# **Information Source Reliability Method Applied to MACE**

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# Introduction

The practice of incorporating Interbull sire evaluations into national evaluation systems has become common place. The reliability of the estimated Interbull breeding value is required to determine appropriate weighting for foreign information included in the national evaluation system. Too much weight is given to the foreign information when the MACE reliability is overestimated. Concerns relating to over-estimation of the MACE reliabilities have been documented by Jones (1997).

The purpose of this study was to develop an approximate method for computing MACE reliability based on the information source (IS) method for calculating breeding value reliabilities (Harris and Johnson, 1998). The IS method was compared with actual reliabilities from the inverse of the MACE equations and the current Interbull approximation (CI) method (Schaeffer and Zhang, 1993).

## **Materials and Methods**

#### Method

The IS method uses the reliability of three information sources: parent average, animal's own records and progeny records. A general equation is required for the reliability of two pieces of information (x and y) in terms of the individual reliabilities:

$$R(x+y) = \frac{R(x) + R(y) - 2R(x)R(y)}{1 - R(x)R(y)}$$
[1]

The calculation of the MACE reliability is broken down into four steps based on a sire-maternal grandsire model:

- 1. Calculate reliability based on progeny records within country
- 2. Incorporate information on progeny's progeny within country
- 3. Combine within country reliabilities across country
- 4. Incorporate information on parent reliability

## Step 1

The reliability of a bull based on progeny for country *j* is calculated using selection index as:

$$R_{j}^{bull}(progeny) = \frac{\overline{n_{j}}h_{j}^{2}}{4 + (\overline{n_{j}} - 1)h_{i}^{2}}$$

where

 $n_j$  is the effective number of daughters in country *j*, and

 $h_i^2$  is the heritability in country *j*.

#### Step 2

The reliability based on progeny does not include grand progeny, great grand progeny, etc. This information can be incorporated by updating the reliability based on progeny for the progeny reliability of each of the bull's progeny (i.e., grand progeny information). The process works from the youngest parent to the oldest parent to allow all generations to be incorporated. The reliability of each bull is updated for each offspring using equation [1] as:

$$R_{j}^{bull}(progeny) = \frac{R_{j}^{bull}(progeny) + \frac{1}{4}R_{ij}^{son}(progeny) - \frac{1}{2}R_{j}^{bull}(progeny)R_{ij}^{son}(progeny)}{1 - R_{j}^{bull}(progeny)\frac{1}{4}R_{ij}^{son}(progeny)}$$

and for maternal grand sons (mgson):

$$R_{j}^{bull}(progeny) = \frac{R_{j}^{bull}(progeny) + \frac{1}{16}R_{ij}^{mgson}(progeny) - \frac{1}{8}R_{j}^{bull}(progeny)R_{ij}^{mgson}(progeny)}{1 - R_{j}^{bull}(progeny)\frac{1}{16}R_{ij}^{mgson}(progeny)}$$

where

 $R_{ii}^{son}(progeny)$  is the progeny reliability for the *ith* 

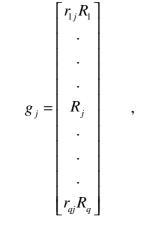
offspring of that bull in country *j* and similarly for *mgson*. This process is repeated for each bull within country.

#### Step 3

Combine the within country reliabilities taking into account the genetic correlations between countries using a multiple trait selection index approach. The reliability for a bull in country j is updated by:

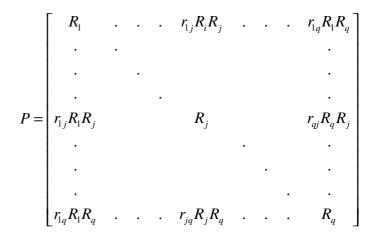
$$R_{j}^{bull}(progeny) = g_{j}^{\prime}.P^{-1}.g_{j}$$

where



 $R_i$  is shorthand for  $R_j^{bull}(progeny)$  obtained within country in step 2

 $R_{ij}$  is the genetic correlation between country *i* and *j* and



## Step 4

Include information on the parents (sire and mgs) in the reliability of the bull. The process works from the oldest bull to the youngest bull to allow all generations to be incorporated, i.e., parents, grand parents, etc. For a given bull, the reliability of a parent of that bull includes information on the bull's progeny. In order to calculate the contribution to the bull's reliability from the parent average (*pa*) this information can be removed from the sire reliability by rearranging equation [1]:

$$R_{j}^{bull}(sire) = \frac{R_{j}^{sire}(pa + progeny) - \frac{1}{4}R_{j}^{bull}(progeny)}{R_{j}^{sire}(pa + progeny) \frac{1}{4}R_{j}^{bull}(progeny) + 1 - \frac{1}{2}R_{j}^{bull}(progeny)}$$

and similarly from the maternal grand sire reliability:

$$R_{j}^{bull}(mgs) = \frac{R_{j}^{mgs}(pa + progeny) - \frac{1}{16}R_{j}^{bull}(progeny)}{R_{j}^{mgs}(pa + progeny)\frac{1}{16}R_{j}^{bull}(progeny) + 1 - \frac{1}{8}R_{j}^{bull}(progeny)}$$

The parent average reliability is then calculated as (assuming the sire and mgs are unrelated):

$$R_{j}^{bull}(pa) = \frac{1}{4} \left[ R_{j}^{bull}(sire) + \frac{1}{4} R_{j}^{bull}(mgs) \right]$$

The total reliability of the bull with one or two parents known and including all information is calculated as:

$$R_{j}^{bull}(pa + progeny) = \frac{R_{j}^{bull}(progeny) + R_{j}^{bull}(pa) - 2R_{j}^{bull}(pa)R_{j}^{bull}(progeny)}{1 - R_{j}^{bull}(progeny)R_{j}^{bull}(pa)}$$

For the oldest animals the sire and dam will be unknown and  $R_j^{bull}(pa + progeny)$  will equal  $R_j^{bull}(progeny)$ since  $R_j^{bull}(pa)$  will equal zero (unknown parents). The process is done for each country.

## **Materials**

The IS method, was compared with the CI method and actual reliabilities computed from the direct inverse of the MACE mixed model equations. The data consisted of the Guernsey sires from the August 1997 Interbull run with data from four countries. The main characteristics of the data are given in Table 1. Two sets of between country genetic correlation matrices were used, the first with high correlations and the second with low correlations and genetic standard deviations. These matrices are given in Table 2. The heritability was set at 0.35 in all countries.

Table 1. Data set characteristics.

	Number
Sires	695
Parentage	
Known sire and mgs	139
Known sire only	218
Known mgs only	15
Unknown sire and mgs	323
Average Progeny number/sire	
Country 1	13.1
Country 2	13.1
Country 3	14.7
Country 4	18.3

Table 2. The between country genetic correlation matrices. Genetic standard deviations on the diagonal.

	Matrix 1				
	Country 1	Country 2	Country 3	Country 4	
Country 1	420	0.93	0.96	0.94	
Country 2		275	0.93	0.94	
Country 3			766	0.91	
Country 4				236	
	Matrix 2				
	Country 1	Country 2	Country 3	Country 4	
Country 1	275	0.93	0.80	0.83	
Country 2		766	0.77	0.81	
Country 3			158	0.90	
Country 4				191	

# **Results and Discussion**

Table 3 contains the accuracy of each approximate method. Clearly the IS method is considerably better than the CI method in all of the accuracy measures. No under-estimation was observed with the CI method. The over estimation is greater when there are lower genetic correlations between countries. Figures 1 and 2 illustrate the relationship among the IS and CI approximate reliabilities and actual reliabilities for genetic correlation matrix 2, respectively.

	Correlation Matrix 1		Correlation Matrix 2	
	CI	IS	CI	IS
Average reliability <sup>1</sup>	0.772	0.762	0.694	0.672
Average absolute bias	0.011	0.004	0.023	0.007
Largest absolute bias	0.119	0.024	0.343	0.053
Regression Slope <sup>2</sup>	0.985	0.999	0.968	0.999
Correlation with true value	0.987	0.998	0.961	0.997
Standard deviation of the bias	0.017	0.005	0.042	0.011

Table 3. Accuracy of the approximate methods for calculating reliability.

<sup>1</sup>Actual average Correlation Matrix 1 = 0.761

Correlation Matrix 2 = 0.671

<sup>2</sup>Coefficient for simple linear regression with the intercept constrained to 0.0

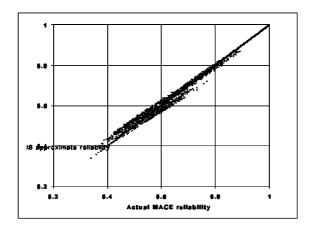


Figure 1. The relationship between the IS approximate reliability and the actual reliability for genetic correlation matrix 2.

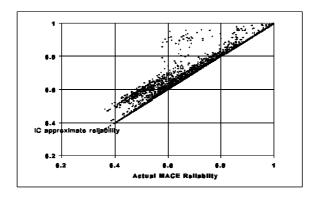


Figure 2. The relationship between the CI approximate reliability and the actual reliability for genetic correlation matrix 2.

Table 4 provides the average absolute bias and correlation between actual and approximate reliability for each country for matrix 2. The smallest biases occurred in country 2 which had the largest genetic standard deviation and contained a large majority of the sires and maternal grand sires of the bulls with progeny information. The larger biases occurred in the countries with the lower genetic correlations with country 2. The IS method outperformed the CI method in all countries. The IS method was considerably better in countries 3 and 4 where the CI method showed considerable over estimation.

 Table 4.
 Accuracy of the approximate methods for calculating reliability for genetic correlation matrix 2 for each country.

	IS Method			
	Country 1	Country 2	Country 3	Country 4
Average reliability <sup>1</sup>	0.715	0.780	0.575	0.618
Average absolute bias	0.005	0.001	0.011	0.010
Largest absolute bias	0.037	0.037	0.053	0.046
Correlation with true value	0.997	0.999	0.992	0.994
	CI Method			
	Country 1	Country 2	Country 3	Country 4
Average reliability <sup>1</sup>	0.730	0.784	0.611	0.651
Average absolute bias	0.016	0.003	0.037	0.037
Largest absolute bias	0.177	0.195	0.343	0.290
Correlation with true value	0.981	0.993	0.916	0.931

<sup>1</sup>Actual average country 1 = 0.715country 2 = 0.781country 3 = 0.574country 4 = 0.614

The IS method for calculating reliabilities from MACE is a significant improvement over the current method used by Interbull particularly for countries such as New Zealand and Australia which have lower genetic correlations with European and North American countries. The IS method presented for the multiple trait sire-maternal grand sire model could easily be adapted to fit other multiple trait models.

## Acknowledgements

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#### References

- Harris, B.L. & Johnson, D.L. 1998. Technical Note: Approximate reliability of genetic evaluations under an animal model. Submitted, J. Dairy Sci.
- Jones, L.P. 1997. A simple approximation to the reliability of Interbull proofs for foreign bulls. *Proc.* 1997 Interbull meeting, Vienna, Austria.
- Schaeffer, L.R. & Zhang, W. 1993. Multi-traits across country evaluation of dairy sires. *Proc. Open Session Interbull Ann. Meeting*, Denmark 8.