

# What's New in PIGBLUP?

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## 1 Introduction

PIGBLUP is a microcomputer-based system using the BLUP methodology to assess the genetic merit and extent of environmental influences on the performance of individual pigs.

The Estimated Breeding Values (EBV's) generated by BLUP for the traits chosen by the breeder for analysis are then combined by PIGBLUP to form a single \$EBV for each animal. This \$EBV can be used as an overall measure of the animal's worth to the breeder for the market he is targeting.

With Version 2.1 of PIGBLUP a Genetic Audit module has been added to provide the breeder with breeding program diagnostics. This module assesses how effective the breeder's selection practices have been in maximising genetic gain towards the defined breeding objective. In addition to the breeder being able to monitor the genetic and environmental trends of the breeding program, a Mate Selection module is also available now to calculate suggested matings which balance maximising genetic gain with minimising the effects of inbreeding on the herd.

To assist the user in understanding PIGBLUP's data requirements, determine inputs, drive the system, and make better use of the output, this paper gives an overview of how PIGBLUP implements BLUP technology, the PIGBLUP menu system and the analytic modules it supports. Enhancements and upgrades to various components of the system will then be more understandable and users will be able to get maximum benefit from their system.

Finally, some proposed future additions to the system will be suggested for consideration.

## 2 Previous PIGBLUP Versions

### 2.1 *Version 1.0*

Version 1.0 of PIGBLUP was released in 1989 and calculated EBV's on just three traits:

- ADG - Lifetime Average Daily Gain
- BF - Back Fat
- NBA - Number Born Alive (Calculated using a single trait repeatability model.)

## **2.2 *Version 1.1***

Version 1.1 was introduced in 1990 with two more traits available for analysis:

- FCR - Feed Conversion Ratio, and
- TADG - Average Daily Gain over a test period.

## **2.3 *Version 2.1***

The most recent release (Sept 1992) is Version 2.1 which expanded the set of available traits with

- CFAT - Carcase Fat
- CMUS - Carcase Muscle, and
- LMY - Lean Meat %

(The breeder is restricted to choosing at most two of these three traits in an analysis.)

System resources needed for computing increase with the square of the number of traits being analysed. In order to analyse an increased number of traits and animals within the PC environment an improvement in the method of setting-up of the mixed model equations in the computer was necessary. AGBU developed the implicit representation of the mixed model equations to achieve this goal. Benchmarking runs of this algorithm show that the new representation uses only 14% of the memory previously required at the cost of a 5% increase in run time.

Tools have also been introduced to assess the breeding program (the Genetic Audit) and to recommend matings to the breeder (the Mate Selection module).

## **3. PIGBLUP Version 2.1**

### **3.1 *Data Requirements***

The data submitted to PIGBLUP by the breeder's herd recording system needs to be formatted and sorted properly and all possible checks made so that the data is valid. Users are reminded (see the User Manual) that PIGBLUP requires that

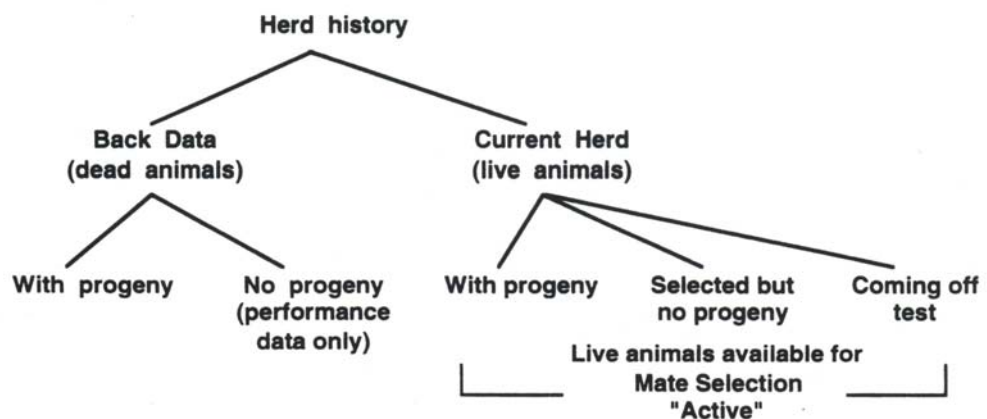
- animals are uniquely identified, are
- sorted by date of birth, and
- sorted by parity within animal.

As breeders use a number of different information management systems (e.g., Herman, MIPS, Pigmania, Pigchamp, AIMS, Pigman, TAPS & Fannplan), a good deal of effort has gone into working with these software groups in developing their

interfaces to the PIGBLUP system. Although the final goal is the same for each of these programmers (namely the PIGBLUP format), they each have had to do things somewhat differently to get there as file structures will invariably be different for the different recording systems. A standalone data checking program, PIGCHECK, which carries out a thorough check of the submitted data is being developed. Suspect values are flagged in addition to outright errors and are written to an error log. The user will be able to check data files using this program before trying to analyse data using PIGBLUP. Potentially, this will save user time and the need to contact ABRI for support.

### 3.2 *Flagging Animals*

In past versions of PIGBLUP, flagging was used only to maintain animals in the output that had been selected, but had yet to have progeny. With the addition of the Genetic Audit and Mate Selection modules, flagging has been extended to identify potential animals for mating by placing an 'A' in the appropriate column of the Type 1 PIGBLUP record. This is meant to include only the current herd as seen in Figure 1. Some recording systems have been flagging either all animals or all animals who went on to become parents. Some of the latter animals are dead and no longer available for mating. Also, having extra animals marked as 'active' can slow down run times and may even cause the limits for numbers of boars and sows to be exceeded. The herd recording system needs the facility to flag as 'active' only live animals from the current herd in the PIGBLUP data extract and to be able to update this in a timely fashion



**Figure 1.** Herd data used by PIGBLUP for analysis

### 3.3 *Menu System*

The PIGBLUP menu system serves a number of purposes:

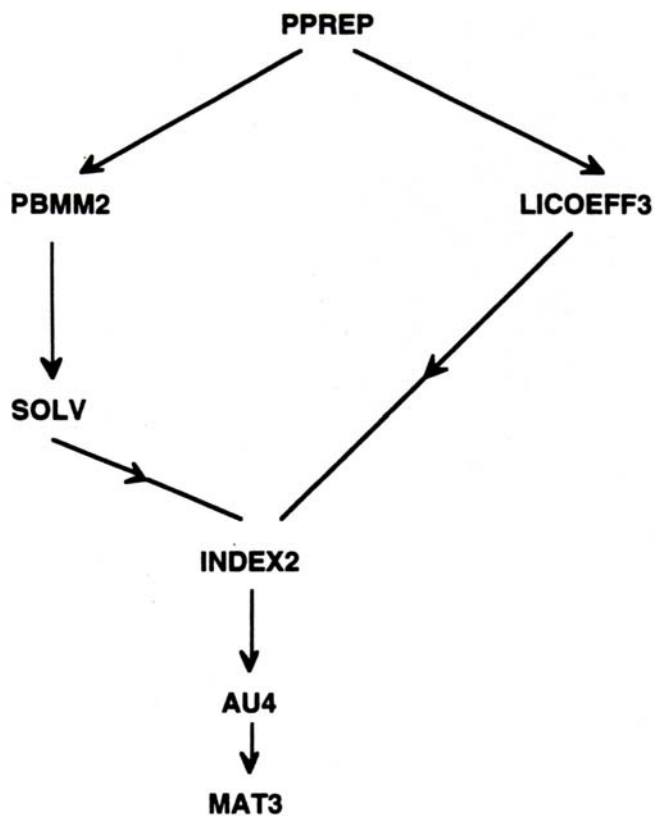
- It provides a mechanism to smoothly and safely integrate the various modules that make up the PIGBLUP suite;
- It removes responsibility from the user for management of the files for a number of herds/breeds. This avoids possible confusion as to which files pertain to which herd/breed and to protect against accidental deletion of files;
- It provides a degree of protection against input of inappropriate values and settings which might otherwise result in irrelevant analysis and wasted time;
- It monitors each stage of the analysis with a view to determining whether conditions are satisfied for initiation of the next stage of analysis;
- It provides an environment in which to view, graph and/or print results from the analyses.

Users of versions prior to Version 2.1 will find in the new version:

- The Menu system is more robust. Better error checking and trapping now catches most errors and allows their cause to be identified more reliably than previously.
- Confirmation is now sought when file or directory deletion is requested and when the user tries to ESCape from the system.
- Emphasis has been given to making operation consistent over all menus so that it is easier to learn and is more predictable in its effects.
- Some functions have been stream-lined to make editing or viewing easier - this is most apparent in Mate Selection.
- Scrolling - both forwards and backwards - is now possible in most menus in which files or long lists are examined.
- Printing is now possible from within PIGBLUP to either a disk file (for later printing) or to an on-line printer. (At present, you must wait for the printer to finish printing before PIGBLUP will allow you to do other things.)
- Users can now define the maximum size of a user-defined management group.
- Number Born Alive can now be selected or de-selected for analysis. Previously, it was always selected.

### 3.4 *Running PIGBLUP*

PIGBLUP works by having the Menu program PBLUP cascade through each of the analytical modules as it progresses. The menu program then waits for the launched module to complete, check whether conditions are satisfied for moving to the next stage of the analysis, and take the appropriate steps.



**Figure 2.** PIGBLUP Analytic Modules

At present, when you chose the analysis date prior to running a PIGBLUP analysis, PIGBLUP resets the system date to that value. This situation will be remedied in the next release of PIGBLUP. When you choose the analysis date, it will be written to a file which is passed - with other information - to the analytic modules. This change will have the added benefit of the date being retained between sessions. As most users use today's date when they run PIGBLUP, "today" will be a valid date; whenever you run PIGBLUP, the current analysis date will be automatically used for the analysis.

Fundamental to use of BLUP is the requirement that we group animals which have performed under the same or similar conditions when comparing performance. PIGBLUP assigns pigs to management groups in two ways: the user-defined management group and user-recorded management group. The former is an implicit grouping of animals - that is, groups are derived using the maximum group size values chosen by the breeder and the maximum number of weeks for a group - while the latter is an explicit grouping.

A major enhancement of PIGBLUP's analytic capability has been made with the ability to define user management groups. This feature gives the breeder greater flexibility in defining management groups such that the animals are assigned appropriately.

User management groups should be created by the breeder to indicate differing environments affecting the performance of animals. Animal, production, carcass and reproductive groups can be so defined.

It is important that the number of animals belonging to each management group be neither too few nor too many: with too few members, there is the possibility of poor estimates of the effect of that management group on an animal's performance (with too few different sires and dams, genetic effects can be confused with environmental ones); and, too many animals may result in a lost opportunity to sharpen the resolution by tighter grouping of animals. PIGBLUP allows the user to vary the minimum and maximum grouping sizes. PIGBLUP automatically initiates a new group when the maximum group size is exceeded.

PIGBLUP uses data on performance, management groups and relatives, together with information on the correlations between various traits, to calculate EBV's. PIGBLUP does this in two separate runs - one for production and one for reproduction. This is done for computing ease and assumes that production and reproductive traits are not correlated. In other words, knowing how many pigs/litter a sow has gives little or no information on her genetic potential for growth or carcass characteristics.

A major advantage of BLUP is that it permits the EBV's for all selected traits to be computed simultaneously. As a result, all genetic and environmental effects are estimated more accurately.

The EBV's calculated in this way are the most accurate currently available. As the EBV's of sire and dam may be combined to estimate the genetic merit of their progeny, there is an immediate benefit from this increased accuracy.

BLUP solves the mixed model equations by making an initial guess at the solution and adjusting the "solution" at each iteration so that it moves towards the correct answer. The larger the set of equations to be solved, the slower this process is. If the solution has not converged within the allocated number of iterations (default 600), you have a choice of either increasing the number of iterations allowed or reducing the correction factors that should be used. At each iteration, an adjustment is

computed for each term in the solution. If the correction factor is one, the whole of the adjustment is added to the term in the previous solution. A correction factor greater than zero but less than one ( 0.9 say) says that only that proportion of the computed adjustment is to be added (0.9 of the adjustment say). The effect of reducing the correction factor is to take smaller but surer steps at the penalty of needing more iterations to reach convergence. Presently, you can use an editor to alter the correction factors held in the file SOL V.PAR but you are unable to alter the maximum number of iterations allowed. The next version will make both factors editable from the 'Run PIGBLUP' menu.

After each module has completed, version 2.1 checks for conditions that would invalidate further processing before commencing the next stage in the analysis. This helps to avoid wasting time.

### **3.5 \$INDEX**

Once the EBV's for all selected traits have been computed for each animal, the breeder is faced with the question of how to use them. If only one trait was analysed, there is no problem: all animals can be compared on the basis of that single number. However, when a number of traits have EBV's, the breeder has to weigh the importance of each trait to his breeding objective when deciding the overall genetic merit of an animal for his breeding objective. PIGBLUP provides \$INDEX as a tool to assist the breeder in this process.

Decisions regarding genetic merit must occur within the context of a target market. PIGBLUP uses two sub-objectives - a growing/finishing sub-objective and a sow sub-objective - when calculating marginal values for each trait.

The growing/finishing sub-objective takes account of economic and production information to calculate pertinent costs and returns for this aspect of the enterprise. Marginal values for each production trait may then be calculated.

Similarly, the sow sub-objective uses the supplied costs to derive the marginal value of reproductive traits from producing an extra pig.

\$INDEX finally combines these sub-objectives to calculate the \$EBV. This index can be used by the breeder as an objective measure on which to base selection and culling decisions. PIGBLUP does not remove the decision making from the breeder; it is a tool for use by the breeder in decision making. (Note that, at present, carcass traits are not used in the \$EBV calculation.)

### **3.6 Genetic Audit**

Having calculated the trait EBV's and the \$EBV, PIGBLUP performs a genetic audit to aid the breeder in determining the effectiveness of his breeding program. Various measures are calculated:

- The percent of animals selected versus those tested (for both the current year and the 5 previous years) provides a measure of the selection intensity of his breeding program. No account is taken of "pre-selection" occurring through the breeder choosing to omit measurements on some animals.
- Selection differentials for traits enable the breeder to assess the relative selection emphasis and intensity for analysed traits.
- The average generation interval for boars and sows provides an indication of the rate at which animals are being turned over.
- Average annual inbreeding provides a handle on this aspect of his breeding program.

### **3.7 Mate Selection**

Since BLUP uses information from all known relatives, there is an increased risk of inbreeding in the herd - especially when a trait of low heritability is being selected. Inbreeding can be ameliorated by increasing the number of boars used and including production traits in addition to reproduction traits in the breeding objective. PIGBLUP has a Mate Selection module which can be used to suggest matings in a particular week. This module uses linear programming to maximise the average EBV's of progeny while minimising their average inbreeding coefficients. The breeder can set the relative emphasis given to these two effects according to his/her concern.

### **3.8 Output**

The stages described above generate a large volume of useful information for the breeder. Graphs of genetic and environmental trends allow the breeder to gain a perspective on how well his breeding program is progressing.

The genetic trends indicate how each EBV has changed relative to that of the base animals. In addition, the relative genetic mean for the herd at various times can be ascertained.



The environmental trends depict the change of conditions under which animals have had to perform over time. The genetic and environmental trends together give an indication of the average production level at various times. A decrease in the environmental trend could be caused by the animals' having endured a deleterious environmental change (eg a severe heat spell or a disease outbreak) or could be due to there having been too few animals in the group for reliable estimation. (A corollary is that an increase in the trend could also arise from poor estimation. This highlights the need for the breeder to take account of these factors when interpreting his output.)

#### **4 Possible Future Short-Term Enhancements**

It is hoped that interaction with participants at this clinic will give the PIGBLUP team other suggestions for possible future enhancements and upgrades. The following are some potential short-term enhancements suggested by the developers and the PIGBLUP Consultative Group.

Introduced Animal groups address the problem which arises when animals from outside the herd are introduced for breeding at various times throughout the breeding program. Current versions treat these animals as though they come from the same genetic base when, in all likelihood, they would be more superior to the base animals the more recently they were introduced. The effect of this limitation is that those animals and their progeny are penalised in the estimation of their EBV's. An option is being developed to enable these animals to be grouped according to period of introduction. Improved EBV estimates should result.

The present \$INDEX is non-linear and based on profit equations. It appears as a "black box". This makes extrapolation of trends by the breeder more difficult. A desired gains approach would give breeders more flexibility as to the amount of selection emphasis put on each trait. Actual weightings used in the calculation of the index should be able to be reviewed by the breeder. It is desirable that a breeder be able to restrict change to a genetic trait should he desire.

Introduce a pricing method for lean meat yield so carcass EBV's can be incorporated in the \$INDEX.

Presently, a maximum of 900 EBV's are able to be sorted. This could be increased to about 4000 and, in addition, allow any trait to be selected as the one on which to sort output.

Currently, the vertical scale on trend graphs is calculated automatically. The ability to fix scale limits may be desirable in order to draw attention to the amount of gain achieved rather than just its trend. Also, we could provide greater flexibility in the defining of years to be considered in the Genetic Audit.

The Mate Selection module currently suggests alternative sires for mating should the primary sire be rejected for some reason. Frequently, the suggested alternative sires are the same for many of the sows. Extra conditions to address this shortcoming should be investigated.

21 day litter weight will be added as a selectable trait for analysis.

The restriction to a maximum of 520 weeks of data should be relaxed or, if possible, removed. Also, it should be possible to choose to analyse only the last n years of data in a PIGBLUP run.

Depending on the demand from breeders, a Windows compatible version of PIGBLUP could be developed.

