

Animal Model Evaluation in Finland: Experience with Two Algorithms

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ABSTRACT

Two algorithms to solve large-scale animal model equations were implemented in Finland using iteration on data. In the first procedure, the breeding values were solved using second-order Jacobi iteration, and, in the second, the breeding values were solved by successive overrelaxation iteration. In both algorithms, the iteration was by Gauss-Seidel for effects other than breeding values.

The second-order Jacobi algorithm was modified to be 20% more memory efficient. The successive overrelaxation algorithm for breeding values was implemented to use less memory than the second-order Jacobi algorithm. Correlations between solutions after 300 rounds and intermediate solutions during the iteration were calculated to compare the algorithms. The algorithm with successive overrelaxation of breeding values converged to the final solutions faster. However, the second-order Jacobi iteration took less time per round than the successive overrelaxation algorithm.

(Key words: breeding value prediction, animal models, iterative methods)

Abbreviation key: ARHS = adjusted right-hand sides, MME = mixed model equations, RAM = random access memory, SOR = successive overrelaxation.

INTRODUCTION

Estimation of genetic merit of animals in modern animal breeding relies on solutions of the mixed model equations (MME). Schaeffer

and Kennedy (6) and Misztal (3) introduced algorithms to solve MME without explicitly forming the equations. In these methods, the data files are read each round of iteration, and the MME are never explicitly formed. Both Gauss-Seidel and second-order Jacobi algorithms have been used for the iteration.

The method of iteration on data has been applied to large-scale national dairy cattle evaluations in various countries, e.g., the US (9), Canada (5), and Italy (1). Although iteration on data greatly reduces the computational requirements, particularly memory, the practical implementations have required a super computer or a very large-scale main frame computer (5, 9).

The first iteration on data concept by Schaeffer and Kennedy (6) was based on Gauss-Seidel algorithm. Their implementation required multiple copies of data files, one for animal effects and another for major fixed effects, to be read once within each round of iteration. In addition, a pedigree file was read repeatedly. Such programs were dependent on an efficient input-output capabilities of computers. Misztal replaced Gauss-Seidel by Jacobi iteration (3). That yielded simpler programming and required only one copy of the observation and relationship files to be read per round of iteration. To enhance a poor convergence rate with the plain Jacobi iteration, the practical applications have been based on second-order Jacobi (1, 5, 9). Nevertheless, the convergence characteristics of the Gauss-Seidel algorithm or the same with overrelaxation (successive overrelaxation, SOR) have been considered to be superior to the second-order Jacobi iteration.

In Finland, the goal was to implement an animal model on a workstation to reduce the expense of evaluations. This paper presents two new approaches for solving animal model equations. Both algorithms use Gauss-Seidel iteration to solve environmental effects. Breeding value solutions are obtained with either

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second-order Jacobi or SOR iteration. The implementation based on Jacobi iteration is designed to use less memory than the earlier versions. With our approach to compute SOR the old multiple data file requirement is relaxed, and the need for random access memory (RAM) is less than with the Jacobi algorithm. The methods are compared with respect to their evaluation time and convergence characteristics.

MATERIALS AND METHODS

Model

The evaluation model was

$$y_{ijklm} = c_i + m_j + h_k + a_l + p_l + e_{lm} [1]$$

where

- y_{ijklm} = observation m for cow l ,
- c_i = age at calving \times lactation number \times days open effect,
- m_j = season of calving \times year effect,
- h_k = random herd-year effect,
- a_l = random additive breeding value of animal,
- p_l = random permanent environment effect, and
- e_{lm} = residual effect.

Animal effect a_l included the effect of genetic groups (7). Groups were assigned only to animals that had unknown parents, and other animals were tied to groups through the inverse of the relationship matrix.

In matrix notation, the model can be written as

$$y = Ws + Xh + Za + Zp + e \quad [2]$$

where vector s contains the fixed effects, h the herd-year effects, and vectors a and p correspond to the effects of animal breeding values and permanent environments, respectively. Matrices W , X , and Z are design matrices of appropriate size. Matrix notation in Equation [2] is used to illustrate the algorithms. Variance ratios to residual over herd-year, permanent environmental effect, and breeding value are denoted as γ , λ_p , and λ_a , respectively.

Algorithms

The two algorithms had similar execution steps for iterating fixed, herd-year, and permanent environmental effects. These effects were solved using Gauss-Seidel iteration. Breeding values were solved by second-order Jacobi iteration in one algorithm and SOR iteration in the other.

The evaluation programs used two data files, one for each sex. The cow file consisted of one record for each cow. The record contained parent identification and the cow's production data. The sire file contained parent identification only. An additional file to store the mate identifiers was needed in the SOR algorithm.

Data were preprocessed to be as directly usable as possible for the evaluation programs. Animals were renumbered separately according to sex. Records in the cow file were sorted according to herd. Herd-year effects were renumbered within herd. Thus, during the evaluation, data could be processed one herd at a time. There was no preadjustment of observations, but, at most, three first lactation records in sequence were accepted. To simplify the algorithms, second and third lactation records produced in a herd different from the first lactation were excluded from the data in the study.

The Second-Order Jacobi Algorithm. The method of solving MME was similar to the algorithm described by Wiggans et al. (8). However, the adjusted right-hand sides (ARHS) of the breeding values (8) were initialized using solutions of the previous iteration round (Veijo Vilva, 1990, personal communication). Thus, only the latest breeding value solutions needed to be stored.

Vectors (length of the vector in parenthesis) were defined:

- a = solution of breeding values (number of animals),
- p = solution of permanent environment effect (number of cows),
- d = diagonal of $Z'Z + \lambda_a A^{-1}$ (number of animals),
- $(Z'y)_{adj}$ = ARHS for animal equations (number of animals),
- $(W'y)_{adj}$ = ARHS of fixed effect equations (total number classes in fixed effects),

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