

Addressing topics raised by workshop participants

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Use of \$INDEX: What is the correct weighting of traits?

A number of participants asked to discuss the different avenues available in PIGBLUP to put the correct weighting on individual traits. A first step in fine tuning the \$INDEX for each breeder's specific needs is to evaluate where the current emphasis of the \$INDEX is. PIGBLUP provides information about the \$INDEX under Statistics of EBVs. This screen is reached through the following steps:

1. Main Menu
2. Generate Output
3. EBVs for traits and \$INDEX
4. Sort output by \$INDEX (it doesn't matter on which trait you sort the output)
5. Limit output by : in order to show EBVs for 10% classes of the whole data set fill in the following details:

The screenshot shows a dialog box titled "PIGBLUP Limit Output by H5NB1". It contains the following fields and values:

Field	Value
Animal Identification	[Empty]
Date of Birth	[Empty]
\$Index EBU	[Empty]
Day of Test	[Empty]
Percent of Animals: Selected (%)	100
Class Size (%)	10

Buttons: Cancel, OK

6. Sex class displayed: if the data set is large enough choose "Gilts" or "Young boars". This guarantees that results are not influenced by any past selection decisions. However, for smaller data sets it might be necessary to choose "All sexes"
7. Select Output: Choose statistics to screen. This will provide you with the following page (based on testau1.dat):

Top	Bttm	Find	Next	Goto	Help	Quit	Line:	1
DERIVED Approximate Index Weights:								
	ADG	BF	NBA					
	0.369	-13.443	4.996					
(The derived index weights represent the approximate change in the index per unit increase in the EBU's.)								
	ADG	BF	NBA1	NBA2	NBA	\$Inx		
CORRELATIONS:								
ADG	...	0.038	0.018	0.024	0.023	0.509		
BF	-0.030	-0.039	-0.037	-0.833		
NBA1	0.837	0.931	0.137		
NBA2	0.979	0.153		
NBA	0.153		
SELECT	10%							
Means	25.02	-1.471	0.099	0.129	0.117	28.88		
S.D's	17.0	0.544	0.351	0.385	0.352	5.57		
Counts	232	232	232	232	232	232		
SELECT	20%							

1. Meaning of output

Firstly, the approximate index weights are presented for each trait included in the \$INDEX. These index weights represent the economic worth of changing each trait by one unit and keeping all other traits constant. The basis of the \$INDEX is one litter. In this example the \$INDEX is (on average) derived as:

$$\text{\$INDEX} = 0.369 * \text{EBV_ADG} - 13.443 * \text{EBV_BF} + 4.996 * \text{EBV_NBA}$$

For each animal the \$INDEX is derived as the sum of individual trait EBVs for ADG, BF and NBA multiplied by their respective index weight. The EBV for NBA is the weighted sum of the EBVs for NBA in the first parity (NBA1) and later parities (NBA2). For example, a boar with EBVs of +50g ADG, -1.5mm BF and +0.1 NBA would have a \$INDEX of:

$$\begin{aligned} \text{\$INDEX} &= 0.369 * 50 + (-13.443) * (-1.5) + 4.996 * 0.1 \\ &= \text{A\$39.114} \end{aligned}$$

If this boar is mated to a sow with the same \$INDEX then their litter would have an economic superiority of A\$39.114 in comparison to the base population.

Secondly, correlations between individual traits and the \$INDEX are shown. In this example, correlations between the EBVs for ADG, BF, NBA1, NBA2 and NBA with the \$INDEX are 0.509, -0.833, 0.137, 0.153 and 0.153, respectively. These correlations show that the \$INDEX is mainly based on backfat and growth rate. Little emphasis is put on litter size.

In the section, "Limit output by", the whole data set was divided into 10% classes based on \$INDEX value. As a result, means for individual traits and the \$INDEX are shown for each 10% class below the table of correlations among EBVs. In this

example, the top 10% of all animals have a mean EBVs for ADG, BF, NBA1, NBA2 and NBA of 25.02 g/day, -1.471 mm, 0.099 piglets, 0.129 piglets and 0.117 piglets, respectively. The mean \$INDEX is A\$28.45.

2. Evaluating different indices

The effect of changing production, economic and marketing inputs on the \$INDEX is best evaluated by setting up a “Buyers own index”. Individual settings can then be changed and evaluated through the procedure described above. Once the desired index has been achieved settings should be changed in the main set up of PIGBLUP. The impact of changes to production, economic and marketing data on the relative weights of different in the \$INDEX has been discussed in detail during the 1997 pig genetics workshop. Given that a number of PIGBLUP users have asked about this topic these summaries are included in the appendix of these workshop notes.

Implementation of eye muscle area calculations?

Although eye muscle area is used overseas, Australian work has focussed on muscle depth. The Australian prediction equation to predict lean meat content of the carcass developed by Drewe Ferguson is based on muscle depth and does not include eye muscle area. Hermes (1996) compared muscle depth recorded on the live animal with real time ultrasound with muscle depth recorded in the abattoir with the Hennesy Chong machine. The abattoir measurement was found to be much less reliable indicated by a large environmental variation and a low heritability. In contrast, muscle depth recorded on the live animal had a heritability of 0.22, which makes it useful in selection procedures to improve carcass quality.

Efficient data collection

PIGBLUP requires accurate data records. Inaccuracies can be introduced during either the on-farm measurement of animals or input into the herd recording system.

There is a trade-off between the accuracy of measurements taken on-farm and the number of animals recorded. If the breeder can afford to set-aside a certain amount of time each week for taking measurements on animals, the only way to increase the number of animals recorded is to decrease the time required to take a measurement. There are two conflicting effects of increasing the proportion of animals measured:

- an increase in the number of animals available for selection;
- a decrease in the time allowed to measure each animal.

The more animals measured the better, accuracy of evaluation and selection pressure are increased. However, decreasing the time taken to record each animal can result in more recording errors, which has a negative impact on the accuracy of the genetic evaluations.

From the starting point that not all animals can be recorded, due to cost, how can breeders choose the animals to measure? Weigh all animals, but only scan a subset based on the weight of the animals. Given a constant age of animals at recording, the

largest animals are most likely to end up as those considered for selection, and therefore it is more important that these animals have ultrasonic backfat measurements than the lighter animals at the same age.

The use of automated on-farm recording systems, such as the PIGVIEW system being developed at AGBU and Bunge Meat Industries, can reduce the number of data measurement errors resulting from time limitations – both in accuracy of the measurement and recording of the observed values (ie the system stores the values straight from the scales and scanning equipment into a computer file, rather than relying on transcription of handwritten data).

Storage and management of data is not carried out by PIGBLUP, or PIGVIEW. This is the task of your herd recording software. Accurate input of the data is very important. One method of achieving this is multiple data entry. In multiple data entry, every data point is input twice *independently* and then repeated entries for the same value are compared. This reduces the possibility of having incorrectly typed data values stored. We are aware of no herd recording system that implements multiple data entry. It is also important that the herd recording system is able to query extreme values and verify dates and time period lengths. Warnings and data errors reported by the herd recording software should be investigated. To help with this process, the programs PIGCHECK and PIGWEED are included with PIGBLUP. These programs perform data checking and error removal from PIGBLUP data files. In the longer term, it is sensible to correct problems identified by PIGCHECK in your herd recording system.

How to set up PICKMATE?

The various steps to install PICKMATE are described in the PIGBLUP manual V4.00 on pages 7-1 to 7-2. After PICKMATE has been installed it is necessary to run the Mate Selection Module in PIGBLUP (section 6 in the manual). The Mate Selection Module provides the necessary files to run PICKMATE. However, it is necessary to export the appropriate files from the Mate Selection Module into the PICKMATE data directory. Further information on running PICKMATE is presented in the manual. However, the various steps of installing and running PICKMATE will be demonstrated to individual users during the workshop.

References

Hermesch, S. 1996. Genetic Parameters of Lean Meat Yield, Meat Quality, Reproduction and Feed Efficiency Traits for Australian Pigs. PhD Thesis, University of New England, Armidale, Australia.