Frequently Asked Questions:
Multi-breed Genetic Evaluation powered by BOLT

By IGS Genetic Evaluation Team

The new genetic evaluation, Multi-breed Genetic Evaluation powered by BOLT, offers groundbreaking advances in the prediction of EPDs for the IGS group. Here are some frequently asked questions and answers to help you better understand the new evaluation.

1. What are the key features of the Multi-breed Genetic Evaluation powered by BOLT?

- Faster and more automated system allowing for frequent genetic evaluations.
- Improved use of genomic data with Single-step.
- Improved methodology for predictions of all traits.
- More accurate accuracy.
- More flexibility to add additional traits or change methods for future improvements.

2. How is IGS's single-step approach different from blending for genomic evaluation?

The blending approach uses separate steps to calculate genomically enhanced EPDs. This approach requires two steps. The first step is to estimate the effects of DNA markers through a process called "training" or "calibration". These effects are then used to calculate molecular breeding values (MBVs) on genotyped animals. The MBVs are then combined with traditionally calculated EPDs to enhance the accuracy of the traditionally calculated EPDs. The blending process is only performed on genotyped animals.

Befitting its name, the single-step approach calculates genomically enhanced EPDs in one step — using DNA, pedigree information, and phenotypes simultaneously. As a result, the DNA information not only improves the accuracy of prediction on genotyped animals, but also on the relatives and contemporaries of the genotyped animals. In a sense, all animals are genomically enhanced under the single-step approach.

There are also issues inherent in the blending process that are solved with single-step. Similar to the fact that only reporting phenotypes on a selected group of animals in your herd can lead to less informative (and more biased) EPDs with traditional evaluation, problems can exist with blending as it only involves genotyped animals — and genotyped animals tend to be highly selected. However, because single-step includes information from non-genotyped as well as genotyped animals, the issues are corrected.

3. How is the Multi-breed Genetic Evaluation powered by BOLT different than other single-step models used in other genetic evaluations?

It is well established that DNA markers vary greatly in their effect on traits — ranging from a large to no impact. To leverage this biological fact in a statistically advantageous manner, the BOLT single-step method only utilizes markers that have a meaningful impact on the traits of interest, while ignoring those that have little to no effect. By using this approach, BOLT reduces the statistical "noise" and thereby increases the accuracy of prediction. By circumventing the "noise," BOLT-generated EPDs tend to be more accurate than EPDs generated by organizations that are relegated to using all markers in their single-step evaluation.

4. How many DNA markers are being used?

The Multi-breed Genetic Evaluation powered by BOLT uses a subset of weighted markers based on a research study performed by Drs. Mahdi Saatchi and Dorian Garrick, while they were scientists at Iowa State University. Drs. Saatchi and Garrick first used the 50,000 markers to determine a subset of weighted markers that are highly associated with economically relevant traits in beef cattle with consistent effects across breeds. Because the IGS evaluation is for multiple breeds, it is important to remove markers with inconsistent effects or no effects in different breeds.

The Saatchi and Garrick research also found that utilizing genotypes on animals of multiple breeds consistently increased the accuracy of prediction within a particular breed when compared to limiting DNA utilization to only animals of a particular breed.

5. Why are some traits influenced by markers and others are not?

The genetic architectures of various traits are different. Some are controlled by few genes with large effects and some are controlled by many small effects genes. In the current DNA profilers, there are some markers with high correlations with corresponding genes for some traits and low correlations with others. That's why we see the different DNA added values for different traits. It is hard to change the genetic architecture of a trait. But, new DNA profilers or future technologies may help to improve the value of DNA information for such traits.

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Furthermore, some maternal traits, like Maternal Calving Ease and Milk, are difficult to predict with genomics because there are so few females genotyped. Increasing the number of cows and heifers genotyped will improve the ability to use genomics to predict maternal traits.

6. Will genomic testing replace the need to submit phenotype records?

No, reporting actual records is critical. The value of genomic predictions increases as the amount of phenotypic information increases. Furthermore, at this point, animals cannot achieve high accuracy with genomic data alone. High accuracy EPDs are only achievable by collecting many phenotypic records on offspring.

7. How do we know predictions via BOLT are better than the previous system (Cornell software)?

The IGS evaluation team has conducted a series of validations to compare the BOLT system to the Cornell system. BOLT-derived EPDs had higher correlations to birth, weaning and yearling weights (0.34, 0.29, and 0.26, respectively) than the Cornell derived EPDs (0.27, 0.19, and 0.20, respectively). Furthermore, there was a larger difference in average progeny performance (birth, weaning, and yearling) of the top 1% compared to the bottom 1% animals in the BOLT derived EPDs compared to the Cornell calculated EPDs. Both validations suggest the BOLT EPDs align better with the actual phenotypes than the Cornell EPDs.

8. Why do some animals have substantial changes in their indexes?

Though the correlations between the previous (Cornell derived) EPDs/indexes and the BOLT derived EPDs/indexes are relatively strong, there will be some animals that happen to move in a consistently favorable or unfavorable direction in a number of EPDs. Because indexes are comprised of several EPDs, even though movement in individual EPDs may be considered small, movement in the same direction across EPDs may yield sizable movements in the index value. This is particularly true for animals that have consistent movement in traits that are drivers of a particular index. Though in a large population like ours we would expect to see several animals with substantial index movement, these animals will be the exception to the rule.

9. How does BOLT improve our calculation of accuracy?

"True" accuracy can be thought of as the gold standard of accuracy. It is statistically unbiased, and therefore the ultimate measure of accuracy. True accuracy is the accuracy resulting from direct calculation. Unfortunately, even with the massively powerful computing capacity now in existence, the direct calculation of accuracy is not possible on datasets the size of ours. Because we cannot calculate accuracy directly, other approaches to accuracy calculation have been developed.

In our Cornell evaluation platform, and all others in existence other than BOLT, the calculation of the accuracy associated with each EPD is achieved through "approximation" methods. It has long been known these methods are a very crude approach to the calculation of accuracy — tending to overestimate accuracy.

Another approach to the calculation of accuracy is via "sampling" methodology. Sampling is shown to be a more accurate predictor of accuracy. In fact, the results of this method were reported to be virtually identical to true accuracy. Unfortunately, due to its computationally intense nature, sampling has long been thought an infeasible approach to the calculation of accuracy on large databases.

BOLT, however, has changed the landscape in this area. By employing unique computing strategies that leverage both software and hardware efficiencies, BOLT performs what was previously unthinkable — utilizing a sampling methodology to calculate what is essentially true accuracy.

Because BOLT can calculate true accuracy, we can put more confidence in our accuracy metrics. Put another way, unlike with approximation, we can count on the predicted movements associated with possible change holding true over time. This was not the case with our Cornell system nor any other system in existence.

10. Why do the carcass EPDs generally have an increase in accuracy with BOLT while this is not a case for other traits?

You will notice that while the Multi-breed Genetic Evaluation powered by BOLT will generally produce lower accuracies than the Cornell system for growth and calving ease traits, the opposite is true for carcass traits.

One reason behind the differing accuracy outcomes is several years ago the evaluation team developed a way to temper inflated accuracies in the Cornell carcass evaluation. Unfortunately, this was not possible for growth traits.

Another reason is that the Cornell system only used the carcass and its corresponding ultrasound trait (e.g., marbling score and IMF) to predict carcass EPDs, while records on several additional correlated traits are leveraged with the BOLT system.

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A new feature of the BOLT evaluation is a new approach to the calculation of Carcass Weight EPDs. Due to limitations, our previous Carcass Weight EPDs did not incorporate actual carcass weights. They were predicted through an index of birth, weaning, and yearling weights. Besides using prior growth records (weaning, post weaning), the new approach also includes actual carcass weights. This feature will undoubtedly lead to a more accurate prediction of carcass weight.

11. What can I do to improve the predictions on my herd?

Whole Herd Reporting — If you haven't already, you should consider enrolling your entire herd with a breed association total herd reporting program as it offers the most complete picture of the genetics involved in your herd.

Proper contemporary groups — It is important for the genetic evaluation that you group, to the best of your ability, animals that were treated uniformly. Proper reporting of contemporary groups ensures better predictions for all.

Take data collection and reporting seriously — Phenotypes are the fuel that drives the genetic evaluation. Take pride in collecting accurate data. If possible, try to collect additional phenotypes like mature cow weight, cow body condition score, feed intake, and carcass data.

Use genomics — DNA testing adds more information to what we know about an animal. The more genotypes we collect, the better we can predict DNA-tested animals in the future. Also, the more relatives genotyped, the better we can predict their relatives in future generations. Therefore, to ensure your bloodlines are well represented in the predictions, genotype your animals. ◆