

Recursive Models For Analysis Of Growth And Ultrasound Carcass Traits In Nelore Cattle

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Introduction

In animal breeding, multiple-trait mixed models are usually used to analyze several traits measured on an individual (Meyer (2005)), longitudinal series of measurements of a trait (Forni et al. (2009)), or observations of the same trait in different environments (Corrêa, M.B.B., Dionello, N.J.L., and Cardoso, F.F. (2010)). With un-structured (co)variance matrices (UN-MT), the number of (co)variance parameters grows quadratically with the number of traits. With many correlated phenotypes, residual and genetic covariance matrices are close to singular, making convergence of estimation algorithms difficult (e.g., Meyer (2005)). Factor analysis (e.g., de los Campos and Gianola (2007)), principal components (e.g., Kirkpatrick and Meyer (2004)) and structural equation models (SEM, e.g., Gianola and Sorensen (2004)) can be used to arrive at more parsimonious models. Gianola and Sorensen (2004) discussed the use of recursive and simultaneous equation models acting on phenotypes; here, we consider recursive models (RM, a special case of SEMs) acting on genetic and residual effects separately, and use these models to estimate (co)variance parameters for growth and ultrasound carcass traits in Nelore beef cattle.

Material and methods

Data collection. Data (n=2,700), provided by the Nelore Breeding Program - Nelore Brazil (PMGRN), were collected from 2002 to 2004 on ten farms located in six Brazilian states. Animals were born from 2000 to 2002. The following real-time ultrasound carcass measures were collected: longissimus muscle area (LMA) and backfat thickness (BF), both obtained from a cross-sectional image on the longissimus dorsi muscle, measured between the 12th and 13th ribs; and rump fat thickness (RF), measured at the intersection between the gluteus medium and biceps femoris muscles located between the hooks and pin bones. Backfat thickness was evaluated at the 3/4 position from the chine bone end of the longissimus muscle, using the cross-sectional ribeye image. Other traits recorded included: body weight (BW), hip height (HH), both measured at the date of ultrasound scanning, and 450-days of

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age standardized scrotal circumference (SC). With the exception of SC, traits were measured in animals ranging 480 to 629 days of age.

Statistical analyses. Data were analyzed using a sire model, $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \boldsymbol{\varepsilon}$ where \mathbf{y} , $\boldsymbol{\beta}$, \mathbf{u} and $\boldsymbol{\varepsilon}$ denote vectors of observations, systematic effects, additive sire effects and model residuals, respectively, and \mathbf{X} and \mathbf{Z} are the corresponding incidence matrices. Systematic effects included: contemporary groups (defined as animals of the same sex (except for SC), born in the same herd, year and season, and reared within the same management group), age of animal at scanning (linear effect, except for SC), and age of dam (linear and quadratic effects for BF, RF, HH, and BW). The joint distribution of random effects was: $p(\boldsymbol{\varepsilon}, \mathbf{u}) = N[\boldsymbol{\varepsilon} | \mathbf{0}, \mathbf{I} \otimes \mathbf{R}_0] N[\mathbf{u} | \mathbf{0}, \mathbf{A} \otimes \mathbf{G}_0]$, where \mathbf{R}_0 and \mathbf{G}_0 are within-subject and within-sire residual and additive (co)variance matrices, respectively. Using RM, sire effects can be described as, $\mathbf{u}_i = \mathbf{B}_u \mathbf{u}_i + \boldsymbol{\xi}_{u,i}$, where \mathbf{u}_i is the random effect of the i^{th} sire, $\mathbf{B}_u = \{b_{u,ij}\}$ is a strictly lower-triangular matrix, i.e., $b_{u,ij} = 0$ for all $i \leq j$, whose non-zero entries define recursive effects, and $\boldsymbol{\xi}_{u,i}$ is a vector of random effects whose (co)variance matrix is: $Cov(\boldsymbol{\xi}_u) = \mathbf{A} \otimes \boldsymbol{\Psi}_u$ where $\boldsymbol{\Psi}_u = Cov(\boldsymbol{\xi}_{u,i})$ is a diagonal matrix. The reduced form model is $\mathbf{u}_i = (\mathbf{I} - \mathbf{B}_u)^{-1} \boldsymbol{\xi}_{u,i}$, therefore, $Cov(\mathbf{u}_i) = \mathbf{G}_0 = (\mathbf{I} - \mathbf{B}_u)^{-1} \boldsymbol{\Psi}_u (\mathbf{I} - \mathbf{B}_u)^{-1}$. Similarly, using RM for residuals, \mathbf{R}_0 can be represented as $\mathbf{R}_0 = (\mathbf{I} - \mathbf{B}_\varepsilon)^{-1} \boldsymbol{\Psi}_\varepsilon (\mathbf{I} - \mathbf{B}_\varepsilon)^{-1}$, where \mathbf{B}_ε is a strictly lower-triangular matrix defining recursive effects between model residuals and $\boldsymbol{\Psi}_\varepsilon$ is diagonal. A fully recursive model (FRM) occurs when all lower-triangular entries of \mathbf{B}_u and of \mathbf{B}_ε are non-zero, i.e., all $b_{u,ij}$ and $b_{\varepsilon,ij}$ with $i > j$ are parameters to be estimated. This model has as many (co)dispersion parameters as the UN-MT, and there is a one to one map from the unknowns in $\{\mathbf{B}_u, \boldsymbol{\Psi}_u, \mathbf{B}_\varepsilon, \boldsymbol{\Psi}_\varepsilon\}$ to those in $\{\mathbf{G}_0, \mathbf{R}_0\}$. Therefore, the FRM is just a re-parameterization of UN-MT. Various degrees of parsimony can be obtained by setting some of the lower-triangular entries of \mathbf{B}_u and \mathbf{B}_ε to zero. Models in this study differed in how \mathbf{B}_u and \mathbf{B}_ε were structured. Model 1 is a FRM, and based on the results of this model two more models were generated. In Model 2 (REC1) the ij^{th} entry of \mathbf{B}_ε was zeroed-out if $sd_{ij}^{-1} |\hat{b}_{ij}| < 1.96$ or $i \leq j$, where \hat{b}_{ij} and sd_{ij} are the posterior mean and posterior standard deviation of the ij^{th} entry of \mathbf{B}_ε obtained from the FRM, respectively. Using this, relative to FMR, a total of 6 recursive effects were zeroed-out. In Model 3 (REC2) we remove any effect in \mathbf{B}_u and \mathbf{B}_ε whose posterior mean in FRM was smaller than 0.15, in absolute value. REC2 has 15 recursive effects (10 in \mathbf{B}_ε and 5 in \mathbf{B}_u) less than FRM. All models were implemented in a Bayesian framework. Inferences were based on 160,000 samples from the posterior distribution obtained after discarding 40,000 samples as burn in, and thinned every 10th iteration. Convergence was checked by inspection of trace plots of dispersion parameters.

Results and discussion

Descriptive statistics of ultrasound carcass and growth traits in Nelore cattle are presented in Table 1.

Table 1: Ultrasound carcass and growth traits in Nelore cattle

Traits ^a	No. of records	Mean \pm SD ^b	No. of sires	No. of dams	No. CG ^c
LMA, cm ²	2,770	48.05 \pm 8.36	231	2,552	243
BF, mm	2,577	1.87 \pm 1.07	226	2,397	253
RF, mm	2,566	2.95 \pm 1.94	226	2,384	252
SC, mm	1,340	245.87 \pm 30.22	106	1,009	88
HH, cm	2,349	136.06 \pm 5.04	226	2,308	250
BW, kg	2,942	339.69 \pm 65.98	236	2,683	302

^a LMA = longissimus muscle area; BF = backfat thickness; RF = rump fat thickness; SC = standardized scrotal circumferences at 450 days of age; BW and HH = weight and hip height obtained at the time of scanning, respectively. ^b SD = standard deviation. ^c No.CG = number of contemporary groups.

Table 2 gives estimates of heritabilities, and of genetic (above diagonal) and residual correlations (below diagonal) obtained from the FRM. The patterns of residual and genetic correlations were slightly different. Recursive models acting separately on \mathbf{u}_i and $\boldsymbol{\varepsilon}_i$ (as opposed to recursion on phenotypes) allow these patterns to be captured. The different patterns of genetic and residual correlations (see Table 2) can be interpreted using estimates of recursive effects. Table 3 gives estimates of genetic (above diagonal) and residual (below diagonal) recursive effects obtained from the FRM.

Table 2: Estimates of heritability (diagonal), genetic (above diagonal) and residual (below diagonal) correlations obtained from the fully-recursive model (FRM).

Traits ^a	LMA	BF	RF	BW	HH	SC
LMA	0.25 \pm 0.05	0.19 \pm 0.19	0.06 \pm 0.20	0.42 \pm 0.14	-0.15 \pm 0.17	0.24 \pm 0.20
BF	0.14 \pm 0.02	0.44 \pm 0.09	0.65 \pm 0.10	0.05 \pm 0.17	-0.49 \pm 0.13	0.07 \pm 0.23
RF	0.11 \pm 0.02	0.57 \pm 0.01	0.35 \pm 0.08	0.10 \pm 0.17	-0.40 \pm 0.15	0.04 \pm 0.18
BW	0.49 \pm 0.02	0.22 \pm 0.02	0.15 \pm 0.02	0.31 \pm 0.07	0.39 \pm 0.15	0.11 \pm 0.19
HH	0.11 \pm 0.02	-0.01 \pm 0.02	-0.03 \pm 0.02	0.42 \pm 0.02	0.44 \pm 0.09	-0.21 \pm 0.23
SC	0.20 \pm 0.04	-0.02 \pm 0.07	0.02 \pm 0.07	0.39 \pm 0.04	0.20 \pm 0.05	0.48 \pm 0.12

^a See Table 1 for abbreviations.

Genetic parameters estimated with REC1 and REC2 (not shown) were similar to those reported in Table 2. Except for a lower genetic correlation between BW and SC, our estimates of genetic parameters were close to those described in the literature for Nelore cattle, using UN-MT (Cyrillo et al. (2001); Yokoo et al. (2008)), and for Angus cattle, using principal components (Meyer (2005)). The number of records of SC used in this study is limited (1,340), and this may, partially, explain differences from previous findings. The posterior mean of the log-likelihood and the estimated number of effective parameters (Spiegelhalter et al. (2002)) were: -18712.1, -18712.3, -18748.6 and 447.5, 443.3, 440.2, for FRM, REC1 and REC2, respectively. Thus, FRM and REC1 fitted the data similarly, and

both were considerably better than REC2. As expected, the effective number of parameters was largest in FRM. The Deviance Information Criterion (DIC, Spiegelhalter et al. (2002)) of FRM, REC1 and REC2 were: 37871.8, 37867.9 and 37937.4, therefore DIC favored REC1 over the other two models.

Table 3: Estimates of genetic (above diagonal) and residual (below diagonal) recursive effects from the fully-recursive model (FRM) in Nelore cattle.

Traits ^a	LMA	BF	RF	BW	HH	SC
		Recursive effects				
LMA		0.40±0.40	-0.13±0.27	0.48±0.18	-0.54±0.27	0.23±0.48
BF	0.21±0.03		0.56±0.12	-0.08±0.12	-0.23±0.16	-0.09±0.32
RF	0.04±0.03	0.55±0.02		0.10±0.14	-0.24±0.19	-0.06±0.30
BW	0.45±0.02	0.09±0.02	0.01±0.02		0.83±0.25	0.34±0.49
HH	-0.14±0.03	-0.05±0.02	-0.04±0.02	0.60±0.03		-0.41±0.40
SC	0.03±0.06	-0.10±0.06	0.02±0.05	0.48±0.06	0.03±0.06	

^a See Table 1 for abbreviations.

Conclusion

Recursive models applied to genetic and residual effects can be used to arrive at more parsimonious representations of genetic and residual (co)variance matrices. This reduces the number of parameters to be estimated, with important computational advantages, and may yield useful interpretations of the underlying patterns of (co)variability. Moreover, unlike recursive models acting on phenotypes, these models do not impose crossed-restrictions between genetic and residual (co)variance matrices. Results from this study indicate that beef cattle growth and ultrasound carcass traits may be successfully analyzed with recursive models.

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