

A **COMPARISON** BETWEEN

BLUP breeding values and **traditional** indices:

A **REVISIT**

DR JAPIE VAN DER WESTHUIZEN

SA STUD BOOK AND ANIMAL IMPROVEMENT ASSOCIATION

The use of BLUP breeding values as a means of comparing the genetic merit of livestock became common practice in animal breeding globally.

Traditionally, especially for beef cattle (but also small stock and to a lesser degree for dairy cattle), individual animals were compared based on their own performances within their contemporary (test) groups. The performance of each individual was then compared to the group mean and expressed as a “ratio”. The resultant calculation is also usually multiplied by 100.

In South Africa this ratio, expressed relative to 100, is popularly called an INDEX. To equalise the “playing field”, pre-corrections are usually made for the age of the animal and the age (and sometimes parity) of the dam of the animal (for maternally influenced traits, such as weaning weight). Comparison groups are usually separated for different sexes.

In many cases, Breeders’ Societies set subminimum values on the eligibility of animals to be considered as breeding contenders, based on these Indices.

BLUP breeding values (also called EBVs, EPDs, ETAs or otherwise), the more accurate predictions of genetic merit, resulted from the initial theoretical developments of Professor Charles Henderson at Cornell University. Due to constraints in computing power, initial genetic merit predictions were based on Sire models and mainly applied in dairy populations. As the abilities of computers exploded (in terms of memory expansion, storage capacity and speed of calculation) and alternative algorithms developed to deal with large matrices, model development and application lead to more accurate predictions of genetic merit for possible breeding animals. Current practices are usually based on so-called “Animal Models”, taking all relationships and measurements into consideration.

BLUP breeding values basically address the serious shortcomings in the prediction of genetic merit of animals considered as replacements or to be culled. Indices only consider performance within their own comparison groups but do not account for the most important question, namely: “will these differences in measured performance result in similar values in the offspring and other circumstances?”

Furthermore, the question also remains if these differences in performances result in the superiority (or inferiority) of the sire or the dam of individuals.

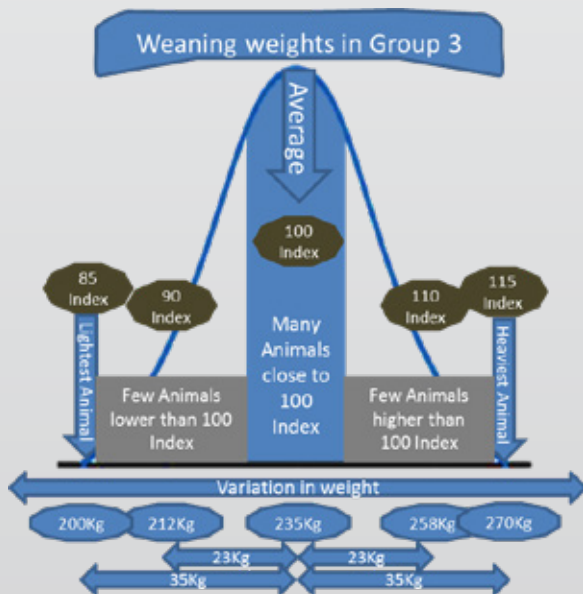
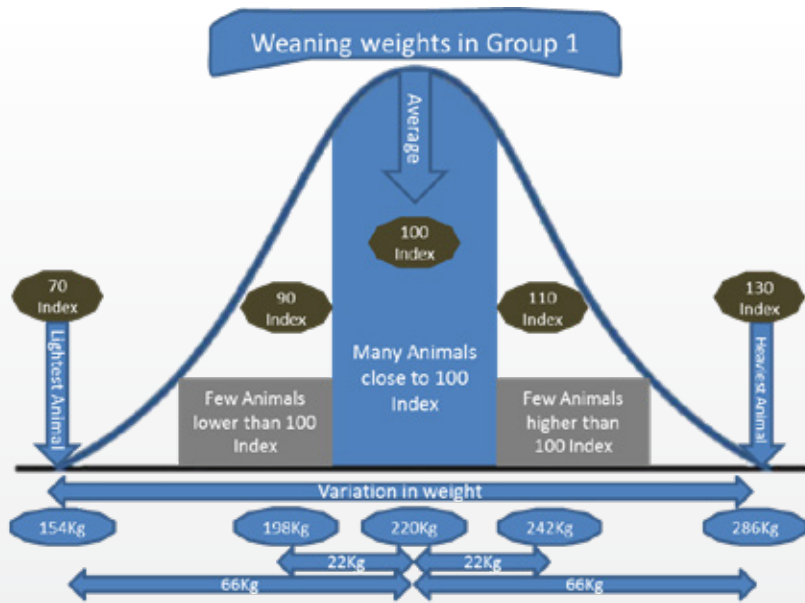


Figure 1 depicts the expected differences in the ranges of indices in three groups of calves recorded for weaning weight.

Differences in the variation of weaning weights in three different measurements (contemporary) groups with the same mean.

From Figure 1 it is clear that the spread or variation in the different contemporary groups is different, resulting in differences in the prediction ability of indices. Group dynamics, as caused by environmental differences, are random and by chance. In relying on indices, this is not taken into consideration at all. It also has a built-in bias and influences selection decisions unfairly, especially where breeds insist on sub-minimums (independent culling levels) for animals to be deemed fit as replacements in the breed.

This last question was one of the driving forces of Henderson to develop a system where the mating bias built into simple averages of performance among the progeny of different bulls could be accounted for. Simply put, one bull's progeny could outperform another simply because he was mated to superior cows and not because of his superior genetic merit. These and the other major factor leading to bias in favouring some animals over others, namely differences in environmental (non-genetic) effects, make BLUP breeding values more appropriate in predicting the genetic merit of livestock.

Why are Indices stable but BLUP breeding values change from one evaluation to the next?

Intuitively, users of predictions describing the genetic merit of animals will put more trust in so-called "stable" values. These often lead to a degree of scepticism in BLUP breeding values due to regular adjustments in predictions. The basis of prediction

between the two methods needs better understanding before conclusions on their usability can be drawn.

Per definition, the “breeding value” of an animal refers to the number of additive genes it has, favouring the trait of interest. In layman’s terms, this could be explained as “how much of its superiority (or inferiority) in measurement is due to its genes that can be transferred to its progeny?” One could also say: “The animal’s value as a parent, compared to the same values of other animals eligible as parents”.

Indices, as defined by the measurement of an animal relative to its contemporaries, are calculated only once when the animal is measured or recorded. It is never again updated, irrespective of how the animal is breeding (in comparison to other parents). The values calculated also assume that this relative value or superiority can be transferred in its entirety to the progeny of the chosen animal.

To explain: an animal with a 110 weaning index is deemed to be a superior parent, even if the average value of its progeny is 95. In effect this assumes that the heritability is 100% (therefore no environmental influence on the expression of the trait), neglecting the fact that all quantitative traits are influenced by genetic differences as well as influence from the environment.

It is also known that all animals receive a random sample of genes from both parents. This means that the first assumption would be that the average genetic merit of all animals in the population (breed) will be the “Parent Average” of all parents used but each individual animal will deviate somewhat from that average (due to Mendelian sampling).

Indices do not take the parents’ genetic merits into account. The assumption is that all animals within the contemporary (measurement) group will be of equal genetic merit before measurement. Put differently, the prediction of an animal’s genetic merit, using indices, assumes that the average genetic levels of all measurement groups are equal. This assumption is obviously also false.

One very distinct difference between genetic merit predictions based on indices and BLUP breeding values occurs with maternally influenced traits such as birth and weaning weights. When calculating an index for such traits the maternal influence on the expression

(measurement) is ignored. Selection making use of such traits is therefore very inefficient, especially in cases where the maternal and direct components are (genetically) negatively correlated.

Modern BLUP models split these two effects effectively and even provide for the so-called permanent (dam) environmental effects (and in pigs even the random litter effects), increasing the accuracy of genetic merit prediction.

The stability of breeding value predictions with the traditional indices (or ratios) therefore does not make them more accurate. Many of the assumptions are not as sound as for BLUP breeding values. In fact, BLUP breeding values take many more sources of information into account. Adjustments are the result of an increase in the accuracy of prediction, something that never happens in the case of indices.

One can in fact say that relying on indices gives a false sense of security, especially on a global (breed) scale.

Figure 2 illustrates the difference between indices from different contemporary groups, with different group means and variation in weights, and BLUP breeding values (especially where BLUP breeding values are standardised, like the Breeding value indices by SA Stud Book).

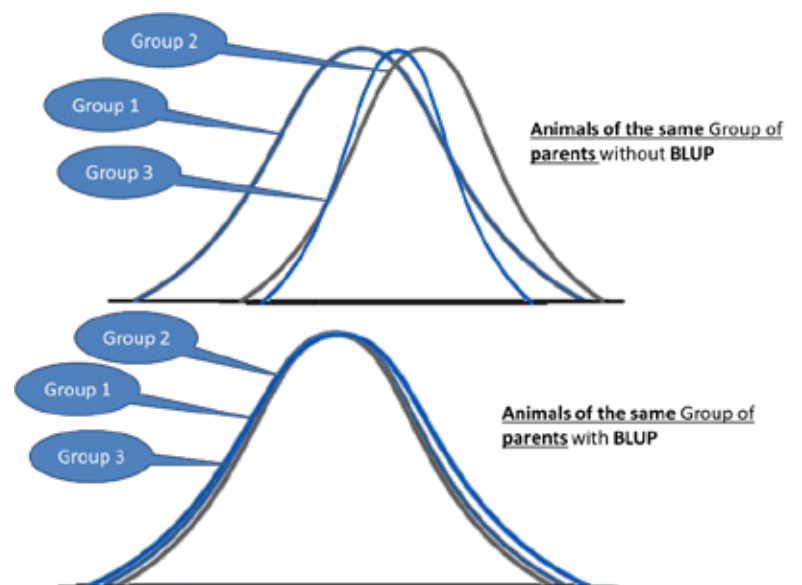
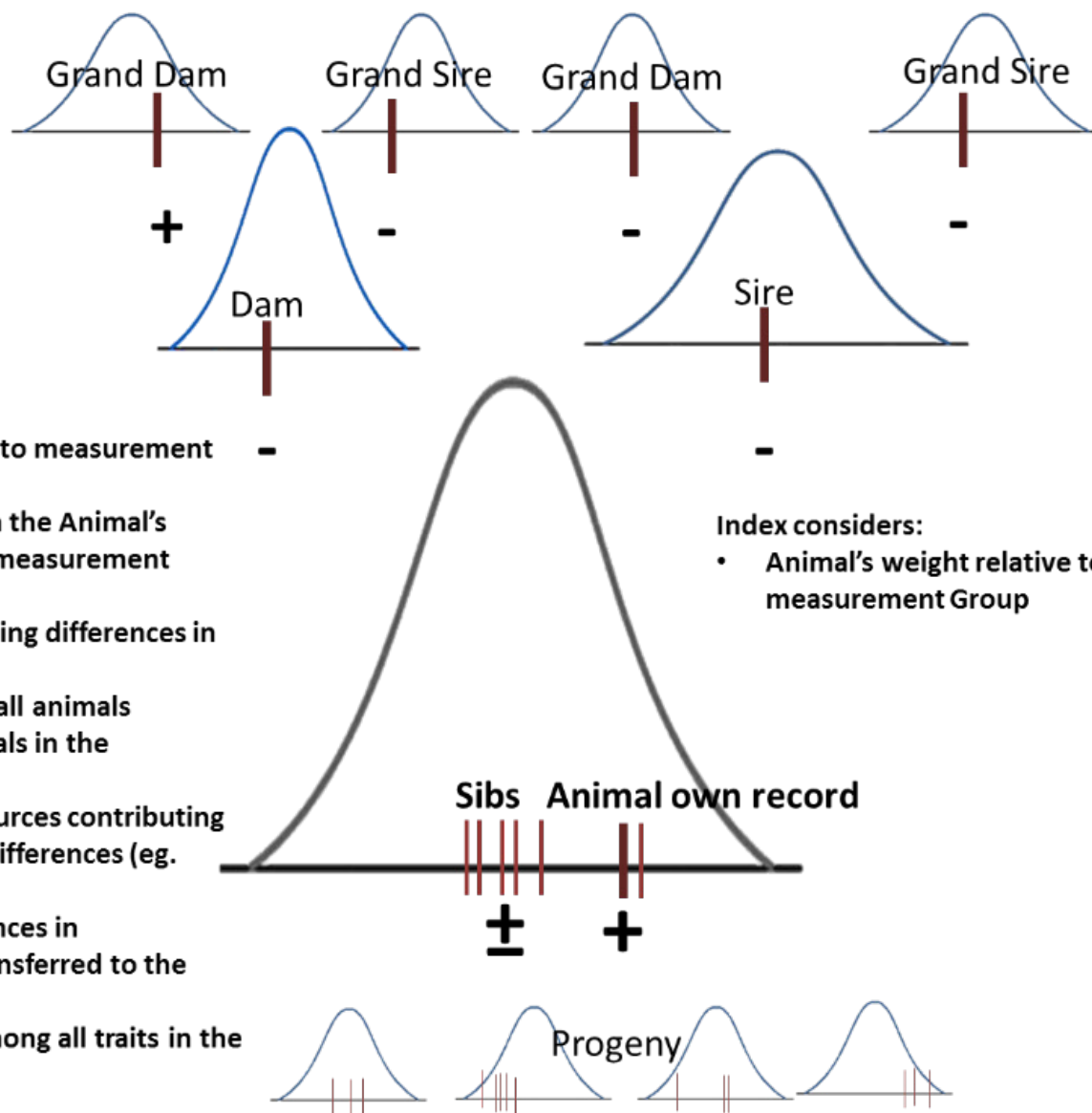


Figure 2. Differences in the way group means and variation in weights are considered by traditional index (ratio) calculations and BLUP breeding value predictions.

Figure 3



BLUP considers:

- Animal's weight relative to measurement Group -
- Weight of each animal in the Animal's lineage relative to their measurement groups -
- Non-genetic factors causing differences in performance -
- The relationship among all animals -
- Genetic level of all animals in the measurement group -
- Separation of genetic sources contributing towards measurement differences (eg. Direct vs Maternal) -
- What part of the differences in measurement can be transferred to the progeny of the animal +
- Genetic relationships among all traits in the model used +

Index considers:

- Animal's weight relative to measurement Group -

In conclusion, Figure 3 summarises the main differences between the consideration of sources of information in the prediction of genetic merit between traditional indices and BLUP breeding values.

Figure 3. Illustration of the difference between the sources of information used in calculating a traditional index (ratio) versus a BLUP EBV

The next steps

Traditional indices for individual traits and the application of independent culling levels (minimum standards) considered in selection programs for livestock made a valuable contribution towards the breeding of livestock in the past. BLUP breeding values have, however, now become the accepted norm to predict genetic merit.

The next enhancement is also becoming common practice, namely the inclusion of genome information to increase the predictive accuracy, especially for young animals and for traits only measurable in one sex (such as milk and female fertility) can only be recorded very late in life (such as herd life) or is very difficult or expensive to measure (like feed intake, carcass, and meat quality-related traits).

A very important development is the use of so-called "Selection Indices" (NOT TO BE CONFUSED WITH THE TRADITIONAL INDICES!) where BLUP breeding values are combined into a single economic value based on input costs and prices realised for the product of the production system. The Logix Cow value, Growth Value and Production value are such values, making provision for the selection of more profitable animals. ■