

Tips for making better use of PIGBLUP

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Introduction

Breeders may not always make best use of the various features of PIGBLUP since they are unaware of specific settings available in the system. This is especially the case for newly developed features but may also apply to system settings that have been part of PIGBLUP since its early development. For example, fitting genetic groups for introduced animals may have only become important as their data set has grown and the use of AI boars from other herds has increased.

It is the aim of this document to provide tips for making better use of PIGBLUP. A number of PIGBLUP features are outlined including the use of spline functions in the \$Index, fitting genetic groups for introduced animals, obtaining across-breed EBVs and making better use of PBSAMA.

Using your own payment grid

1. Setup of the Traditional PIGBLUP \$Index

The original profit function in PIGBLUP allows users to incorporate their own specific payment grid. The setup of payment grids is outlined in section 11 of the PIGBLUP manual and an example is provided below. A number of comments have been added to the payment grid to outline its structure. This file called demo520.grd has to be put in the PIGBLUP home directory (ie. C:\PIGBLUP\PBV520). In addition, the file paygrids.txt, also located in the PIGBLUP home directory must include a reference to this payment grid by adding the line "demo520="Demo520",SUM,demo520.grd,".

# V5.20 Demo Payments Grid	
# demo520.grd	<u>Note:</u> these comments have to be omitted in the real file
%	increment is expressed in %
increment	the premium/discount is a % increment ie. -5%
ALL	valid for both sexes
Weight Classes:	
3	There are 3 weight classes
1.0	factor for conversion to metric carcase weight
60.0 86.0	the upper levels for the three weight classes
#	Note only 2 are required (3 minus 1)
Depth Classes:	
7	Number of depth classes
1.0	factor for conversion to mm
10 12 14 15 16 17	upper limits for depth classes (N - 1)
0 -3 -6 -9 -12 -15 -18	discount in % for each fat depth, 1. weight range
0 -2 -4 -6 -8 -10 -12	discount in % for each fat depth, 2. weight range
0 -1 -2 -3 -4 -5 -6	discount in % for each fat depth, 3. weight range

Once the specific payment grid has been setup in this way, it is available in the *Payment System window* of the Traditional PIGBLUP \$Index setup (see manual page 6-11). PIGBLUP then fits a curve to model the specific payment grid. In Version 5.20 it is possible to use spline for this. Splines provide greater flexibility in modelling grids and do not make assumptions about the shape of the curve.

It is still necessary to specify an average carcass price if a payment grid has been setup. However, the settings for premiums in the *Economics window* are not used anymore.

A range of economic, production and marketing parameters are incorporated in the profit function. However, the emphasis being placed on individual traits is largely driven by a few key parameters:

- The *Cost_Feed* setting has the biggest impact on the economic importance of feed conversion ratio (*Economics window*).
- The *Non_Feed_Costs* setting influences the emphasis placed on growth rate (*Economics window*).
- The mean back fat level defined under the *Production window* affects the emphasis placed on back fat together with the payment grid specified.
- PIGBLUP models the price grid at the target weight specified in the *Production window*.
- The emphasis on litter size is mainly determined by *Market* settings.

2. Evaluation of \$Index settings

The profit function in PIGBLUP does not provide economic values for each trait. Economic values quantify the change in profit if one trait is changed by one unit. However, approximate economic weights are derived for growth rate, back fat, feed conversion ratio (if the data are available for this trait) and litter size through regression of the \$Index on trait-EBVs. These are shown in the '*Derived weights*' window for display of EBVs. In addition, correlations between the \$Index and trait-EBVs are listed. This information should be compared for different settings.

Please note, unselected animals (young boars or gilts) should be chosen for evaluation of the economic emphasis placed on each trait. In addition, the pool of young animals should be large and it is recommended to increase the maximum age for implicit flagging to 365 days for this procedure.

Fitting genetic groups for introduced animals

1. Background

A genetic analysis within an individual herd makes use of all the information available from within the individual herd. If records are available for a number of years, then the amount of information available for boars selected on farm is larger than the information available for animals introduced into the herd, like AI boars. For example, performance records may be available for parents and other relatives of a boar selected on farm. In comparison, a newly introduced AI boar has initially no information available on farm until his progeny have been recorded on farm.

An introduced AI boar is regarded as a ‘base animal’ in the standard analysis and has a starting EBV of zero in each trait until relatives have been recorded on farm. An animal born on farm, on the other hand, has an EBV that is the average of its parents EBVs. If genetic gain has been achieved in individual traits, animals born on farm have superior EBVs to introduced animals, since selection is taken into account.

Performance records are not available on farm to account for selection of introduced animals and by fitting genetic groups in BLUP analyses according to Westell et al., (1988) it is attempted to account for the genetic merit of introduced animals. The solutions (estimates) of genetic groups are the average genetic merit of so-called “phantom parents” of introduced animals. It is assumed that these phantom parents have a similar genetic merit. Introduced AI sires are therefore often assigned to genetic groups based on the year of entry. This approach has also been adopted in PIGBLUP. The “first” EBV of an animal is the average of its parents, which explains why starting EBVs of each AI boar are the solutions (estimates) of the genetic group effect at the time the boar enters the herd if genetic groups are fitted.

Fitting genetic groups will change EBVs in comparison to an analysis that does not fit genetic groups. However, comparison of EBVs per se derived from different analyses does not provide any information about the best model that should be used for genetic analysis. For example, Quaas (1988) stated that complex grouping strategies for base animals may lead to some unsuspected confounding with other fixed effects, which may be difficult to detect for large real-life data sets. One approach is to use mean progeny performance of sires to determine which set of EBVs of sires is the best predictor of differences in performance of progeny in the given data set. For such an analysis EBVs have to be derived using data that are independent of the progeny performance data of these boars. Often the data are not sufficient for such an analysis and the ‘sensibility’ of genetic group solutions may be the only (subjective) criterion that is used in the decision making process.

2. Settings in PIGBLUP

Information about introduced animals is available in the PIGBLUP manual on pages 6-7 and 6-8. Whether genetic groups are fitted for introduced animals is set in PIGBLUP within the *Setup Menu* under the *Model Tab* by ticking ‘*Group introduced animals (IA)*’. Directly beneath this is ‘*Number of years in first Introduced Animals group*’,. This setting determines the number of years that form the genetic base for introduced animals. Subsequent genetic groups are then formed for each year if there are at least 5 sires and 25 parents available or if the number of animals is greater than 400.

The type of genetic groups, fixed versus random, is set in PIGBLUP under *Setup Menu* and *Solve Tab* and can be set separately for production and reproduction traits. The default setting is zero (fixed genetic group). However, if analyses are slow to converge or genetic group effects are ‘unbelievable’ random genetic groups may be preferable (see PIGBLUP manual 6-8).

3. Genetic group solutions

Solutions for genetic groups are shown in the run.log file directly underneath the changes in the convergence criterion for production and reproduction traits. They are in the order of traits analysed. Four production traits are shown in the example, growth rate, back fat, feed conversion ratio and juvenile IGF1. The first genetic group with 206 animals is set to zero. Three other genetic groups have been formed. Note the favourable trend in solutions for genetic groups over time.

```

Convergence: 0.00001010    940
Convergence: 0.00000999    944
Diagonal and Final Group Solutions
1st Group unconstr.:
18.08933  2.12103  0.04948  11.42882
Group Solutions (breed x trait): 4
  206  0.00000  0.00000  0.00000  0.00000
   26  24.82380  0.05412 -0.06072 -6.23457
   29  29.92692 -0.86993 -0.09938 -12.40108
   30  63.26509 -1.34352 -0.22358 -27.56098

```

Example of genetic group solutions for production traits as shown in run.log file

4. Fixed versus random genetic groups

Sometimes solutions for genetic groups seem reasonable for production traits but are ‘unbelievable’ for reproduction traits. Genetic group solutions for litter size in the first parity are shown for fixed and random genetic groups in the Table below.

The base genetic group is always zero with a minimum of 200 animals. Group solutions were largest for fixed genetic groups ranging from +1.74 to -1.14 piglets between yers. These solutions are reduced for random genetic groups. The reduction will be larger for larger parameters. Using random genetic groups with a low parameter increased the required number of iterations considerably. The number of iterations decreased for larger values used as the setting for random genetic groups and estimates of genetic groups were closer to zero.

Table 1. Solutions for fixed and random genetic groups for litter size in the first parity

Parameter	Fixed		Random	
	0	1	10	30
Base (N:206)	0	0	0	0
(N: 26)	0.94	0.79	0.37	0.17
(N:29)	1.74	1.31	0.50	0.21
(N:29)	-1.14	-0.35	0.10	0.06
Iterations (N)	652	2821	737	426

5. Conclusion

Genetic groups for introduced animals may be fitted when a large number of animals are introduced into the herd over a number of years. In some situation, fitting fixed genetic groups may lead to ‘unbelievable’ solutions of genetic groups, which are most often observed for reproductive traits due to limited data available. Fitting random genetic groups with larger parameter values decreases solutions for genetic groups. Breeders should get as much information as possible about the genetic merit of introduced animals and genetic groups solutions should reflect the average genetic merit of introduced animals.

Across-breed analysis

1. Analysis of multiple purebred lines

Pigs from different breeds or lines are usually kept in the same environment. Combining a number of breeds into one analysis may be beneficial in smaller herds due to larger contemporary group sizes. PIGBLUP enables multiple breed genetic evaluations if users specify multiple breeds in the setup.

Each breed will be assigned a separate genetic group with the first breed in the list set to zero. Other breeds are then expressed relative to the first breed listed. Genetic group solutions for breed are shown in the run.log file as outlined above.

2. Analysis of purebred and crossbred data

Data preparation for joint analysis of purebred and crossbred data is outlined in the PIGBLUP manual on page 6-5. Consider joint analysis of two purebred lines and the resulting crossbred offspring. Briefly, three breeds will have to be defined for this scenario; all parents must have a record of type 1 to define their breed code and crossbred data should be assigned to a different user-defined management group than purebred animals to avoid potential bias due to heterosis.

Separate genetic groups will be defined for the two purebred populations. In contrast, the crossbred offspring originate from the two purebred populations and no separate genetic group is required.

PBSAMA explained

1. General setup

The PBSAMA module is called from the *Post Analysis / Mate Selection / Selection and Mate Allocation* button. This opens a separate window which blocks access to other PIGBLUP features. As a first step, the maximum number of permutations should be increased substantially to 200,000. This setting is accessed from *Edit* and then *Optimisation Parameters*.

If status information is available, *Status Group Codes* need to be set, which is accessed from the *Edit* screen as well. PBSAMA will show the status codes available from the data, which need to be linked to status 'Groupings'. Note, it is possible to link multiple status codes to one 'Grouping'.

Previous 'Selected Animals List' and 'Mating List' are stored under *Previous*. By default, up to six lists are stored in the directory 'prev' on the PC, which is a sub-directory of the 'pbsama' directory. The 'pbsama' directory is placed within each breed directory once pbsama has been activated. These lists are normal text files and can be edited with other programs.

General settings for PBSAMA are defined in the file 'samaset.ini' located in the PIGBLUP directory and the number of lists stored can be modified by changing the appropriate parameter in samaset.ini [NToStore=6].

2. Practical guidelines

There is no unique solution for a selection list or a mating list. PBSAMA maximises the objective function, which is defined by the different weightings given to its components (see PBSAMA manual page 1-2), and alternative results may give same or similar objective function. Therefore, it is recommended to explore results for components of the objective function by placing minimal weight on components of objective function to reduce increase in relationships between animals and inbreeding of offspring (mate list only). These settings may be repeated to better evaluate the 'base setting'. The weights on relationships and inbreeding may then be increased to evaluate the resulting changes to components of the objective function.

The objective function is defined as the sum of genetic merit (\$Index) of animals considered for selection or mating minus relationship between these animals and the relationship with other animals, if status information is available. In addition, the objective function for mate allocation can include the inbreeding level of offspring and the variance in genetic merit of offspring. Currently, a weighting of 1 to 10 can be placed on each component. However, these components are not scaled and differ substantially in magnitude. Work is underway to develop a more appropriate range for each weighting factor. Breeders are able to modify the default range of each weighting factor and are encouraged to contact AGBU staff for further details.

The group of animals available for selection should be large enough to ensure selection intensities of less than 5% for boars and less than 20% for gilts. This will be easier to achieve if batch farrowing is practiced. Similarly, mate lists may be derived every three weeks including all current farrowings and gilts in the gilt pool.

3. Results

Selected Animals List provides a list of boar(s) and gilts suggested for selection. The summary of the objective function provides the total and average genetic merit for males (M) and females (F). The genetic merit represents the \$Index. If multiple indexes have been setup, the \$Index that is written to the file read back into the herd recording system (custom.inx file) is used. The weight on the total genetic merit is always one and cannot be changed.

The example shown below does not include any status information and only relationships among candidates are incorporated into the objective function. A weight of three has been used for relationship among candidates. The total genetic merit was \$216 for boars with an average of \$72 for the three boars. The total relationships among candidates were 3.58 among males, 31.8 among females and 4.45 among males and females. The average relationships among candidates are shown in the row below.

Selected Animals List
Created on: 13/10/2006 4:47:32 PM

Boars	Gilts
BOAR007899	SDW0007683
BOAR007962	SDW0007695
BOAR008033	SDW0007733
	SDW0007741
	SDW0007748
	SDW0007760
	SDW0007762
	SDW0007766
	SDW0007803
	SDW0007811
	SDW0007918
	SDW0007921
	SDW0007934
	SDW0007966
	SDW0008038

Summary of objective function for this list

Term	Weight	Male	Female	MxF
Total genetic merit	1.00	216.	963.	
Average genetic merit		72.0	64.2	
Relationships among candidates	3.00	3.58	31.8	4.45
Av. Rel. among candidates		0.398	0.141	0.989E-01

Mating List shows list of sows/gilts along with the preferred boar for mating. The next column shows the \$Index of the resulting litter along with the inbreeding level of the offspring. In addition, alternative boars are shown for each sow. The summary of objective function for this list follows the format of the Selected Animal List. In addition, the sum of inbreeding coefficients and the variance in \$Index of offspring resulting from suggested matings are shown. A number of constraints can be put in place by the user shown at the bottom of each mating list.

PIGBLUP Selection and Mate Allocation						
PBSAMA Edit Previous Help						
Mating List						
<i>Created on: 19/10/2006 5:01:18 PM</i>						
Sow/Gilt	Preferred	EBV	F	Alternate 1	Alternate 2	
SOW0006099	BOAR003392	24.1	0.00			
SOW0006012	BOAR003392	25.4	0.03	BOAR006445		
SOW0006122	BOAR004943	61.5	0.00	BOAR006445	BOAR003392	
SOW0006659	BOAR004943	56.6	0.00	BOAR006445	BOAR003392	
SOW0006000	BOAR003392	18.9	0.06	BOAR006445		
Average		37.3	0.02			
Summary of objective function for this list						
Term	Weight	Male	Female	MxF		
Total genetic merit	1.00	211.	162.			
Average genetic merit		42.2	32.4			
Relationships among candidates	3.00	13.0	6.63	1.06		
Av. Rel. among candidates		0.520	0.265	0.425E-01		
Total offspring inbreeding	5.00			0.938E-01		
Offspring variance	2.00			403.		
Optimisation constraints						
Minimum and maximum allowed usage of boars						
Boar	Minimum	Maximum				
BOAR006445	0	3				
BOAR003392	1	5				
BOAR004943	0	2				
Enforced matings						
Sow	Boar					
SOW0006000	BOAR003392					
Disallowed matings						
Sow	Boar					
SOW0006099	BOAR006445					
Help Print OK						

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References

- Quaas, R. L. (1988). "Additive genetic model with groups and relationships." *Journal of Dairy Science* **71**: 1388-1345.
- Westell, R. A., R. L. Quaas, and L. D. van Vleck (1988). "Genetic groups in an animal model." *Journal of Dairy Science* **71**: 1310-1318.