PREDICTION OF BREEDING VALUE AND ESTIMATION OF VARIANCE COMPONENTS IN SPAIN BY MIXED MODELS.


1992. Changes in the model:

- New definition of Contemporary Groups.

- Days-open effect.

- Heterogeneity of variance correction.


- Genetic grouping (origin by sex and age).
CONTEMPORARY GROUP (CG). TREATMENT AND DEFINITION.

RESULTS FROM SIMULATION (UGARTE et al., 1992).

C.G. RANDOM IMPLIES SOME GOOD PROPERTIES:

- ↓ PREDICTION ERROR VARIANCE.


- ↑ GENETIC CORRELATION BETWEEN
  PREDICTED AND TRUE BREEDING VALUE.
RESULTS FROM REAL DATA. (BEN GARA AND ALENDÁ, 1992).

G.C. RANDOM IMPLIES:

* GOOD PROPERTIES:

- 1 CORRELATION PEDIGREE INDEX - YD

- 1 EFFECTIVE NUMBER ($N_e$)/REAL NUMBER ($N_r$)

- 1 $N_e/\sigma^2$.

* BAD PROPERTIES:

- 1 CORRELATION PREDICTED B.V. - C.G. EFFECT.

B.V. OF BULLS USED IN POSITIVE C.G. EFFECTS ARE OVERESTIMATED.
ERROR VARIANCE ($\sigma^2$), COEFFICIENT OF DETERMINATION (CD) AND RATIO OF EFFECTIVE SIZE ($N_e$) AND ERROR VARIANCE FOR THE MODELS THAT CONSIDERED HERD-YEAR AND HERD-YEAR-MOBILE SEASON AS FIXED OR RANDOM.

<table>
<thead>
<tr>
<th>MODEL</th>
<th>$\sigma^2_0$</th>
<th>CD</th>
<th>$N_e/\sigma^2_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>HERD-YEAR</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FIXED</td>
<td>1,465,300</td>
<td>.42</td>
<td>.044</td>
</tr>
<tr>
<td>RANDOM</td>
<td>1,310,610</td>
<td>.48</td>
<td>.050</td>
</tr>
<tr>
<td><strong>HERD-YEAR-SEASON (MOBILE)</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FIXED</td>
<td>1,026,250</td>
<td>.62</td>
<td>.057</td>
</tr>
<tr>
<td>RANDOM</td>
<td>1,026,500</td>
<td>.62</td>
<td>.061</td>
</tr>
</tbody>
</table>
WITHIN HERD CORRELATION BETWEEN PEDIGREE INDEX (PI = 1/2 B.V. SIRE + 1/2 B.V. DAM) AND YIELD DEVIATION (YD) FROM HERD CONTEMPORARY.

<table>
<thead>
<tr>
<th>MODEL</th>
<th>CORRELATION PI - YD</th>
</tr>
</thead>
<tbody>
<tr>
<td>HERD-YEAR FIXED</td>
<td>.28</td>
</tr>
<tr>
<td>RANDOM</td>
<td>.38</td>
</tr>
<tr>
<td>HERD-YEAR-SEASON (MOBILE) FIXED</td>
<td>.27</td>
</tr>
<tr>
<td>RANDOM</td>
<td>.40</td>
</tr>
</tbody>
</table>

EXPECTED WITHIN HERD CORRELATION PI - YD = .42
CORRELATION BETWEEN SIRE PREDICTED BREEDING VALUE (BV) AND CONTEMPORARY GROUP (CG) ESTIMATED EFFECTS.

<table>
<thead>
<tr>
<th>MODEL</th>
<th>CORRELATION BV - CG</th>
</tr>
</thead>
<tbody>
<tr>
<td>FIXED HERD-YEAR</td>
<td>.07</td>
</tr>
<tr>
<td>RANDOM</td>
<td>.34</td>
</tr>
<tr>
<td>FIXED HERD-YEAR-SEASON (MOBILE)</td>
<td>.14</td>
</tr>
<tr>
<td>RANDOM</td>
<td>.36</td>
</tr>
</tbody>
</table>
CONCLUSIONS:

1. USE OF C.G. AS RANDOM EFFECTS IN H-FRIESIAN EVALUATION IN SPAIN IS NOT RECOMMENDED ($H, + YS(H), ?$).

2. MOBILE HYS DEPENDING ON HERD SIZE IMPLEMENTED FOR NEXT EVALUATION.
HETEROGENEITY OF VARIANCE CORRECTION

- MANAGEMENT GROUPS (MG) WITH AT LEAST 30 OBSERVATIONS WERE CREATED FROM SIMILAR CONTEMPORARY GROUPS (C.G.) WITH A MAXIMUM OF 3 C.G.

- STANDARD DEVIATION FOR MG ($\sigma_{MG}$):

$$\sigma_{MG} = \left[ \frac{N_i V_i + 30 P V_i + 5N_{i-1} V_{i-1} + 5N_{i+1} V_{i+1}}{N_i + 30 + 5N_{i-1} + 5N_{i+1}} \right]^{1/2}$$

$N_i$ = NUMBER OF OBSERVATIONS IN MG$_i$.
$V_i$ = VARIANCE OF MG$_i$.
$P V_i$ = PREDICTED VARIANCE OF MG$_i$.

$$P V_i = (C V_{pop} \cdot \mu_i)^2$$

$C V$ = COEFFICIENT OF VARIATION  (0.19 IN SPANISH POPULATION)
$\mu_i$ = PHENOTYPIC MEAN OF MG$_i$

(BAGNATO AND JENSEN PERSONAL COMMUNICATION)
IMPROVEMENT OF COMPUTING ALGORITHMS

- G.S. (100 ITERATIONES) CURRENTLY USED TO SOLVE BLUP-ANIMAL MODEL MME.

- G.S. SLOW TO CONVERGE
- UNCERTAINTY ABOUT STOPPING POINT

- SIMULATION APPLIED TO:

- COMPARE NUMERICAL ACCURACY OF 6 ITERATIVE PROCEDURES:
  - GAUSS-SEIDEL (GS)
  - JACOBI-CONJUGATE GRADIENT (JCG)
  - SUCCESSIVE OVERRELAXATION (SOR)
  - SYMMETRIC SOR - CONJUGATE GRADIENT (SSORCG)
  - BLOCK (200 ECUATIONS) (BLO)
  - BLOCK (FIXED EFFECTS + 200 EQ) (BLOF).

- STUDY "ACCURACY OF PREDICTIONS" DURING ITERATION UNDER THE 6 PROCEDURES

- DETERMINE STOPPING CRITERIA BY COMPARING PROGRESS OF ACCURACY OF PREDICTIONS AND ESTIMATED GENETIC TREND WITH NUMERICAL CRITERIA USED TO MONITOR CONVERGENCE.
- DATA SETS:

- 2 SIZES (5000, 20000)

- SELECTED vs UNSELECTED

- NUMERICAL CRITERIA:  
  \[ C_d = \frac{\|b^{n-1} - b^a\|}{\|b^a\|} \]  
  (Cb = y)

  \[ Md = \max |b^{n-1} - b^n| \]

  \[ Cp = \frac{\|b^n - b\|}{\|\Delta\|} \]

- ACCURACY OF EVALUATION:  
  \[ \rho_n \]

- MSD = \[ \frac{\sum (Q_i - u_i)^2}{n} \]
  (u_i = additive genetic value)
  (n = number of animals evaluated)

- ESTIMATED GENETIC TREND (b)
CONCLUSIONS:

- JCG and blocking allow more numerical accuracy but larger memory (4x) and CPU time (4-5x) required.

- Fixing ranking does not require high numerical accuracy ($C_d \geq 10^{-3}$).

- Obtaining stable MSD and $\beta$ required more numerical precision ($C_d \geq 10^{-4}$).

- Slightly slower convergence for smaller and selected data sets.

- Possible shift to JCG for future evaluations.
Changes in Cd during iteration

(size: 5000; selected pop'n)
Correlation between real and predicted breeding value for bulls during iteration

(size: 5000; selected pop'n)
Mean Squared Difference between real and predicted breeding value (MSD) for bulls during iteration

(size: 5000; selected pop'n)
Estimated genetic trend (b) during iteration

(size: 5000; selected pop'n)
Estimated genetic trend (b) whenCd changed one digit of accuracy

(size: 5000; selected pop'n)