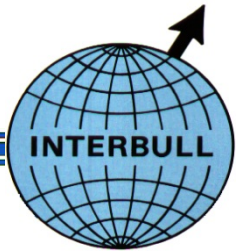


Interbull Technical Workshop and Industry Meeting
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Session: International Genetic Correlations



Across Country Genetic Correlations:
From Estimation to Utilization

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Outline

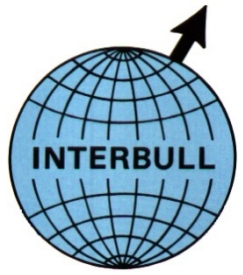
Across Country Genetic Correlation

- 1- An anecdote**
- 2- A review of scientific developments**
- 3- The practice**
- 4- The effects**

- 5- Some personal remarks**



An Anecdote



An anecdote





A Review of Scientific Developments



A review of scientific developments (1)

Multiple-Country Comparison of Dairy Sires

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and Poultry Science
University of Guelph
Guelph, ON, Canada N1G 2W1

To ana-
lyze the data with the multiple-trait model,
estimates of residual and sire variances and the
genetic correlation between the two countries
need to be available.



A review of scientific developments (2)

Estimation of Genetic (Co)variance Components for International Evaluation of Dairy Bulls

Sigurdsson, A., Banos, G. and Philipsson, J. (INTERBULL Centre, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Box 7023, S-750 07 Uppsala, Sweden).
 Estimation of genetic (co)variance components for international evaluation of dairy bulls. Accepted January 12, 1996. *Acta Agric. Scand., Sect. A, Animal Sci.* 46: 129–136, 1996. © 1996 Scandinavian University Press.

Agust Sigurdsson*,
Georgios Banos and
Jan Philipsson
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 Animal Breeding and Genetics,
 Swedish University of Agricultural
 Sciences, Box 7023, S-750 07
 Uppsala, Sweden

$$\mathbf{G}_{ij}^{(k+1)} = \frac{[\hat{\mathbf{u}}_i^{(k)} \mathbf{T}_{uu} \hat{\mathbf{u}}_j^{(k)} - \hat{\mathbf{g}}_i^{(k)} \mathbf{T}_{gg} \hat{\mathbf{g}}_j^{(k)} + \text{tr}(\mathbf{T}_{uu} \mathbf{W}_{ij}^{uu(k)}) + 2\text{tr}(\mathbf{T}_{gu} \mathbf{W}_{ij}^{ug(k)}) + \text{tr}(\mathbf{T}_{gg} \mathbf{W}_{ij}^{gg(k)})]}{q}$$



A review of scientific developments (3)

A Method To Estimate Correlations Among Traits In Different Countries Using Data On All Bulls

L. Klei¹⁾ and K. A. Weigel²⁾

¹⁾ Holstein Association USA, Inc. Brattleboro, Vermont, USA

²⁾ University of Wisconsin, Madison, Wisconsin, USA

$$G_o^{(t+1)} = G_o^{(t)} + G_o^{(t)} \sum_{[m]} \left\{ H_{[m]} (G_o^{(t)})^{-1} \hat{S}_{[m]} \cdot G_o^{(t)} \right. \\ \left. - q_{[m]} G_o^{(t)} \right) H_{[m]}^T \Big\} G_o^{(t)} / q$$



A review of scientific developments (4)

MACE for Ayrshire Conformation: Impact of Different Uses of Prior Genetic Correlations

Thomas Mark¹, Per Madsen², Just Jensen² and Freddy Fikse¹

¹Interbull Centre, Uppsala, Sweden

²Danish Institute of Agricultural Sciences, Foulum, Denmark

$$r_G = \frac{\frac{r_{G_{ays}}}{\sigma_{r_{G_{ays}}}^2} + \frac{r_{G_{hol}}}{\sigma_{r_{G_{hol}}}^2}}{\frac{1}{\sigma_{r_{G_{ays}}}^2} + \frac{1}{\sigma_{r_{G_{hol}}}^2}} = \frac{CB_{ays} r_{G_{ays}} + \frac{CB_{hol} r_{G_{hol}}}{d^2}}{CB_{ays} + \frac{CB_{hol}}{d^2}}$$



A review of scientific developments (5)

J. Dairy Sci. 86:677–679

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A Simple Method for Weighted Bending of Genetic (Co)variance Matrices

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1. Determine matrix of eigenvectors, \mathbf{U}_n , and diagonal matrix of eigenvalues, \mathbf{D}_n , of \mathbf{V} . Hence, $\mathbf{V}_n = \mathbf{U}_n \mathbf{D}_n \mathbf{U}_n'$, where n denotes iteration number;
2. Replace \mathbf{D}_n with Δ_n , where $\delta_{i,i} = \varepsilon$, for $d_{i,i} < \varepsilon$, and $\delta_{i,i} = d_{i,i}$, otherwise. Set the value of ε to a small positive real number;
3. Calculate a new covariance matrix: $\mathbf{V}_{n+1} = \mathbf{V}_n - [\mathbf{V}_n - \mathbf{U}_n \Delta_n \mathbf{U}_n'] \odot \mathbf{W}$ (where \odot is the Hadamard product);
4. Repeat until \mathbf{V}_{n+1} is positive definite.



A review of scientific developments (6)

J. Dairy Sci. 88:1214–1224

© American Dairy Science Association, 2005.

Data Subsetting Strategies for Estimation of Across-Country Genetic Correlations

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A review of scientific developments (7)

Rank reduction models

- Works from France
- Works from Finland



A review of scientific developments (8)

Bentler-Weeks formulation of SEM

$$\eta_{q \times 1} = B_{q \times q} \eta_{q \times 1} + \gamma_{q \times r} \xi_{r \times 1}$$

Diagram illustrating the Bentler-Weeks formulation of SEM. The equation is $\eta_{q \times 1} = B_{q \times q} \eta_{q \times 1} + \gamma_{q \times r} \xi_{r \times 1}$. Red arrows point from descriptive labels to the corresponding terms in the equation:

- Vector of DVs points to $\eta_{q \times 1}$.
- Regression coefficients between DVs points to $B_{q \times q}$.
- Regression coefficients between DVs and IVs points to $\gamma_{q \times r}$.
- Vector of IVs points to $\xi_{r \times 1}$.

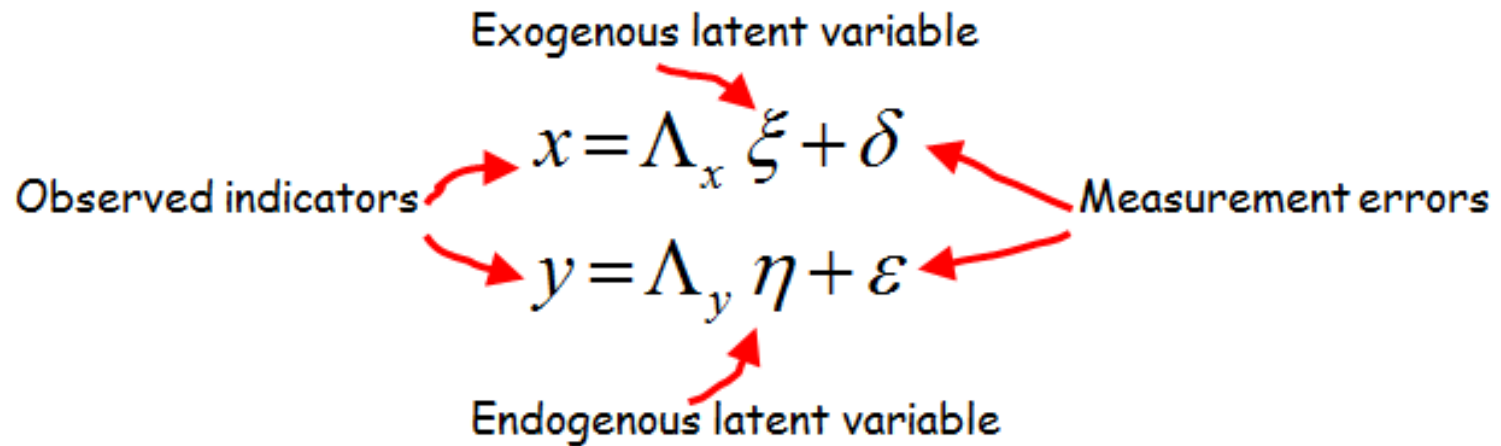
$\Phi_{r \times r}$ = Covariance matrix of IVs

Parameters to estimate are B , γ and Φ (use ULS, GLS, ML, ...)

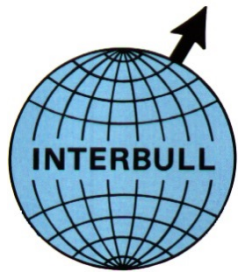


A review of scientific developments (9)

LISREL Notation

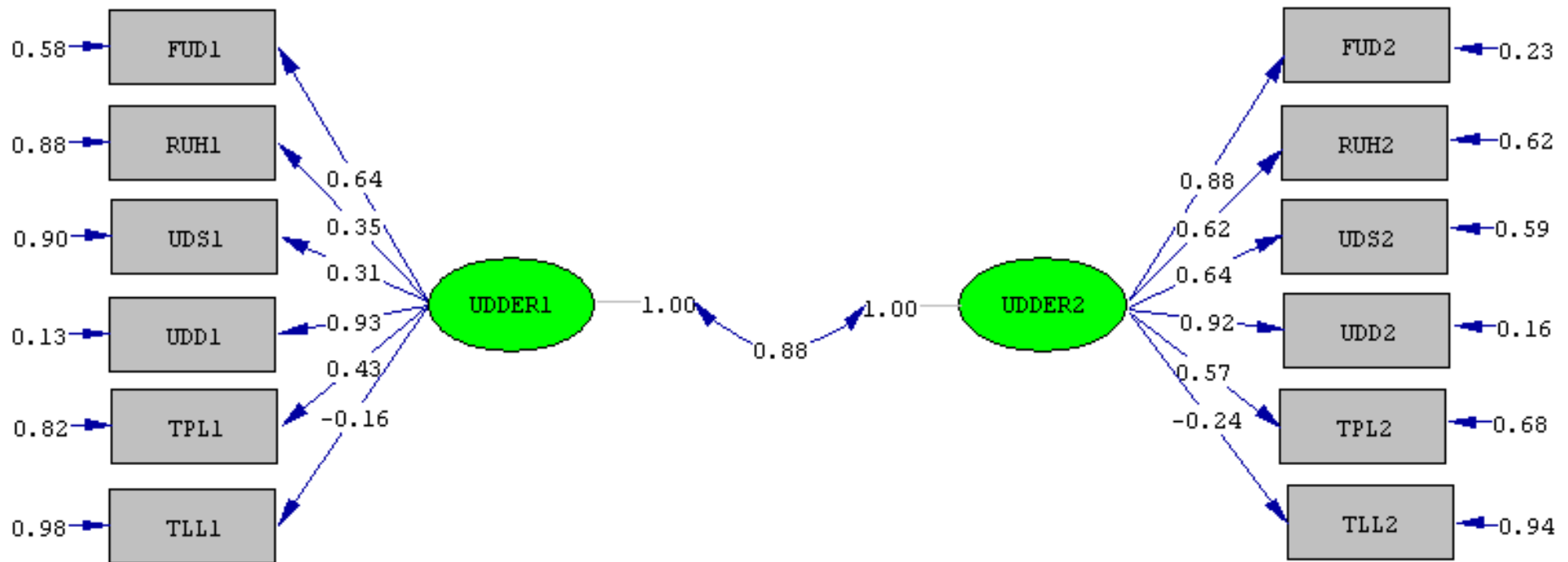


$E(\eta) = E(\xi) = E(\varepsilon) = E(\delta) = 0$ $\xi \varepsilon \delta \eta \delta \delta \xi \varepsilon$
 ε uncorrelated with ξ , δ and η
 δ uncorrelated with ξ , ε and η
 $\Theta_\varepsilon = E(\varepsilon\varepsilon')$, $\Theta_\delta = E(\delta\delta')$



A review of scientific developments (10)

SEM for Udder traits in AYS (implemented in LISREL)





The Practice



The practice (1)

What are the problems?

- **Computational problem**
 - **CPU (RAM) requirement;**
 - **CPU time requirement;**

- **Structural problem**
 - **Poorly linked populations**



The practice (2): Structural problem (1)

Out of 12997 across country genetic correlations:

Number of correlations	Number of common bulls
230	1
82	2
99	3
49	4
95	5
45	6
140	7
113	8
106	9



The practice (3): Structural problem (2)

Out of 960 across country genetic correlations with $CB < 10$:

Breed	CB < 10
BSW	67
GUE	39
HOL	200
JER	71
RDC	493
SIM	90



The practice (4)

Across Country Genetic Correlations (Estimation):

- * Use **country subsetting**,
- * 3-5 countries in a subset,
- * Use the USA as the "link-provider"
- * Use **bull subsetting** (only CB + $\frac{3}{4}$ sibs)
- * Use REML (KW98 Package) to estimate r_G for subsets
- * Combine r_G sub-matrices in full sized r_G matrix

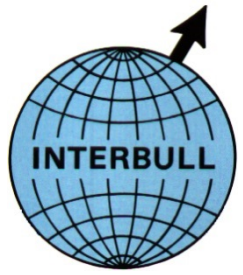
(Only 26 HOL-traits combinations (out of 171))



The practice (5)

Across Country Genetic Correlations (Post-processing)

- * Harmonize r_G values across evaluations
- * Form groups of countries
 - Impose "windows" within/across groups of countries
 - Regress towards median r_G within group
- * Use HOL r_G values from HOL for other breeds
- * Weigh current estimate and previously used r_G values
- * Bend the r_G matrix



The Effects



The Effects (1)

There were 12997 genetic correlations during 1409t

Comparison between 1409t and 1401t

- * 1896 E r_G values changed > 0.05 (about 14.6%)
- * 820 W r_G values changed > 0.05 (about 6.3%)
- * 746 P r_G values changed > 0.05 (about 5.7%)

E = Estimated; W = windowed; P = Post-processed



The Effects (2)

There were 12997 genetic correlations during 1409t

Correlation between old & new E r_G values: 0.787

Correlation between old & new W r_G values: 0.808

Correlation between old & new P r_G values: 0.840

E = Estimated; W = windowed; P = Post-processed



The Effects (3)

There were 12997 genetic correlations during 1409t

Correlation between	E & W	r_G values: 0.813
Correlation between	E & P	r_G values: 0.675
Correlation between	W & P	r_G values: 0.800

E = Estimated; W = windowed; P = Post-processed



The Effects (4)

There were 12997 genetic correlations during 1409t

# of r_G values changing > 0.05 between E & W:	3193
# of r_G values changing > 0.05 between E & P:	3659
# of r_G values changing > 0.05 between W & P:	1198

E = Estimated; W = windowed; P = Post-processed



Some personal remarks



Some personal remarks

- 1- The main problem is the poor link between populations;**
- 2- This problem is not going away;**
- 3- We manipulate the estimated r_G values too much;**
- 4- We have to find better (and simpler) methods.**



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