Solving Mace Equations

L. Klei
Holstein Association USA, Inc., Brattleboro, Vermont, USA.

Introduction

Mace involves the analysis of performance information on traits in different countries. Correlations among these traits are usually high. As a result the genetic (co)-variance matrix among the traits in the different countries is close to singular. The mixed model equations associated with the Mace model have therefore the potential of being close to singular. Singularity of a matrix can be shown by computing eigenvalues of the matrix and observing whether one or more of them are zero. Near singularity is indicated by one or more eigenvalues close to zero.

Computing Mace involves solving a large system of linear equations. To avoid problems associated with direct solving this matrix, iterative techniques are used. The method mostly used is iteration on data which as described by Schaeffer and Kennedy (1986) is a Jacobi iteration (Quaas, pers. comm., 1989). This method is easy to program and requires relatively little computer memory. This method performs well when the matrix is diagonally dominant (Golub and Van Loan, 1987). However, this is not the case in a near singular matrix. Another approach is Gauss-Seidel iteration (Golub and Van Loan, 1987). The application of this method uses the actual mixed model equations to obtain solutions iteratively. The convergence condition for this method is positive definiteness of the matrix involved. This is the case for Mace mixed models. It is relatively easy to modify iteration on data to perform Gauss-Seidel iterations instead of Jacobi iterations (Jansen and Sullivan, pers. comm.).

This papers compares solutions from the two iterative methods to solutions obtained from directly solving the equations.

Method

Let the mixed model equations be represented by:

$$\mathbf{Cx} = \mathbf{y}$$

Exact solutions for **x** can be obtained through an LU decomposition of **C** such that:

$$\mathbf{LUx} = \mathbf{y}$$

and to solve this compute:

$$\mathbf{x} = \mathbf{U}^{-1}\left(\mathbf{L}^{-1}\mathbf{y}\right)$$

The structure of **L** and **U** makes it possible to obtain the solutions without actually computing the inverses. Computation of solutions through the LU decomposition were obtained using FSPAK, a sparse matrix computation package developed by Perez-Enciso et al. (1994).

Jacobi iteration in round (k+1) is represented in terms of **x**, **y**, and **C** by:

$$x_i^{(k+1)} = \left(y_i - \sum_{j=1}^{i-1} c_{ij} x_j^{(k)} - \sum_{j=i+1}^{n} c_{ij} x_j^{(k)} \right) c_{ii}^{-1}$$

Notice that the Jacobi update for the solutions in $(k+1)^{th}$ round are based on solutions from the k^{th} round. With some effort it can be shown that in order for the Jacobi iteration to converge the matrix **C** has to be diagonally dominant. This means that the condition

$$\max_i \sum_{j \neq i} \left| c_{ij} / c_{ii} \right| < 1$$

has to hold. The speed of convergence is directly related to the degree of dominance of the diagonal, c_{ii} (Golub and Van Loan, 1985).

Gauss-Seidel iteration is very similar to Jacobi iteration with the exception that $x_j^{(k+1)}$ replaces $x_j^{(k)}$ in

$$\sum_{j=1}^{i-1} c_{ij} x_j^{(k)}$$

This method in round (k+1) can therefore be written as

$$x_i^{(k+1)} = \left(y_i - \sum_{j=1}^{i-1} c_{ij} x_j^{(k+1)} - \sum_{j=i+1}^{n} c_{ij} x_j^{(k)} \right) c_{ii}^{-1}$$

It can be shown that Gauss-Seidel iteration will converge as long as the matrix **C** is positive definite (Golub and Van Loan, 1985).

For this study both Jacobi and Gauss-Seidel iterations were used in a block diagonal form where each block, $\mathbf{C_{ij}}$, consisted of the part of matrix **C** pertaining to animals i and j, as well as $\mathbf{x_i}$, and $\mathbf{y_i}$ are those solutions and right hand sides pertaining to animal i. To obtain the formulas for the block diagonal form simply replace the scalars in the previous two formulas with the corresponding vectors and matrices.

Table 1. Genetic correlations for stature.

	CAN	NLD	DEU	ITA	FRA
USA	.9760	.9219	.9057	.9685	.9154
CAN		.9303	.9164	.9645	.9236
NLD			.9541	.9197	.9462
DEU				.9160	.9248
ITA					.9193

USA - Stature CAN - Stature
NLD - Stature DEU - Stature
ITA - Stature FRA - Sacrum Height

Table 2. Genetic correlations for rear udder width

	CAN	NLD	DEU	ITA	FRA
USA	.8986	.7383	.7380	.8238	.6579
CAN		.6375	.6261	.7767	.5654
NLD			.8562	.5851	.7661
DEU				.6032	.7125
ITA					.4114

USA - Rear Udder Width CAN - Rear Attachment Width
NLD - Rear Udder Height DEU - Rear Udder Height
ITA - Rear Udder Width FRA - Rear Udder Height

Material

Mace solutions were computed for Stature, Rear Udder Width, and Final Score in six countries, Canada (CAN), France (FRA), Germany (DEU), Italy (ITA), The Netherlands (NLD), and the United States (USA) using the most recent genetic evaluations from each country that were available in in November 1997. Since not all traits are measured in all countries trait combinations were determined by computing proof correlations and taking the trait that had highest correlation with the USA trait. Correlations for these traits are in Table 1 through Table 3.

Table 3. Genetic correlations for final score.

	CAN	NLD	DEU	ITA	FRA
USA	.8723	.7756	.7550	.8455	.7823
CAN		.6682	.6220	.7411	.8034
NLD			.5555	.7322	.6417
DEU				.6817	.5271
ITA					.6525

USA - Final Score CAN - Conformation
NLD - Final Score DEU - Body Type
ITA - Final Score FRA - Type Composite

Solutions were computed using the LU decomposition, Jacobi iteration (3000 and 12000 rounds) and Gauss Seidel iteration (1000 rounds). Results of the iterative methods were compared based on averages, standard deviation and distributions of differences with the direct method of obtaining solutions (LU). Starting values for the iterative techniques were the genetic evaluations from each country.

Results

The total linear system of equations consisted of 220,416 equations (36,579 bulls, 156 phantom groups and 6 countries). Solutions were expected to be between -4 and +4.

Eigenvalues for the correlation structures of the three traits can be found in Table 4. As expected trait combinations in which many of the same traits were involved were closer to singularity, eigenvalues closer to zero, than those that used traits with different definitions.

Comparisons of solution of the iterative methods with those obtained through LU decomposition are expressed in the following tables as LU decomposition - iterative solution. As a result, positive values show that the iterative method over-predicts the true solutions, while negative values under-predict.

Table 4. Eigenvalues.

Stature	Rear Udder Width	Final Score
.0227	.0769	.0824
.0328	.1380	.1817
.0452	.1816	.2394
.0751	.3294	.3970
.1566	.7943	.5223
5.6677	4.4798	4.5772

Table 5. Mean and standard deviation of the difference between the iterative solution and the LU solution Differences are expressed as iterative solution - LU solution.

Method	Stature		Rear Udder Width		Final Score	
	mean	st.dev.	mean	st.dev.	mean	st.dev.
GS	.006	.026	.022	.041	.015	.024
J3000	.125	.325	.132	.332	.098	.224
J12000	.061	.166	.053	.153	.052	.111

GS - Gauss-Seidel iteration (1000 rounds)
J3000 - Jacobi iteration (3000 rounds)
J12000 - Jacobi iteration (12000 rounds)

Table 6. Extreme deviations of the difference between the iterative solution and the LU solution. Deviations are expressed as iterative solution - LU solution.

Method	Stature		Rear Udder Width		Final Score	
	negative	positive	negative	positive	negative	positive
GS	-.289	.294	-.053	.498	-.038	.287
J3000	-.439	3.452	-.586	3.600	-.230	2.291
J12000	-.241	1.771	-.314	1.696	-.110	1.117

GS - Gauss-Seidel iteration (1000 rounds)
J3000 - Jacobi iteration (3000 rounds)
J12000 - Jacobi iteration (12000 rounds)

From Table 5 it can be seen that all three iterative approaches have a tendency to over-estimate the solutions obtained through LU. It is also clear from this table that of the two iteration methods Gauss-Seidel needs the fewest iteration rounds to reach the same values as obtained from the LU decomposition. Combining this information with the information in Table 6 and Table 7 it can also be observed that many more rounds of Jacobi iteration are needed to obtain the same precision as what is achieved by Gauss-Seidel iteration. From the previous three tables it can also be observed that it would be beneficial to go additional rounds of iteration for both iterative methods.

Table 7. Percentage of solutions within deviation range classes. Deviations are expressed as iterative solution - LU solution.

Range		Stature			Rear Udder Width			Final Score		
		GS	J3000	J12000	GS	J3000	J12000	GS	J3000	J12000
<	*-.40*		*.0*			*.0*				
-.40	*-.30*		*.1*			*.0*	*.0*			
-.30	-.20	.0[1)]	.1	.0		.1	.0		.0	
-.20	-.10	.8	.3	.2		.4	.1		.1	.0
-.10	-.05	1.6	.5	.3	.0	.9	.5		.4	.2
-.05	**.00**	**23.0**	**22.5**	**22.7**	**25.6**	**25.8**	**28.5**	**25.2**	**24.4**	**24.0**
.00	**.05**	**71.8**	**38.2**	**50.0**	**61.3**	**34.6**	**42.7**	**67.7**	**37.0**	**45.5**
.05	.10	1.9	9.8	10.2	10.1	6.4	10.8	6.2	10.1	12.3
.10	.20	.9	9.4	9.0	2.1	7.3	12.6	.9	11.1	13.8
.20	.30	.1	8.0	3.6	.4	10.8	1.5	.0	9.8	1.7
.30	*.40*		*3.4*	*1.0*	*.3*	*7.2*	*.7*		*2.7*	*.8*
.40	*.50*		*2.8*	*1.1*	*.1*	*2.1*	*1.0*		*.6*	*.9*
.50	*1.00*		*3.0*	*1.3*		*2.4*	*1.1*		*2.7*	*.4*
1.00	>		*1.9*	*.7*		*1.9*	*.6*		*.9*	*.5*

1) .0 indicates that at least one solution fell in this category but less than .1 percent of all solutions qualified

GS - Gauss-Seidel iteration (1000 rounds)
J3000 - Jacobi iteration (3000 rounds)
J12000 - Jacobi iteration (12000 rounds)

A recurring question associated with computing is how much memory is needed and how long does it take. Table 8 shows the approximate memory and time requirements needed to complete iteration. Even though the cost of iteration for Gauss-Seidel on a per round basis (~5 seconds) is approximately five times higher when compared with Jacobi iteration this is offset by the gains in increased rate of convergence. On a CPU time basis LU decomposition is competitive with Gauss-Seidel, however for this method memory becomes the limiting factor. Keep in mind that none of the programs were developed to have optimal memory and time requirements and that these number are just a general indication.

Table 8. Timing and memory requirements of the different methods.

Method	LU	Gauss-Seidel	Jacobi	
rounds		1000	3000	12,000
CPU time	60m	84m	53m	212m
Max memory	372 Mb	60 Mb	16 Mb	16 Mb

Conclusions

1. Results of this study show the importance of an adequate number of iteration for obtaining solutions from systems of equations when iterative techniques are used to solve them. It might be necessary to, occasionally, compare results from iterations with direct solutions to validate the stopping criteria.

2. Rates of convergence depend on the iteration technique used.

3. Gauss-Seidel iteration is a good alternative to iteration on data even though memory requirements are increased.

Acknowledgments

Financial support for this research was received from the National Association of Animal Breeders.

Literature cited

Golub, G.H. & Van Loan, C.F. 1987. *Matrix Computations*. 5th Printing. The Johns Hopkins University Press. Baltimore. Maryland.

Schaeffer, L.R. & Kennedy, B.W. 1986. Computing strategies for solving mixed model equations. *J. Dairy Sci. 69*, 575.

Perez-Enciso, M., Misztal, I. & Elzo, M.A. 1994. FSPAK: An interface for public domain sparse matrix routines. In *Proc. 5th. World Congress on Genetics Applied to Livestock Production.* Vol. 22:87.