Dams had an average of 6.7 records but an average of 4.7 records were included in cow indexes. The discrepancy arises because early records of old dams were made before indexing was done by USDA. The average repeatability of dams was 40 percent with a range of 23 to 44. PD's for sires and maternal grandsires had average repeatabilities of 92 and 86 percent, respectively. All pedigree index information was based on the most recent proofs as of November, 1974 and not information available when progeny tested sire's first daughters appeared in the data.

Another form of pedigree grouping which is used in the Northeast is to group by stud affiliation. Different studs may tend to select different kinds of bulls in some way that is not reflected in their pedigree indexes. These may include type, show winnings, fat test, etc. Bulls evaluated in this data set were grouped by studs; however, since most studs had relatively few bulls represented, studs were combined based on the author's opinion of similar selection philosophies. For instance, cooperatives were usually considered together. Bulls not stud identified were also grouped separately. Grouping was thus by stud type. The distribution of bulls by stud identification is given in Table 5.

The time period in which the bull was born was also a criteria for grouping along with stud affiliation or pedigree index. The following is a description of 7 groupings compared in this study where abbreviations

Table 5. Stud affiliation of tested bulls

Stud code	Identification	Number
1	Select Sires	1
2	Carnation-Genetics	32
3	Tri-state	6
4	Kansas	18
5	Minnesota Valley	1
6	Midwest	22
7	American Breeders Service	32
8	Curtiss	29
9	Other coops	20
0	No stud identification	40

represent model definitions where grouping was as described.

1. SMG--Bulls were grouped by Index 1 into 10 groups. The range of each group was about 80 kg with groups at the extremes tending to be larger because of fewer bulls.
2. SCI--Bulls were grouped by Index 2 into 10 groups of approximately 95 kg.
3. STYR--Bulls were grouped by stud type within period of birth.

   Assignment of stud type was as follows:

Stud type	Stud codes
I	1,2,8
II	4,7
III	0,3
IV	5,6,9

   Birth periods were 1952-60, 1961-63, and 1964-68. There were 12 groups.
4. BRTH--Grouping was by birth year of bull. Group 1 included bulls born from 1952 through 1957, group 2 included sires born from 1958 through 1960, and 8 additional groups were by one year increments starting in 1961 and ending with 1968. There were 10 groups.
5. SMGB--Index 1 was used to group bulls within periods of birth. Periods of birth were 1952-60, 1961-63, and 1964-68. There were 13 groups.
6. SCIB--Index 2 was used to group bulls within period of

birth. Periods of birth were 1952-60, 1961-63, and 1964-68. There were 14 groups.

7. RELB--Grouping was combined with the uses of additive relationships. Bulls were assigned to groups identical to BRTH. There were 10 groups.

All 7 groupings were used for obtaining sire estimates for milk. Only group definitions SMG, BRTH, and RELB were compared for fat. Milk indexes were used for obtaining sire estimates for milk and a fat index was used when SMG was used to obtain fat estimates.

Relationships between sires

Relationships between sires was included in two evaluations for milk and fat. One method considered relationships alone and a second combined uses of the relationship matrix with grouping. Grouping was by year of birth identical to group definition 4.

All but 31 sires were related to at least one other tested sire in the data set used. The order of the coefficients matrix was increased by 62 or 31 percent over the original 201 sires. Inbreeding was not considered in creating the inverted relationship matrix.

METHODS AND PROCEDURES

Background

Several features of the mixed model for obtaining BLUP are:

1. It requires just a simple modification of regular least squares. Variance ratios are added to diagonals of the sire equations.
2. Nuisance variables may be absorbed by a simple algebraic process.
3. Solutions are easily obtained by direct inversion when the number of equations are less than approximately 200.
4. When the number of equations is large, solutions may be obtained by iteration.

Henderson (1974) discussed the choice of model. He pointed out the data chosen may partially determine the model and vice versa. He also stressed that the more complete a model is the less chance for bias, but adding unimportant elements to the model results in greater computational cost and larger sampling variances. Assuming the correct model is chosen, sire estimates are best linear unbiased predictions (BLUP). As simple a model as possible which accounts for important sources of variation is desired. Such a model was incorporated into sire evaluation in the Northeast and has been used successfully for several years. It is:

$$Y_{ijk\ell} = \mu + h_i + g_j + s_{jk} + e_{ijk\ell} \qquad (1)$$

where

$Y_{ijk\ell}$ is a first lactation, 2X, 305 day, ME record of ℓ^{th} daughter of the k^{th} sire in the j^{th} group and the

i^{th} herd-year-season,

μ is a constant,

h_i is the i^{th} herd-year-season,

g_j is the j^{th} group included to account for genetic trend by regressing sires to an appropriate group mean instead of zero or μ,

s_{jk} is the k^{th} sire nested in the j^{th} group,

e_{ijkl} are mutually uncorrelated random variables.

Only first lactation records are used. This eliminates bias due to non-random culling of daughters. It also considerably reduces computational problems because if multiple records of cows are included, selection must be accounted for.

The effects of the model must be assumed fixed or random. Herd-year-seasons might logically be considered random because a new sample of data would be from a new set of herds, years, and seasons. However, certain breeders tend to use better bulls than others and this is reflected in the herd-year-season means. Treating herd-year-seasons as fixed effects eliminates this bias due to sire selection. Genetic differences between herds, other than what is accounted for by sires of herdmates, are absorbed along with herd-year-seasons. An additional refinement in sire evaluation would be to correct for genetic herd differences as measured through the cow.

Sire effects are their transmitting ability relative to some base population. In the model, sires are considered random for two reasons. First, they are the result of a sampling process, the random segregation of genes. Secondly, the purpose of estimating sire effects is to predict future daughter performance. When computing sire effects under the assumption that they are random, only a simple modification of least square's normal equations is required. The variance ratio (σ_e^2/σ_s^2) is added to the diagonal of the sire equations (this will be shown later). This is often referred to as augmenting the diagonal to simultaneously regress sire means for number of daughters, distribution of daughters, and imperfect heritability.

The estimated transmitting ability of a bull from this model is $\hat{g}_j + \hat{s}_{jk}$. Sires are nested in groups and deviate about its mean. The group constant reflects the mean of a subpopulation of bulls. It is important that bulls be assigned to a group which reflects his genetic ability because $\hat{g}_j$ is part of his estimated transmitting ability. This is most important when a bull has few daughters because they have small influence in determining his group constant. Also, $\hat{g}_j$ contributes relatively more to estimating a sire's transmitting ability when he has few daughters than when he has many. Groups are considered fixed effects.

The mixed model was described in general in the Review of Literature. For model (1), it is:

$$Y = Hh + Gg + Ss + e$$

where

Y is a vector of daughter records, n x 1;

H is a known fixed matrix, n x r;

h is a column vector of environmental effects, r x 1;

G is a known fixed matrix, n x q;

g is a column vector of genetic group effects, q x 1;

S is a known fixed matrix, n x p;

s is an unknown vector of random sire effects, $E(s) = 0$, $V(s) = Q\sigma_e^2$, s is p x 1 and Q is p x p;

e is a n x 1 non-observable random vector, $E(e) = 0$, $V(e) = R\sigma_e^2$, $Q^{-1} = I\sigma_e^2/\sigma_s^2$;

and assuming $R = I$, $RQ^{-1} = I\sigma_e^2/\sigma_s^2$.

The above equations then are:

$$\begin{bmatrix} H'H & H'G & H'S \\ G'H & G'G & G'S \\ S'H & S'G & S'S + I\dfrac{\sigma_e^2}{\sigma_s^2} \end{bmatrix} \begin{bmatrix} \hat{h} \\ \hat{g} \\ \hat{s} \end{bmatrix} = \begin{bmatrix} H'Y \\ G'Y \\ S'Y \end{bmatrix}$$

Solutions cannot be obtained directly from these equations because of the large order of the coefficients matrix. The procedures for creating mixed model equations and obtaining solutions are given in the following sections. Examples of these procedures are in the Appendix.

Procedures for creating equations

1. Absorbing h into s

At this point, a simplified model is considered which ignores groups. It is:

$$Y_{ik\ell} = h_i + s_k + e_{ik\ell} \qquad (2)$$

where

the factors are identical to model (1) except that groups are ignored and h_i refers to a herd-year instead of herd-year-season.

Note that the mean μ is included with the herd-year effect, $h_i = \mu + \text{herd-year}_i$. The group equations can be created after absorption which will be shown later. They are simply combinations of the absorbed sire equations.

Absorption is an algebraic process whereby a set of effects are solved for in terms of the remaining effects of the model. For model (2), herd-years are solved for in terms of sires. Various other terms have been applied to this technique including "sweep out". It is necessary because of the impossibility of directly obtaining solutions when the number of equations is greater than several hundred. In this study several thousand herd-years are involved.

Lentz et al. (1969) showed by example how absorption could be accomplished as herd-years were read into the computer sequentially. The absorbed coefficients for model (2) are:

$$C_s = \begin{bmatrix} \sum_i (n_{i1\cdot} - \frac{n_{i1\cdot}^2}{n_{i\cdot\cdot}}) & -\sum_i \frac{n_{i1\cdot} n_{i2\cdot}}{n_{i\cdot\cdot}} & \cdots & -\sum_i \frac{n_{i1\cdot} n_{ip\cdot}}{n_{i\cdot\cdot}} \\ -\sum_i \frac{n_{i2\cdot} n_{i1\cdot}}{n_{i\cdot\cdot}} & \sum_i (n_{i2\cdot} - \frac{n_{i2\cdot}^2}{n_{i\cdot\cdot}}) & & \vdots \\ \vdots & & \ddots & \vdots \\ -\sum_i \frac{n_{ip\cdot} n_{i1\cdot}}{n_{i\cdot\cdot}} & \cdots & & \sum_i (n_{ip\cdot} - \frac{n_{ip\cdot}^2}{n_{i\cdot\cdot}}) \end{bmatrix} \tag{3}$$

where

C_s is the absorbed coefficients matrix or sire equations after absorption,

$n_{ik\cdot}$ is the number of daughters of sire k in herd-year i,

$n_{i..}$ is the total number of progeny in herd-year i,

p is the total number of sires.

A characteristic of these equations is that they sum to zero by row or column. The diagonal element is equal to the sum of the off-diagonals times minus one.

The right hand sides after absorption are:

$$R_s = \begin{bmatrix} \sum_i (Y_{i1.} - n_{i1.}\overline{Y}_{i..}) \\ \sum_i (Y_{i2.} - n_{i2.}\overline{Y}_{i..}) \\ \cdot \\ \cdot \\ \cdot \\ \sum_i (Y_{ip.} - n_{ip.}\overline{Y}_{i..}) \end{bmatrix} \qquad (4)$$

where

R_s are the absorbed right hand sides,

$Y_{ik.}$ is the sum of lactation records for the daughters of the k^{th} sire in the i^{th} herd-year,

$Y_{i..}$ is the mean of all lactation records in the i^{th} herd-year.

The computations are relatively easy. The first step is to sort daughter records by year of freshening within herd. This way, herd-years can be absorbed one at a time as they are read into the computer. In addition, sires are sorted within herd-years so that sire codes may be identified more efficiently. The second step is to identify all sires in the data set. They are then sorted by sire's registration number and coded 1 to p, the total number of sires. The registration number and code for each sire is read in and stored in the computer.

The appropriate arrays are then zeroed out. The largest of these is the coefficients matrix, C_s, whose dimensions are p x p when full stored. If double precision is used, the required core is $8p^2$ (a double precision computer word is 8 bytes long). For p equal to 200, the required core for just storing that array is 320,000. Since core time is expensive, a more economical way of handling the coefficients matrix is required. An acceptable alternative is to use direct access to a supporting disk. This reduces the required array area to just p double precision words because only one sire equation needs to be in the computer at one time. Besides reducing run cost due to core time, turn around time is reduced because less core needs to be reserved.

The next step in the absorption process is to read in the first record and initialize herd and year. Immediately, the second record is read in and a subroutine called to check whether a new herd-year has been encountered. If so, the program branches to the subroutine where the actual algebra of absorption takes place. If the herd-year does not change, a subroutine is called to match sire's registration number with his code. Following this, a counter for number of daughters of that sire in that herd-year subclass is incremented by one. Herd-year sums and total sums of squares can also be accumulated.

After all herd-years have been absorbed, each row of the coefficients matrix is checked to see that it sums to zero. Finally, the absorbed sire equations and right hand sides are written out on tape by rows. Total and herd-year sums of squares and number of records and herd-years can also be written out.

2. Adding variance ratios

Until now, sires have been treated as if they were fixed. In the next step, after group equations are created, the ratio of the error variance to the sire variance (σ_e^2/σ_s^2) is added to the diagonal of the absorbed sire equations thus regressing for imperfect heritability, and number and distribution of daughters. By doing this, sires are treated as if they were random. The value used in this study was 15 which corresponds to a heritability of .25. Adding the variance ratios eliminates any rank deficiency so that no restriction on the sire equations are required to obtain unique solutions.

3. Creating group equations

A separate computer program creates the group equations which were previously ignored. This can be done after absorption because sires are totally nested in groups. Groups are merely combinations of the sire equations. It is not necessary to use direct access because the sire coefficients matrix, C_s, may be handled one row at a time. A p by g matrix F of 0's and 1's is constructed in the computer where p and g are the number of sires and groups, respectively.

$$F_{pxg} = \begin{bmatrix} 1 & 0 & 0 & \ldots \\ 0 & 0 & 1 & \ldots \\ 0 & 0 & 1 & \ldots \\ 0 & 1 & 0 & \ldots \\ \cdot & & & \\ \cdot & & & \\ \cdot & & & \end{bmatrix}$$

The sire identification code from 1 to p and its predetermined group code from 1 to g is read into the computer and the value 1 assigned to that position in F. All other values in that row of F are assigned the value 0. For example, sire number 2 is assigned to group 3. The position $F_{2,3}$ is assigned the value 1 while all other positions in row 2 of F are 0.

Matrix multiplication of C_s times F results in the p x g matrix C_g.

$$\underset{pxp}{\begin{bmatrix} C_s \end{bmatrix}} \underset{pxg}{\begin{bmatrix} F \end{bmatrix}} = \begin{bmatrix} C_g \end{bmatrix}$$

where

Cg is the group portion of the sire equations.

These equations are created one sire at a time. After each equation is created, it is checked to see that it still sums to zero. Fifteen is then added to the diagonal of each sire equation which is now one by p + g and is written out on tape.

Next, the rows and columns of C_g are interchanged to get C_g'.

$$\begin{bmatrix} C_g \end{bmatrix} \longrightarrow \begin{bmatrix} C_g' \end{bmatrix}$$

A g x g matrix J is formed by multiplying C_g' times F.

$$\underset{gxp}{\begin{bmatrix} C_g' \end{bmatrix}} \underset{pxg}{\begin{bmatrix} F \end{bmatrix}} = \underset{gxg}{\begin{bmatrix} J \end{bmatrix}}$$

The group equations are:

$$\begin{bmatrix} C_g' \end{bmatrix} \begin{bmatrix} J \end{bmatrix}$$

A check is made to see that they sum to zero. They are then written out on tape.

The final step is to create the group right hand sides for milk and fat. This is done by premultiplying the absorbed right hand sides by F′.

$$\begin{bmatrix} F' \end{bmatrix} \begin{bmatrix} R \end{bmatrix} = \begin{bmatrix} K \end{bmatrix}$$

The full right hand sides are:

$$\begin{bmatrix} R \\ \hline K \end{bmatrix}$$

They are checked to see that they sum to zero and are then written out on tape. The equations are now ready for solution. They are:

$$\left[\begin{array}{c|c} C_s + I15 & C_g \\ \hline C_g' & J \end{array}\right] \begin{bmatrix} \hat{s} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} R \\ \hline K \end{bmatrix} \qquad (5)$$

4. Considering relationships among sires

The accuracy of prediction of sire's transmitting ability can be increased by considering the additive relationships among sires. This is reflected in lower prediction error variances and may result in fewer groups being required. Considering relationships the resulting equations are:

$$\begin{bmatrix} C_s + A^{-1}15 \end{bmatrix} \begin{bmatrix} \hat{s} \end{bmatrix} \begin{bmatrix} R \end{bmatrix} \qquad (6)$$

or

$$\left[\begin{array}{c|c} C_s + A^{-1}15 & C_g \\ \hline C_g' & J \end{array}\right] \begin{bmatrix} \hat{s} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} R \\ \hline K \end{bmatrix} \qquad (7)$$

when groups are considered where submatrices are as previously defined and A^{-1} is the inverse of the relationship matrix.

Until recently, it was not practical to use this procedure because obtaining the inverse of the relationship matrix (A) was difficult when the number of sires was large. However, Henderson (1975) has discovered simple methods of creating the inverse of the relationship matrix directly from a list of sires and dams of sires to be evaluated assuming the population is non-inbred. The mixed model equations required are increased by the number of identified parents. The equations now are:

$$\left[\begin{array}{c|cc} C_s + W_{11}15 & W_{12}15 & C_g \\ \hline W_{12}'15 & W_{22}15 & 0 \\ \hline C_g' & 0 & J \end{array}\right] \left[\begin{array}{c} \hat{s} \\ \hat{f} \\ \hline \hat{g} \end{array}\right] = \left[\begin{array}{c} R \\ 0 \\ \hline K \end{array}\right] \tag{8}$$

where

$$A^{-1} = \begin{bmatrix} W_{11} & W_{12} \\ W_{21} & W_{22} \end{bmatrix} = \begin{bmatrix} A_{11} & A_{12} \\ A_{12}' & A_{22} \end{bmatrix}^{-1}$$

and $\hat{f}$ is BLUP of future progeny of untested sires and dams. Absorbing the equations for identified parents would result in equations identical to (8); however, this again is not practical if the number of equations is large. It is feasible to solve all equations iteratively simultaneously obtaining pedigree estimates for identified parents.

If all parents are known, the number of sire equations is increased by a factor of three. For the data set used in this study where all sires and dams are known, the increase in equations would be from 201 to 603. Henderson (1975) has shown that under certain assumptions, dams may be excluded. In addition, any untested sire having only one tested son and no tested maternal grandsons, and any untested maternal grandsire having only one tested grandson may be excluded. The resulting solutions are identical to (7). The assumptions are:

1. Non-inbred population.
2. Relationships are restricted to the sires and maternal grandsires of all males with tested progeny.
3. All dams of progeny tested sons have only one such son.
4. Records on dams are not included.

In this study, the simplified procedure was used. Pedigrees including sires and maternal grandsires for all tested bulls were listed and screened to meet the required criteria. Sires and maternal grandsires were coded so that all sires were numbered from 1 to n. Tested sires were numbered from 1 to 201 and an additional 62 individuals were numbered from 202 to 263.

The inverse of the relationship matrix was created on disk. Contributions were made to A^{-1} by the method described by Henderson (1975) where p, s, and g are the coded numbers of tested sire, his sire, and his maternal grandsire, respectively.

1. If s and g are both known, add:

   1/11 to (g,g);

   2/11 to (g,s) and (s,g);

   -4/11 to (g,p) and (p,g);

4/11 to (s,s);

-8/11 to (s,p) and (p,s);

16/11 to (p,p).

2. If s is known and g is unknown, add:

   1/3 to (s,s);

   -2/3 to (s,p) and (p,s);

   4/3 to (p,p).

3. If g is known and s is unknown, add:

   1/15 to (g,g);

   -4/15 to (g,p) and (p,g);

   16/15 to (p,p).

4. If g and s are both unknown, add:

   1 to (p,p).

After completing the computation of A^{-1}, it is written out on tape and later added to the already created sire equation.

Obtaining solutions to mixed model equations

Although it is desirable to obtain solutions by the direct inverse, it is seldom practical in sire evaluation. The time and thus the expense of inverting the coefficients matrix increases more than linearly with increasing size of matrix. In this study, numerous solutions to as many as 273 equations were required, thus iteration was used.

For the modified least squares equations of interest, iteration has proven to be a practical and economical way of obtaining solutions. Characteristic of the sire equations is that they are diagonally dominant and their right hand sides sum to zero. These features make iteration extremely efficient. Experience has shown that solutions obtained by this process are very close to those by direct inversion, however, more feasible for a large number of equations.

The sire and group equations to be solved are of the form:

$$AB = K$$

where

A is the coefficients matrix,

B is the vector of unknown variables to be estimated,

K is the vector of right hand sides.

The iteration procedure can be developed as follows: Initial values of B are estimated by dividing the right hand sides by the diagonal of the coefficients matrix. The initial values are substituted into the original equations and multiplied times the coefficients matrix to yield estimated right hand sides after one round.

$$AB_1 = K_1$$

Second and later solutions are as follows:

$$\hat{B}_1{}^2 = (K_1 - A_{12}\hat{B}_2{}^1 - A_{13}\hat{B}_3{}^1 - \cdot \cdot \cdot \cdot - A_{1n}\hat{B}_n{}^1)/A_{11}$$

$$\hat{B}_2{}^2 = (K_2 - A_{21}\hat{B}_1{}^2 - A_{23}\hat{B}_3{}^1 - \cdot \cdot \cdot \cdot - A_{2p}\hat{B}_p{}^1)/A_{22}$$

$$\begin{array}{c}\cdot\\\cdot\\\cdot\end{array}$$

$$\hat{B}_p{}^2 = (K_p - A_{p1}\hat{B}_1{}^2 - A_{p2}\hat{B}_2{}^2 - \cdot \cdot \cdot \cdot - A_{p(p-1)}\hat{B}^2_{p-1})/A_{pp}$$

where

the upper subscript of B represents the number of iterations

p is total number of equations.

$Q = \sum_i (\hat{K}_i - K_i)^2$ is computed and used as a criteria whether or not to terminate the iteration process. When Q is close to 0, the process is terminated.

As was pointed out earlier, there is a rank deficiency in the group equations. However, iterated solutions are obtained without making any restriction on the coefficients. The equations are consistent (a set of solutions exist) and that is all that is required. If desirable, a restriction may be applied to the final solutions which would be identical to those if that same restriction had been applied to the coefficients matrix before iteration.

The computing strategy is to read the coefficients matrix onto disk and use direct access calling on only one sire equation at a time.

Methods of comparing solutions

The purpose of sire evaluation is to predict the performance of future daughters of a bull. If genetic trend is adequately accounted for, the prediction of daughters at any point in time can be used. Correlations may be computed as measures of the predictive ability of the different grouping strategies or alternatives.

A second criteria for comparing sire evaluations is that of the rank correlations of bulls by different evaluations. Spearman rank correlations are computed between all evaluations. While these correlations are not highly sensitive, they do indicate in general how closely different evaluations rank a particular group of bulls.

A third method of comparing ranks commonly used in livestock judging contest has some appeal. Its basis is that one position switches in rank resulting in smaller penalty than multiple switches. In livestock judging, the "true" ranking and cuts are determined by an official judge or committee of judges. The "official" for comparing ranks of sire estimates were based on the correlations between evaluations and additional daughter records. Cuts were the actual differences between adjacently ranked bulls measured in kg. An example of penalties for misrankings is given below:

official 1 2 3 4
cuts 1 2 4
placing 1--2 1 3 4 score = - 1
placing 2--1 2 4 3 score = - 4
placing 3--4 3 2 1 score = -23

A complete reversal of ranks results in a large penalty while for single switches in rank the penalty depends on the differences between adjacently ranked bulls. To help interpret scores, they will be computed as a percent of complete reversal of ranks. The penalty will be a percent of the largest possible penalty.

RESULTS AND DISCUSSION

Estimated transmitting abilities for 201 bulls were computed for milk and fat production using different mixed model definitions. Ten model definitions for milk and six for fat were compared. Modified contemporary comparisons computed by USDA were also compared; however, they were generally based on more daughters. The model definitions and modified contemporary comparison were coded for easier reference in this section. These codes are listed in Table 6. Codes for models with grouping correspond to more detailed descriptions of grouping in the data description. Estimated transmitting abilities will simply be referred to as sire estimates.

Group solutions

Tables 7 and 8 list group solutions for milk production and Table 9 lists group solutions for fat. All information used in assigning sires to groups was what was available as of November 1974. In practice, whatever criteria is used to group sires must be information which is available when a bull's first daughters freshen. The attitude taken in this study, however, was to use the latest and most complete pedigree indexes available when data were analyzed. The resulting sire estimates, where pedigree indexes were used for grouping, are based on information which would necessarily not have been available or very complete at the time of grouping.

All grouping was done linearly with regard to the criteria for grouping. For instance, where an index was used as the only grouping

Table 6. Codes for the modified contemporary comparison and mixed model definitions

Codes	Definitions
PD74	Modified Contemporary Comparisons obtained from USDA
NGRP	No grouping
NGIO	No grouping and off-diagonals ignored
SMG	Grouping was by a pedigree index of sires' and maternal grandsires' PD's
SCI	Grouping was by a pedigree index of sires' PD and dam's cow index
STYR	Grouping was by stud year
BRTH	Grouping was by birth year of the sire
SMGB	Same as SMG but within periods of birth
SCIB	Same as SCI but within periods of birth
RELB	Grouping was by birth year and relationships between sires were considered
REL	Relationships only are considered

Table 7. Group solutions for milk[a]

Group number	Model definitions			
	SMG	SCI	BRTH	RELB[b]
1	-198	-283	-206	-199
2	-193	-288	- 20	- 17
3	- 49	-146	- 19	- 14
4	-130	-165	- 1	0
5	- 79	44	27	39
6	- 86	- 89	45	38
7	50	33	52	54
8	159	83	95	117
9	170	241	26	18
10	178	154	27	36

[a] Solutions are in kg.

[b] Group average.

Table 8. Group solutions for milk[a]

Group number	Model definitions					
		STYR		SMGB		SCIB
1	I	-182	1	-136	1	-171
2		- 87		-227		-192
3		-170		- 62		-123
4	II	- 11		69		111
5		122	2	-184	2	-350
6		210		- 34		- 69
7	III	-260		57		12
8		- 68		157		81
9		- 11	3	-147		134
10	IV	-157		- 98	3	-393
11		- 77		- 87		-128
12		172		193		190
13				160		18
14						204

[a] Solutions are in kg.

Table 9. Group solutions for fat[a]

Group number	Model definitions		
	SMG	BRTH	RELB[b]
1	-9.2	-5.4	-5.0
2	-5.4	0.3	.3
3	-2.1	-2.2	-2.4
4	.4	-1.4	-1.2
5	-4.5	0.5	1.1
6	1.2	2.6	3.2
7	-1.6	2.0	2.0
8	3.5	6.1	5.7
9	7.8	-4.2	-5.1
10	10.9	1.3	1.6

[a] Solutions are in kg.

[b] Group average.

criteria, group 1 would include sires with the most negative indexes and the last group would include highest indexes. Thus, it is expected that group solutions will follow somewhat linearly in magnitude with respect to group number. This, of course, is true if the criteria for grouping does in fact separate bulls into different and predictable subpopulations. Group solutions for SMG and SCI for milk do reflect large differences as a result of grouping (Table 7). The ranges from highest group to lowest group are 376 and 529 kg for SMG and SCI, respectively. Since first lactation milk production has a heritability of about .25, it is not surprising that grouping sires using these indexes alone should result in distinct group solutions. Regressions of group solution on group number are 45 kg for SMG and 56 kg for SCI. Group solutions did not increase linearly with group number, but they were not grossly misplaced. For instance, a large negative group solution was not associated with a high group number and vica vera.

While the regressions of group solution on group number were positive and large for both SMG and SCI, there were rather large changes for adjacent groups both in magnitude and direction. There are several possible reasons for these differences. First, indexes used as grouping criteria were not based on equivalent information. While most PD's of sires were modified contemporary comparisons thus reflecting a common base, the majority of maternal grandsire's (MGS) PD's were based on the old herdmate comparison. Cow indexes were based on older PD's and usually not all of a cow's records. Secondly, the first group and last group were based on a wider range of indexes. For SCI, group solutions for the first two and last two groups are reversed in magnitude. McGilliard (1974) found that when predicting daughter performance from dam's estimated average transmitting abilities (EATA), daughters from dam's with extreme EATA's produced closer to the mean than expected. Extremely high cow indexes may be due to exceptional feeding or other treatment relative to herdmates. Another possible explanation is that very high performance may be the result of epistatic gene action. Gene segregation may break up desirable gene combinations thus contributing to poor prediction of progeny performance. This is not true for males whose merit is measured totally through his progeny.

Bulls were also grouped by their birth year to see the extent to which genetic subpopulations could be distinguished (Table 7). Differences in group solutions are less striking for BRTH than for SMG or SCI. The very oldest bulls, those born from 1952-57, were much poorer for milk production than all others. The overall range in group solutions is 301 kg; however, the range for sires from groups 2 through 10 spanning 10 years was only 115 kg. The regression of group solution on group number was 19 kg. Just grouping by birth year of bull was not as effective in creating distinct subpopulations as grouping by pedigree index.

Four groupings were tried which combined consideration of period of birth and pedigree knowledge. What was thought to be most crude was for model STYR where sires were grouped according to type of stud (Table 8). Those thought to be natural service bulls were grouped separately as well. The four types of studs as defined in the data description had means over all years of:

I	-146 kg
II	107 kg
III	-113 kg
IV	109 kg

Linear trends in group solutions can be seen in all stud types. This grouping strategy was effective in determining distinct subpopulations of bulls even though explicit knowledge of a bull's pedigree was not considered. It should be reiterated that studs were subjectively determined and included a selected group of sires. Inference about selection goals, aims, or success of the studs with bulls in this study is not recommended. Few bulls per stud were represented and then only bulls meeting criteria of this study. It was the author's opinion that stud year groups were defined such that their group solutions would rank II, IV, III, I. The actual rank was IV, II, I, III but top and bottom pairs were not very different.

Index 1 and 2 were used to group bulls within birth periods. These model definitions were SMGB and SCIB and their group solutions are presented in Table 8. The three birth periods are represented by numbers 1, 2, and 3 in the table. Within each birth period, group solutions increased. Group means by birth period are given in Table 10. Means for each later period are larger. Differences within birth periods are larger than between periods.

When additive relationships were included in the model along with grouping, group averages (GA) were used for comparison instead of group solutions (Table 7). This is because sires within groups no longer sum to zero due to variance and covariances of related bulls (i.e., $\sum_{j=1}^{i}(\hat{g}_i + \hat{s}_{ij})/n$ no longer equals $\hat{g}_i$). The regression of group average on group number was 19. Differences in group averages for RELB and group solutions for BRTH are similar.

Three group definitions were tried for fat production (Table 9). SMG, BRTH, and RELB had regressions of 1.82, 0.50, and 0.45 kg of group solution on group number. The effect of grouping was similar to that for milk production.

Another way of examining the effect of grouping on sire estimates is using a between and within group analysis. Table 11 gives the proportion of variation between and within groups for milk and fat. F tests for groups are also presented. Grouping is highly significant ($P < .01$) for all definitions except BRTH and RELB which are significant ($P < .05$). Grouping usually accounted for about 25 percent of the variation where pedigree indexes were used and for STYR. Highest between group variation is 34 percent for SCIB and lowest is for BRTH for both milk and fat.

Keown (1974), Shaeffer _et al_. (1975), and Everett _et al_. (1975) have all shown distinct differences in group solutions. In this study, group year differences were less dramatic than the other types of groupings tried. This may be due to the way in which bulls were selected. Using data of daughters of bulls with very complete pedigrees was probably too restrictive; however, it seemed necessary to make fair comparisons of the use of pedigree indexes for grouping. The results of grouping in this study indicate that using pedigree indexes to define homogenous subpopulations is very effective. The use of pedigree indexes for grouping could

Table 10. Group means by time period for SMGB and SCIB[a]

Period	SMGB	SCIB
1	-89	-94
2	- 1	-48
3	4	-29

[a] Group means are in kg.

Table 11. Proportion of variation due to grouping

	Model definitions	df	Between groups	Within groups	F
Milk	SMG	9	25	75	6.1**
	SCI	9	32	68	6.8**
	STYR	11	25	75	6.0**
	BRTH	9	5	95	2.1*
	SMGB	12	25	75	6.1**
	SCIB	13	34	66	8.5**
	RELB	9	5	95	2.1*
Fat	SMG	9	24	76	7.3**
	BRTH	9	8	92	2.7**
	RELB	9	9	91	2.5**

*Significant at .05.

**Significant at .01.

eliminate the need for more crude grouping criteria such as stud or region. Also, differences in selection criteria from stud to stud would influence groups less. The net effect would be the need for fewer groups which in turn would be larger in terms of number of bulls and daughters. Groups would be better estimated and thus less likely to change when additional daughters are evaluated.

It should again be emphasized that in practice assigning bulls to groups must be done on a priori knowledge. There will always be large variation within groups, when the best information possible is known. The smallest percent of within group variation was 66 percent in this study. A best grouping strategy would be one which resulted in maximum between group variation with the restriction that information used in grouping is available when first daughters are evaluated and differences between groups represent genetic differences. For this reason, a within group sire deviation that is large, either positive or negative, does not mean that a sire was misgrouped. He is simply different than other bulls, whose grouping criteria was the same, due to sampling of his daughters, inaccuracies of his pedigrees, or gene segregation from his sire and dam.

Another factor which affects the magnitude of $\hat{s}_{ij}$ is the accuracy with which that bull is evaluated. Bulls whose evaluations are based on few daughters are regressed closer to their group solution. The group solution, largely determined by other bulls, has a great deal of influence on the sire estimates. Powell and Freeman (1974) derived the approximate expression $(1-b)(G_w - G_r)$ where G_w and G_r represent the means for "wrong" and "right" groups and b is the diagonal of the coefficients matrix. Bulls with large numbers of daughters are little affected by whatever group to which they are assigned because 1-b approaches zero. For example, if b equals .95, $G_w - G_r$ would have to be 1000 kg for an estimate to change by as much as 50 kg. This does not mean that grouping is not important and essential for these bulls. Two factors are involved in the concept of grouping. First, the assignment of bulls with relatively few daughters to groups is important to improve accuracy. We try to estimate the genetic merit of a bull based on his pedigree. An estimate with large error means that a bull's prediction will change more than if the original pedigree estimate had been a good one. But grouping, whether right or wrong, is still essential if genetic trend exists in the population. The second factor is that all daughters of a bull, no matter when they enter production, will be regressed to the same mean. To accomplish this, identical restrictions must be used from one evaluation to another when new daughters and new groups are added. Older groups must be maintained at least until the accuracy of prediction of all bulls in the group is close to one.

Thus, nationwide use of the mixed model is difficult because vast numbers of bulls must be re-evaluated each time to maintain group solutions and comparisons. Solving these latter problems requires sophisticated computer technology, statistical methodology, or a combination of both.

<u>Comparison of sire estimates by different mixed model definitions</u>

Sire estimates for milk and fat are presented in Tables 12 and 13. Where different group definitions were used, the prediction of sire's transmitting ability is $(\hat{g}_i + \hat{s}_{ij}) - (\hat{g}_{i'} + \hat{s}_{i'j'})$ or

Table 12. Sire estimates for milk

Sire Code	PD74	NGRP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
1	99	-263	-203	-302	-251	-353	-353	-292	-305	-374	-272
2	-189	-142	-35	-104	-109	-100	-192	-112	-105	-173	-127
3	351	421	453	417	437	436	378	408	437	359	408
4	-520	-490	-484	-464	-481	-445	-523	-481	-484	-510	-476
5	212	92	151	131	66	25	-6	134	45	29	134
6	-147	-437	-398	-482	-523	-514	-515	-516	-486	-528	-446
7	-78	-111	-119	-78	-88	-64	-134	-88	-84	-120	-96
8	95	-15	46	-64	7	-43	-149	-55	45	-149	-8
9	-147	6	71	15	5	-5	-33	1	-19	-59	-10
10	34	-226	-231	-239	-235	-201	-260	-241	-242	-244	-213
11	-87	-146	-102	-231	-255	-269	-299	-311	-272	-301	-141
12	-571	-237	-244	-263	-263	-257	-322	-265	-286	-326	-229
13	-143	-145	-131	-180	-185	-184	-179	-170	-168	-193	-118
14	-151	-85	-41	-97	-74	-126	-119	-97	-71	-98	-58
15	-146	-210	-122	-234	-205	-268	-255	-208	-191	-264	-214
16	50	-269	-263	-285	-377	-272	-358	-321	-330	-313	-213
17	-123	-178	-111	-149	-154	-162	-284	-146	-240	-290	-181
18	172	163	93	169	126	192	151	144	144	171	182
19	-216	-320	-297	-387	-371	-330	-346	-371	-380	-350	-323
20	-175	-113	-51	-154	-121	-202	-119	-191	-165	-125	-116
21	11	-195	-148	-210	-219	-250	-204	-223	-220	-207	-195
22	-52	0	49	-25	-32	-7	-16	-23	-27	-33	-19
23	546	341	224	364	363	348	330	361	375	326	334
24	-470	-158	-142	-191	-187	-164	-184	-183	-195	-169	-149
25	94	67	-11	97	85	117	58	82	86	69	78
26	544	331	362	323	321	343	320	319	315	320	326
27	-218	-55	-75	-63	-66	-38	-78	-70	-83	-84	-58
28	-439	-184	-152	-253	-230	-259	-203	-232	-255	-208	-183
29	256	-92	-28	-113	-114	-104	-114	-129	-128	-126	-119
30	-113	95	125	57	47	90	84	65	66	77	86
31	-205	23	-34	96	71	41	-2	50	72	-12	18
32	-157	-95	-64	-67	-82	-48	-113	-84	-83	-94	-75
33	-88	-89	-40	-103	-119	-77	-96	-103	-124	-89	-84
34	-248	-304	-350	-342	-351	-287	-331	-390	-372	-333	-312
35	177	-38	4	-61	-28	-56	-56	-62	-71	-70	-51
36	-37	-128	-103	-139	-144	-130	-141	-141	-152	-147	-143
37	-120	-268	-227	-294	-316	-287	-287	-295	-338	-301	-281
38	-202	-74	-127	-87	-92	-48	-84	-87	-84	-79	-75
39	128	86	204	41	38	-26	72	-7	5	65	83
40	362	421	475	438	476	439	404	431	446	405	417
41	-242	-265	-135	-303	-372	-348	-271	-341	-320	-262	-266
42	-269	-343	-463	-353	-361	-321	-348	-368	-365	-351	-348

Table 12. (Continued)

Sire Code	PD74	NGEP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
43	204	224	288	217	230	199	215	217	233	209	222
44	188	137	73	158	143	171	133	152	136	146	146
45	-295	-361	-416	-363	-369	-341	-372	-376	-365	-369	-359
46	-20	-131	-247	-102	-118	-82	-140	-125	-119	-126	-118
47	-172	-236	-176	-211	-237	-342	-250	-253	-298	-252	-225
48	252	372	287	380	360	356	365	357	351	350	357
49	54	14	9	17	29	41	7	12	14	14	18
50	209	159	174	213	237	184	152	204	204	139	149
51	-7	52	61	97	116	81	44	71	86	129	111
52	-60	-26	-57	5	-39	-67	-34	10	-48	-37	-28
53	-64	198	156	239	151	162	196	238	184	193	200
54	150	-86	-60	-97	-74	-82	-96	-97	-73	-112	-107
55	177	48	-57	54	66	80	44	41	69	52	51
56	378	466	385	538	565	455	457	500	512	386	407
57	-250	-208	-104	-298	-335	-307	-232	-283	-287	-276	-229
58	204	152	163	141	151	166	147	144	148	135	130
59	160	338	281	376	366	389	329	364	368	344	355
60	-155	-67	-31	-111	-182	-93	-77	-80	-105	-90	-73
61	176	165	158	214	221	142	167	210	203	162	165
62	-194	-53	0	-52	-47	-68	-57	-52	-40	-53	-47
63	282	214	75	250	241	264	215	241	240	237	235
64	-101	-111	-124	-253	-324	-135	-118	-254	-384	-156	-140
65	-219	-306	-368	-296	-301	-268	-308	-310	-297	-297	-302
66	-44	-111	-144	-113	-98	-91	-114	-111	-106	-126	-128
67	-222	-70	-132	-79	-37	5	-63	-70	-26	-87	-105
68	111	-34	-119	4	19	43	-36	0	12	-22	-23
69	342	198	174	240	232	177	192	234	226	186	197
70	-305	-279	-333	-273	-275	-289	-275	-269	-267	-272	-276
71	-179	-257	-208	-279	-275	-292	-251	-234	-242	-237	-251
72	-6	58	97	44	41	84	56	65	60	46	42
73	-189	-203	-195	-130	-161	-170	-211	-172	-161	-229	-202
74	-24	-133	-109	-151	-151	-155	-138	-163	-131	-133	-138
75	-147	-194	-219	-149	-195	-223	-190	-168	-175	-190	-186
76	-29	24	48	48	36	-14	21	50	-4	88	87
77	-72	-152	-67	-130	-111	-190	-149	-130	-129	-152	-156
78	101	72	155	60	56	37	76	26	86	85	47
79	98	-60	-50	-21	-39	-34	-57	-49	-41	-61	-71
80	-108	-278	-215	-307	-264	-317	-276	-292	-293	-266	-273
81	336	97	-79	131	125	148	100	125	124	113	102
82	651	704	720	731	734	692	708	724	730	700	696
83	267	-323	-326	-369	-386	-353	-311	-324	-338	-299	-329
84	141	86	104	71	75	69	87	69	94	54	56

Table 12. (Continued)

Sire Code	PD74	NGFP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
85	100	122	159	158	181	135	113	152	151	73	90
86	159	71	-19	35	54	146	78	32	-10	100	77
87	252	357	251	374	384	406	361	371	380	364	352
88	-37	-8	-35	64	38	-38	1	60	37	-8	-24
89	83	302	296	236	350	269	309	197	279	336	240
90	448	303	188	315	330	352	305	323	316	300	292
91	57	8	73	-32	43	-29	16	-10	-23	32	3
92	-2	-16	-9	-24	-13	0	-22	-14	-4	-29	-30
93	-250	-319	-275	-335	-330	-352	-320	-331	-315	-324	-325
94	-10	20	-67	49	58	80	25	44	51	40	25
95	-34	-21	0	-25	5	-40	-22	-18	1	-27	-23
96	-82	141	211	71	39	103	149	72	19	142	114
97	137	106	5	107	139	177	112	112	103	148	128
98	-22	-277	-416	-267	-299	-200	-269	-314	-277	-226	-278
99	199	-168	-311	-166	-110	-102	-159	-161	-117	-148	-166
100	309	218	105	294	317	251	227	284	284	248	225
101	-142	-47	-41	-80	-41	-21	-54	-67	-48	-17	-47
102	-392	-369	-369	-427	-465	-372	-370	-418	-500	-351	-366
103	-297	-209	-142	-250	-237	-250	-208	-248	-220	-215	-215
104	99	90	56	182	146	58	109	176	148	138	109
105	242	392	364	425	410	422	394	402	407	362	355
106	-284	-212	-275	-155	-174	-240	-203	-160	-178	-214	-221
107	687	647	579	672	670	689	648	665	667	658	651
108	-302	-106	3	-140	-159	-167	-111	-213	-111	-111	-110
109	272	130	133	99	157	163	139	123	147	124	103
110	485	871	925	802	898	820	885	854	882	760	685
111	475	313	147	371	357	380	322	361	351	342	329
112	-927	-605	-543	-674	-711	-644	-588	-669	-743	-584	-607
113	-365	16	71	-78	-45	5	33	-58	-42	-47	-42
114	4	-46	-116	-9	-5	-65	-38	-13	-11	-37	-45
115	-88	75	125	58	119	63	80	-25	45	107	70
116	80	-77	-61	5	0	-149	-60	13	13	-53	-67
117	260	-19	-14	44	28	17	-7	3	24	-12	-36
118	278	-39	-50	62	-68	8	-17	0	-12	-57	-81
119	-258	11	74	1	30	-46	23	-9	69	17	8
120	357	242	182	326	353	351	260	314	331	316	296
121	421	239	123	306	304	327	250	295	308	258	242
122	87	49	62	127	127	48	69	135	144	29	18
123	-172	-234	-179	-303	-324	-279	-227	-313	-358	-259	-263
124	-202	-102	-117	-147	-69	-87	-74	-153	-108	-147	-164
125	-6	-142	-78	-130	-128	-183	-144	-134	-117	-144	-139
126	-203	-43	81	-136	-184	125	-21	-111	-252	-68	-110

Table 12. (Continued)

Sire Code	PD74	NGRP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
127	-308	-23	1	71	54	-96	0	56	81	186	173
128	191	105	114	84	126	230	114	82	105	80	22
129	228	361	386	406	335	537	381	472	473	406	387
130	-186	-9	80	134	59	14	30	149	-15	34	-17
131	473	571	670	631	598	687	588	632	563	612	601
132	-164	-83	-95	-153	-182	-151	-67	-132	-232	-63	-74
133	293	289	189	331	322	352	285	321	326	306	311
134	294	-157	-140	17	75	-143	-119	-5	36	-130	-162
135	158	37	26	36	84	222	62	4	155	48	24
136	-559	-462	-390	-515	-525	-523	-455	-504	-549	-470	-463
137	-243	-138	-137	-195	-230	-213	-117	-179	-167	-106	-122
138	-185	-43	12	-17	-7	-107	-31	24	-38	-48	-53
139	-459	-412	-336	-471	-518	-289	-393	-442	-458	-425	-454
140	-322	58	98	114	272	64	93	226	57	79	41
141	-124	-51	20	-89	-42	-115	-66	-118	-23	-69	-48
142	236	103	-27	143	135	159	99	133	139	117	123
143	-190	-87	-94	-174	-136	-103	-47	-147	-118	-42	-72
144	-49	391	429	486	490	579	414	498	511	376	354
145	-75	201	239	94	130	199	223	118	136	150	134
146	-113	55	126	-23	-7	-19	70	11	6	63	50
147	-68	-58	-95	-205	-232	-71	-21	-135	-289	-29	-76
148	229	52	-28	118	94	151	67	123	61	59	49
149	163	15	89	17	36	-38	13	48	10	-17	-9
150	-8	-56	-63	-192	-163	-33	-20	-159	-140	-27	-60
151	223	114	-28	155	152	173	113	147	152	132	133
152	19	-248	-212	-173	-171	-253	-184	-93	-242	-133	-206
153	192	-10	34	149	77	-5	31	160	-10	111	78
154	-170	-1	19	-44	-92	1	57	-61	-76	109	33
155	-201	-179	-198	-173	-214	-240	-145	-191	-213	-134	-178
156	-502	-371	-301	-414	-433	-296	-355	-405	-399	-356	-371
157	443	563	572	632	653	587	593	640	640	645	606
158	-68	222	228	155	175	248	261	319	178	326	273
159	288	185	198	272	265	326	224	262	289	215	170
160	-6	44	99	24	49	23	62	5	70	71	46
161	261	171	37	207	205	232	170	205	209	186	187
162	142	165	176	151	189	127	188	159	227	167	146
163	-60	-132	-90	-181	-77	-247	-57	-195	-128	-19	-111
164	703	560	450	606	598	626	562	598	603	574	571
165	-416	-278	-167	-364	-381	-361	-219	-336	-359	-205	-258
166	-92	-188	-146	-228	-229	-180	-142	-239	-72	-150	-203
167	-313	-39	28	63	10	-91	14	93	-33	10	-39
168	295	371	247	393	381	434	372	389	392	374	373

Table 12. (Continued)

Sire Code	PD74	NGFP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
169	205	199	51	237	232	264	196	237	229	212	217
170	434	551	597	541	559	648	552	522	592	544	549
171	-152	57	72	36	9	-45	74	-10	234	-37	-10
172	-98	189	235	81	188	101	213	123	261	210	143
173	-322	-213	-191	-208	-204	-247	-212	-190	-208	-179	-170
174	-176	-216	-94	-283	-268	-288	-212	-268	-258	-261	-237
175	69	-52	-54	-105	-94	-115	-41	-74	-79	-81	-75
176	-60	-250	-207	-277	-276	-316	-246	-281	-185	-263	-257
177	-166	54	71	0	120	-66	74	-15	254	235	250
178	98	-14	13	-115	-74	304	2	-83	177	12	20
179	-245	-96	-11	-177	-208	-173	-88	-139	-255	-112	-104
180	39	1	-10	-55	23	-57	12	-21	80	-1	0
181	-5	-44	-83	43	35	-94	-33	33	54	1	13
182	339	161	32	202	194	218	159	194	198	178	183
183	-48	-152	-133	-234	-205	-231	-140	-188	-201	-184	-176
184	-689	-615	-645	-689	-735	-630	-603	-652	-791	-659	-658
185	-108	14	-4	-105	-159	-73	27	-76	-240	-102	-66
186	-192	31	85	-29	-69	-33	39	-15	-17	4	8
187	254	242	255	416	341	133	258	428	245	272	264
188	-387	-277	-247	-303	-238	-337	-268	-305	-275	-249	-247
189	-178	35	23	18	-77	-65	52	-31	-52	27	33
190	-248	-95	-136	-148	-145	-115	-83	-138	-140	-92	-93
191	-453	-217	-155	-308	-282	-293	-194	-282	-275	-209	-217
192	247	270	279	357	302	424	277	364	363	276	280
193	382	386	436	370	373	342	389	366	439	321	327
194	-60	27	10	37	12	-9	36	21	16	81	84
195	383	283	147	330	323	348	282	322	327	303	306
196	83	88	135	200	198	-4	114	191	233	183	181
197	356	274	181	327	330	345	281	331	342	265	270
198	51	-56	-11	-29	-11	-123	-49	19	-45	-60	-58
199	-3	-137	-199	-67	-93	-185	-127	-62	-123	-168	-153
200	108	-30	-150	45	59	72	-26	36	51	15	23
201	101	-29	-197	42	34	65	-26	31	44	40	43

Table 13. Sire estimates for fat

Sire Code	PD74	NGRE	NGIO	SMG	BRTH	RELB	REL
1	9.2	-5.5	-4.1	-6.6	-7.7	-8.5	-5.9
2	-3.1	-5.4	-1.6	-4.5	-6.6	-6.6	-5.5
3	22.4	23.9	25.4	23.7	22.9	22.9	23.8
4	-6.7	-7.3	-4.8	-6.6	-8.0	-8.1	-7.5
5	2.4	1.6	3.6	2.2	-0.9	0.8	3.3
6	14.9	16.0	14.2	18.5	17.9	18.1	16.2
7	-7.2	-8.3	-7.5	-7.4	-8.7	-8.7	-8.3
8	-4.0	-3.1	-1.5	-4.9	-6.5	-6.6	-3.1
9	7.8	7.4	10.4	7.8	6.5	6.1	7.1
10	0.5	11.1	10.3	11.3	11.9	11.5	10.8
11	-5.4	-4.8	-3.2	-9.3	-8.7	-8.1	-4.1
12	12.2	-8.4	-9.3	-9.2	10.5	10.2	-7.8
13	13.6	12.2	12.5	13.5	13.1	13.6	11.9
14	-3.6	-2.0	-1.6	-2.5	-2.8	-2.9	-2.2
15	6.0	-0.4	1.5	-1.3	-1.7	-1.6	-0.3
16	1.9	10.6	-8.4	10.8	12.9	11.9	-9.5
17	1.9	-0.8	0.7	-0.5	-3.5	-3.4	-0.9
18	1.4	0.6	-1.8	1.0	0.5	1.4	1.4
19	8.7	-2.3	-2.0	-4.6	-2.7	-2.9	-2.5
20	11.0	5.9	7.5	4.0	6.0	6.3	6.3
21	7.4	-0.6	0.3	-1.0	-0.7	-0.8	-0.5
22	3.3	1.7	3.8	1.2	1.5	1.0	1.1
23	21.0	13.0	9.2	13.5	13.0	13.1	13.0
24	20.8	-3.2	-2.1	-4.2	-3.6	-3.5	-3.1
25	0.1	-1.5	-1.6	-0.7	-1.5	-1.5	-1.6
26	7.8	0.7	1.2	0.4	0.4	0.6	0.8
27	-2.6	-0.8	-1.7	-1.1	-1.0	-1.7	-1.4
28	-5.8	-0.4	0.2	-2.7	-0.5	-0.6	-0.4
29	1.0	10.7	-9.3	11.7	11.0	11.5	11.6
30	-4.5	0.8	2.7	-0.4	0.8	0.4	0.4
31	-2.6	-0.5	-4.4	2.4	-0.7	-0.9	-0.7
32	-7.2	-3.2	-0.8	-2.4	-3.4	-3.1	-2.9
33	1.9	0.2	1.6	-0.2	0.0	-0.1	-0.1
34	-0.4	-8.7	11.8	11.1	-9.0	-9.2	-9.1
35	8.7	-2.5	-1.6	-3.2	-2.6	-2.9	-2.8
36	-7.6	10.5	10.1	10.8	10.6	11.0	11.1
37	1.0	-6.7	-4.4	-7.6	-6.8	-7.0	-7.0
38	-9.9	-3.8	-5.2	-3.9	-4.2	-2.0	-4.0
39	6.4	0.8	2.5	-1.5	-0.0	0.3	1.2
40	16.0	15.5	17.3	15.8	15.3	15.2	15.2
41	-9.9	12.1	-8.4	14.4	12.8	14.0	13.6
42	-8.1	-9.0	11.7	-9.5	-9.4	-9.8	-9.4

Table 13. (Continued)

Sire Code	PD74	NGRP	NGIO	SMG	BRTH	RELB	REL
43	10.5	11.1	13.8	10.8	10.9	10.8	11.1
44	-6.3	-5.2	-6.6	-4.6	-5.5	-5.2	-5.0
45	12.2	13.9	16.4	14.2	14.2	14.3	14.0
46	-2.2	-6.0	-6.5	-5.2	-6.2	-6.2	-6.0
47	11.3	13.3	13.2	12.2	14.1	12.3	11.1
48	13.7	22.7	20.4	23.1	22.3	21.3	21.9
49	-1.7	-2.1	-2.0	-2.0	-2.4	-2.3	-2.0
50	-6.3	-1.1	-0.5	0.1	-1.6	-1.9	-1.5
51	8.3	10.1	10.9	11.8	9.5	12.8	12.9
52	-1.7	-2.9	-4.5	-2.3	-3.6	-3.7	-3.0
53	-7.6	4.0	1.3	4.8	3.5	3.0	3.1
54	-3.6	-7.7	-6.6	-8.0	-8.0	-8.4	-8.2
55	6.9	-0.6	-3.2	-0.5	-0.8	-0.7	-0.5
56	17.8	21.0	17.4	23.9	20.2	18.6	19.8
57	-5.4	-5.7	-3.4	-7.7	-7.0	-6.3	-3.8
58	11.9	12.3	13.6	12.2	12.3	11.5	11.3
59	0.5	7.2	7.6	8.3	7.1	7.2	7.3
60	-6.3	-3.6	-1.9	-5.3	-5.0	-5.4	-4.5
61	6.9	5.5	4.0	7.5	5.3	5.4	5.6
62	12.6	-6.9	-4.5	-7.0	-7.2	-7.0	-6.7
63	9.6	4.8	0.6	6.1	4.7	5.2	5.3
64	-2.2	-3.9	-3.8	-8.7	-5.3	-5.9	-5.1
65	-9.0	11.1	12.4	10.8	11.3	11.4	11.4
66	2.4	-0.7	-1.7	-0.7	-0.8	-1.6	-1.7
67	-9.9	-3.6	-5.1	-4.0	-3.5	-4.9	-5.0
68	4.6	-0.6	-3.7	0.2	-1.1	-0.5	-0.2
69	13.3	7.3	6.0	8.3	7.0	6.7	7.0
70	-9.9	-9.1	11.7	-9.0	-9.0	-8.8	-9.0
71	-1.3	-3.7	-2.6	-4.4	-3.6	-2.6	-2.7
72	1.9	6.4	7.1	6.1	6.2	6.2	6.3
73	15.8	10.4	-9.0	-7.5	11.1	-9.3	-8.4
74	11.7	14.6	13.0	15.7	15.0	15.1	15.0
75	-3.6	1.7	-0.6	3.6	1.6	2.1	2.3
76	3.3	1.7	2.6	1.9	1.1	3.3	3.5
77	6.4	2.5	4.7	3.5	2.5	2.8	2.8
78	0.1	-0.7	2.2	-1.0	-0.7	-1.7	-2.3
79	0.1	-2.0	-2.1	-0.3	-2.0	-1.4	-1.5
80	12.6	13.8	12.4	14.8	13.9	12.1	12.0
81	11.0	1.9	-3.2	3.2	2.0	2.2	2.0
82	31.0	29.2	28.9	30.2	29.3	29.1	29.0
83	3.3	-9.9	10.5	12.7	-9.6	-9.7	10.4
84	-4.9	-8.3	-8.9	-8.8	-8.6	-9.3	-9.3

Table 13. (Continued)

Sire Code	PD74	NGRP	NGIO	SMG	BRTH	RELB	REL
85	13.7	12.0	13.3	13.6	11.5	10.8	11.3
86	2.8	-2.3	-4.5	-2.8	-2.2	-2.0	-2.2
87	10.5	12.1	9.0	12.6	12.2	12.0	11.7
88	2.4	1.4	0.3	4.3	1.6	2.2	1.9
89	-1.3	1.9	0.1	-1.9	2.1	2.8	0.7
90	15.1	11.3	7.9	11.7	11.3	11.3	11.2
91	1.0	-1.2	1.3	-2.8	-1.2	-1.0	-1.3
92	15.4	-9.3	10.0	-9.5	-9.4	-9.7	-9.6
93	-9.5	16.5	16.2	17.1	16.6	16.7	16.6
94	15.5	14.3	12.2	15.1	14.4	14.7	14.4
95	10.1	6.1	6.7	6.0	5.8	5.8	6.0
96	-1.3	7.9	10.2	5.6	8.0	7.4	7.1
97	5.5	2.9	-0.4	2.9	3.0	3.4	3.2
98	-9.0	14.6	18.6	14.0	14.4	14.5	15.6
99	5.1	10.6	14.8	10.5	10.0	-9.8	10.6
100	5.1	6.8	2.6	9.8	7.1	7.4	7.0
101	12.2	-6.8	-5.8	-7.9	-7.0	-7.2	-7.8
102	-8.6	-9.0	-9.2	10.0	-8.8	-8.5	-8.8
103	-6.7	-7.6	-5.8	-9.1	-7.4	-7.5	-7.7
104	6.0	6.7	5.6	10.5	7.7	8.1	6.7
105	16.4	20.2	18.5	21.6	20.1	19.3	19.3
106	-8.1	-4.4	-8.1	-2.1	-3.8	-4.5	-5.1
107	19.6	18.8	17.1	19.7	18.9	19.1	18.8
108	-6.7	-3.9	-0.8	-4.9	-3.4	-3.1	-3.7
109	5.1	3.7	4.2	2.0	4.5	4.7	3.6
110	16.4	31.8	33.2	28.0	33.1	25.6	22.7
111	17.4	14.0	9.3	15.6	14.6	15.1	14.6
112	31.3	21.7	20.0	23.0	20.6	20.4	21.7
113	-7.2	8.4	9.9	6.4	9.1	7.9	8.0
114	0.1	3.2	-0.2	4.6	3.6	3.8	3.3
115	-1.3	-4.8	-2.6	-4.9	-4.6	-4.5	-5.2
116	0.5	-2.0	-2.4	1.4	-1.2	-1.3	-1.9
117	2.8	1.0	1.4	3.7	2.0	1.9	0.6
118	1.0	-1.3	-1.9	3.0	0.2	-2.5	-3.9
119	1.0	7.8	9.3	7.6	8.3	8.2	7.8
120	11.0	6.7	4.6	10.1	7.4	8.8	8.1
121	18.3	14.2	10.4	16.0	14.7	14.5	14.0
122	-1.7	-2.9	-3.9	0.2	-2.1	-3.8	-4.3
123	1.0	-3.7	-3.6	-5.2	-2.9	-2.3	-3.0
124	-9.5	-3.9	-3.9	-5.1	-2.7	-7.3	-8.1
125	3.3	-1.8	0.0	-1.7	-1.8	-1.7	-1.5
126	14.0	-8.8	-5.7	10.7	-8.3	-8.7	-9.8

Table 13. (Continued)

Sire Code	PD74	NGFP	NGIO	SMG	BRTH	RELB	REL
127	-9.5	3.2	3.6	5.4	4.0	11.0	10.0
128	-3.6	2.3	3.0	1.8	2.9	0.6	-1.2
129	-6.7	6.7	9.1	7.5	7.6	8.2	7.3
130	10.4	-2.1	0.5	3.9	-0.4	-1.5	-3.5
131	16.4	14.9	17.5	17.4	15.5	16.3	15.8
132	-4.5	-4.2	-4.3	-5.5	-3.5	-3.7	-4.2
133	2.4	1.9	1.2	3.0	2.1	2.2	2.0
134	5.5	-5.0	-4.4	-1.2	-3.4	-3.6	-5.1
135	6.4	2.9	2.5	3.3	4.0	3.5	2.4
136	-9.5	-7.7	-6.0	-9.0	-7.5	-7.1	-6.8
137	10.4	-7.2	-9.2	-8.1	-6.5	-5.8	-6.6
138	-8.6	0.1	1.3	0.6	0.6	1.1	0.6
139	-9.9	10.6	-8.2	12.6	-9.7	11.1	12.5
140	13.1	1.8	2.3	2.5	3.3	3.3	2.1
141	14.5	-9.6	-7.4	11.6	10.4	10.3	-9.3
142	1.0	-2.5	-4.2	-1.5	-2.5	-2.5	-2.5
143	-5.4	-3.1	-3.5	-4.7	-2.7	-1.8	-1.7
144	-3.6	10.8	11.3	14.7	11.8	10.4	9.3
145	-2.6	8.2	10.0	6.0	9.2	6.2	5.2
146	-2.2	2.9	4.4	0.2	3.6	3.5	2.9
147	2.8	7.3	8.3	1.8	7.8	7.7	7.2
148	10.5	3.5	0.8	6.1	4.1	4.6	4.0
149	10.5	2.3	4.3	2.0	2.5	2.2	2.1
150	1.4	-4.0	-4.1	-6.6	-2.6	-2.7	-4.1
151	14.6	11.4	10.6	12.5	11.8	12.0	11.7
152	1.4	-4.2	-2.9	-2.4	0.2	0.9	-3.0
153	3.7	-0.9	0.2	5.8	1.0	2.6	0.9
154	-2.6	2.0	1.4	0.5	6.1	8.0	4.0
155	-2.6	-5.6	-6.7	-5.1	-3.4	-3.9	-6.5
156	12.8	5.0	7.6	4.3	6.4	6.6	5.4
157	13.3	19.1	19.8	21.9	21.2	21.7	19.7
158	1.9	12.8	13.2	10.5	15.6	17.4	14.4
159	-0.4	-0.1	0.7	1.8	2.5	2.6	0.2
160	0.1	6.4	6.8	5.8	7.7	7.8	6.6
161	2.8	1.9	0.6	2.9	2.3	2.3	2.0
162	19.2	10.5	10.1	9.4	11.9	11.1	9.9
163	0.1	-7.2	-6.3	-9.0	-2.0	-1.5	-6.3
164	6.9	4.0	2.6	5.2	4.5	4.4	3.9
165	10.4	11.6	-9.0	15.7	-7.7	-6.2	-9.4
166	-0.4	3.5	5.2	2.1	7.0	6.9	3.7
167	12.2	-0.9	0.5	3.0	2.8	3.8	0.9
168	14.6	16.3	15.2	17.0	16.8	16.6	16.2

Table 13. (Continued)

Sire Code	PD74	NGPP	NGIO	SMG	BRTH	RELB	REL
169	-2.2	-2.7	-4.8	-1.7	-2.8	-2.7	-2.5
170	6.4	12.1	12.7	12.0	10.9	11.2	12.9
171	-5.4	1.5	2.2	1.4	-1.9	-3.8	1.6
172	-5.8	-2.1	-3.5	-7.4	-4.6	-4.5	-2.4
173	12.6	11.6	11.4	11.7	12.2	10.4	-9.1
174	-2.6	-5.7	-2.8	-8.0	-7.2	-7.4	-4.6
175	-7.6	-7.6	-9.2	-9.4	-9.2	10.4	-8.4
176	-1.3	-9.3	-8.7	10.3	10.8	11.3	-9.4
177	-4.0	1.4	1.7	-0.6	2.6	9.9	8.4
178	4.6	-0.3	0.9	-6.0	-4.2	-4.5	0.3
179	-5.4	-0.6	1.0	-3.4	-2.5	-4.6	-2.2
180	-5.8	-5.3	-6.0	-7.2	-6.8	-7.4	-5.5
181	-9.9	-5.6	-7.8	-3.5	-5.0	-5.0	-5.6
182	2.8	-3.4	-5.4	-2.4	-3.5	-3.6	-3.3
183	-3.1	-9.0	-9.0	11.7	10.9	12.3	-9.9
184	25.8	16.0	16.4	18.3	17.6	19.2	17.0
185	-0.8	0.5	-0.3	-1.7	1.3	1.5	1.5
186	-6.3	-2.3	-1.7	-4.5	-1.9	-2.5	-3.5
187	7.8	7.8	8.9	15.0	4.0	0.9	5.5
188	15.8	-6.2	-5.1	-7.0	-5.7	-5.3	-6.2
189	-6.3	1.4	1.2	1.5	-2.2	-3.1	1.4
190	-9.9	-6.8	-7.7	-8.4	-6.2	-5.9	-6.6
191	-7.2	-4.5	-3.1	-6.6	-3.2	-2.8	-4.1
192	7.8	7.7	7.7	11.3	5.7	4.3	6.8
193	13.7	13.7	15.3	13.1	13.9	12.1	11.3
194	6.0	9.1	7.7	9.6	9.5	11.1	10.5
195	13.3	10.5	9.2	11.7	10.7	10.6	10.4
196	2.8	3.2	4.7	5.8	0.4	4.1	8.4
197	4.2	4.9	1.7	7.0	5.2	5.6	5.2
198	0.1	-4.1	-3.4	-3.7	-3.6	-4.1	-4.7
199	-4.0	-3.7	-6.9	-0.9	-3.4	-4.5	-4.6
200	9.6	4.9	2.8	7.6	5.3	6.1	5.5
201	1.4	-0.9	-4.0	0.9	-0.5	1.1	0.7

$(\hat{g}_i + \hat{s}_{ij}) - (\hat{g}_i + \hat{s}_{ij'})$. Where no grouping was used, the estimate of sire's transmitting ability was $\hat{s}_i - \hat{s}_{i'}$. All sire estimates were forced to sum to zero after solution as shown in the Appendix. To visually check how sire estimates compare, the difference between any two sires of interest should be observed and not their actual magnitude. Table 14 lists variances of sire estimates for different model definitions for milk and fat. For both milk and fat estimates, grouping has increased the variance of sire estimates. For milk, the least variance was when no grouping was used and off-diagonals were ignored (NGIO). Largest variance was for sire estimates by SCIB which is 37 percent more than NGIO. The least variance for fat estimates is for REL and the largest for PD74. Variances for all models where grouping was used are comparable except for BRTH. The variances of PD74 for either milk or fat are large. This is expected since herdmate deviations are regressed less due to large numbers of daughters.

The actual ranks of all bulls are presented in Tables 15 and 16 for milk and fat, respectively. Rankings for mixed model definitions are fairly close while PD74 tends to be most different. Among mixed model definitions, ranks by NGIO tend to be most different. Ranks by other mixed model definitions are most homogenous.

Rank and product-moment correlations were computed to examine the relationship between sire estimates by the different models. Tables 17 and 18 list these correlations for all levels for milk and fat, respectively. Overall correlations are expected to be high because most bulls were evaluated with a large number of daughters. Rank correlations among

Table 14. Variances for different model definitions for milk and fat

	Model definition	Variance
Milk	PD74	68,791
	NGRP	56,060
	NGI0	52,620
	SMG	67,434
	SCI	70,740
	STYR	69,111
	BRTH	58,646
	SMGB	67,382
	SCIB	71,824
	RELB	59,546
	REL	55,687
Fat	PD74	88.3
	NGRP	76.2
	NGI0	75.2
	SMG	88.8
	BRTH	80.3
	RELB	76.6
	REL	74.8

Table 15. Ranks of sire estimates for milk.

Sire Code	PD74	NGFP	NGIC	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
1	72	180	171	181	170	193	191	178	181	195	182
2	156	148	110	128	131	129	159	133	128	156	143
3	19	10	8	12	11	12	14	13	13	15	9
4	197	199	199	196	196	197	199	197	196	198	199
5	44	58	43	55	71	79	97	55	80	85	50
6	139	197	195	198	198	198	198	199	197	199	196
7	120	140	143	118	125	112	144	126	126	137	131
8	75	98	77	115	97	105	152	112	81	150	94
9	140	90	70	94	98	90	110	93	104	116	97
10	87	171	178	167	166	156	175	167	163	170	167
11	122	151	136	164	171	172	183	182	171	185	148
12	199	174	179	171	172	168	187	171	175	188	173
13	136	150	148	154	153	152	155	152	149	160	139
14	141	128	114	125	119	138	141	129	118	131	116
15	137	166	145	165	157	170	174	161	153	177	168
16	85	181	182	177	191	173	193	185	184	186	166
17	133	157	140	144	143	145	181	144	162	181	159
18	56	44	58	44	58	42	46	52	55	45	41
19	166	190	185	193	189	187	189	191	192	190	189
20	150	141	117	147	137	157	140	158	147	138	138
21	89	162	159	161	161	165	163	163	158	162	162
22	110	92	75	106	107	91	99	107	108	106	99
23	4	18	27	21	17	23	18	20	17	20	18
24	195	155	155	156	154	146	157	155	154	155	150
25	76	66	101	62	64	60	73	64	65	72	66
26	5	20	15	27	28	26	21	28	27	23	21
27	167	118	127	114	115	103	128	119	124	125	114
28	192	159	161	169	164	169	162	164	168	163	160
29	34	132	106	132	134	132	136	136	140	140	141
30	130	57	49	75	79	63	61	69	73	69	63
31	165	82	109	63	69	77	96	74	69	96	87
32	144	134	124	117	124	109	135	124	125	130	125
33	124	131	112	127	136	120	132	130	138	127	129
34	173	187	191	188	186	176	188	193	191	189	188
35	54	107	91	113	106	110	118	115	119	122	112
36	106	142	137	139	140	139	148	143	145	148	149
37	132	179	177	178	181	175	182	179	185	184	186
38	162	125	147	122	127	108	130	125	127	123	124
39	65	61	29	84	83	96	67	97	94	73	65
40	16	9	7	10	10	11	10	11	11	9	8
41	170	178	151	184	190	191	178	189	183	175	181
42	178	192	198	189	187	186	190	190	189	191	192

Table 15. (Continued)

Sire Code	PD74	NGRP	NGIC	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
43	48	31	17	37	38	40	35	38	37	38	35
44	52	49	66	46	52	47	50	49	59	50	48
45	180	193	197	190	188	189	195	192	190	194	193
46	100	143	180	126	135	121	146	135	136	141	140
47	149	173	164	162	168	190	172	169	180	172	172
48	36	14	18	16	18	19	16	22	20	16	13
49	83	87	89	93	90	76	92	87	89	89	88
50	45	46	36	39	35	43	45	41	43	52	46
51	97	72	72	61	62	65	77	67	66	56	57
52	113	103	120	95	109	116	111	89	115	108	103
53	115	37	41	34	50	50	38	34	46	39	37
54	61	129	121	124	120	122	133	128	121	136	134
55	53	75	119	76	70	66	78	77	71	77	71
56	15	8	13	8	7	10	8	8	8	10	10
57	176	164	138	180	185	183	170	176	176	180	174
58	47	47	38	52	49	48	48	53	53	54	53
59	58	19	19	17	16	17	19	19	18	17	15
60	143	123	108	131	150	126	127	122	129	128	122
61	55	43	40	38	39	55	43	39	44	47	45
62	160	117	94	111	114	117	119	111	111	113	110
63	28	34	63	32	34	32	36	33	35	33	33
64	127	138	146	170	183	140	139	170	193	153	147
65	168	188	192	179	180	171	184	181	179	182	187
66	107	139	157	133	130	124	137	132	130	139	144
67	169	124	149	120	108	85	123	118	107	126	133
68	66	106	144	97	93	75	112	95	91	101	101
69	20	38	37	33	36	45	40	36	41	40	38
70	183	186	189	173	175	179	179	173	170	179	184
71	153	177	173	175	176	180	173	165	164	169	177
72	94	67	57	80	81	64	75	70	75	79	77
73	157	163	167	135	146	148	165	153	146	168	163
74	102	145	139	145	142	144	145	150	142	143	145
75	138	161	176	143	155	159	158	151	150	159	161
76	103	81	76	78	85	93	87	73	96	64	62
77	118	152	126	137	133	154	153	137	141	152	152
78	69	64	42	73	75	78	64	82	64	65	74
79	74	122	115	102	110	100	121	110	112	118	120
80	128	185	175	165	173	185	180	177	178	178	183
81	22	56	129	54	59	53	57	57	60	59	60
82	3	2	2	2	2	2	2	2	2	2	1
83	31	191	188	192	193	194	185	186	186	183	191
84	63	62	54	69	67	69	60	68	63	76	70

Table 15. (Continued)

Sire Code	PD74	NGRP	NGIC	SMG	SCI	STYP	BRTH	SMGB	SCIB	RELB	REL
85	70	51	39	45	45	56	54	48	51	70	61
86	59	65	103	88	76	54	63	80	99	63	68
87	37	17	22	18	13	16	17	16	16	13	17
88	105	94	111	70	84	101	94	71	84	95	102
89	79	23	15	36	21	31	22	42	31	19	32
90	9	22	32	28	24	21	23	24	26	27	25
91	82	89	65	109	80	97	88	99	105	83	92
92	91	99	97	104	105	87	105	102	97	105	104
93	175	189	183	187	184	192	186	187	182	187	190
94	99	83	125	77	74	67	85	76	79	80	81
95	104	101	95	105	99	104	104	105	95	103	100
96	121	48	28	67	82	61	47	66	87	51	56
97	64	53	90	59	53	44	55	62	62	49	54
98	101	183	196	172	179	155	177	184	174	167	185
99	49	156	187	149	132	130	154	149	134	149	155
100	23	33	53	30	29	34	32	31	30	32	34
101	135	114	113	121	111	95	117	117	116	99	109
102	190	194	193	195	195	196	194	195	198	192	194
103	181	165	156	168	167	166	164	168	159	166	169
104	71	59	73	43	51	73	56	45	52	53	58
105	39	11	14	11	12	15	11	14	14	14	14
106	179	167	184	148	149	162	161	148	151	165	171
107	2	3	5	3	3	3	3	3	3	3	3
108	182	137	92	140	145	147	134	162	132	134	135
109	30	50	47	60	47	49	49	58	54	57	59
110	6	1	1	1	1	1	1	1	1	1	2
111	7	21	45	19	19	18	20	21	21	18	19
112	201	200	200	200	200	201	200	201	200	200	200
113	188	84	68	119	113	84	81	113	113	111	107
114	90	113	141	100	101	114	113	101	100	109	108
115	123	63	50	74	61	72	62	108	82	62	69
116	80	126	122	96	100	142	122	86	90	114	119
117	33	100	102	81	91	81	98	92	86	97	105
118	29	108	116	72	116	83	100	94	101	115	128
119	177	88	64	98	89	107	86	98	72	87	91
120	17	29	33	26	20	22	29	29	23	24	24
121	12	30	51	29	30	28	31	30	28	31	31
122	77	74	71	56	56	74	69	54	56	84	86
123	148	172	165	182	182	174	169	183	187	173	180
124	163	136	142	141	118	123	126	146	131	147	154
125	96	149	128	136	138	151	150	139	133	146	146
126	164	110	61	138	152	59	103	131	166	120	136

Table 15. (Continued)

Sire Code	PD74	NGFP	NGIC	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
127	184	102	93	68	77	128	95	72	67	42	43
128	51	54	52	65	57	37	52	65	61	67	84
129	42	16	12	14	23	9	13	10	10	8	11
130	155	95	62	53	72	82	83	50	102	82	98
131	8	4	3	5	6	4	5	5	7	5	5
132	145	127	134	146	151	143	125	138	160	119	123
133	26	24	31	23	27	20	24	26	25	25	22
134	25	154	154	92	68	141	142	96	85	142	153
135	60	77	82	87	65	38	72	91	49	78	82
136	198	198	194	199	199	199	197	198	199	197	198
137	171	147	153	158	163	158	138	154	148	133	142
138	154	111	87	101	102	133	108	83	110	112	113
139	194	196	190	197	197	178	196	196	195	196	197
140	186	68	56	58	32	71	59	37	76	68	78
141	134	115	84	123	112	136	124	134	106	121	111
142	40	55	104	51	54	51	58	56	57	58	55
143	158	130	132	152	139	131	115	145	135	110	121
144	109	12	11	9	9	8	9	9	9	11	16
145	119	35	24	64	55	41	34	61	58	48	51
146	131	70	48	103	103	94	68	88	93	74	72
147	117	121	135	159	165	118	102	140	177	104	127
148	41	73	105	57	63	52	70	60	74	75	73
149	57	85	59	91	66	102	90	75	92	98	95
150	98	120	123	157	147	99	101	147	143	102	117
151	43	52	107	47	48	46	53	51	50	55	52
152	88	175	174	151	148	167	156	127	165	144	165
153	50	96	79	50	66	89	82	46	98	60	67
154	147	93	85	110	126	86	74	114	122	61	80
155	161	158	169	150	160	161	151	159	157	145	158
156	196	195	186	194	194	182	192	194	194	193	195
157	10	5	6	4	4	7	4	4	4	4	4
158	116	32	26	48	46	35	28	27	47	21	27
159	27	40	30	31	33	29	33	32	29	35	44
160	95	76	55	89	78	80	71	90	70	71	75
161	32	41	78	40	40	36	42	40	42	41	39
162	62	42	35	49	43	58	41	47	40	46	47
163	114	144	131	155	122	163	120	160	139	100	137
164	1	6	9	6	5	6	6	6	5	6	6
165	191	184	163	191	192	195	168	188	188	161	179
166	125	160	158	163	162	150	149	166	120	151	164
167	185	109	81	71	95	125	89	63	109	91	106
168	24	15	23	15	14	13	15	15	15	12	12

Table 15. (Continued)

Sire Code	PD74	NGRP	NGIC	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
169	46	36	74	35	37	33	39	35	39	36	36
170	11	7	4	7	8	5	7	7	6	7	7
171	142	69	67	86	96	106	65	100	36	107	96
172	126	39	25	66	44	62	37	59	32	37	49
173	187	168	166	160	156	164	166	157	156	157	156
174	151	169	133	176	174	177	167	172	169	174	175
175	81	116	118	130	129	135	114	120	123	124	126
176	112	176	172	174	177	184	171	174	152	176	178
177	146	71	69	99	60	115	66	103	33	34	30
178	73	97	86	134	121	30	93	123	48	90	85
179	172	135	100	153	159	149	131	142	167	135	132
180	86	91	98	112	92	111	91	106	68	94	93
181	93	112	130	82	87	127	109	79	77	93	89
182	21	45	80	41	42	39	44	43	45	44	40
183	108	153	150	166	158	160	147	156	155	158	157
184	200	201	201	201	201	200	201	200	201	201	201
185	129	86	96	129	144	119	84	121	161	132	118
186	159	79	60	108	117	98	79	104	103	92	90
187	35	28	21	13	22	57	30	12	34	29	29
188	189	182	181	183	169	188	176	180	172	171	176
189	152	78	83	90	123	113	76	109	117	86	79
190	174	133	152	142	141	134	129	141	144	129	130
191	193	170	162	186	178	181	160	175	173	164	170
192	38	27	20	22	31	14	27	18	19	28	26
193	14	13	10	20	15	27	12	17	12	22	20
194	111	80	88	85	94	92	80	84	88	66	64
195	13	25	44	24	26	24	25	25	24	26	23
196	78	60	46	42	41	88	51	44	38	43	42
197	18	26	34	25	25	25	26	23	22	30	28
198	84	119	99	107	104	137	116	85	114	117	115
199	92	146	170	116	128	153	143	116	137	154	151
200	67	105	160	79	73	68	106	78	78	88	83
201	68	104	168	83	88	70	107	81	83	81	76

Table 16. Ranks of sire estimates for fat.

Bull Code	PD74	NGFP	NGIC	SMG	BFTH	RELB	REL
1	35	150	138	148	164	168	152
2	126	149	105	133	154	155	150
3	2	3	3	4	3	3	2
4	154	163	147	147	165	165	162
5	76	76	56	73	99	86	63
6	195	198	195	200	200	199	198
7	158	168	165	154	170	169	168
8	134	125	103	138	153	154	126
9	42	36	23	37	43	49	39
10	95	187	184	183	188	187	186
11	142	144	124	171	169	164	136
12	187	170	180	170	181	179	165
13	192	192	192	191	192	193	191
14	131	112	104	120	123	122	112
15	53	92	72	107	106	104	94
16	81	185	171	181	191	189	180
17	80	101	85	97	132	127	99
18	85	85	111	85	84	80	79
19	37	118	115	134	122	123	117
20	27	47	41	59	47	46	46
21	43	95	91	103	96	95	96
22	66	75	55	84	78	83	81
23	3	16	31	18	17	16	16
24	199	127	117	130	139	128	125
25	102	108	106	100	104	102	106
26	41	84	80	89	86	87	84
27	124	100	109	105	100	105	102
28	145	91	92	121	92	93	95
29	92	186	181	185	185	188	190
30	136	82	60	96	82	89	89
31	123	93	143	72	95	96	98
32	157	126	101	119	131	125	121
33	79	87	71	94	89	91	92
34	105	171	139	182	172	172	173
35	36	119	107	124	119	121	120
36	161	182	183	180	182	183	188
37	91	157	141	157	155	157	161
38	178	134	151	128	141	111	133
39	50	83	64	109	90	90	80
40	12	10	9	12	12	12	11
41	177	191	170	194	190	194	194
42	163	174	188	173	175	177	178

Table 16. (Continued)

Bull Code	PD74	NGRF	NGIO	SMG	BFTH	RFLB	REL
43	31	24	13	28	26	27	25
44	150	147	161	135	148	145	143
45	186	195	198	193	195	195	195
46	118	155	159	142	150	151	153
47	182	193	194	188	194	191	187
48	19	4	4	5	4	5	4
49	114	114	114	114	115	112	110
50	149	105	98	93	105	109	103
51	38	28	20	24	29	17	17
52	113	123	146	116	136	131	123
53	160	53	75	55	62	67	65
54	130	167	160	161	166	166	167
55	46	94	125	98	97	94	97
56	7	5	8	3	6	8	5
57	141	154	127	158	157	153	131
58	24	18	14	22	18	21	23
59	94	39	40	35	39	42	36
60	148	130	113	144	146	147	139
61	45	48	54	41	50	53	49
62	190	160	145	151	159	156	159
63	34	52	86	44	53	54	53
64	117	137	133	164	147	150	146
65	167	188	190	179	187	186	189
66	75	99	110	101	98	103	107
67	176	129	150	129	135	143	144
68	60	97	132	90	101	92	93
69	22	38	45	36	42	44	41
70	175	176	187	168	173	171	172
71	111	132	119	131	137	117	119
72	78	44	42	46	45	48	47
73	198	181	175	156	186	174	170
74	183	196	193	196	197	197	196
75	129	73	100	62	77	77	69
76	65	74	62	77	80	65	61
77	49	64	49	63	70	68	67
78	101	98	68	104	94	106	114
79	100	111	116	95	110	99	104
80	189	194	191	195	193	190	192
81	26	69	126	65	75	75	74
82	1	2	2	1	2	1	1
83	64	180	185	190	177	175	184
84	137	169	173	165	168	173	175

Table 16. (Continued).

Bull Code	PD74	NGRP	NGIC	SMG	BFTH	RELB	REL
85	18	21	15	17	23	28	22
86	72	117	144	122	113	110	113
87	30	20	33	20	19	20	20
88	74	79	90	57	76	76	75
89	110	71	94	113	73	69	86
90	14	23	36	26	24	22	24
91	90	106	77	123	103	97	101
92	196	177	182	174	176	176	181
93	171	200	197	198	198	198	199
94	13	12	18	14	15	14	13
95	32	46	44	48	48	51	48
96	109	32	24	52	33	41	40
97	55	62	98	70	64	64	64
98	166	197	200	192	196	196	197
99	58	184	196	177	179	178	185
100	57	40	61	32	40	40	42
101	185	159	154	159	158	159	164
102	165	173	177	175	171	167	171
103	153	165	155	169	161	163	163
104	52	43	46	30	35	35	44
105	11	6	6	7	7	6	7
106	162	142	168	115	140	139	147
107	4	8	10	8	8	7	8
108	152	136	102	137	128	124	130
109	56	55	53	76	54	55	60
110	10	1	1	2	1	2	3
111	8	14	29	13	14	13	12
112	201	201	201	201	201	201	201
113	156	30	27	43	31	37	34
114	99	60	96	56	61	61	62
115	108	145	120	139	143	141	148
116	93	110	118	82	102	98	109
117	71	81	74	61	74	78	88
118	89	107	112	67	87	116	132
119	88	33	28	39	32	34	35
120	25	42	50	31	38	32	33
121	6	13	22	11	13	15	15
122	112	122	134	91	112	133	138
123	87	131	131	143	125	113	124
124	170	135	135	141	121	160	166
125	63	109	95	111	107	107	105
126	193	172	153	178	167	170	182

Table 16. (Continued)

Bull Code	PD74	NGRP	NCIC	SMG	BFTH	RELB	REL
127	169	58	57	53	57	26	28
128	128	65	58	80	65	88	100
129	151	41	32	40	37	33	37
130	181	115	89	60	91	101	129
131	9	11	7	9	11	11	10
132	135	140	140	145	133	132	137
133	73	70	79	66	72	74	72
134	54	146	142	106	130	130	145
135	48	61	65	64	58	62	68
136	168	166	156	167	162	158	160
137	180	162	179	162	152	148	157
138	164	88	76	87	83	82	87
139	174	183	169	189	178	184	193
140	191	72	66	71	63	66	71
141	194	179	164	184	180	180	176
142	86	120	139	108	116	114	118
143	140	124	130	136	120	108	108
144	127	25	19	16	21	30	30
145	122	31	26	47	30	47	54
146	116	63	51	92	60	63	66
147	70	37	35	78	34	39	38
148	29	57	83	45	56	56	56
149	28	66	52	75	69	73	70
150	84	138	137	149	118	119	134
151	16	22	21	21	22	19	19
152	83	141	122	118	88	84	122
153	62	103	93	51	81	71	82
154	121	67	73	88	46	36	57
155	120	151	162	140	129	135	156
156	23	49	39	58	44	45	52
157	21	7	5	6	5	4	6
158	77	17	16	29	10	9	14
159	104	89	84	79	68	70	91
160	98	45	43	50	36	38	45
161	69	68	87	69	71	72	73
162	5	27	25	34	20	24	29
163	97	161	158	166	111	100	155
164	44	54	63	54	55	57	58
165	179	189	174	197	163	152	177
166	103	56	47	74	41	43	59
167	184	104	88	68	66	60	83
168	15	9	12	10	9	10	9

Table 16. (Continued)

Bull Code	PD74	NGRP	NGIC	SMG	BFTH	RELB	REL
169	115	121	148	110	124	118	116
170	47	19	17	23	25	23	18
171	139	77	67	83	108	134	76
172	144	113	129	155	144	140	115
173	188	190	186	187	189	182	174
174	119	153	121	160	160	161	141
175	159	164	178	172	174	181	169
176	107	178	172	176	183	185	179
177	133	78	69	99	67	31	31
178	59	90	82	146	142	138	90
179	138	96	81	125	117	142	111
180	143	148	157	153	156	162	149
181	173	152	167	126	145	144	151
182	68	128	152	117	134	129	127
183	125	175	176	186	184	192	183
184	200	199	199	199	199	200	200
185	106	86	97	112	79	79	77
186	147	116	108	132	109	115	128
187	40	34	34	15	59	85	51
188	197	156	149	152	149	146	154
189	146	80	78	81	114	126	78
190	172	158	166	163	151	149	158
191	155	143	123	150	126	120	135
192	39	35	38	27	49	58	43
193	17	15	11	19	16	18	21
194	51	29	37	33	28	25	26
195	20	26	30	25	27	29	27
196	67	59	48	49	85	59	32
197	61	50	70	42	52	52	55
198	96	139	128	127	138	136	142
199	132	133	163	102	127	137	140
200	33	51	59	38	51	50	50
201	82	102	136	86	93	81	85

Table 17. Rank and product-moment correlations between model definitions of all bulls evaluated for milk[a]

	PD74	NGRP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
PD4		.726	.624	.755	.758	.749	.710	.748	.750	.710	.721
NGRP	.788		.945	.965	.964	.966	.990	.965	.958	.976	.986
NGIO	.698	.959		.893	.895	.883	.934	.896	.890	.913	.924
SMG	.810	.977	.921		.985	.947	.957	.992	.967	.959	.967
SCI	.803	.976	.923	.989		.946	.957	.982	.980	.961	.966
STYR	.800	.971	.906	.960	.956		.958	.945	.941	.949	.952
BRTH	.772	.993	.951	.972	.971	.967		.960	.950	.986	.977
SMGB	.800	.977	.925	.994	.987	.960	.976		.961	.961	.966
SCIB	.800	.970	.919	.977	.985	.956	.967	.972		.954	.963
RELB	.772	.982	.933	.971	.971	.959	.990	.974	.966		.987
REL	.786	.988	.940	.978	.975	.961	.982	.976	.971	.990	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

Table 18. Rank and product-moment correlations between model definitions of all sires evaluated for fat[a]

	PD74	NGRP	NGIO	SMG	BRTH	RELB	REL
PD74		.735	.695	.724	.719	.715	.729
NGRP	.791		.965	.969	.981	.968	.989
NGIO	.749	.976		.924	.946	.933	.958
SMG	.785	.978	.943		.967	.955	.961
BRTH	.776	.989	.964	.971		.990	.973
RELB	.769	.976	.949	.962	.989		.978
REL	.786	.987	.963	.971	.978	.986	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

mixed model definitions range from .883 to .990 for milk and .933 to .999 for fat. Product moment correlations are slightly higher. Correlations for PD74 with mixed model definitions are lower than among definitions. They range from .624 to .758 and .698 to .810 for rank and product-moment correlations, respectively, for milk. For fat, rank correlations range from .695 to .735 and product-moment correlations range from .749 to .791. Correlations tended to be highest between model definitions which were similar such as SMG and SCI or NGRP and REL. BRTH estimates are highly correlated with no grouping.

Observing rank and product-moment correlations for all bulls, it is hard to discern any large differences in ranks by any definition. As was explained in the previous section, the effect of grouping depends on the number and distribution of daughters. For this reason, correlations were computed for just those sires with limited information. The basis for this was the magnitude of the sire diagonal before augmenting by 15. This number reflects the contribution of a bull's daughters to his sire estimate and depends on the number and distribution of daughters by herd-year. For the absorbed coefficients matrix, C_s, the sire diagonal is:

$$\left(n_{ij\cdot} - \frac{n_{ij\cdot}^{2}}{n_{i\cdot\cdot}}\right)$$

From this, it can be shown that any one daughter of a bull can never have the full value of one. Table 19 shows the influence of various numbers of daughters and herdmates in a herd-year to the sire diagonal. When the number of daughters and herdmates are equal, the sire diagonal is equal to

Table 19. Effect of number and distribution of daughters on the sire diagonal of the coefficients matrix

Number of daughters of sire j in herd-year i	Number of daughters of other bulls herd-year i	$n_{ij} - \frac{n_{ij}^2}{n_{i..}}$
1	1	.50
1	2	.67
1	5	.83
1	10	.91
1	100	.99
2	1	.67
5	1	.83
10	1	.91
100	1	.99
2	2	1.00
5	5	2.50
10	10	5.00
100	100	50.00

one-half the number of daughters in that herd-year. With 100 herdmates, the contribution of one daughter of a bull to the sire diagonal is nearly one. Also, if 100 daughters of a bull are compared to only one daughter of another bull, the contribution to its sire diagonal is still only about one.

Cumulative classes of bulls were formed whose sire diagonal from C_s was less than or equal to 10, 15, 20, and 25, respectively. Each higher class included those bulls in the lower class or classes. Of the original 201 bulls, there was a cumulative total of 24, 33, 49, and 70 bulls in each class as illustrated in Table 20.

Rank and product-moment correlations by classes are presented in Tables 21 through 24 for milk and Tables 25 through 28 for fat. Correlations among model definitions for classes of bulls were less than for all bulls. This may be due to sampling to some extent but it also seems to reflect real differences in how models were defined.

To compare the influence of grouping, correlations between NGRP and model definitions with grouping will be discussed for the classes of bulls. The lower the correlations, the greater the effect of grouping for that class of bulls. In general, correlations were lower for each class with smaller sire diagonals. For milk, BRTH is the only grouping model with ranks highly correlated (.980) with NGRP for bulls whose sire diagonal is less than or equal to 10 (Table 21). However, the rank correlations for RELB, which is a combination of birth year grouping and accounting for relationships, is only .834 with NGRP. Rank correlation for relationships alone (REL) is .916. The combination of grouping and relationships was

Table 20. Cumulative classes of bulls based on magnitude of sire diagonal in C_s

Class	Sire diagonal	Number of bulls
1	≤10	24
2	≤15	24 + 9 = 33
3	≤20	24 + 9 + 16 = 49
4	≤25	24 + 9 + 16 + 21 = 70

Table 21. Rank and product-moment correlations between model definitions for bulls whose sire diagonal was less than or equal to 10 for milk[a]

	PD74	NGRP	NGIO	SMG	SCI	STRR	BRTH	SMGB	SCIB	RELB	REL
PD74		.010	.060	.143	.174	.128	.040	.139	.185	.185	.143
NGRP	.177		.957	.813	.750	.829	.980	.789	.725	.834	.916
NGIO	.173	.972		.874	.805	.839	.956	.827	.770	.882	.924
SMG	.395	.815	.861		.896	.726	.837	.969	.801	.792	.801
SCI	.313	.804	.850	.918		.689	.808	.883	.881	.800	.765
STYR	.261	.766	.754	.609	.632		.843	.713	.691	.794	.803
BRTH	.174	.950	.920	.809	.817	.771		.817	.762	.893	.923
SMGB	.348	.798	.836	.969	.904	.649	.824		.795	.770	.780
SCIB	.298	.726	.779	.757	.842	.655	.740	.718		.746	.756
RELB	.236	.874	.879	.793	.828	.711	.927	.794	.766		.938
REL	.242	.901	.904	.807	.802	.680	.867	.784	.775	.943	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

Table 22. Rank and product-moment correlations between model definitions for bulls whose sire diagonal was less than or equal to 15 for milk[a]

	PD74	NGRP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
PD74		.233	.274	.394	.402	.380	.206	.424	.409	.300	.303
NGRP	.507		.969	.863	.848	.877	.968	.843	.839	.885	.946
NGIO	.487	.989		.885	.881	.885	.924	.866	.853	.885	.941
SMG	.601	.919	.923		.932	.823	.868	.982	.858	.836	.834
SCI	.546	.918	.928	.959		.805	.851	.927	.918	.849	.844
STYR	.531	.927	.916	.869	.857		.869	.815	.806	.834	.853
BRTH	.478	.979	.966	.915	.914	.919		.843	.809	.935	.922
SMGB	.577	.914	.919	.985	.953	.881	.921		.853	.823	.819
SCIB	.544	.898	.907	.904	.932	.879	.889	.888		.793	.842
RELB	.478	.935	.932	.905	.915	.879	.965	.910	.892		.934
REL	.502	.959	.955	.917	.917	.892	.942	.911	.914	.967	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

Table 23. Rank and product-moment correlations between model definitions for bulls whose sire diagonal was less than or equal to 20 for milk[a]

	PD74	NGRP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
PD74		.419	.389	.502	.496	.489	.391	.520	.505	.428	.424
NGRP	.587		.965	.912	.904	.912	.964	.901	.878	.910	.953
NGIO	.543	.987		.902	.886	.907	.917	.879	.852	.883	.920
SMG	.648	.941	.931		.955	.860	.903	.984	.912	.901	.910
SCI	.613	.941	.933	.971		.843	.905	.951	.946	.906	.901
STYR	.606	.936	.920	.896	.886		.898	.864	.829	.854	.858
BRTH	.568	.983	.965	.934	.937	.932		.897	.879	.950	.929
SMGB	.631	.939	.929	.985	.963	.902	.940		.901	.899	.902
SCIB	.624	.923	.912	.934	.955	.895	.917	.918		.870	.892
RELB	.559	.946	.929	.930	.938	.894	.968	.936	.919		.954
REL	.576	.962	.947	.942	.939	.896	.947	.939	.933	.975	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

Table 24. Rank and product-moment correlations between model definitions for bulls whose sire diagonal was less than or equal to 25 for milk[a]

	PD74	NGRP	NGIO	SMG	SCI	STYR	BRTH	SMGB	SCIB	RELB	REL
PD74		.469	.418	.520	.526	.522	.435	.529	.541	.467	.476
NGRP	.612		.962	.918	.909	.931	.972	.918	.893	.933	.963
NGIO	.570	.982		.880	.868	.899	.934	.880	.842	.901	.921
SMG	.662	.946	.923		.962	.882	.901	.984	.920	.907	.918
SCI	.638	.948	.927	.975		.870	.901	.954	.954	.914	.915
STYR	.632	.944	.920	.909	.905		.914	.881	.856	.880	.885
BRTH	.587	.985	.967	.938	.944	.938		.907	.874	.960	.941
SMGB	.641	.947	.927	.986	.969	.914	.948		.908	.918	.922
SCIB	.653	.934	.913	.946	.964	.911	.927	.932		.886	.908
RELB	.589	.958	.940	.938	.956	.908	.974	.946	.931		.968
REL	.611	.970	.950	.948	.946	.910	.956	.948	.942	.980	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

Table 25. Rank and product-moment correlations between model definitions for bulls whose sire diagonal was less than or equal to 10 for fat[a]

	PD74	NGRP	NGIO	SMG	BRTH	RELG	REL
PD74		.135	.101	.149	.226	.279	.195
NGRP	.252		.914	.721	.799	.697	.909
NGIO	.271	.961		.781	.721	.620	.883
SMG	.268	.772	.816		.740	.651	.715
BRTH	.191	.792	.751	.663		.920	.787
RELG	.206	.687	.645	.542	.907		.792
REL	.276	.889	.858	.675	.737	.823	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

Table 26. Rank and product-moment correlations between model definitions for bulls whose sire diagonal was less than or equal to 15 for fat[a]

	PD74	NGRP	NGIO	SMG	BRTH	RELB	REL
PD74		.168	.143	.221	.271	.289	.211
NGRP	.525		.941	.811	.854	.774	.936
NGIO	.519	.988		.834	.813	.748	.916
SMG	.500	.905	.906		.838	.746	.784
BRTH	.500	.942	.934	.868		.946	.836
RELB	.456	.869	.860	.799	.949		.842
REL	.482	.937	.927	.854	.882	.915	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

Table 27. Rank and product-moment correlations between model definitions for bulls whose sire diagonal was less than or equal to 20 for fat[a]

	PD74	NGRP	NGIO	SMG	BRTH	RELB	REL
PD74		.303	.280	.341	.325	.310	.292
NGRP	.576		.958	.894	.908	.860	.952
NGIO	.545	.989		.896	.873	.837	.938
SMG	.561	.935	.930		.895	.838	.863
BRTH	.542	.959	.950	.905		.963	.882
RELB	.496	.905	.894	.858	.959		.897
REL	.536	.950	.939	.900	.915	.947	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

Table 28. Rank and product-moment correlations between model definitions for bulls whose sire diagonal was less than or equal to 25 for fat[a]

	PD74	NGRP	NGIO	SMG	BRTH	RELB	REL
PD74		.423	.415	.404	.409	.402	.413
NGRP	.604		.959	.913	.940	.902	.967
NGIO	.580	.981		.888	.907	.877	.949
SMG	.582	.941	.919		.918	.883	.897
BRTH	.571	.967	.949	.920		.971	.922
RELB	.544	.923	.906	.888	.968		.932
REL	.580	.960	.944	.918	.935	.959	

[a] Upper half contains rank correlations, lower half contains product-moment correlations.

effective in lowering the rank correlations with NGRP compared to model definitions BRTH or REL. The lowest rank correlations are for grouping models SCI and SCIB. The effect of grouping on ranks of bulls is large for this class of bulls. Rank correlations of mixed model sire estimates with those by PD74 are close to zero for NGRP, NGIO, and BRTH. Highest rank correlation with PD74 is for SCIB and RELB.

Correlations among models are higher for each class of bulls (Tables 21 through 24). For the largest class of bulls (sire diagonal ≤ 25), correlations are similar to those for all bulls. Looking at correlations by classes verifies that the influence of grouping is greatest for bulls with fewer daughters.

The same overall trends in correlation were found for fat as for milk when computed by classes (Tables 25 through 28). For the first class where the sire diagonal was less than or equal to 10, BRTH was not as highly correlated with NGRP as it was for milk. The correlations for RELB were smaller than for either BRTH or REL. Grouping alone or in combination with relationships had a large influence on rankings of bulls with smaller sire diagonals. Using correlations by classes of bulls to examine changes in rank by different model definitions was effective for both milk and fat.

Testing sire estimates

The predictability of sire estimates by the different model definitions was tested by correlations with an independent set of daughter records. These records were not included in the original evaluation of sires because they had no herdmates in any herd-year. Tested records were adjusted for average age and month of calving, twice a day milking, and 305 day length lactation but not for environmental effects. Herdmate deviations were not used because they require that the average merit of herdmate's sires is either zero or that herd averages can be adjusted for genetic merit of herdmate's sire. It did not seem reasonable to test sire estimates with deviations where estimates of herdmate's sire must be assumed. Environmental covariances will bias correlations of sire estimates with test daughters but these should be identical for each model definition. This is because environmental effects were accounted for in the same way for each model and the same records were used to test sire estimates by the different model definitions. In fact, the same basic set of sire equations after absorption were used but with modification by grouping strategy or accounting for relationships.

Correlations of test daughters with sire estimates by the different mixed model definitions are presented in Tables 29 and 30 for milk and fat, respectively. Correlations were computed by classes depending on the magnitude of the sire diagonal as was described in the previous section (Table 20).

For milk, there are differences among model definitions. These differences are most pronounced for class 1, where fewer daughters were represented. Differences among model definitions are small for class 4; however, STYR exceeds all others. In all classes STYR is most predictive. This is surprising because of the subjective way in which the model was defined compared to the more objectively determined models by pedigree index. When it was first observed, it was hypothesized that STYR being

Table 29. Correlations between sire estimates by different model definitions with daughters not evaluated for milk

Model definition	Class[a] 1	2	3	4
N[b]	(20)	(22)	(25)	(27)
NGRP	.10	.17	.22	.16
NGIO	.01	.17	.22	.18
SMG	.11	.23	.27	.19
SCI	.06	.18	.22	.16
STYR	.20	.29	.32	.24
BRTH	.01	.17	.23	.16
SMGB	.12	.24	.28	.21
SCIB	.15	.25	.26	.19
RELB	-.02	.16	.21	.15
REL	-.04	.14	.21	.14

[a] Classes defined in Table 20.

[b] Average number of daughters tested per bull.

Table 30. Correlations between sire estimates by different model definitions with daughters not evaluated for fat

Model definition		Class[a]			
	N[b]	1 (20)	2 (22)	3 (25)	4 (27)
NGRP		.11	.18	.19	.13
NGIO		.13	.19	.20	.16
SMG		.11	.19	.20	.14
BRTH		.08	.18	.19	.13
RELB		.00	.13	.15	.10
REL		.01	.12	.14	.09

[a] Classes defined in Table 20.

[b] Average number of daughters tested per bull.

more predictive may be due to grouping within birth periods. This was the reason for computing sire estimates by the model definition BRTH. However, test correlations for this model were very similar to NGRP. It may point out the importance of grouping natural service sires separately which was not done for models determined by pedigree indexes.

The models with grouping by pedigree indexes have the next largest correlations. SMGB and SCIB are slightly better than SMG and SCI. If the indexes used in SMG and SCI were to a common base, thus fully accounting for genetic trend, then these model definitions should be as predictive as SMGB and SCIB. They are not which may be due to sampling but may also be because sire's and MGS's PD's, and CI's used did not fully account for genetic trend.

REL and RELB are the least predictive for the set of bulls tested. It should still be desirable to use relationships in mixed model sire evaluations to lower prediction error; however, grouping is still essential. For this set of data, grouping by stud-year or pedigree index along with an accounting for relationships would be desirable.

Correlations for fat are presented in Table 30 and are not very definitive. Again, use of relationships are least predictive.

Rank deviations

The results of examining changes in rank by the number and degree of switches in rank are presented in Table 31 for milk. In one case, PD74 was considered optimum because it was computed from the most complete information. In the second case, STYR was considered optimum because it was most predictive of mixed model evaluations. Deviations are listed as

Table 31. Changes in rank for rank deviations

	PD74 optimum		STYR optimum	
	Deviation	Percent of reverse in ranks	Deviation	Percent of reverse in ranks
PD74	0	0	639707	3.57
NGRP	696560	4.13	86582	.48
NGIO	967709	5.73	296461	1.66
SMG	622581	3.69	133228	.74
SCI	618458	3.66	134750	.75
STYR	641605	3.80	0	0
BRTH	734765	4.35	103135	.58
SMGB	644741	3.82	136392	.76
SCIB	639479	3.79	136563	.76
REL	741777	4.39	126438	.71
RELB	713602	4.23	118589	.66

a percent of a complete reversal in ranks. For instance, if 1-2-3-4 is correct, a complete reversal is 4-3-2-1. These results indicate much larger differences between any of the mixed model definitions and PD74 than among model definitions. Ignoring the off-diagonals of the coefficients matrix resulted in the largest difference from the evaluations considered optimum. This agrees with Keown (1974) who found that sire estimates varied more when the merit of herdmate's sires were ignored compared to when different methods of grouping were tried.

Relationships between sire estimates and pedigree indexes

Correlations were computed between sire estimates by different model definitions and pedigree indexes. They are presented in Tables 32 and 33 for milk and fat, respectively. Expected correlations were computed by a method similar to that of Searle (1964). The expected correlation between a progeny test of a bull and the progeny test of his sire is $\frac{1}{2}\sqrt{\beta\beta'}$ where β is the expected regression of a sire's transmitting ability on his daughter deviation. Assuming one record per daughter and every daughter in a different herd, $\beta = \frac{nh^2}{4 + (n-1)h^2}$. Since PD's used were based on multiple records and daughters were distributed across herds, repeatability computed by the USDA was used for β. Repeatability is a regression which weights daughter deviations according to number of records and distribution of daughters across herds. β' is the regression of the son's transmitting ability on his daughter's deviations. When computing expected correlations for PD74 (first line of Tables 32 and 33), β' is the USDA repeatability. For the mixed model, where evaluations were usually based on fewer daughters, β' was $\frac{n'}{n' + 15}$ where n' is the magnitude

Table 32. Correlations between indexes and sire estimates by different model definitions for milk

Model definitions	Sire PD	Dam CI	MGS PD	Index 1	Index 2
PD74	.45	.24	.23	.49	.50
NGRP	.34	.23	.14	.36	.41
NGIO	.27	.21	.10	.28	.34
SMG	.47	.25	.20	.49	.53
SCI	.46	.30	.20	.48	.55
STYR	.37	.22	.13	.38	.43
BRTH	.33	.24	.14	.35	.41
SMGB	.46	.25	.19	.48	.51
SCIB	.45	.30	.18	.47	.54
RELB	.38	.23	.16	.40	.44
REL	.39	.22	.16	.41	.45
Expected Correlation PD	.44	.29	.21		
Mixed Model	.43	.29	.21		

Table 33. Correlations between indexes and sire estimates by different model definitions for fat

Model definitions	Sire PD	Dam CI	MGS PD	Index 1	Index 2
PD74	.35	.29	.27	.43	.47
NGRP	.35	.21	.12	.36	.41
NGIO	.33	.20	.10	.33	.38
SMG	.43	.21	.14	.43	.46
BRTH	.34	.23	.14	.35	.41
RELB	.39	.23	.15	.41	.45
REL	.42	.21	.13	.42	.45
Expected Correlation PD	.44	.29	.21		
Mixed Model	.43	.29	.21		

of the sire diagonal of the sire equations after absorption. Expected correlations are the average of each son-sire pair. Son-dam and son-maternal grandsire expected correlations were computed similarly. Cow indexes have a repeatability computed by USDA. Expected correlations are presented at the bottoms of Tables 32 and 33 which contain observed correlations. Those labelled PD74 apply to the first line of the table while those labelled mixed model apply to the remainder of the table.

The observed correlations for PD74 are close to their expected correlations. Son-sire and son-maternal grandsire observed correlations are slightly higher than expected while son-dam correlations are lower. The agreement between observed and expected is much greater for this set of data than for Vinson and Freeman (1972). Indexes used in this study were the most recent available for bulls where Vinson and Freeman used indexes computed when initial selection of the bull was made. Correlations are in better agreement with Butcher (1973). His pedigree data was the most recent as of the time of his study.

For milk, highest observed correlations are for model definitions where pedigree indexes were used for grouping and PD74 (Table 32). Lowest correlations with all indexes are for NGIO. Correlations for Index 1 and Index 2 are similar with those for Index 2 being slightly higher. Correlations between pedigree indexes and REL were higher than they were with NGRP but not as high as most grouping models. This is further evidence that some combinations of grouping along with the relationship matrix is desirable. Birth year, however, appears to be a poor choice of grouping for this set of data. Correlations for STYR with pedigree indexes are less than might be expected based on tested daughters. Son-dam correlations deviate most from expected.

Table 33 lists correlations for fat sire estimates with pedigrees indexes for fat. REL estimates are highly correlated with sire's PD. Lowest correlations are for NGIO just as for sire estimates for milk. Most correlations were lower than for milk.

Regressions of sire estimates on the pedigree indexes were also computed and are presented in Tables 34 and 35. Expected regressions are $\frac{1}{2}\beta$ where β was defined as previously described for correlations. Regressions are highest for sire estimates where pedigree indexes were used to determine groups. For instance, where sire's PD was used as a criteria for grouping, SMG and SMGB regressions are greatest. Regressions of sire estimates on dam's CI are largest when the CI was used as part of the criteria for grouping. Sire estimates do reflect the use of pedigree information whether through the use of pedigree indexes in grouping, considering relationships among tested bulls, or stud identification.

Table 34. Regressions of sire estimates on pedigree indexes for milk

	Dependent variables				
	Sire PD	Dam CI	MGS PD	Index 1	Index 2
PD74	.47 (.07)[a]	.17 (.05)	.19 (.06)	.28 (.04)	.32 (.04)
NGRP	.40 (.08)	.18 (.06)	.13 (.06)	.23 (.04)	.29 (.05)
NGIO	.33 (.08)	.17 (.06)	.10 (.07)	.19 (.05)	.25 (.05)
SMG	.50 (.07)	.18 (.05)	.17 (.06)	.29 (.04)	.34 (.04)
SCI	.48 (.07)	.22 (.05)	.16 (.06)	.28 (.04)	.35 (.04)
STYR	.39 (.07)	.16 (.05)	.11 (.06)	.22 (.04)	.27 (.04)
BRTH	.38 (.08)	.19 (.05)	.13 (.06)	.22 (.04)	.29 (.04)
SMGB	.49 (.07)	.18 (.05)	.16 (.06)	.28 (.04)	.33 (.04)
SCIB	.47 (.07)	.21 (.05)	.15 (.06)	.27 (.04)	.34 (.04)
RELB	.43 (.07)	.18 (.05)	.14 (.06)	.25 (.04)	.30 (.04)
REL	.46 (.08)	.18 (.06)	.14 (.06)	.26 (.04)	.32 (.05)
Expected Regressions	.46	.20	.21		

[a] Standard errors are in parentheses.

Table 35. Regressions of sire estimates on pedigree indexes for fat

	Dependent variables				
	Sire PD	Dam CI	MGS PD	Index 1	Index 2
PD74	.35 (.06)[a]	.23 (.05)	.20 (.05)	.20 (.03)	.27 (.04)
NGRP	.36 (.07)	.18 (.06)	.10 (.06)	.18 (.03)	.25 (.04)
NGIO	.34 (.07)	.17 (.06)	.08 (.06)	.17 (.03)	.24 (.04)
SMG	.40 (.06)	.17 (.05)	.10 (.05)	.20 (.03)	.27 (.04)
BRTH	.34 (.07)	.19 (.06)	.11 (.06)	.17 (.03)	.25 (.04)
RELB	.39 (.07)	.19 (.06)	.11 (.06)	.20 (.03)	.27 (.04)
REL	.43 (.07)	.18 (.06)	.10 (.06)	.22 (.03)	.29 (.04)
Expected Regressions	.46	.20	.21		

[a] Standard errors are in parentheses.

SUMMARY

Two hundred and one Holstein bulls were evaluated for estimated transmitting ability of milk and fat using several variations of the mixed model. Variations in model definitions were in the use of knowledge of the bull's pedigree. Pedigree information used included birth year, stud identification, two pedigree indexes, and the additive relationships among bulls. Pedigrees were provided by the Holstein Friesian Association of America. Incorporating pedigree information into the mixed model was by grouping, by addition of the inverted relationship matrix to the sire equations, or a combination of both. A total of ten model definitions for milk and six for fat were compared by how they rank bulls and predict daughter records. All evaluations were based on first lactation official DHI records from Iowa, Missouri, and Kansas.

The purpose of including the group effect in the mixed model is to account for genetic trend. However, determining in what group a bull should be included is primarily for increasing accuracy of estimating his transmitting ability. This is because the random sire effect from the mixed model is regressed close to the mean of the group in which he has been placed. With few daughters, the sire's deviation is regressed close to the group mean. The ability to predict the group solutions was examined to see the extent to which genetic subpopulations could be distinguished by including a group effect in the mixed model. The greatest degree of variation due to grouping was 34 percent for an index based on sire's PD and dam's cow index within period of birth (SCIB). Grouping by

stud year (STYR) was as effective in determining distinct genetic subpopulations as an index based on sire's and maternal grandsire's PD (SMG and SMGB). The least variation due to grouping was 5 percent for milk and 8 percent for fat when birth year was the criteria for grouping. Pedigree indexes were effective in predicting distinct genetic subpopulations.

Ranks of sire estimates by the different model definitions were compared by rank and product-moment correlations. All model definitions were highly correlated with each other. Similar model definitions had highest correlations between them. Correlations for the BRTH, REL and RELB models with NGRP were high. The lowest correlations among mixed model definitions were when the off diagonals of the sire coefficients matrix were ignored thus not accounting for genetic merit of herdmates sires. When correlations were computed for classes of bulls determined by the magnitude of sire diagonals, differences in ranking were accentuated but similar model definitions were still most highly related.

Predicting ME production of daughters not previously used in obtaining group solutions was also done by classes determined by the magnitude of the sire diagonal. Of the mixed model definitions, STYR was always most predictive followed by the indexing models. REL and RELB were always poorest. Relationships cannot be used alone in place of grouping for this set of data. Birth year was a poor choice of grouping to be used alone or in combinations with relationships. An improvement would be to account for relationships among bulls in combination with grouping by a pedigree index.

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APPENDIX

Examples of procedures

A simple example will be used to demonstrate procedures used to obtain sire estimates with a mixed model, as was done in this study. Characteristics of absorption, grouping, accounting for relationships, and obtaining solutions will be illustrated. Examples are taken from Henderson (1975).

1. Model

Consider the simple model:

$$Y_{ikl} = h_i + s_k + e_{ikl} \qquad (1)$$

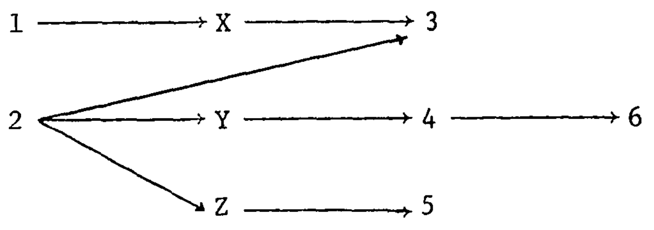
where

h_i is a fixed environmental effect and includes the mean μ,

s_k is a random sire effect,

e_{ijkl} are mutually uncorrelated random variables.

The following sires with tested progeny and their known parents are represented by the following path diagram. Sires 2, 3, 4, 5, and 6 have tested offspring. X, Y, and Z are female offspring.



(2)

2. Absorption

The distribution or progeny by sire for the first 3 h_i's are:

	h_1		h_2		h_3	
	N	Sum Y	N	Sum Y	N	Sum Y
s_2	2	27,000	1	13,000	3	38,000
s_3	1	15,000	0	0	0	0
s_4	0	0	1	12,000	0	0
s_5	0	0	3	40,000	0	0
s_6	2	30,000	0	0	0	0

N is number of progeny

At the start, the coefficients matrix is 5 x 5 and all values are zero and the right hand sides vector is 5 x 1 and all zero.

$$\begin{aligned} 0s_2 + 0s_3 + 0s_4 + 0s_5 + 0s_6 &= 0 \\ 0s_2 + 0s_3 + 0s_4 + 0s_5 + 0s_6 &= 0 \\ 0s_2 + 0s_3 + 0s_4 + 0s_5 + 0s_6 &= 0 \\ 0s_2 + 0s_3 + 0s_4 + 0s_5 + 0s_6 &= 0 \\ 0s_2 + 0s_3 + 0s_4 + 0s_5 + 0s_6 &= 0 \end{aligned} \tag{3}$$

Using the algebra for absorption found on pages 43 and 44 of the text, the equations after absorption of h_1 are:

$$\begin{aligned} 1.20s_2 - .40s_3 - 0s_4 - 0s_5 - .80s_6 &= -1800 \\ -.40s_2 + .80s_3 - 0s_4 - 0s_5 - .40s_6 &= 600 \\ - 0s_2 - 0s_3 + 0s_4 - 0s_5 - 0s_6 &= 0 \\ - 0s_2 - 0s_3 - 0s_4 + 0s_5 - 0s_6 &= 0 \\ -.80s_2 - .40s_3 - 0s_4 - 0s_5 + 1.20s_6 &= 1200 \end{aligned} \tag{4}$$

All rows and columns sum to zero as do the right hand sides. The results of absorbing h_2 are:

$$\begin{array}{rrrrrrrrrrrrrr}
2.00s_2 & - & .40s_3 & - & .20s_4 & - & .60s_5 & - & .80s_6 & = & -1800 & + & 0 & = -1800 \\
-.40s_2 & + & .80s_3 & - & 0s_4 & - & 0s_5 & - & .40s_6 & = & 600 & + & 0 & = 600 \\
-.20s_2 & - & 0s_3 & + & 80s_4 & - & .60s_5 & - & 0s_6 & = & 0 & - & 1000 & = -1000 \\
-.60s_2 & - & 0s_3 & - & 60s_4 & + & 1.20s_5 & - & 0s_6 & = & 0 & + & 1000 & = 1000 \\
-.80s_2 & - & .40s_3 & - & 0s_4 & - & 0s_5 & + & 1.20s_6 & = & 1200 & + & 0 & = 1200
\end{array} \tag{5}$$

All rows and columns still sum to zero as well as the right hand sides. Absorbing h_3 results in no contribution to the coefficients or right hand sides because only sire 2 has any offspring represented. This can be shown from the algebra of absorption. The diagonal for sire 2 is:

$$\left(n_{31\cdot} - \frac{n_{31\cdot}^{2}}{n_{3\cdot\cdot}}\right) = 3 - \frac{(3)^2}{3} = 0 \tag{6}$$

The off-diagonals are of the form

$$-\frac{n_{31\cdot}n_{3j\cdot}}{n_{3\cdot\cdot}} = \frac{3 \text{ x } 0}{3} = 0 \tag{7}$$

Continuing through the absorption process the following equations may result if the same six sires are used in more herds.

$$\underbrace{\begin{bmatrix} 18.26 & -3.51 & -2.40 & -6.32 & -6.03 \\ -3.51 & 23.21 & 0 & -11.21 & -8.49 \\ -2.40 & 0 & 33.24 & -16.23 & -14.61 \\ -6.32 & -11.21 & -16.23 & 33.76 & 0 \\ -6.03 & -8.49 & -14.61 & 0 & 29.13 \end{bmatrix}}_{C_s} \underbrace{\begin{bmatrix} \hat{s}_2 \\ \hat{s}_3 \\ \hat{s}_4 \\ \hat{s}_5 \\ \hat{s}_6 \end{bmatrix}}_{S} = \underbrace{\begin{bmatrix} -3{,}444 \\ 50{,}461 \\ 84{,}498 \\ -61{,}645 \\ -69{,}870 \end{bmatrix}}_{R_A} \tag{8}$$

3. Creating Group Equations

The model now becomes:

$$Y_{ijkl} = h_i + g_j + s_{jk} + e_{ijkl} \tag{9}$$

where g_j is the j^{th} group effect.

Groups will be created from the absorbed sire equations and right hand sides as was described in the text. Assigning sires 2 and 3 to group 1 and sires 4, 5 and 6 to group 2 results in the following F matrix:

$$F = \begin{bmatrix} 1 & 0 \\ 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 0 & 1 \end{bmatrix} \tag{10}$$

The result of multiplying C_s times F produces C_g and the following sire equations:

$$\left[\begin{array}{ccccc|cc} 18.26 & -3.51 & -2.40 & -6.32 & -6.03 & -14.75 & 14.75 \\ -3.51 & 23.21 & 0 & -11.21 & -8.49 & -19.70 & 19.70 \\ -2.40 & 0 & 33.24 & -16.23 & -14.61 & 2.40 & -2.40 \\ -6.32 & -11.21 & -16.23 & 33.76 & 0 & 17.53 & -17.53 \\ -6.03 & -8.49 & -14.61 & 0 & 29.13 & 14.52 & -14.53 \end{array}\right] \tag{11}$$

Note that these sire equations still sum to zero.

To create the group equations, the transpose of G is multiplied times F resulting in J.

$$J = \begin{bmatrix} 34.45 & -34.45 \\ -34.45 & 34.45 \end{bmatrix} \tag{12}$$

The group equations are $\left[\; C\hat{g} \;\middle|\; J \right]$ or

$$\left[\begin{array}{ccccc|cc} -14.75 & -19.70 & 2.40 & 17.53 & 14.52 & 34.45 & -34.45 \\ 14.75 & 19.70 & -2.40 & -17.53 & -14.52 & -34.45 & 34.45 \end{array}\right] \tag{13}$$

and they also sum to zero.

The group right hand sides are the sum of sire right hand sides of the sires assigned to groups 1 and 2.

$$\begin{aligned} -3{,}444 + 50{,}461 &= 47{,}017 \\ 84{,}498 - 61{,}645 - 69{,}870 &= -47{,}017 \end{aligned} \tag{14}$$

Augmenting the diagonal

Ignoring the relationship among sires, the ratio of error variance to sire variance (assumed to be 15) is added to the diagonal of the sire equations. The resulting equations are:

$$\begin{bmatrix} 33.26 & -3.51 & -2.40 & -6.32 & -6.03 & 14.75 & -14.75 \\ -3.51 & 38.21 & 0 & -11.21 & -8.49 & 19.70 & -19.70 \\ -2.40 & 0 & 48.24 & -16.23 & -14.61 & -2.40 & 2.40 \\ -6.32 & -11.21 & -16.23 & 48.76 & 0 & -17.53 & 17.53 \\ -6.03 & -8.49 & -14.61 & 0 & 44.13 & -14.52 & 14.52 \\ 14.75 & 19.70 & -2.40 & -17.53 & -14.52 & 34.45 & -34.45 \\ -14.75 & -19.70 & 2.40 & 17.53 & 14.52 & -34.45 & 34.45 \end{bmatrix} \begin{bmatrix} \hat{s}_2 \\ \hat{s}_3 \\ \hat{s}_4 \\ \hat{s}_5 \\ \hat{s}_6 \\ \hat{g}_1 \\ \hat{g}_2 \end{bmatrix} = \begin{bmatrix} -3{,}444 \\ 50{,}461 \\ 84{,}498 \\ -61{,}645 \\ -69{,}870 \\ 47{,}017 \\ -47{,}017 \end{bmatrix} \tag{15}$$

Considering additive relationships among sires

The additive relationship matrix A is:

$$A = \begin{bmatrix} 1.0 & .5 & .25 & .25 & .125 \\ .5 & 1.0 & .25 & .125 & .125 \\ .25 & .25 & 1.0 & .0625 & .5 \\ .25 & .125 & .0625 & 1.0 & .03125 \\ .125 & .125 & .5 & .03125 & 1.0 \end{bmatrix} \qquad (16)$$

Since the order is small, A^{-1} can be easily computed for this example. The result of multiplying A^{-1} times 15 is:

$$15A^{-1} = \begin{bmatrix} 21.4545 & -9.5455 & -2.7273 & -4.0 & 0 \\ -9.5455 & 20.4545 & -2.7273 & 0 & 0 \\ -2.7273 & -2.7273 & 21.3636 & 0 & -10.0 \\ -4.0 & 0 & 0 & 16.0 & 0 \\ 0 & 0 & -10.0 & 0 & 20.0 \end{bmatrix} \qquad (17)$$

The sire equations considering relationships but ignoring groups are:

$$\begin{bmatrix} 39.7145 & -13.0555 & -5.1273 & -10.32 & -6.03 \\ -13.0555 & 43.6645 & -2.7273 & -11.21 & -8.49 \\ -5.1273 & -2.7273 & 54.6036 & -16.23 & -24.61 \\ -10.32 & -11.21 & -16.23 & 49.76 & 0 \\ -6.03 & -8.49 & -24.61 & 0 & 49.13 \end{bmatrix} \qquad (18)$$

The right hand sides, of course, do not change. Several differences should be noted from equations (15) where relationships were not considered. The diagonals of (18) are always at least as large as (14) as are the off-diagonals. There will thus be more regression to the mean by the diagonals.

However, adjustment for sires of herdmates will be greater because the off-diagonals are larger. Note also when considering relationships that sire 3 is adjusted by sire 4 where no adjustment was made before.

Rows and columns no longer sum to zero.

Since it is not feasible to obtain an inverse directly for large order matrices, the simple method for writing the inverse directly from a list of parents discovered by Henderson will be shown. The pedigree of known parents for this example is:

Bull	Sire	Maternal grandsire
1	0	0
2	0	0
3	2	1
4	1	2
5	0	2
6	4	0

Using the simple procedure given in the methods section, A^{-1} is:

$$\begin{bmatrix} 1+1/11+4/11 & 2/11+2/11 & -4/11 & -8/11 & 0 & 0 \\ 2/11+2/11 & 1+4/11+1/11+1/15 & -8/11 & -4/11 & -4/15 & 0 \\ -4/11 & -8/11 & 16/11 & 0 & 0 & 0 \\ -8/11 & -4/11 & 0 & 16/11+1/3 & 0 & -2/3 \\ 0 & -4/15 & 0 & 0 & 16/15 & 0 \\ 0 & 0 & 0 & -2/3 & 0 & 4/3 \end{bmatrix} \tag{19}$$

which, when multiplied by 15, equals:

$$15A^{-1} = \begin{bmatrix} 21.8182 & 5.4545 & -5.4545 & -10.9091 & 0 & 0 \\ 5.4545 & 22.8182 & -10.9091 & -5.4545 & -4.0 & 0 \\ -5.4545 & -10.9091 & 21.8182 & 0 & 0 & 0 \\ -10.9091 & -5.4545 & 0 & 26.8182 & 0 & -10.0 \\ 0 & -4.0 & 0 & 0 & 26.0 & 0 \\ 0 & 0 & 0 & -10.0 & 0 & 20.0 \end{bmatrix} \qquad (20)$$

The equations ignoring groups are:

$$\begin{bmatrix} 21.8182 & 5.4545 & -5.4545 & -10.9091 & 0 & 0 \\ 5.4545 & 41.0782 & -14.4191 & -7.8545 & -10.32 & -6.03 \\ -5.4545 & -14.4191 & 45.0282 & 0 & -11.21 & -8.49 \\ -10.9091 & -7.8545 & 0 & 60.0582 & -16.32 & -24.61 \\ 0 & -10.32 & -11.21 & -16.23 & 49.76 & 0 \\ 0 & -6.03 & -8.49 & -24.61 & 0 & 49.13 \end{bmatrix} \begin{bmatrix} s_1 \\ s_2 \\ s_3 \\ s_4 \\ s_5 \\ s_6 \end{bmatrix} = \begin{bmatrix} 0 \\ -3{,}444 \\ 50{,}461 \\ 84{,}498 \\ -61{,}645 \\ -69.870 \end{bmatrix} \qquad (21)$$

Obtaining solutions

Solutions for (8), (15), (18), and (21) are given in Table A.1. These solutions illustrate several characteristics of mixed model solutions. Solutions for coefficients (8), where 15 was added to all diagonal elements, sum to zero. This can be used as a check that the solution was correctly computed.

The estimates from (15) were computed two ways: by iteration as was done in this study and by a direct solution (Dgelg). In the latter case, a Lagrange multiplier was used so that $\Sigma\Sigma(\hat{g}_i + \hat{s}_{ij}) = 0$. Solutions obtained by Dgelg were after imposing a restriction on groups such that they summed to zero. No restrictions were applied to groups when solutions were obtained by iteration. It can be verified, however, that solutions

Table A.1. *Solutions to examples*

	Coefficient matrices				
	(8)	(15)		(18)	(21)
		Iteration	Dgelg		
$\hat{s}_1$					762
$\hat{s}_2$	- 256	- 540	- 540	94	94
$\hat{s}_3$	852	540	540	951	951
$\hat{s}_4$	1178	1341	1341	1098	1098
$\hat{s}_5$	- 710	- 486	- 486	- 647	- 647
$\hat{s}_6$	-1064	- 855	- 855	- 697	- 697
$\hat{g}_1$		- 592	464		
$\hat{g}_2$		-1365	- 309		

obtained in both ways are consistent.

Iteration $\hat{g}_1 - \hat{g}_2 = -593 - (-1365) = 773$

Dgelg $\hat{g}_1 - \hat{g}_2 = 464 - (-319) = 773$

To obtain group solutions by iteration identical to Dgelg, the following is done:

$$X = \sum_{ij}\sum(\hat{g}_i + \hat{s}_{ij})$$

$$Y = X/\text{number of sires}$$

$$\hat{g}_i = \hat{g}_i - Y$$

For the example:

$$X = [-592 + (-540)] + (-592 + 540) + (-1365 + 1341) +$$

$$[-1365 + (-486)] + [-1365 + (-855)] = -5279$$

$$Y = -5279/5 = -1056$$

$$\hat{g}_1 = -592 - (-1056) = 464$$

$$\hat{g}_2 = -1365 - (-1056) = -309$$

Sires within groups also sum to zero.

for $g_1 \longrightarrow \hat{s}_i + \hat{s}_2 = -540 + 540 = 0$

for $g_2 \longrightarrow \hat{s}_1 + \hat{s}_2 = 1341 - 486 - 855 = 0$

Solutions for (18) and (21) are identical; however, solutions no longer sum to zero. For (21), there is an estimate for sire 1 who had no progeny. This is a pedigree estimate.