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Model-based Approaches to Improving Accuracy of Genetic Evaluations and Rewarding High Quality Data

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Motivation for the Topic

- Donnell Brown asked us to address some provocative questions about data quality, specifically with respect to contemporary group formation and weighing conditions.
  - Bob Weaber just addressed those issues
  - Part of Donnell's framing of the problem was an enumeration of things computers can't do.

I am going to propose some ways we could address Donnell's concerns through better genetic evaluation models

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"Things That Annoy Me About National Cattle Evaluation"

- The following slide is taken directly from a presentation I gave in this committee 4 years ago with the above title

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Why Don't We Reward Breeders for Submitting High Quality Information?

- Breeders who submit high quality information could have higher accuracies.
- Those who do not or where there is evidence of bias could have lower accuracies and their animals EPDs could correspondingly be shrunken more toward the mid-parent mean.
- This could be done statistically as part of the evaluation.

How to Reward Breeders for Submitting High Quality Data

- Apply a lower residual variance to records submitted by breeders with evidence of high quality
  - This is a parameter in all genetic evaluations
  - It reflects the amount of random noise in the data
  - It is generally assumed the same for all records, regardless of source.
  - Not all evaluation software could accommodate heterogeneous residual variance, but it does not inherently increase the computational burden.

What Would Rewards for Submitting High Quality Data Be?

- Higher accuracy EPDs for the same amount of information submitted.
- Greater influence than breeders with low quality on evaluations of animals used in multiple herds

Example

- Donnell made the excellent point that weighing conditions and variation in fill could significantly impact "environmental noise" (= residual variance).
  - Particularly relevant to weight traits.
  - Breeders who use better weighing conditions should have lower residual variance and should reap the benefit of higher accuracy

How Would Heterogeneous Residual Variance be Determined?

- Estimated directly on a per-breeder basis in the evaluation.
  - Improper contemporary group formation would be reflected here
- Possibly adjusted up or down based on indirect diagnostics
  - Would basically compare ranking based on within-herd with breed-wide ranking
  - These might have greater power to detect cheating
  - Lack of phenotypic variation, especially for birth weight
  - **NOT** based on subjective opinion of Breed Improvement Director

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Robust Prediction

- "Outliers" are shrunk toward the mean more than observations with residuals close to 0.
- While not intended to completely replace rule-based data edits, it could reduce reliance on them.

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Computational Feasibility

- Primary obstacle is whether the software used for genetic evaluation is designed to accommodate these models.
- Impact on computing time and memory requirements should not be excessive.

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Fitting Weigh Order or Time in the Model

- Could adjust out some of the residual variance due to variation in fill.
  - Within group regression on time or order
- Could be easily accomplished by breeders who capture weights automatically from electronic scale and IDs.
- More important for larger contemporary groups.
  - Preferable to splitting calves from one pasture into arbitrary contemporary groups.

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Accommodating More Frequent Weights Through Use of Random Regression Model for Growth

- Use as many weights as are available and at whatever ages they were taken.
  - No edits for weights taken out of range.
- Predicts growth curves
- It is more computationally intensive than our current standard analyses of weight traits.

Conclusions

- Accounting for data quality in genetic evaluations could improve accuracy of the resulting evaluations directly.

- The greater impact could be indirect, e.g. providing incentives for breeders to follow the practices Bob described to improve data quality.

Questions?

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