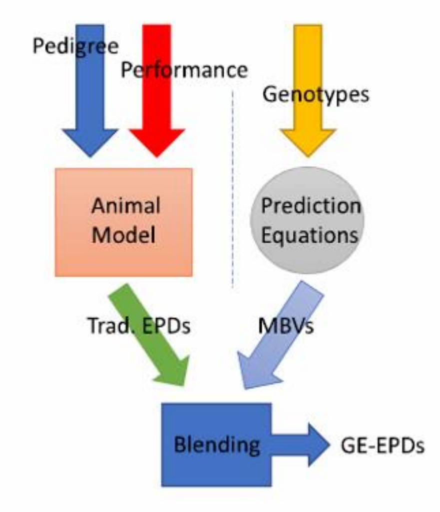
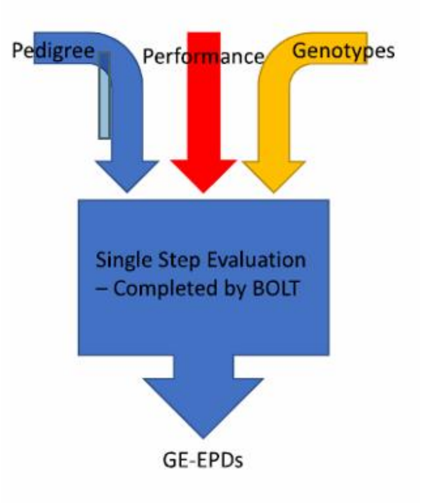
# *New* EPDs arriving December 2017 – the nuts & BOLTs!

The new BOLT (Biometric Open Learning Technology) moves away from a post-run blending of genomic data and uses a Single Step Analysis to better incorporate this important data.

Old system



New system:



- The Single Step model is different than the Traditional Multistep model because:
  - Multistep model assumes that all traits are correlated
  - Single Step will decouple certain traits from being correlated, which decreases the amount of correlated trait data and will provide the farmer and rancher with a better estimation on the actual trait of interest

- **Single Step Models (BOLT) are made up of the following data:**
  - BW, WW, YW & MM EPDs
    - Come from a model which includes data from BW, WW & YW phenotypes
  - SC EPDs
    - Come from a model which included SC and WW phenotypes
  - CW & CREA (C stands for Carcass)
    - Come from a model which includes BW, CW, CREA and Scan REA (SREA) phenotypes
  - CFAT & CMARB EPDs (C stands for Carcass)
    - Come from a model which includes BW, CW, CFAT, CMARB, Scan Fat(SFAT) & Scan IMF (SIMF) phenotypes
  - MCW EPDs
    - Comes from a model which included MCW and WW phenotypes
  - CE & MCE EPDs
    - Comes from a model which included BW, CE & MCE observations
  - SCF EPDs
    - Comes from a model which includes SCF observations
  - UDDER & TEAT EPDs
    - Comes from a model which includes Udder and Teat observations

Four Key Points that will drive change in AHA/CHA EPDs

- BOLT Handles Genomics Better
  - BOLT incorporates Genomics into the evaluation in a more correct fashion when compared to how we utilized Genomics in the past
  - Only the most influence markers for each trait are used; this improves the accuracy of the genomic prediction
- BOLT separates Traits
  - In the past other traits had influence over the trait of interest through correlations in each evaluation
  - Individual traits have been separated, as much as possible, from other traits, to allow for better selection on the trait of interest
- BOLT Uses a Data Cut Off to Remove Bias
  - Performance data has been cutoff at 2001, any data recorded before that date has been removed from the evaluation
  - This will have an effect on the accuracy of old bulls and potentially their EPDS, if they have no progeny born since 2001
  - This did not change the ranking of bulls, however it removes potential bias that could be seen in the data, before whole herd reporting began
- BOLT Calculates Accuracy Differently
  - In the past, our genetic models could only estimate accuracy, this was the best tool at the time, however with BOLT accuracy can be calculated and not estimated

o **The Growth model** is relatively unchanged and the results show that animals can have some movement dependent on genomic influence or data that is included (or removed) in the evaluation, but for the vast majority of animals the resultant BOLT EPDs will be quite similar to previous EPDs

Most Noticeable Changes

- Largest changes you will notice are in CE and MCE; this change is due to 2 things:
  - We are using **<u>MORE</u>** calving observations:
    - In the past if a calf crop was all scored as Unassisted, the data could not be used in the evaluation, because the evaluation needed variation to determine a deviation from average
    - BOLT used a different method and can use all data, even data that is uniform across a calf crop
- The resulting calving ease EPDs (CE & MCE) in the BOLT analysis will have a larger range of possible values than we saw before, this means that better CE/MCE bulls will have larger values than previous, and bulls that have poorer CE/MCE will have a more negative EPDs than previous
  - This will allow you to select harder for cattle that deviate more on CE however maintain their performance

  - We are only using 2 yr old data
    - The definition of CE remains the same as previous; the difficulty in calving observed at a heifers first calving
    - Data from older cows has been removed from the evaluation as this data did not actually add any power to the analysis
    - Even with removing the older cows, we are still using **<u>MORE</u>** data than before because of the inclusion of data with no variation

        - Accuracies have seen a more significant change as in the case of older, currently unused bulls, some (and possibly all) of their progeny records have been removed from the analysis, however the change in accuracy on a population basis has been quite small

    - As well BOLT provides ACTUAL Accuracies, the previous analysis provided *estimated* Accuracies

- **FMI, MPI and RFI**
    - FMI, MPI and RFI are indices that are calculated post-EPD run, based on economic drivers that determine the proportion of each trait that is accounted for in the index
    - All these will have to be revamped in order to account for the changes in the model from previous to now
    - CHA will be working revamp these indexes and reintroduce them to the Analysis, until that time we will not be reporting any index values for FMI & MPI.

NEW! **SCF** - **Sustained Cow Fertility** (replacing STAYABILITY)
This trait predicts a female's ability to stay in the herd through the age of twelve (ten calving's after calving as a two-year-old heifer). The EPD is reported on a probability scale meaning that a higher EPD for a sire means his daughters are more likely to remain fertile and produce more calves throughout their lifetime. Because of the limited number of phenotypes collected that have a corresponding genotype, the genomic component is not included in this model.

NEW! **Udder & Teat**
Both UDDR and TEAT EPDs are reported on the scoring scale. Differences in sire EPDs predict the difference expected in the sires' daughters' udder characteristics when managed in the same environment. For example, if sire A has a UDDR EPD of 0.4, and sire B has a UDDR EPD of -0.1, the difference in the values is 0.5, or one-half of a score. If daughters of sires A and B are raised and managed in the same environment, you would expect half a score better udder suspension in daughters of sire A, compared to sire B.
Likewise, if sire A has a teat size EPD of 0.4, and sire B has a teat size EPD of -0.1, the difference in the values is 0.5, or one-half of a score. If daughters of sires A and B are raised and managed in the same environment, you would expect half a score smaller teat size in daughters of sire A, compared to sire B. Just like with the scoring system, the higher the EPD the better for both traits.

In summary, CHA is confident that we are now using the most robust and progressive genetic evaluation available that will help identify Hereford genetics that are the most profitable for the commercial Industry.

More details from the American Hereford Association Genetic Evaluation Updates