had no effect (P>0.10) on ADG or feed intake over the 6-wk experiment. However, due to numerical differences in feed intake and ADG, feed efficiency was improved (P<0.05) for pigs fed Diet 3. There was no effect (P>0.10) of diet type on Ca digestibility. Phosphorus, DM, CP and energy digestibilities were lowest (P<0.05) for pigs fed Diet 4. The digestibility of P was similar for pigs fed Diets 1, 2 and 3. Pigs fed Diet 2 had a higher DM digestibility compared to pigs fed Diet 1 (P<0.05), but were similar to those fed Diet 3. Pigs fed Diet 3 had a higher CP digestibility than those fed Diets 1 or 2 (P<0.05). However, pigs fed Diet 3 had a slightly lower energy digestibility than pigs fed Diets 1 or 2 (P<0.05). The results of this study indicate that hulless or hulled barley can be incorporated into swine diets at levels of at least 40% and yield performance similar to corn-SBM based diets, if diets are formulated to the same nutrient specifications.

Key Words: Pig, Barley, Digestibility

452   Energy and nitrogen balance of pigs fed four corn grains. R.W. Fent*, S.D. Carter, M.J. Rincker, and B.W. Senne, *Oklahoma State University, Stillwater.*

Six sets of four littermate barrows (27.5 kg) were used to evaluate four corn grains (A, B, C, and D) in an energy and nitrogen balance experiment. Corns A and B were nearly isogenic with A being normal corn, while B was a high-oil variety. Corns C and D were also normal varieties. Pigs were housed individually and allotted to four dietary treatments based on weight and litter. Experimental diets (1.0% Lys) consisted of corns A, B, C, or D (90.48%) with casein (5.04%), crystalline amino acids, and a vitamin/mineral source. Pigs had ad libitum access to water and an effort was made to equalize feed intake within replicate. A 7-d adjustment period to the diets was followed by a 5-d collection of feces and urine. Data are reported on a DM basis unless otherwise noted. GE concentration and CP content of corns A, B, C, and D were: 4,462, 4,761, 4,594, and 4,601 kcal/kg and 8.73, 9.14, 9.47, and 9.02%, respectively. GE intakes for pigs fed diets containing A, B, C, and D were 5,452, 5,291, 5,387, and 4,965 kcal/d. However, fecal and urine GE excretions (kcal/d) were similar (P>0.10) across all treatments. The DE for the diets containing A, B, C, and D were 3,924, 4,186, 4,061, and 3,990 kcal/kg while ME were 3,868, 4,127, 4,006, and 3,935 kcal/kg, both varying (P<0.04) depending on source of corn. However, no differences (P>0.10) were seen in DE:GE (.886, .887, .894, and .885) or ME:GE (.874, .875, .882, and .873). Nitrogen absorption and retention were not affected by corn source. Previously, we determined the ME

of casein to be 4,560 kcal/kg and, thus, the casein in the diet (5.04%) supplied 230 kcal/kg. Subtraction of the ME provided by casein from the ME of the diets resulted in ME concentrations of 3,600, 3,842, 3,660, and 3,625 kcal/kg (as-fed basis) for corns A, B, C, and D. This correction resulted in slight differences (P<0.10) in ME:GE (.901, .905, .909, and .890) for the corn grains. These results indicate that although ME concentrations varied for the four corn grains, the differences observed were attributed to initial variation in GE concentration.

Key Words: Corn, Metabolizable energy, Pigs

453   Swine digestible energy evaluations of Bt (MON810) and Roundup Ready®corn compared with commercial varieties. A.M. Gaines*, G.L. Allee, and B.W. Ratliff, *University of Missouri-Columbia.*

Two digestible energy experiments were conducted to compare nutritional value of insect protected (containing CrylA (b) protein, Bt) corn, glyphosate-tolerant (Roundup Ready, RR) corn (containing maize EPSPS protein), their near-isogenetic parents (BtC and RRC) and three commercial corn hybrids (C1, C2, and C3). Twenty crossbred barrows (26.4±2.8 kg) were placed in metabolism crates allowing for separate collection of feces in two collection periods. Pigs were assigned to one of the five dietary treatments in a complete randomized design. Fecal matter was collected and feed disappearance recorded for the five-day periods. Both fecal material and feed were analyzed for dry matter and gross energy values to determine digestible energy coefficients for each of the experimental hybrids. There were significant differences (P≤.05) in digestibility coefficients (88.1%, 87.7%, 86.2%, 87.3%, and 87.6% for Bt, BtC, C1, C2, and C3, respectively). However, Bt was not different than its near-isogenic parent (BtC). Twenty additional crossbred barrows (25.5±2.9 kg) were placed in metabolism crates in two collection periods and assigned to one of the five dietary treatments in a complete randomized design. Fecal matter was collected and feed disappearance recorded for the five-day periods. There were significant differences (P≤.05) in digestible energy coefficients (87.3%, 88.4%, 86.0%, 88.6%, and 88.0% for RR, RRC, C1, C2, and C3, respectively). However, RR was not different from its near-isogenic parent (RRC). In conclusion, Bt and RR corn digestible energy coefficients values are not different from their near isogenetic parents; however, there were differences among the other three commercial corn hybrids tested.

Key Words: Corn, Energy, Swine

ASAS/ADSA Breeding and Genetics: Quantitative Methods

454   Use of matrix exponentials to enforce the positive definite constraint of covaraince matrices. S.D. Kachman*, *University of Nebraska.*

Restricted maximum likelihood estimates of covariance matrices must be positive definite. Enforcing the positive definite constraint for unstructured covariance matrices is a challenge. Matrix exponentials provide a means of reducing the positive definite constraint to a symmetry constraint. An unstructured covariance matrix $\mathbf{V}$ can be written as the exponential of a matrix $\mathbf{A}$. A matrix exponential is defined as $\mathbf{V}=\exp(\mathbf{A})=\Sigma_{i=1}^{\infty}\mathbf{A}^i$. Provided that $\mathbf{A}$ is symmetric and finite the covariance matrix $\mathbf{V}=\exp(\mathbf{A})$ is positive definite. By taking a spectral decomposition of $\mathbf{A}=\mathbf{PDP}$' and iterating on $\mathbf{D}$ as opposed to $\mathbf{A}$, the required derivatives are dramatically simplified. The partial derivative of $\mathbf{V}$ with respect to δ_{ij}, element ij of $\mathbf{D}$, is $\mathbf{P}\Delta_{ij}\mathbf{P}$' where Δ_{ij} is matrix of zeros except for elements ij and ji which are equal to $[\exp(\delta_{ii})-\exp(\delta_{jj})]/[\delta_{ii}-\delta_{jj}]$. The derivative reduces to $\exp(\delta)$ when $\delta_{ii}=\delta_{jj}=\delta$.

Key Words: Mixed Model, REML

455   Use of partial augmentation to improve the Monte Carlo sampling of variance components. R.A.A. Torres Jr and Richard L. Quaas, *Animal Science Department - Cornell University.*

The use of Gibbs Sampling (GS) to estimate variance components (Σ) for some highly parameterized mixed linear models (animal models) results in chains with very slow mixing. Sampling all location parameters (θ) together may not be enough to overcome the slow mixing. Procedures to sample from the marginal distribution of dispersion parameters have

been suggested but they can be too computationally burdensome for certain applications. Sampling from the marginal distribution of variance components involves evaluating the likelihood as in derivative-free REML estimation, where the determinant of the mixed model equations is obtained using factorization techniques for sparse matrices. This factorization involves reordering the system of equations and results in an arrow shaped system ($\mathbf{C}$). This shape is the useful feature exploited here. The upper left-hand block ($\mathbf{C}_{11}$), corresponding to the tail of the arrow, is usually very large and very sparse and its determinant can be computed at a much lower cost than that for the entire system. Our approach is to sample Σ from its distribution marginal with respect to location parameters at the tail of the arrow (θ_1), but conditional to those at the head of the arrow (θ_2). To do so, we compute $\pi(\Sigma$—$\theta_2,\mathbf{y})$ which is proportional to the target distribution and requires the Cholesky factor of $\mathbf{C}_{11}$ only and use it in a Metropolis-Hastings (MH) algorithm to obtain a sample of Σ. For a system of 255,325 equations, 75,699 were avoided by combining additive and cow effects for non-parents, what is possible as we use MH for sampling Σ. $\mathbf{C}_{11}$ was assigned 168,000 equations as a high increase in computation resulted if more equations were included. This resulted in augmenting only with 11,626 parameters, which is about 4.5% of the number of augmented parameters in the usual implementation of the GS. Such approach is a compromise between marginal sampling and full conditional sampling of dispersion parameters. It is capitalizes on the shorter chain needed with full conditional sampling (lower autocorrelations) and the computational ease of marginalization.

Key Words: Markov Chain Monte Carlo, Covariance function, Test-day model

456 Least Squares Lehmann-Scheffe superior to other methods for estimating variance components and heritability. W.D. Slanger* and J.W. Carlson, *North Dakota State University.*

Least Squares Lehmann-Scheffe (LSLS) estimators (Slanger, 1996) of two variance components and heritability were compared with those of ANOVA (=Henderson's Method 3 (H3)), MINQUE, ML, and REML. Model was fixed herd by random sire with interaction. Thirty-nine progeny were distributed over 3 herds and 4 sires. There were 15,000 computer simulation replications per each of 96 combinations of designs (n=6), heritabilities (.05, .20, .50, .70), ratios of sire variance to interaction variance (3:1, 1:3), and distributions (normal and chi-square with 3 df). The designs ranged from almost balanced to very unbalanced. Nonzero estimates of variance components and heritability were used in the comparisons presented here. Results for the normal distribution are presented here since normal and chi-square results were approximately the same for all 96 combinations. LSLS was superior to the other four methods, and the more unbalanced the design the more superior was LSLS. For instance, the relative mean square errors for heritability estimators averaged over the 48 combinations were 1.0, 2.7, 2.4, 2.2, and 2.8 for LSLS, H3, MINQUE, ML, and REML, respectively. The analogous percentages of nonzero estimates of heritability were 44, 29, 28, 17, and 28%. For the most unbalanced design, the relative mean square errors for sire variance estimators averaged over the eight combinations were 1.0, 7.6, 9.5, 4.3, and 7.3, for LSLS, H3, MINQUE, ML, and REML, respectively. The analogous percentages of nonzero estimates of sire variance were 67, 64, 61, 40, and 51%. Distributions of all LSLS estimators were superior in that the percentages of estimates within plus and minus 50% the value of the parameter were almost always greater for LSLS than all other methods. Estimator performances were approximately the same whether the variance ratio was 3:1 or 1:3. Results are substantive evidence that LSLS is superior to the compared methods for estimating variance components and heritability and justify efforts to make the procedure computationally efficient.

Key Words: Estimation, Variance components, Heritability

457 Correlations between clinical mastitis at different stages of lactation in Norwegian Cattle using a multivariate threshold model. Y. M. Chang*[1], R. Rekaya[2], D. Gianola[1], B. Heringstad[3], and G. Klemetsdal[3], [1]*Department of Animal Sciences, University of Wisconsin, Madison,* [2]*Department of Dairy Science, University of Wisconsin, Madison,* [3]*Department of Animal Science, Agricultural University of Norway.*

Clinical mastitis records on 13,070 first-lactation cows from 1,868 herds, progeny of 250 sires, were analyzed. The interval ranging from 30 days pre-calving to 150 days post-partum was divided into 6 periods of equal length. Within period, it was checked whether mastitis occurred or not. Mastitis incidence was 4.3% and 10.6% in the first two periods, and ranged between 1.9% and 2.1% subsequently. The objective was to infer genetic and residual correlations between mastitis in the 6 periods. An hexavariate analysis was carried out with a Bayesian threshold model, assuming that mastitis (presence vs. absence) was a different trait in each period. Using a multivariate normal link, unobserved mean liabilities were modeled as a linear function of year, age-season of calving, herd, and sire effects. All residual variances were set equal to one. For cows culled before 150 days, missing liabilities were included in an augmented posterior distribution. Gibbs sampling was used to draw from posterior distributions of interest, and an algorithm was devised to collect samples from the residual correlation (covariance) matrix. Heritability of clinical mastitis was 0.12, 0.09, 0.11, 0.09, 0.08 and 0.09 for the 6 periods. Genetic correlations were positive and small (0.03 ± 0.27), except between periods 1 and 3 (-0.07) and periods 1 and 6 (-0.18). Most posterior coefficient of variations were larger than 100%, and zero was included in 95% credibility sets for all genetic correlations, illustrating lack of precision of inferences . Results may suggest that different genes are involved in the expression of clinical mastitis in different periods. Residual correlations ranged between -0.11 and 0.44, and were smaller for non-adjacent intervals.

Key Words: Clinical mastitis, Heritability, Threshold model

458 An assessment of threshold models with Student t distributed liabilities for the analysis of calving ease. K. Kizilkaya*[1], P. Carnier[2], G. Bittante[2], A. Albera[3], and R. Tempelman[1], [1]*Michigan State University, East Lansing, MI, USA,* [2]*University of Padova, Legnaro, Italy,* [3]*Associazione Nazionale Allevatori Bovini di Razza Piemontese, Carru, Italy.*

A heavy-tailed Student t residual distribution may be specified as an alternative to the Gaussian distribution for the conceptual underlying liability variables in a regular threshold model. This threshold-t model specification is an attempt to confer outlier-robustness properties for the analysis of ordered categorical data, e.g. calving ease. However, it is not known how well various Bayesian model choice criteria would be able to correctly discern between a threshold-t and a regular threshold model specification in animal breeding and what implications model choice might have on breeding value inference. We assess these issues using MCMC methods in a simulation study and in an application to calving ease data. For each of three populations, underlying liabilities were generated for 1000 progeny from 50 sires, with each sire mated to 5 dams. Each population was characterized by a residual scale (variance) parameter of 1.00 and a genetic variance of 0.50 for normally distributed genetic effects. The residual effects were Student t distributed with degrees of freedom being 4, 20, or infinity (i.e. Gaussian) for the three populations, respectively. Underlying liabilities were converted to ordinal data with four categories based on the same threshold parameter values (relative to the overall mean) of -0.25, 0.25 and 1.25 for all populations. The data was analyzed using threshold animal models with either normal or Student t distributed residual specifications on the liability scale. Model choice, as based on various pseudo-Bayes factor criteria, was correctly assigned in all three cases. The regular threshold and threshold-t sire maternal-grandsire models were also applied to data on calving ease scores in Italian Piedmontese cattle. The Bayes factor criteria ($>$100) appeared to heavily favor a threshold-t specification; nevertheless, the rank correlation on posterior means of breeding values between a threshold-t and regular threshold model analyses exceeded 0.98.

Key Words: Threshold Model, Model Choice

459 Bayesian inference in linear mixed model using Dirichlet process prior. Romdhane Rekaya*, *Dept. of Dairy Science, University of Wisconsin.*

Practice of hierarchical modeling has exploded in the last decade both in applied statistics and in animal breeding. Such explosion is a result of 1) the great capacity of hierarchical modeling in solving complex problems by breaking them into submodels (parts) that can be solved more easily and then assembled in a natural way and 2) the development of Markov Chain Monte Carlo methods (MCMC) to overcome the computational complexity. In hierarchical models, as with all parametric models, specification of distributions for parameters and often hyperparameters is required. Usually a considerable uncertainty is associated with those distributions leading to inevitable concerns about the sensitivity of the resulting inferences to the assumed forms of component distributions. Hence, a nonparametric or semi-parametric modeling that avoids the prior specification of distribution forms is a logical choice to assess such uncertainty. A nonparametric model using Dirichlet process prior was implemented for a small data set to assess the sensibility of assuming normality for the distribution of the additive breeding values. 5621 first lactation milk yield records and 7094 animals in the pedigree were used to compare a nonparametric hierarchical model with a standard mixed liner model. Posterior mean of heritability was 0.32 and 0.31 using standard mixed linear model and nonparametric hierarchical model, respectively. No significant differences were observed on the posterior means of the genetic and residual variances using both models. The posterior mean of the "degree of belief" or precision parameter on the baseline prior of the distribution of additive breeding values was 13 strongly supporting the normality of such distribution. In animal breeding applications using mixed linear model, it looks more reasonable to assume uncertainty over the distribution of the error terms given the possibility of outlying observations.

Key Words: nonparametric, Dirichlet, Bayesian

460 Bayesian analysis of skewed Gaussian models: an application to reproductive traits in dairy cattle. G. J. M. Rosa*[1,2], R. Sartori[2], M. C. Wiltbank[2], and D. Gianola[2], [1]*UNESP - Botucatu, SP/Brazil,* [2]*UW - Madison, WI.*

A normal distribution is assumed often in statistical analysis. If the assumption does not hold, e.g., when data are skewed, Gaussian-based methods may lead to erroneous inference. Alternatives include data transformations, non-parametric methods or assumptions meeting the skewness requirement. Here, the approach of Fernández and Steel (*JASA* **93**: 359-371, 1998) was adopted for modeling skewed Gaussian distributions. An extra parameter, controlling allocation of mass to both sides of the mode, is required. Data were from an experiment with Holstein cows aimed to study whether or not high milk yield affects embryo quality. Twenty-seven dry and 28 lactating cows (40-100 days post-partum) were synchronized and bred by AI. Five days after insemination, embryos were evaluated for embryonic cell nuclei cycles (ECC, estimated from embryonic cell counts) and number of accessory sperm (NAS). A Bayesian framework (with diffuse priors) was adopted; a Gibbs sampler with Metropolis-Hastings steps was used to carry out the analyses. Gaussian and skewed models with different assumptions about homogeneity of scale and skewness parameters were compared using Bayes factors. Single chains were run for each model, with 300,000 iterations for posterior inferences, after burn-in. There was skewness to the left and to the right, respectively, of the distributions of ECC and of NAS. Bayes factors gave stronger support to models having a homogeneous scale parameter, but different skewness parameters for the two groups, for both traits. No differences were found for NAS between groups of cows. ECC was more skewed in lactating cows, as some embryos had very few cycles. The skewed Gaussian methodology offers a flexible alternative for analysis of biological data.

Key Words: Skewed distribution, Bayesian inference, Reproductive traits

461 Bayesian inference on uncertain paternity for prediction of genetic merit. F. F. Cardoso* and R. J. Tempelman, *Michigan State University, East Lansing, MI/US.*

A simulation study was used to compare the performance of three different genetic evaluation methods when 30% of non-parent animals (i.e. without progeny) have uncertain paternity due to the use of multiple sires in mating groups. One method was best linear unbiased prediction based on Henderson's average numerator relationship matrix (ANRM). The other two methods were Bayesian and used the data to infer upon the probability of an individual with uncertain paternity being sired by any one of a number (2, 3, or 4) of candidate sires. One of these methods was an empirical Bayes (EBAYES) procedure and the other was a fully Bayesian procedure based on the use of Gibbs sampling (GIBBS). Ten simulated populations were generated at each of three different levels of heritability (h^2): .10, .30 and .50. Each population consisted of four generations of phenotypic selection and included 20 sires, 100 dams and 500 non-parent animals in total. The methods were compared by mean squared error of prediction (MSEP), mean bias (MBIAS) and rank correlation (RANK) between estimated and true breeding values. Mean posterior probabilities of true sires (MPPTS) for individuals with uncertain paternity were generally of similar magnitude under EBAYES and GIBBS. For either Bayesian method, the MPPTS were significantly greater (P<.05) than the corresponding prior probabilities (inverse of number of candidate sires) at h^2 equal to .30 and .50; however, these differences were not very large (+3.1 to +7.1%). At h^2 equal to .10, the MPPTS were generally not different from the prior probabilities (P>.05). There were no significant differences in genetic evaluations between the three methods in terms of MSEP, MBIAS and RANK (P>.05) for all three heritabilities. These results indicate that there may be little power in field data to infer upon candidate sire assignments for individuals with uncertain paternity. Under these and similar situations, ANRM may be satisfactorily used for genetic evaluations, particularly in light of the savings in computing resources compared to EBAYES and GIBBS methods.

Key Words: Multiple sires, Genetic evaluation, Gibbs sampling

462 Two-step and random regression analyses of weight gain of Canadian beef bulls. Flavio Schenkel*, Stephen Miller, Janusz Jamrozik, and James Wilton, *University of Guelph, Guelph, ON, Canada.*

Objective was to compare a two-step (TS) model and a joint procedure via random regression model (RR) for evaluating weight gain of 25,315 bulls, weighed every 28 days on 140 day test. TS analysis consisted of fitting fixed linear regressions to weights of each bull on days of measurement to determine gain on test. In the second step, mixed model analyses of gain estimated variance components and breeding values (EBV), including fixed effects of breed, test group and starting age, and random effects of weaning herd-year group (WHY) and of animal (additive genetic). The RR model included the same effects as the TS mixed model analyses, with additional random animal permanent environment (PE) effect. Fourth order Legendre polynomials of days on test were fitted for all fixed and random effects in the model, except for breed. Breed effects and residual variances were estimated for each measurement period. Variance components and EBV's for gain were obtained from the estimated covariance function and random regression coefficients for weight. RR heritability (h^2) estimates for gain on test increased over time, being maximum at end of test (0.377) and similar to TS procedure (0.376). PE variance ratio estimates also increased over time and were higher than h^2. WHY variance ratio estimates kept constant over time, being slightly higher at end of test (0.076) than TS (0.069). Genetic correlations between gain up to different days on test given by RR were high (from 0.81, between 28 and 140 day gain on test, to 0.99, between 112 and 140 day gain on test). Genetic correlations between gain on discrete 28 day intervals were moderate to high (e.g., 0.53 and 0.86 between the last 28 days on test and the first and fourth 28 days, respectively). Rank correlation between EBV's for 140 day gain by the two procedures was 0.97, 0.83, and 0.67 for all bulls, the 5% best (highest RR EBV's), and the 1% best bulls, respectively. Results indicate that, despite similar h^2 estimates, the two procedures rank top bulls quite differently for 140 day gain on test. RR model accounted for changes over time of genetic and environmental effects on the test weight gain curve of the bulls.

Key Words: Weight Gain, Beef Cattle, Random Regression

463 Predictions of 305-day lactation yields in cows by ARMA models. N.P.P. Macciotta*[1], D. Vicario[2], G. Pulina[1], and a. Cappio-Borlino[1], [1]*Universit di Sassari, Italia,* [2]*Italian association of Simmental cows breeders* .

This study deals with ARMA models, a family of stochastic models originally developed in the context of time series analysis, used to predict Test Day (TD) yields of milk production traits in dairy cows. The main feature of ARMA models is their ability to take account both of the average lactation curve of a homogeneous group of animals and of the residual individual variability that may be explained in terms of probability models, such as Autoregressive (AR) and Moving Average (MA) processes. Furthermore, the standard method of ARMA estimation includes several diagnostic tools such as Fourier transform, autocorrelation and partial autocorrelation functions, that are helpful in identifying the most appropriate model structure. Data were TD of milk production traits (milk, fat and protein yields) of 6,000 Italian Simmental cows, with 8 TD records per lactation. Homogeneous groups were formed according to parity (1st, 2nd and 3rd calving) and data were fitted to a Box-Jenkins ARMA model. Different situations of missing data were simulated and cumulated 305-d yields were calculated by TIM using all actual (actual yields) or actual plus forecasted (estimated yields) TD yields. Accuracy of predictions is remarkable also when a few actual TD records are available. As an example, in third parity cows the correlations between actual and estimated yields are 0.88 for milk and protein and 0.84 for fat when 6 out of 8 TD records are predicted. Accuracy rapidly increases with the number of actual TD available: correlations are about 0.96 for milk and protein and 0.93 for fat when 4 out of 8 TD records are predicted. In comparison with the standard method of projecting lactations in progress by extension factors, ARMA modelling do not compress the variance of predictions. Furthermore, ARMA models can be easily implemented in data recording softwares also at farm level.

Key Words: Milk Production Traits, ARMA Models, Test Day

464   Establish confidence intervals for daily milk yield measures by robust bootstrap. P. M. Saama*[1] and I. L. Mao[2], [1]*Michigan State University, East Lansing, MI,* [2]*National Institute of Agricultural Science, Denmark.*

Prior to statistical analyses of daily milk yield data, outliers due to equipment malfunction or confirmed milk recording errors should be removed. However, those outliers that are caused by health status, body condition, stress, energy balance, or BST would be valid data. Hence, using the central limit theorem (CLT) to establish confidence intervals (CI) for yield measures could be misleading. The "ordinary" bootstrap performs poorly in these situations. This study demonstrates the use of a robust bootstrap resampling algorithm to construct CI for daily milk yield. The double bootstrap algorithm advances the notion that CI can be constructed from a function of the sample and the mean whose distribution is independent of the mean, the sample, or any other unknown parameter using pivotal quantities. In the algorithm, the mean of the data is computed. Then the first stage bootstrap sample (F) of size n is obtained from the observed data, with replacement (WR). The difference between the mean of F and the mean of the observed data is divided by the SE of the mean (SEM) of F, is a pivotal quantity that provides a robust bootstrap-t distribution of the mean daily yield. Then, the second stage bootstrap sample (G) of size n is randomly drawn WR from F. The difference between the mean of this bootstrap sample and the mean of F is now divided by the SEM of G. The first and second stage bootstraps are repeated B and K times, respectively. The CI for the mean can be obtained from the percentiles of the bootstrap distributions. Daily milk records for 89 first lactation cows from a Michigan herd were used for demonstration with B=500 and K=500. The distribution was skewed to the right at peak and in late lactation. The 95% CI given by the CLT were widest. The ordinary bootstrap gave narrow CI while the bootstrap-t and double bootstrap methods gave relatively stable CIs. After computing 99% confidence intervals using this approach, data that do not fall within the limits of that interval could be removed prior to statistical analysis.

Key Words: Milk yield, Variation, Bootstrap

465   Determination of covariance functions for lactation traits on dairy cattle using random-coefficient regressions on B-splines. R.A.A. Torres Jr and Richard L. Quaas, *Animal Science Department - Cornell University .*

Covariance functions for dairy cattle have been specified either by a multi-trait analysis of records within an interval of the lactation followed by extrapolation or by direct modeling of observations throughout the lactation using random-coefficient regressions. Here we present an approach using regressions on B-splines that is an extension of the within interval multi-trait analysis where the intervals are specified by the knots. It allows local fitting behavior and simultaneous modeling of every day of the lactation. The approach was applied to 296,601 test day records from 36,520 cows for milk yield, 180,474 records from 27,320 cows for fat and protein yield and 135,336 records from 26,628 cow for somatic cell score coming from 13 large dairy herds from New York State during 1989 through 1997. A longitudinal model with cows as subjects was used together with other effects to adjust for environmental effects and a heteroskedastic independent residual. Inferences about the dispersion parameters were made from the samples of a Markov Chain Monte

Carlo procedure. For milk yield the 3 largest eigenvalues of the covariance function for the cow specific effect accounted for at least 85%, 11% and 2.5% of the total variance and the respective eigenfunctions were close to constant, linear and quadratic functions, with slight discrepancy at the extremes causing variance reduction. For fat and protein yield the first eigenvalue accounted for at least 94.88% and 96.20% of the total variance, respectively. This shows that a repeatability model with heterogeneous variance to account for smaller variation, mostly at the beginning of the lactation, should suffice for these traits. Somatic cell score had at least 5 eigenvalues accounting for more than 1% of the total variance. For this trait too, the first 3 eigenfunctions closely followed the constant, linear and quadratic functions.

Key Words: Covariance functions, Test-day model, B-splines

466   Comparison of random regression test-day models using Bayes factors. Pedro Lopez-Romero*[1], Romdhane Rekaya[2], Yu-Mei Chang[2], Daniel Gianola[2], and Maria J. Carabao[1], [1]*Departamento de Mejora Gentica y Biotecnologa. INIA. Madrid-Spain,* [2]*Department of Animal Sciences. University of Wisconsin. Madison, WI- USA.*

Test-day milk yields (TD) from Spanish Holstein cows were analised with a set of random regression models (RR), including Wilmink (W) and Ali-Schaeffer (A) functions, and Legendre polynomials (L) of varying order on additive (3 and 5)and permanent (3,5 and 6) effects. Data were 47,982 completed first lactations. L were selected from a previous study, where a wider range of L models was evaluated using REML, assuming constant residual variance (CRV). Model performance had been assesed via goodness of fit, predictive ablility, and behaviour of estimated daily variance and of correlations involving yields at different parts of lactation. These RR were revisited from a Bayesian perpective, allowing for heterogeneous residual variance (HRV) between 3 intervals. Gibbs Sampling was used to draw from marginal posterior distributions. The log-marginal likelihood (LML) was estimated for each model using the harmonic mean of likelihood values. Estimated LMLs can be used to compute the Bayes Factors (LBF). LBFs were greater than 150 in all cases, showing a very strong evidence in the Jeffreys's scale. The A model did not reach the convergence after 460,000 iterations. L models reached the convergence very fast since orthogonal polynomials lower the correlation between samples. The most plausible specification was an L model of 3rd order for additive effects, and of 6th order for permanent effects. Further analysis was done for 3 L models of order 3 for additive 3,5 and 6 for permanent effects, assuming CRV. A better performance than for its corresponding HRV counterpart was noted for the 5th and 6th order models for permanent effect.

MODEL	LML (x10^9)	RV		
		5-75d	76-265d	266-335d
L(3,3)	-4.906	15.53	10.06	9.24
L(3,5)	-4.798	13.10	9.40	8.30
L(5,5)	-4.796	13.12	9.41	8.38
L(3,6)	-4.782	12.69	9.31	8.29
W	-5.663	21.94	17.11	28.07
L(3,3)	-4.912		10.96	
L(3,5)	-4.781		9.81	
L(3,6)	-4.770		9.58	

Key Words: Test day models, random regression, Bayes factor

ASAS/ADSA Food Safety: Microflora Survalence

467   Effect of Shipping Stress in Beef Cattle on Prevalence Levels of Enterohemoragic E. coli and Salmonella spp. from the Feedlot to the Packing Plant. A.R. Barham[1], B.L. Barham*[1], A.K. Johnson[1], D.M. Allen[2], J.R. Blanton, Jr.[1], and M.F. Miller[1], [1]*Texas Tech University,* [2]*Excel Corperation.*

Two hundred steers and heifers, from ten pens were used to determine prevalence of Enterohemoragic E. coli (EHEC) and Salmonella spp. (SAL) prior to and after shipping to a packing plant. Two samples were collected per animal: ventral midline hide swab and fecal sample, two weeks prior to transportation and at the packing plant. Samples were collected from all trucks before loading animals. EHEC and SAL tests were conducted following USDA & FSIS approved protocols.

Prevalence levels were generated using the frequency procedure in SAS (1995). Changes in prevalence levels were analyzed using the T-test procedure in SAS (1995). Overall prevalence of EHEC on hides and in feces at the feedlot were 18% and 9.5% respectively and 4.5% and 5.5% at the packing plant. Results indicated a numerical decrease in EHEC prevalence from feedlot to packing plant for hides and feces (P>.05). Overall prevalence of SAL on hides and in feces at the feedlot were 6% and 18% respectively, while prevalence at the packing plant was 87% and 43%. Data indicated an increase in SAL prevalence from feedlot to packing plant with the only significant increase seen on hides (P<.0001). Twenty percent of pens at the feedlot had positive EHEC feed samples while no feed samples were positive for SAL. Water samples taken at the feedlot indicated 10% of the pens were positive for both EHEC and SAL.