

Rick Bourdon, a Red Angus breeder currently involved in teaching and research at CSU, has designed this series (continued from last month's Journal) to help breeders understand and use available performance information.

A Series

Beef Cattle Breeding

by Dr. Richard Bourdon, Colorado State University

Part Nine

Sire Evaluation IV: The Animal Model

This article is the last in this series on sire evaluation and the last article to deal with how cattle are measured. The subject is the animal model, a statistical method which many experts consider the ultimate technique for genetic evaluation.

The animal model has not yet been used by breed associations. It is still somewhat experimental, and no one knows exactly what form the model will take when it is applied to actual field data. The discussion which follows may be a bit premature, but my intention is to show some of the possibilities for genetic evaluation in the near future.

As was the case for the sire evaluation methods outlined in the last article, the animal model will be described in terms of its abilities to overcome sire evaluation problems. The following is a list of characteristics we would expect to find in an ideal sire evaluation model:

1. Produces valid comparisons among sires.
2. Accounts for level of competition among sires.
3. Accounts for non-random mating.
4. Accounts for culling for poor performance.
5. Accounts for genetic trend.
6. Uses all available information.
7. Separates the growth component from maternal breeding value.

8. Accounts for reranking of sires in different environments.

9. Accounts for bad data.

The animal model is one of the class of models known as BLUP (Best Linear Unbiased Prediction) models. As such, it retains the advantages of the BLUP sire effects model discussed earlier (last month). It keeps track of which animals were compared in which contemporary groups, and in so doing accounts for level of competition among sires. It uses the numerator relationship matrix, a table of pedigree relationships which creates genetic ties among herds, years and contemporary groups. This allows sires which have not competed *directly* against each other to compete *indirectly* and increases the amount of information available for estimating any particular sire's breeding value or EPD. The animal model produces inbreeding coefficients as computational byproducts. Finally, the model emphasizes the *distribution* of progeny among contemporary groups, a characteristic which can help alleviate some of the bias caused by non-random mating or preferential treatment.

The animal model contains some major innovations which give it an advantage over the BLUP sire effects model. First, it evaluates *all* animals in a herd, not just sires. Hence the name "animal" model. The animal model

produces breeding value estimates for sires, dams, replacements—even prospective matings. It is, therefore, much more than a sire evaluation technique; it is an improved method for calculating breeding values in general.

Unlike previous sire evaluation models, the animal model takes into account an individual's own performance information in estimating his breeding value. This is a tremendous advantage because when the heritability of a trait is moderate to high, own performance can contribute a great deal to a breeding value estimate and its accuracy. Young sires with limited progeny or no progeny at all can be compared with older sires, resulting (one would hope) in increased use of younger sires and more rapid turnover of generations. With the animal model, more young sires will be evaluated accurately enough to appear in sire summaries, and these documents will be of more current, as opposed to historical, value.

Because the animal model evaluates dams as well as sires, it can account for non-random mating. The model keeps track of which sires were mated to which dams and adjusts its estimates accordingly. If a sire is mated to only the best producing cows, his EBVs or EPDs for growth will be adjusted downward.

The animal model provides an en-



tirely new way of analyzing weaning weight and calculating maternal breeding values. Weaning weight is divided into three component parts: a **direct effect** reflecting the calf's breeding value for growth to weaning, a **maternal effect** representing the dam's breeding value for milk production and mothering ability (maternal breeding value), and a **permanent environmental effect** reflecting environmental conditions which have permanently influenced a dam's mothering and milking abilities.

This arrangement separates the growth component from maternal breeding value, making it possible to evaluate animals independently for growth and maternal ability. A sire, for example, might have an EPD for *direct* weaning weight of +30 lb. and an EPD for *maternal* weaning weight of +20 lb. His calves would be expected to average 30 lb. above herd average at weaning due to growth inherited from their sire. His daughters' calves would be expected to be 35 lb. above average—15 lb. due to growth inherited from their grandsire and 20 lb. attributable to the maternal ability of their dams.

The inclusion of a component for permanent environmental effects enables the animal model to compute most probable producing ability or MPPA. Producing ability can be defined as a cow's contribution to the weaning weights of her offspring. That contribution includes genes for growth which are transmitted from the cow to her calf and maternal environment provided by the cow. Producing ability can be estimated with the animal model by simply adding a cow's EBV for *maternal* weaning weight, one-half her EBV for *direct* weaning weight (only half her genes for growth are passed to her calf) and her estimate for permanent environmental effect.

Up to this point, we have thought of sire evaluation models in the context of **single trait evaluation**; only one trait is evaluated at a time. The animal model is capable of **multiple trait evaluation**. With multiple trait evaluation, animals are rated for two or more traits simultaneously using estimates of correlations between traits. The multiple trait model has two advantages: it increases the amount of information available for any given breeding value estimate, and more importantly, it reduces the bias caused by culling for poor performance.

To see how the bias caused by culling of poorer performing animals can be overcome by a multiple trait model,

consider the example of a sire whose offspring have been culled heavily at weaning due to low weaning weights. Because they are a select group, his remaining calves will probably be average or better for yearling weight. A single trait model will be blind to the selection which has occurred and will rate the sire low for weaning weight, but average or above for yearling weight. A multiple trait model will adjust the sire's yearling weight EBV for the weaning weights of all his calves, including those that were culled. In this way, the multiple trait model counteracts the effect of culling at weaning and produces estimates for yearling weight similar to those obtainable had no culling occurred.

The animal model is well equipped to account for genetic trend. This ability is a happy consequence of using a full numerator relationship matrix which creates ties between all animals—sires, dams and offspring. Even though two animals may be generations apart, their EBVs computed with the animal model are directly comparable. It is even possible to express all estimates as deviations from the average of foundation animals. When breeding values for all sires and dams, past and present, in a herd are listed in this manner, we get a complete picture of the herd's genetic history.

If sires really do rank differently in different regions or management systems, the only way to fairly compare them is on a within-environment basis. This would mean separate evaluations for each environment—a solution which may not be practical.

The animal model has only modest ability to reduce the bias caused by preferential treatment or inaccurate data. Statistical models operate at the mercy of the data they were designed to analyze; if the data are worthless, so will be the results. No model can overcome the problem of bad data.

All genetic models depend to some extent on quantities which can only be estimated. Even the simplest breeding value calculation, for example, requires an estimate of heritability. Because of its multiple trait characteristics and unique way of handling maternal breeding value, the animal model relies on a number of heritability and correlation estimates. It is particularly vulnerable, therefore, if these estimates turn out to be inaccurate.

The biggest problem with the animal model, and the one which has so far prevented its implementation, is computational difficulty. Applying the animal model to a realistically large set of field data is a computing nightmare. Fortunately, we now have "super computers" which may be able to tackle

Table 1.


Characteristic	BLUP Animal Model
1. Produces valid comparisons among sires.	good
2. Accounts for level of competition among sires.	good
3. Accounts for non-random mating.	good
4. Accounts for culling for poor performance.	good
5. Accounts for genetic trend.	good
6. Uses all available information.	good
7. Separates the growth component from maternal breeding value.	good
8. Accounts for reranking of sires in different environments.	poor
9. Accounts for bad data.	fair

Table 1 rates the animal model for the characteristics we would like an ideal sire evaluation model to have.

As you can see from the table, the animal model is almost, but not quite an ideal method for genetic evaluation. The extent to which valid comparisons among animals are made depends on the degree to which individuals in different herds are related. For practical purposes, this means that the animal model (and other BLUP models) will be most effective when sires have progeny in many herds, i.e., when artificial insemination is used extensively within a breed.

The animal model, with all its power, can do little to overcome the effects of genotype by environment interactions.

such large problems. And another generation of "super computers" is just around the corner.

The animal model is neither perfect nor easy to implement. However, because it makes use of all available information, because it corrects for biases caused by non-random mating, selection and genetic trend, because it estimates maternal ability independent of growth, and because it offers more accurate evaluation of young animals of both sexes, the animal model will be the model of choice in the future. 

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NEXT:
Weighing the traits
—what is the best animal?