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CONFIDENCE REGIONS FOR GENETIC PARAMETERS OF ULTRASOUND SCANS AND ACTUAL CARCASS MEASUREMENTS OF INTRAMUSCULAR FAT

A. Reverter

Animal Genetics and Breeding Unit*, University of New England, Armidale, NSW 2351

SUMMARY

The aim of this study is to investigate the effectiveness of a parametric approach to approximate ellipsoid confidence regions for estimates of heritability (h^2) and genetic correlations (r_g). The procedure requires bootstrapping a series of Method R estimates. An illustrative numerical example is presented using real-time ultrasound scans of intramuscular fat percent (IMF %) on 5,391 yearling bulls and heifers and abattoir measurements of IMF % on 1,397 progeny. A total of 18 Method R estimates of genetic parameters were obtained. Emphasis was given to 1) the moderate (0.297) estimate of r_g between ultrasound scans on yearling bulls and abattoir measurements on steer progeny ($r_{g(Scan\_Bull-Abatt)}$); and 2) the low (0.121) h^2 found for live-scans on bulls ($h^2_{Scan\_Bull}$). Results indicate that, given the model and the size and structure of the data, the estimate of $r_{g(Scan\_Bull-Abatt)}$ should not be affected by the magnitude of the estimate of $h^2_{Scan\_Bull}$. However, a strong negative correlation between $r_{g(Scan\_Bull-Abatt)}$ and h^2 of IMF % at the abattoir could be expected.

Keywords: Confidence intervals, carcass, computing analysis, heritability

INTRODUCTION

Estimates of genetic parameters from multivariate animal models have an associated sampling correlation (r_S) that is rarely reported. Ignoring this r_S may lead to misleading results when making inferences about covariance components. Working with test day milk yield records, Kaiser *et al* (1998) approximated the joint density function for the proportion of phenotypic variance accounted for by gametic imprinting and h^2. The procedure was formally outlined by Reverter *et al* (1998) and is based on bootstrapping a limited number of Method R estimates.

BREEDPLAN, the National Australian genetic evaluation for beef cattle, produces several carcass EBVs including percent intramuscular fat (IMF %). Recent research (Graser *et al.* 1998) has concluded that ultrasound scans of IMF % on heifers are highly correlated with abattoir data from steer progeny. However, this was not as pronounced in bulls. To further investigate this phenomenon, our study focuses on the r_S between estimates of genetic parameters for IMF % across sexes. The inferential and computational effectiveness of a parametric algorithm to approximate ellipsoid confidence regions presented by Reverter *et al* (1998) is explored here with real data.

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[*] AGBU is a joint intitute of Nsw Agriculture and the University of New England

MATERIALS AND METHODS

Data. Abattoir carcass data on Angus steers and heifers were obtained from the Cooperative Research Centre for the Cattle and Beef Industry (Beef CRC). Details of the design of the breeding program and management regimes used by the Beef CRC can be found in Robinson (1995).

Live animal ultrasound scans were from 52 Angus herds that were participants in a research project conducted by the Animal Genetics and Breeding Unit and funded by the Meat Research Corporation. Table 1 presents descriptive statistics for the IMF % records involved in this study. To enhance distinguishing among the different market endpoints, carcass data in Table 1 are given separately for the domestic and the export (namely, Japanese and Korean) markets.

Table 1. Descriptive statistics for intramuscular fat percent (IMF%)

	Trait[A]	N	Mean	STD	Minimum	Maximum
Abattoir						
Domestic	CWT (kg)	578	216.56	27.56	153.50	297.50
	IMF(%)	578	3.51	1.26	1.23	10.08
Export	CWT (kg)	819	304.43	36.28	151.00	421.50
	IMF(%)	819	5.93	2.24	1.83	18.80
Live-Scans						
Bulls	Age (d)	2,857	482.05	92.13	292.00	688.00
	IMF(%)	2,857	3.88	1.46	0.50	12.20
Heifers	Age(d)	2,534	504.91	83.88	325.00	696.00
	IMF(%)	2,534	4.89	1.69	1.00	13.90

[A]CWT = Hot carcass weight, IMF = Intramuscular fat percent.

Genetic parameters. Method R procedures with multiplicative adjustments (Reverter *et al.* 1994) were used to estimate variance components. Eighteen 50 % samples were evaluated with solutions considered converged when the relative change in each variance component was less than 10^{-4}. The mixed-model for the genetic parameter estimation was:

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 \\ 0 & Z_2 & 0 \\ 0 & 0 & Z_3 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \\ u_3 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix}$$

Where y denotes the vector of observations; X is a known incidence matrix relating observations in y with fixed effects in β which includes contemporary group (CG) and a linear covariate; Z is the incidence matrix relating observations in y with random additive genetic effects in u; and e is the vector of random residual effects. Subscripts 1, 2 and 3 indicate abattoir, live-scan bulls and live-scan heifer records on IMF %, respectively. For abattoir records, carcass weight was fitted as a covariate and CG defined as herd of origin, sex, slaughter house and day. Fixed effects for live-scans included CG (defined as herd, paddock and date of measurement) and age as covariates. Ancestors were traced back 2 generations (parents and grand-parents) to give a pedigree with 18,319 relatives.

Confidence regions (CR). The iteration scheme that was used to approximate the 95 % CR is presented in Figure 1. From the initial n = 18 estimates of h^2 and r_g, 1,000 bootstrap replicates ($BOOT_R$) were generated and their respective means (8_R) and variances (S_R) evaluated. Estimates of the global mean (μ) and variance (S) were obtained from the average of 8_R and S_R, respectively. Finally, to determine whether any pair of values in $\mathbf{x}_i$ (containing a h^2 and r_g randomly selected from the entire parameter space) fell in the CR, the generalised squared distance $(\mu-\mathbf{x}_i)^T S^{-1}(\mu-\mathbf{x}_i)$ was computed and compared with $2(n-1)/(n-2)\ F_{2,n-2}(0.05)$.

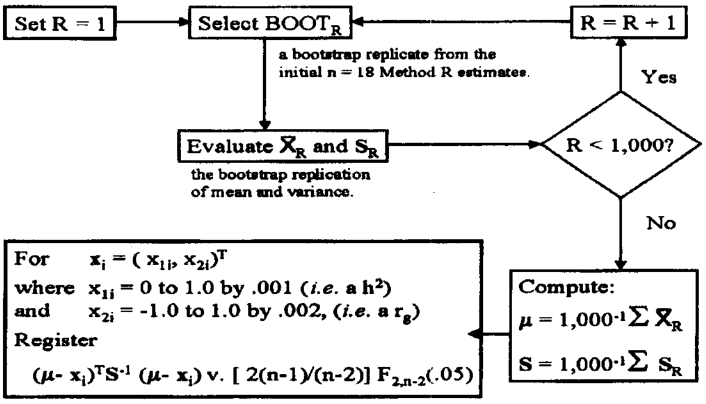

Figure 1. Algorithm to build an approximate 95% confidence region.

RESULTS AND DISCUSSION

Table 2 contains Method R estimates of h^2 and r_g from the average of the 18 independent 50 % random sub-samples. For validation purposes, REML estimates from the VCE 4.2 software (Groeneveld and García-Cortés 1998) are also presented. For Method R, SE were approximated by the STD of the 18 estimates. The SE associated with h^2 is a reflection of the number of records available for each trait. The larger SE associated with r_g were attributed to these parameters being estimated only through relationship as no animals had both live-scan and abattoir measurements.

The moderate estimate of $r_{g1,2}$ of .249 as compared to that for heifers ($r_{g1,3}$ = .668) was attributed to bulls being leaner and expressing marbling to a lesser degree (Graser *et al.* 1998). The approximate r_S's between the estimates were generally low (± .20). However the r_S between the estimates of h^2_1 and $r_{g1,2}$ was highly negative (-.85) which anticipates the difficulty in estimating $r_{g1,2}$ precisely and indicates that more favourable estimates of $r_{g1,2}$ could be associated with low estimates of h^2_1.

Table 2. Method R (MR) and REML estimates of heritability (h^2) and genetic correlation (r_g)^A

	h^2_1	H^2_2	h^2_3	$r_{g1,2}$	$r_{g1,3}$	$r_{g2,3}$
MR	.446 ± .109	.121 ± .048	.297 ± .104	.249 ± .556	.668 ± .301	.598 ± .268
REML	.456 ± .069	.073 ± .027	.335 ± .029	.136 ± .275	.614 ± .152	.770 ± .188

^{A}Subscripts 1, 2 and 3 indicate abattoir, live-scan bulls and live-scan heifer IMF%, respectively.

Figure 2 illustrates the joint 95 % ellipsoids for the estimates of abattoir IMF % h^2 and r_g between live-scan and abattoir IMF % resulting from 95 % CR and for the two sexes. The lengths and slopes of the major and minor axes of the ellipsoids reflect the magnitude of the sample pooled covariance matrices among the estimates as well as their respective ranges.

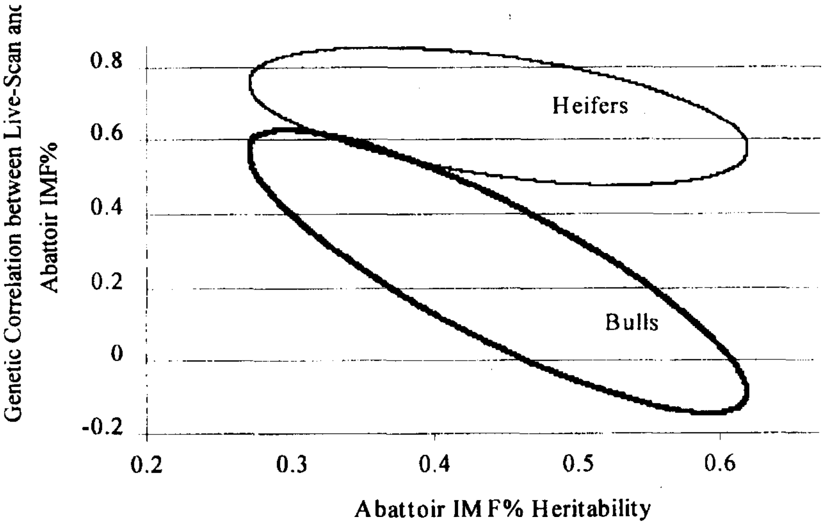

Figure 2. Joint ellipsoids for the estimates of abattoir IMF% h^2 and genetic correlation between live-scan and abattoir IMF% resulting from 95% confidence regions and for the two sexes.

Once the Method R estimates were available, the CR were trivial to construct as only the bootstrap replicates were required. The shape of the resulting ellipsoids provides a rich inferential framework about the sensitivity of the genetic parameter estimates to the structure of the data. Further research is required to explore possible changes in the ellipsoids shape as more data becomes available.

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