Introducing PIGBLUP version 4.20

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Introduction

Version 4.20 adds considerably to the analytical capabilities of PIGBLUP. This new version will be demonstrated at this workshop. The purpose of this paper is to outline the changes that have been implemented and what they mean to the users of the system.

The major change in this release is an upgrade to the analysis of reproduction traits.

Multivariate reproduction analysis

In previous versions of PIGBLUP number born alive (NBA) and 21-day litter weight (LW21D) have been analysed using a univariate repeatability model. This means that:
- the two traits have been analysed separately, with no account being taken of the genetic relationships between them; and,
- repeated records across parities have been treated as records on the same trait.

In our new evaluations five traits are analysed:
- NBA in the first parity (NBA1);
- NBA in second and later parities (NBA2);
- LW21D in the first parity (LW21D1);
- LW21D in second and later parities (LW21D2); and,
- Weaning to conception interval (WCI) between the first and second parity.

By splitting NBA and LW21D into two traits each, we recognise that there is considerable genetic difference between gilt and sow performance for reproduction traits. Evidence for this comes from studies showing a lower genetic correlation between first parity performance and subsequent parity performance than between later parities (see, for example, Tholen *et al*, 1996). This allows us to model the genetics of the sow for NBA and LW21D better by using genetic relationships within and between these traits and also with WCI. It also provides scope for different emphasis to be placed on gilt and sow performance in the breeding objective.

Producing estimated breeding values (EBVs) for WCI gives a route by which the farrowing interval may be genetically reduced. A reduction in the farrowing interval will result in more pigs per sow per year. The reasons for analysing WCI in preference to gestation length or lactation length are that there is very little variation in gestation length and lactation length is usually a management decision. There is therefore very little scope for selecting to decrease these components of the farrowing interval.

1. *Data inputs*

The new reproduction analysis utilises the existing PIGBLUP data formats (version 1.0 and 1.1). As a result of this, WCI should only be analysed if:

- the date at which LW21D was recorded was the weaning date, such that the weighing date in the file is the weaning date, or,
- LW21D is not recorded, but weaning date is entered into the weighing date field in the file.

A new format will be included into PIGBLUP that will have an additional field for weaning date. This will enable people that wean and weigh litters on different days to analyse both traits. The new format will also accommodate four-figure years in date fields (ie 2000 instead of 00).

2. *Estimated breeding values*

Multivariate reproduction of NBA, LW21D and WCI results in the following EBVs:

- NBA in the first parity (NBA1),
- NBA in later parities (NBA2),
- cNBA = w_{NBA1}.NBA1 + w_{NBA2}.NBA2,
- LW21D in the first parity (LW21D1),
- LW21D in later parities (LW21D2),
- cLW21D = w_{LW21D1}.LW21D1 + w_{LW21D2}.LW21D2,
- WCI

There are only three traits that can be selected for reproduction analysis, NBA, LW21D and WCI. Ticking NBA always results in analysis of NBA1 and NBA2, and the creation of the composite EBV (cNBA). This is the same for LW21D.

Both component and composite reproduction EBVs are output and available for importing into your herd-management program. Trends and summary statistics can be viewed for either the component or composite traits.

The weights (w_{NBA1}, w_{NBA2}, w_{LW21D1} and w_{LW21D2}) applied to the first and later parity EBVs to define the composite trait are set in the Economic Limits window in PIGBLUP. While you can input any positive numbers for these weights, internally PIGBLUP adjusts them so that they sum to one (ie $w_{NBA1} + w_{NBA2} = 1$ and $w_{LW21D1} + w_{LW21D2} = 1$). The composite trait is used in the creation of the $INDEX EBV.

Additional improvements

Modifications have been made which do not relate directly to the new reproduction analyses. Some of these changes are in the background, but some will be visible to the user.

1. Mate selection

For a user-supplied boar or sow list, the program automatically runs the genetic audit that has been modified to ensure that the animals in the list are included in the Mate Selection run if they were included in the analysis.

2. Multiple breed handling

As of version 4.10, when multiple breeds are included in an analysis, each breed defines a separate base population. In version 4.20, the order in which the user specifies breeds sets the breed that forms the "true" base population. That is, the base animals in the first breed in the list of breeds to be analysed simultaneously have an average EBV of zero, the average EBV of base animals in the other breeds are expressed relative to this.

When looking at the program outputs (trends, statistics), the user can specify the breed or combination of breeds to be viewed.

3. Screen improvements

In order to aid navigation around the program, each screen has a button or item that can be selected that results in the user returning to the previous screen or menu.

4. Printing of graphs

The user can elect to print graphs either to a printer or to a file. The user needs to know the necessary printer settings to set this option up. PIGBLUP cannot access the Windows printing facility yet.

5. Processing of flags

PIGBLUPs routines that edit and process animal and data flags have been significantly speeded up. For large data sets, this can result in considerable savings when manipulating the flags within PIGBLUP.

6. Variance component verification

The user can modify variance and covariance components within PIGBLUP. Although this facility should still be used with caution, version 4.20 now has the ability to check that the covariance matrices are valid. The user can opt to have the covariance matrices validated, in this case the matrices for all traits and for the current selected set of traits are checked for positive-definiteness. In a two-trait context, this equates to checking that the correlations do not exceed one. For a multiple trait analysis, the procedure is more complex but ensures that all parameters are consistent with one another.

7.   *Limits and trait checking*

Limits on weaning to conception interval and weight at start of test have been included, along with the appropriate tests in the program.

Conclusion

Marked improvements in the analysis of reproduction traits along with improvements in performance and design and a number of minor corrections make PIGBLUP version 4.20 a valuable upgrade from previous versions.

References

Tholen, E., Bunter, K.L., Hermesch, S., and Graser, H.-U. (1996). The genetic foundation of fitness and reproduction traits in Australian pig populations 2. Relationships between weaning to conception interval, farrowing interval, stayability, and other common reproduction and production traits. *Australian Journal of Agricultural Research*, 47:1275-1290.