Properties of BLUP EBVs

Karen Marshall

UNE

IAEA, Korea, April, 2006

Genetic evaluation systems

- Breeder submits phenotypes and pedigree

- Genetic evaluation system returns BLUP EBVs
  - plus other useful information e.g. selection indexes, accuracies, inbreeding coefficients

- Can be
  - Within herds
  - Across herds, within breeds
  - Across herds, across breeds (best)
## Extract from LAMBPLAN report

### Terminals - Top 150

<table>
<thead>
<tr>
<th>Rank</th>
<th>Name</th>
<th>Analogue Date Friday, 15 June 2015</th>
<th>Herd &amp; Abomasum</th>
<th>Breed &amp; Abomasum</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Properties of BLUP EBVs

### Understanding LAMBPLAN EBV's

**How to read a LAMBPLAN report:**

- **EBV:** Estimated Breeding Value.
- **EBV Rank:** The position of the EBV in the ranking.
- **EBV Score:** A value indicating the accuracy of the EBV estimate.
- **EBV Change:** The change in EBV from the previous update.

---

### Properties of BLUP EBVs
Media Releases

16 August 2004

MLA's LAMBPLAN database records one million sheep

MLA's LAMBPLAN database records one million sheep.

The LAMBPLAN database records one million sheep.

At MLA's LAMBPLAN database, the one million sheep have been objectively measured and recorded on Meat and Livestock Australia's LAMBPLAN terminal sire database.

LAMBPLAN manager Dr Alex Ball said this was a great achievement for the national genetic evaluation program LAMBPLAN and the genetic improvement of the Australian prime lamb industry.

"Recording the one million sheep in the LAMBPLAN terminal sire database reinforces the integrity of the system and what it has to offer," Dr Ball said.

"Since 1989, when LAMBPLAN first started operating, the Australian prime lamb industry has seen some phenomenal improvements in live weight growth, increased eye muscle area and decreases in fat."

"In fact genetic improvements have seen post weaning weights of 8-8 month lambs increase by 5.8 kilograms, fat decrease by 0.6mm and eye muscle area improve by 5.3mm."

For the average lamb producer this means an extra $5.60 per lamb produced in carcass value alone.
BREEDPLAN INTERNATIONAL

BREEDPLAN is a modern genetic evaluation system for beef cattle breeders. It is based in Australia, with clients worldwide. BREEDPLAN offers breeders the potential to accelerate genetic progress in their herds, and to provide objective information on stock they sell to commercial breeders.

BREEDPLAN calculates Estimated Breeding Values (EBVs) for a range of traits including:

<table>
<thead>
<tr>
<th>Trait</th>
<th>Weight</th>
<th>Fertility</th>
<th>Concarce</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth weight</td>
<td>Sire's Sire</td>
<td>Sire's Dam</td>
<td>Dam's Concarce</td>
</tr>
<tr>
<td>280-day milk weight</td>
<td>Days to Calving</td>
<td>Gestation length</td>
<td>Calving ease</td>
</tr>
<tr>
<td>200, 400 and 600-day weight</td>
<td>Growth rate</td>
<td>Fat thickness</td>
<td>Muscle mass</td>
</tr>
<tr>
<td>Mature cow weight</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

(Note: EPDs are calculated for North American clients)

Included in the calculation of EBVs are the animal's own performance, the performance of known relatives, the heritability of each trait and the relationship between the different traits in a model-based genetic evaluation model, combining all traits in one analysis.

Properties of BLUP EBVs
Consider the features we want in an EBV

Case study:

A breeder selects a young ram that has a high EBV based on his own phenotype only. The ram has 30 progeny and his EBV drops.

Why?
Consider the features we want in an EBV

Case study:

A breeder is performing assortative mating. He sells his sire with the highest EBV - this sire produces in another herd and his EBV drops.

Why?

Features of EBVs

High accuracy, for high response ‘best’
  • highest correlation between true and estimated breeding value

Lack of any bias, for fair comparison ‘unbiased’
  • true breeding values are distributed around predicted breeding values
BLUP and accuracy

*BLUP maximises EBV accuracy by*

- calculating EBVs using all information sources
  - Information from relatives
  - Information from correlated traits
- using proper index weights
- just the same as a selection index
  
  *(note BLP = selection index)*

---

BLUP and lack of bias

*BLUP ensures EBVs are unbiased*

- unbiased EBVs are a matter of fair comparison
  
  *note selection index (BLP) + unbiased = BLUP*
What ‘fixed effects’ would need to be accounted for so all animals have comparable EBVs?

Herd A

Herd B

Date of birth

Possible causes of bias ‘fixed effects’

Can account for some bias easily e.g.

- Problem: Some animals reared as singles, other as twins
  Solution: Correct phenotypes for effect of rearing type

- Problem: Animals producing in different herds
  Solution: Take phenotypic deviation from herd mean

- Problem: Animals are measured at different ages
  Solution: Correct phenotypic observations for age
Possible causes of bias ‘fixed effect confounded with genetic effect’

- Problem: Animals producing in different herds, and the different herds have different genetic means (no longer can take phenotypic deviation from herd mean)

- Solution: Use reference sires as links between herds, and simultaneously evaluate herd and sire effects

Use of link sires

Progeny means

<table>
<thead>
<tr>
<th>Flock</th>
<th>Sire 1</th>
<th>Sire 2</th>
<th>Sire 3</th>
<th>Sire 4</th>
<th>Sire 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>45</td>
<td>40</td>
<td></td>
<td>45</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td></td>
<td></td>
<td>45</td>
<td>40</td>
<td>50</td>
</tr>
</tbody>
</table>

Sire 1 is superior in flock A, & sire 3 is superior in flock B.

But which sire is the best overall?
Use of link sires

Progeny means

<table>
<thead>
<tr>
<th>Flock</th>
<th>Sire 1</th>
<th>Sire 2</th>
<th>Sire 3</th>
<th>Sire 4</th>
<th>Sire 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>45</td>
<td>40</td>
<td></td>
<td></td>
<td>45</td>
</tr>
<tr>
<td>B</td>
<td></td>
<td></td>
<td>45</td>
<td>40</td>
<td>50</td>
</tr>
</tbody>
</table>

Assuming ewes are of equal merit in flock A and flock B, the sire 5 data indicates that flock B is performing in a better environment.

Thus sire 1 is genetically superior to sire 3, as sire 1 produces the same phenotype despite the worse environment.

In practice

- Linkage between herds / flocks within the major genetic evaluation systems (e.g. LAMBPLAN / BREEDPLAN) is now substantial

- This allows across-flock and even across-breed analysis
Possible causes of bias
'unequal merit of mates'

- Problem: Some sires have better mates

| Sire 1: +300 | Dam 1: +200 | Progeny: +250 |
| Sire 2: +300 | Dam 2: +400 | Progeny: +350 |

*Without information on the dams, sire 2 would 'look better' due to a higher progeny mean*

- Solution: Account for mates by evaluating all animals jointly

*Properties of BLUP EBVs*

---

In practice

- Genetic evaluation systems encourage recording of phenotypes on mates

- If no dam information is provided, the dam is presumed to be 'average'

*Properties of BLUP EBVs*
Possible causes of bias 'selection bias'

- Problem: There is culling and selection
  - worst sires have more progeny culled 'culling bias'
  - animals are from selected parents

<table>
<thead>
<tr>
<th>ID</th>
<th>Sire</th>
<th>Weaning Weight</th>
<th>Progeny mean</th>
<th>Yearling Weight</th>
<th>Progeny mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>101</td>
<td>1</td>
<td>160</td>
<td></td>
<td>300</td>
<td></td>
</tr>
<tr>
<td>102</td>
<td>1</td>
<td>140</td>
<td>140</td>
<td>280</td>
<td>280</td>
</tr>
<tr>
<td>103</td>
<td>1</td>
<td>120</td>
<td></td>
<td>260</td>
<td></td>
</tr>
<tr>
<td>104</td>
<td>2</td>
<td>140</td>
<td></td>
<td>280</td>
<td></td>
</tr>
<tr>
<td>105</td>
<td>2</td>
<td>120</td>
<td>120</td>
<td>260</td>
<td>270</td>
</tr>
<tr>
<td>106</td>
<td>2</td>
<td>100</td>
<td></td>
<td>no record as culled</td>
<td></td>
</tr>
</tbody>
</table>

Sire 2 gets an unfair 'lift' in progeny mean of yearling weight, due to culling at weaning.
Animals are from selected parents

Year 1

350  300  250

Year 2

365  335  310  290

Genetic mean changes as years go by due to selection

Animals born in recent years are expected to be genetically better than those born in past years

If EBVs are calculated as a deviation from the year mean, this wouldn't be accounted for

Properties of BLUP EBVs

Possible causes of bias ‘selection bias’

✧ Problem: There is culling and selection
  • worst sires have more progeny culled ‘culling bias’
  • animals are from selected parents

✧ Solution: Do joint evaluation
  • account for culling bias by evaluating first and later traits jointly
  • account for selection by joint evaluation over years

A feature of BLUP
In practice

❖ Information on culled animals should be included in the evaluation

❖ Similar to links between herds, links between years are required

Genetic trends

As BLUP separates genetic and year effects

genetic trends can be observed by plotting BLUP EBVs over years
In practice

- Genetic evaluation services often provide genetic trends to their clients
- Genetic trends are used as marketing tools
Possible causes of bias ‘unbalanced designs’

- Problem: Some animals have more information than others
  - different number of sibs
  - different number of progeny
  - etc.

- Solution: Construct a ‘customised’ selection index for each animal

  *A feature of BLUP*

Properties of BLUP EBVs

---

In practice

- Optimal weightings are placed on each information source

- Only the EBVs (rather than the index weights) are reported

Properties of BLUP EBVs
Another feature of BLUP

EBVs can be compared directly over age classes

Selection on BLUP EBVs results in optimisation of the generation interval

![Diagram showing proven sires and young sires with a truncation point.]

Another feature of BLUP

BLUP uses family information (and more so at lower heritabilities)

Selection on BLUP EBVs can thus result in higher F than selection on phenotypes alone

Properties of BLUP EBVs
How BLUP works

A joint evaluation of all animals
  • uses all additive genetic relationships
  • uses data on all animals jointly

Works as a linear model
  • corrects different effects for each other
  • jointly estimates animal effects and fixed effects

Has selection index properties
  • each EBV is the result of a customized index

---

BLUP summary

Optimal weights for all information sources
  • lots of different sets exist of optimal weighting factors, BLUP does it automatically

Allows comparisons of EBV's of animals in different herd (possibly with different genetic means)
  • but links need to exist in the data!

Accounts for culling and selection, non-random mating
  • but culled, non selected animals and mates need to be included in the analysis!

Allows selection across age classes – optimises generation interval

Provides an estimate of genetic trend
In practice

Accuracy of BLUP EBVs depends on quality of the data (as well as the trait heritability)

- Accurate phenotypic measurements
- Correct pedigree
- Correct recording of fixed effects & assignment to contemporary groups
- Appropriate data structure (e.g. information on mates, culls)

Remember, if BLUP doesn’t know a piece of information, it cannot account for it

Questions

How easy would it be to cheat the system?

Could an animal have different EBVs when evaluated under more than one evaluation systems?

When is an animal’s EBV likely to change within the one evaluation system?
From a ‘letter to the editor’ submitted to The Land 1999. Indicates a lack of understanding by the breeder.

"Dr Banks criticises [a particular genetic evaluation system] as he believes it is only regarding phenotype — the individual animal — while Lambplan can compare animals across flocks, regions, climates and feed buckets ...

However, as a current user of Lambplan, we can say the question of feed history of our sheep is never asked for, nor recorded so environmental factors have no say."

Properties of BLUP EBVs