

Breeding & Genetics: Statistical methods in animal breeding and genetics

446 Response to selection by marker assisted BLUP with use of approximate gametic variance covariance matrices. L. R. Totir*, R. L. Fernando, and J.C.M. Dekkers, *Iowa State University*.

Under additive inheritance, Henderson's mixed model equations (HMME) provide an efficient approach to obtain genetic evaluations by marker assisted best linear unbiased prediction (MABLUP) given pedigree relationships, trait, and marker data. For large pedigrees with many missing markers, however, it is not feasible to calculate the exact gametic variance covariance matrix required to construct HMME. The objective of this study is to investigate the consequences of using approximate gametic variance covariance matrices on response to selection by MABLUP. Two methods were used to generate approximate variance covariance matrices. The first method (Method A) completely discards the marker information for individuals with unknown linkage phase between two flanking markers. The second method (Method B) makes use of the marker information at only the most polymorphic marker locus for individuals with unknown linkage phase. Data sets were simulated with complete or incomplete marker data for flanking markers with 2, 4, 6, 8 or 12 alleles. Several missing marker data patterns were considered. The genetic variability explained by marked quantitative trait loci (MQTL) was modeled with one or two MQTL of equal effect. Response to selection by MABLUP using Method A or Method B were compared with that obtained by MABLUP using the exact genetic variance covariance matrix, which was estimated using 15,000 samples from the conditional distribution of genotypic values given the observed marker data. For the simulated conditions, the superiority of MABLUP over BLUP based only on pedigree relationships and trait data varied between 0.0% and 10.6% for Method A, between 1.1% and 16.2% for Method B, and between 4.1% and 18.5% for the exact method. The difference between response to selection obtained for the model with one MQTL and the model with two MQTL was small.

Key Words: Marker assisted selection, BLUP, Gametic variance covariance matrix

447 A simulation program using finite loci with infinite possibilities, FLIP. P. L. Spike*¹, R. R. Benson¹, R. L. Fernando¹, J. C. M. Dekkers¹, P. J. Berger¹, and B. R. Skaar¹, *Iowa State University*.

A simulation program was developed in C++ for instructional use in animal breeding and genetics classes and for simulation research. The purpose of the program is to simulate animal performance for a species of choice with multiple traits and multiple breed populations. Animal performance is simulated by combining the effects of a finite number of loci in diploid organisms with random variation. The core of the program consists of "known" alleles assigned to loci on a variable number of pairs of homologous chromosomes and a single pair of sex chromosomes. Alleles can be genes or other unique DNA sequences that may serve as markers. The effects of the "known" gene combinations can be assigned such that both additive and non-additive effects can be defined for both allelic and non-allelic sets of gene pairs. The effects of "known" gene combinations can include the effects of imprinting. Optionally, the program can create additional "unknown" genes to increase the genetic variance-covariance resulting from the "known" genes to a desired level. These "unknown" genes are assumed to be inherited independently. In addition, more "unknown" genes can be added to increase the level of inbreeding depression expected from the "known" genes to a desired level of inbreeding depression. Finally, additional "unknown" genes can be created for use with multiple populations that will increase the levels of heterosis expected from the "known" genes to a desired level of heterosis. Genetic evaluation software will be used to produce genetic evaluations consistent with industry practices. Work continues on the development of a student interface to access animal performance, exchange genetic material among students and incorporate some economic evaluation of student progress.

Key Words: Genetic Simulation, Finite Locus

448 A simple method for joint analysis of multiple binary responses. R. Rekaya* and T. Averill, *The University of Georgia*.

Genetic evaluation for secondary traits has increased considerably worldwide. Several secondary traits (e.g. fertility, health data) are now of crucial economical interest in different genetic improvement programs. Developments in Markov Chain Monte Carlo methods for analysis of binary data made use of the threshold model (TM) as a standard tool to deal with such data. In the animal breeding field, given the theoretical and computational complexity of analysis of multiple binary traits, such analysis was done assuming a Gaussian distribution for the binary traits. In a Bayesian joint analysis of several binary responses using a TM, the major problem resides in the sampling of the residual (co)variance (RCV) matrix as results of the fixation of some of the diagonal elements of such matrix to overcome the identification problem. Hence, several alternative sampling techniques have been proposed based on the partition of the RCV matrix. Although these methods are theoretically sound, some computational and implementation problems can emerge, especially with large number of binary traits. The method we propose overcomes all the computational and implementation problems associated with the sampling of the RCV matrix. It consists in working with the non-identifiable TM. Once draws from the non-identifiable model are obtained, they are transformed to the identifiable scale using the square root of the diagonal elements of the non-identifiable residual variance matrix. Two simulations with 3 and 8 binary traits were conducted to test the proposed method. Based on five replicates, the bias was less than 3 and 2% for the genetic and RCV, respectively, in both cases. Such bias is well within the Monte Carlo error. Compared two actual methods (Metropolis-Hastings or matrix decomposition) used in analysis of multiple binary responses, the proposed method yielded more accurate results (less bias) and was extremely superior from computational point of views. The proposed method was applied to test-day mastitis data where mastitis status in each test-day was treated as different trait.

Key Words: Binary traits, Threshold model, Residual variances

449 Comparison of estimation methods for heterogeneous residual variances with random regression models. S. Tsuruta*¹, I. Misztal¹, and T. Druet², ¹*University of Georgia, Athens GA*, ²*Station de Gntique Quantitative et Applique, INRA, Jouy-en-Josas Cdex, France*.

The objective of this study was to compare estimation methods of heterogeneous residual variances with random regression models. (Co)variance components were estimated with two data sets; milk yields (69,816 test day records for 7354 cows in the first lactation) and final scores (30,041 first records with 1 record per cow) in Holsteins. Up to third order Legendre polynomials for additive genetic effects were included in the models as random regressions on days in milk for milk yields and on year at first calving for final scores. Heterogeneous residual variances were estimated by logarithmic third order polynomials via AI-REML, intervals via Gibbs Sampler, or an extra error effect via REML. In the interval method, ten and five intervals for residual variances were assigned in the models for test day records and for final scores, respectively. Additive genetic variances were not different among heterogeneous residual variance estimation methods. Estimates of heritability and heterogeneous residual variances were similar for all methods except the interval method, in which the data size for each interval may not have been sufficient. Estimating heterogeneous residual variances with an error effect did not require program modifications and was easily applicable to multiple traits, but was computationally about five times more expensive. The extra error method and the logarithmic polynomial method may be better if variations of residual variances are small or regular. Also, the logarithmic method may have better estimating properties due to fewer parameters. When changes of residual variances are irregular, the interval method may be adequate. In practice, less expensive methods such as the interval method with sufficient data or the logarithmic polynomial method may be better choices for estimating heterogeneous residual variances with random regression models.

Key Words: Heterogeneous residual variances, Genetic parameters, Random regression models

450 Plotting covariance functions from random regression models. A. Legarra*¹, I. Misztal¹, and J. Jamrozik², ¹University of Georgia, Athens, GA, ²University of Guelph, Guelph, ON, Canada.

Covariance functions estimated by fitting random regression models can contain artifacts (e.g. very high variances or correlations) due to small data sets, data structure or limitations of random regression models. These functions contain variances along trajectories and covariances between any two points for any given combination of traits. However, their high dimensionality makes it difficult to thoroughly check all these aspects. A library of functions was written in a matrix-algebra package to visualize time-dependent (co)variances and correlations among and within traits for different effects (additive direct and maternal, permanent...). Two sets of parameter estimates were analyzed. The first set, obtained using 4th order Legendre polynomials, is used in routine test-day evaluation of Canadian Holstein for 12 traits: milk, fat and protein yields and somatic cell scores in three parities. Covariance functions generally showed smooth patterns. Correlations decreased regularly with time within the same trait or among production traits. Correlations of yields with somatic cell score exhibited a more undulating shape. Values were generally small and negative, oscillating between 0.19 and -0.25, with high positive values seen only in the extremes of the trajectories. The second set, obtained using cubic Legendre polynomials, was an analysis of sequential weights of animals up to 2 years of age in Brazilian Nellore, fitting direct and maternal effects. Small peaks in the correlation patterns occurred relatively frequently. Correlations among maternal and direct additive effects dependent on the age oscillated between 0.35 and -0.65. Negative values were seen along most of the trajectory, and the value of 0.35 was observed in the correlation between direct additive effect at day 10 and maternal additive effect at day 570. Visual analysis of (co)variances and correlations allows to observe problems and can aid in constructing covariance functions without artifacts.

Key Words: Covariance functions, Random regression

Extension Education: Management and profitability

452 Entrepreneurial characteristics of dairy farming differences between Dutch and Pennsylvania farmers. R.H.M. Bergevoet*¹ and L. A. Holden², ¹Wageningen University, ²Penn State University.

The objective was to investigate the impact of different farming environments, European Union (EU) versus the northeastern US, on the dairy farmer's goals, values, and strategies for success. Dairy farmers in the Netherlands and Pennsylvania completed a common questionnaire assessing their goals, objectives, assessment of their business environment, and perception of success. Netherlands questionnaires (n=256) were completed by mail and Pennsylvania questionnaires were completed in person (n=73). The Mann-Whitney test was used to evaluate differences between groups of farmers. Results indicated that the main reasons for becoming involved in farming for both groups were more freedom, owning a business, and the potential for high income; however the degree of importance of these factors differed ($P < .05$) by group. Both groups placed a higher value on non-economic goals compared to economic goals, but with differing degrees of importance ($P < .05$). Both groups considered the image of their product and the development of the Internet as opportunities and legislation and local planning as threats, but they value consumer's concerns about the environment, animal welfare and food safety differently ($P < .05$). Netherlands farmers considered consumer concerns as opportunities while Pennsylvania farmers viewed them as threats ($P < .01$). Both groups valued farming in an "environment friendly" way, and neither group saw "going organic" as a serious option. Netherlands farmers especially evaluated their success on the criteria: ability to expand, net farm income and cost of production per hundredweight of milk. Pennsylvania farmers placed the most emphasis on net farm income. With different economic systems between the EU and northeastern US, there were common goals, values and business strategies shared by dairy farmers.

Key Words: Goals and objectives, Farmer characteristics, Assessment of environment

451 Joint optimisation of the number of animals to test and to select. M.E. Goddard*, University of Melbourne and Victorian Institute of Animal Science, Australia.

Some species, especially with the aid of modern reproductive technology, can produce a very large number of gametes, so that the number of breeding stock needed to replace the herd does not limit the number that must be selected. Therefore the number selected can be optimised to balance the benefits from intense selection against the disadvantages of small effective population size. The intensity of selection also depends on the number available for selection (the number tested) and this can also be optimised to balance selection intensity against the costs of breeding and testing more animals. By differentiating a formula for the net benefit of selection, expressions for the optimum number to test and to select have been found. The optimum number to select depends largely on the ratio of the benefit from selection to the cost of low effective population size. The optimum number to test depends largely on the ratio of the cost of testing to the benefit from selection. The accuracy of selection can sometimes be increased usually at an increased cost. The approach used makes it possible to optimise the accuracy of selection jointly with the other two variables. As an example, the accuracy of a progeny testing was optimised by optimising the number of daughters per bull. Some of the costs of testing are proportional to the number of bulls tested and some are proportional to the total number of daughters. If these costs are decreased, the optimum solution changes very little in total costs, but the number of bulls increases as the cost per bull decreased and the number of daughters per bull increased as the costs per daughter decreased. In practice there is usually some selection of bulls prior to progeny testing. This can be optimised by optimising the number tested and selected at all stages in the process. Even if selection prior to progeny testing is of low accuracy, the optimum is to select intensely at this stage provided the cost per bull is small compared to the cost of progeny testing. This has implications for the use of DNA markers that might be used to select bulls for progeny testing.

Key Words: Progeny testing, Marker assisted selection

453 Whole farm planning for the production of grass-finished beef. T. M. Johnson*¹, R. E. Morrow¹, C. A. Wells¹, M. L. Thomas¹, and J. K. Apple², ¹National Center for Appropriate Technology, Fayetteville, AR, ²University of Arkansas, Fayetteville.

Beef calves in the US are predominately produced on small farms then transported to feedlots prior to harvest. Some beef producers with adequate resources have been attempting to improve sustainability and capture more value by selling retail beef products; however, challenges exist that must be overcome to make the production of retail beef possible on the farmstead. In Northwest Arkansas, 11 farms participated in a SARE project to evaluate the potential of producing and direct marketing, grass-finished beef. In this pilot study, 50 crossbred calves from 11 producers were moved to a common site and rotationally grazed on wheat, cereal rye and annual rye pastures, from December 3, 2001 until June 25, 2002. No grain was fed. Calf initial weight was 307 ± 10.5 kg. Thirty-four calves were harvested from May 6 to June 25 in four groups when body condition score reached 6 when palpated by hand. Number of days grazed was 175 ± 3.9 d. Harvest weight was 456 ± 11.9 kg with an ADG of 0.86 ± 0.029 kg. The following carcass characteristics were observed: $54.4 \pm 0.28\%$ dressing percent, 249 ± 7.4 kg hot carcass weight, 2.01 ± 0.099 yield grade, with 85% of the carcasses grading select, 12% standard and 3% choice. Carcasses were dry-aged an average of 21-d and the retail yield was 145 ± 4.3 kg. Carcasses were processed into 25 retail cuts, with emphasis on boneless product. Products have been marketed through word of mouth, newspaper advertising, radio features, presentations to civic organizations, and a display booth during a local community fair. Sales during the first six months resulted in 36% of the product being sold. Data from this project has been presented at 11 meetings or workshops for beef producers and will be used in beef marketing publications produced on the ATTRA project. As a result, nine of these producers have formed a limited liability corporation, hired a professional marketing firm, and are pursuing additional marketing opportunities for grass-finished beef.

Key Words: Grass-finished Beef, Marketing, Sustainability