

Multiple Traits

LRS

CGIL

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Intro

- Animals are measured for many economic traits
- Traits have genetic and other correlations
- Can improve accuracy of EBV through correlations, low heritability traits gain more
- Correlations need to be accurate
- MT analyses easier in 2012
- One big analysis versus several small analyses
- Can account to some degree for selection on one trait versus others
- Models for each trait can be different
- All have animal additive genetic effects in common

Simulation

$$y_{1ij} = B_{1i} + a_{1j} + e_{1ij}$$

$$y_{2kj} = C_{2k} + a_{2j} + e_{2kj}$$

OR

$$y_{tijk} = B_{ti} + C_{tk} + a_{tj} + e_{tijk}$$

where values put in for B_{2i} would be 0, and values put in for C_{1k} would be 0.

Parameters

$$\mathbf{G} = \begin{pmatrix} g_{11} & g_{12} \\ g_{12} & g_{22} \end{pmatrix} = \begin{pmatrix} 1 & 2 \\ 2 & 15 \end{pmatrix}$$

$$\mathbf{R} = \begin{pmatrix} r_{11} & r_{12} \\ r_{12} & r_{22} \end{pmatrix} = \begin{pmatrix} 10 & 5 \\ 5 & 100 \end{pmatrix}$$

$$\rho_g = 2/(15)^{.5} = .52,$$

$$\rho_r = 5/(1000)^{.5} = .16$$

$$h_1^2 = \frac{1}{11} = .09$$

$$h_2^2 = \frac{15}{115} = .13$$

Generating Records

$$\begin{aligned}\mathbf{G} &= \mathbf{L}_G \mathbf{L}'_G \\ &= \begin{pmatrix} 1 & 0 \\ 2 & (11)^{.5} \end{pmatrix} \mathbf{L}'_G\end{aligned}$$

$$\begin{aligned}\text{and } \mathbf{R} &= \mathbf{L}_R \mathbf{L}'_R \\ &= \begin{pmatrix} (10)^{.5} & 0 \\ (2.5)^{.5} & (97.5)^{.5} \end{pmatrix} \mathbf{L}'_R.\end{aligned}$$

$$\begin{aligned}\begin{pmatrix} y_{1ij} \\ y_{2kj} \end{pmatrix} &= \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \end{pmatrix} \begin{pmatrix} 6.7 \\ 6.3 \\ 0 \\ 0 \end{pmatrix} + \begin{pmatrix} 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} 0 \\ 0 \\ 25 \\ 40 \\ 55 \end{pmatrix} \\ &+ \begin{pmatrix} \text{Parent Ave. Trait 1=0} \\ \text{Parent Ave. Trait 2=0} \end{pmatrix} + (1)^{.5} \begin{pmatrix} 1 & 0 \\ 2 & (11)^{.5} \end{pmatrix} \begin{pmatrix} .6942 \\ -1.3027 \end{pmatrix} \\ &+ \begin{pmatrix} (10)^{.5} & 0 \\ (2.5)^{.5} & (97.5)^{.5} \end{pmatrix} \begin{pmatrix} -.5324 \\ -.9468 \end{pmatrix}\end{aligned}$$

Data

Animal	Sire	Dam	B-level	C-level	Trait 1	Trait 2
1	0	0	1	1	2.3	39
2	0	0	1	2	2.6	39
3	0	0	1	3	9.8	53
4	0	0	1	1	4.7	4
5	0	0	1	2	5.5	63
6	1	3	2	3	2.5	64
7	1	4	2	2	8.4	35
8	1	5	2	3	8.2	41
9	2	3	2	1	9.0	27
10	2	4	2	1	7.8	32
11	2	5	2	2	2.8	46
12	6	10	2	3	7.4	67

Culling

Animal	Sire	Dam	B-level	C-level	Trait 1	Trait 2
1	0	0	1	1	2.3	
2	0	0	1	2	2.6	
3	0	0	1	3	9.8	53
4	0	0	1	1	4.7	4
5	0	0	1	2	5.5	63
6	1	3	2	3	2.5	
7	1	4	2	2	8.4	35
8	1	5	2	3	8.2	41
9	2	3	2	1	9.0	27
10	2	4	2	1	7.8	32
11	2	5	2	2	2.8	
12	6	10	2	3	7.4	67

Constructing MME

$$\begin{pmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{pmatrix} = \begin{pmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{pmatrix} \begin{pmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 \end{pmatrix} \begin{pmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{pmatrix} + \begin{pmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{pmatrix}$$

$$\text{Var} \begin{pmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{pmatrix} = \begin{pmatrix} \mathbf{A}g_{11} & \mathbf{A}g_{12} \\ \mathbf{A}g_{12} & \mathbf{A}g_{22} \end{pmatrix}$$

$$\text{Var} \begin{pmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{pmatrix} = \begin{pmatrix} \mathbf{I}r_{11} & \mathbf{I}r_{12} \\ \mathbf{I}r_{12} & \mathbf{I}r_{22} \end{pmatrix}$$

if both traits observed on all animals.

May be more convenient to have traits arranged within animals (as in the tables) rather than animals within traits.

MME

$$\begin{pmatrix}
 \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{X}_1 & \mathbf{X}'_1 \mathbf{R}^{12} \mathbf{X}_2 & \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{Z}_1 & \mathbf{X}'_1 \mathbf{R}^{12} \mathbf{Z}_2 \\
 \mathbf{X}'_2 \mathbf{R}^{21} \mathbf{X}_1 & \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{X}_2 & \mathbf{X}'_2 \mathbf{R}^{21} \mathbf{Z}_1 & \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{Z}_2 \\
 \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{X}_1 & \mathbf{Z}'_1 \mathbf{R}^{12} \mathbf{X}_2 & \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{Z}_1 + \mathbf{A}^{-1} \mathbf{g}^{11} & \mathbf{Z}'_1 \mathbf{R}^{12} \mathbf{Z}_2 + \mathbf{A}^{-1} \mathbf{g}^{12} \\
 \mathbf{Z}'_2 \mathbf{R}^{21} \mathbf{X}_1 & \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{X}_2 & \mathbf{Z}'_2 \mathbf{R}^{21} \mathbf{Z}_1 + \mathbf{A}^{-1} \mathbf{g}^{21} & \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{Z}_2 + \mathbf{A}^{-1} \mathbf{g}^{22}
 \end{pmatrix}
 \begin{pmatrix}
 \mathbf{b}_1 \\
 \mathbf{b}_2 \\
 \mathbf{a}_1 \\
 \mathbf{a}_2
 \end{pmatrix}$$

$$= \begin{pmatrix}
 \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{y}_1 + \mathbf{X}'_1 \mathbf{R}^{12} \mathbf{y}_2 \\
 \mathbf{X}'_2 \mathbf{R}^{21} \mathbf{y}_1 + \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{y}_2 \\
 \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{y}_1 + \mathbf{Z}'_1 \mathbf{R}^{12} \mathbf{y}_2 \\
 \mathbf{Z}'_2 \mathbf{R}^{21} \mathbf{y}_1 + \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{y}_2
 \end{pmatrix}$$

MME, No Residual Covariances

$$\begin{pmatrix}
 \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{X}_1 & \mathbf{0} & \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{Z}_1 & \mathbf{0} \\
 \mathbf{0} & \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{X}_2 & \mathbf{0} & \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{Z}_2 \\
 \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{X}_1 & \mathbf{0} & \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{Z}_1 + \mathbf{A}^{-1} \mathbf{g}^{11} & \mathbf{A}^{-1} \mathbf{g}^{12} \\
 \mathbf{0} & \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{X}_2 & \mathbf{A}^{-1} \mathbf{g}^{21} & \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{Z}_2 + \mathbf{A}^{-1} \mathbf{g}^{22}
 \end{pmatrix}
 \begin{pmatrix}
 \mathbf{b}_1 \\
 \mathbf{b}_2 \\
 \mathbf{a}_1 \\
 \mathbf{a}_2
 \end{pmatrix}$$

$$= \begin{pmatrix}
 \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{y}_1 \\
 \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{y}_2 \\
 \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{y}_1 \\
 \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{y}_2
 \end{pmatrix}$$

MME, No genetic correlations

$$\begin{pmatrix}
 \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{X}_1 & \mathbf{X}'_1 \mathbf{R}^{12} \mathbf{X}_2 & \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{Z}_1 & \mathbf{X}'_1 \mathbf{R}^{12} \mathbf{Z}_2 \\
 \mathbf{X}'_2 \mathbf{R}^{21} \mathbf{X}_1 & \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{X}_2 & \mathbf{X}'_2 \mathbf{R}^{21} \mathbf{Z}_1 & \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{Z}_2 \\
 \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{X}_1 & \mathbf{Z}'_1 \mathbf{R}^{12} \mathbf{X}_2 & \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{Z}_1 + \mathbf{A}^{-1} \mathbf{g}^{11} & \mathbf{Z}'_1 \mathbf{R}^{12} \mathbf{Z}_2 \\
 \mathbf{Z}'_2 \mathbf{R}^{21} \mathbf{X}_1 & \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{X}_2 & \mathbf{Z}'_2 \mathbf{R}^{21} \mathbf{Z}_1 & \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{Z}_2 + \mathbf{A}^{-1} \mathbf{g}^{22}
 \end{pmatrix}
 \begin{pmatrix}
 \mathbf{b}_1 \\
 \mathbf{b}_2 \\
 \mathbf{a}_1 \\
 \mathbf{a}_2
 \end{pmatrix}$$

$$= \begin{pmatrix}
 \mathbf{X}'_1 \mathbf{R}^{11} \mathbf{y}_1 + \mathbf{X}'_1 \mathbf{R}^{12} \mathbf{y}_2 \\
 \mathbf{X}'_2 \mathbf{R}^{21} \mathbf{y}_1 + \mathbf{X}'_2 \mathbf{R}^{22} \mathbf{y}_2 \\
 \mathbf{Z}'_1 \mathbf{R}^{11} \mathbf{y}_1 + \mathbf{Z}'_1 \mathbf{R}^{12} \mathbf{y}_2 \\
 \mathbf{Z}'_2 \mathbf{R}^{21} \mathbf{y}_1 + \mathbf{Z}'_2 \mathbf{R}^{22} \mathbf{y}_2
 \end{pmatrix}$$

Residual Matrices and Missing Traits

$$\mathbf{E}_{12} = \begin{pmatrix} 10 & 5 \\ 5 & 100 \end{pmatrix}^{-1}$$

$$\mathbf{E}_1 = \begin{pmatrix} 10 & 0 \\ 0 & 0 \end{pmatrix}^{-}$$

$$\mathbf{E}_2 = \begin{pmatrix} 0 & 0 \\ 0 & 100 \end{pmatrix}^{-}$$

Solutions

$$B_{11} = 5.02$$

$$B_{12} = 6.56$$

$$C_{21} = 20.09$$

$$C_{22} = 49.06$$

$$C_{23} = 51.96$$

Animal Solutions

Animal	Sire	Dam	Trait 1	Trait 2
1	0	0	-.36	-1.68
2	0	0	-.07	1.04
3	0	0	.41	1.17
4	0	0	-.04	-1.49
5	0	0	.06	.96
6	1	3	-.10	-.14
7	1	4	-.20	-2.30
8	1	5	-.14	-.96
9	2	3	.31	1.62
10	2	4	.14	1.13
11	2	5	-.18	.65
12	6	10	.16	1.51

In Practice

Sheep - Growth System

- survival after 24 h
- birthweight, kg
- 50-d weight, kg
- 50-100 d gain, kg
- ultrasound fat, mm
- ultrasound loin, cm

In Practice

Sheep - Ewe Reproduction System

- age at first lambing, d
- number born at first lambing
- number weaned from first lambing
- interval between lambings
- number born at later lambings
- number weaned from later lambings

In Practice

Swine - Test Station Growth

- number of visits to feeder per day
- time spent at feeder per day
- feed consumed per day
- weight per day
- ultrasound fat, mm, at intervals
- ultrasound loin, cm, at intervals

In Practice

Dairy Cattle - Test Day System

- First, second, third and later lactations
- Milk, fat, protein yields and SCS
- Random regressions order 5

In Practice

Dairy Cattle - Fertility System

- First versus second and later calvings
- Age at first calving/Interval calving to first service
- Calving ease
- Stillbirths
- Gestation length/Days Open
- Interval first service to conception
- Non-return rate 56 days
- Number of services
- Calf size

Covariance Estimation

- Scalars to vectors and matrices of order t
- $\mathbf{x}'_i; \mathbf{x} = 5$ to $t \times t$ matrix, invert, and compute Cholesky decomposition.
- Noise is $sol_i = sol_i + \mathbf{L}w$ where w is a vector of random normal deviates.
- Genetic matrix is inverted Wishart,

$$\begin{pmatrix} \hat{\mathbf{a}}'_1 \mathbf{A}^{-1} \hat{\mathbf{a}}_1 & \hat{\mathbf{a}}'_1 \mathbf{A}^{-1} \hat{\mathbf{a}}_2 \\ \hat{\mathbf{a}}'_2 \mathbf{A}^{-1} \hat{\mathbf{a}}_1 & \hat{\mathbf{a}}'_2 \mathbf{A}^{-1} \hat{\mathbf{a}}_2 \end{pmatrix}$$

- Residual matrix, should estimate missing residuals

$$\mathbf{res}'_{k*} = \begin{pmatrix} \mathbf{R}_{oo} & \mathbf{R}_{om} \\ \mathbf{R}_{mo} & \mathbf{R}_{mm} \end{pmatrix} \begin{pmatrix} \mathbf{R}_{oo}^{-1} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \end{pmatrix} \begin{pmatrix} \mathbf{e}_o \\ \mathbf{0} \end{pmatrix}$$

$$\mathbf{S}_e = \left(\sum_{k=1}^N (\mathbf{res}'_{k*} \mathbf{res}_{k*}) + \nu_e \mathbf{R}_e \right)$$

Gibbs Sampling

- Difficult to determine burn-in length, so many parameters
- Start two chains with completely different starting values, same priors and degrees of belief, and with the same random number seed. Eventually the two chains would become the same.
- Maybe too many missing records on a trait, then restrict data to animals with all traits available(?)
- Will give you SE on correlation estimates

Indexes

$$I = w_1 \hat{a}_1 + w_2 \hat{a}_2 + \dots$$

where \hat{a}_i are EBVs and w_i are relative economic weights. Indexes should use EBVs from MT analyses.