# Maternal Effects

LRS

CGIL

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# Definition

Put in figure from ABMethods notes

# Where

- Pre birth effects
- During birth and immediately after
- Care up to weaning
- Rapidly diminishing effects after weaning
- Nearly all species of creatures

# Model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Z}_3\mathbf{p} + \mathbf{e},$$

where

- **y** is the growth trait of a young animal,
- **b** is a vector of fixed factors influencing growth, such as sex of the offspring, or age of dam,
- **a** is a vector of random additive genetic effects (i.e. direct genetic effects) of the animals,
- **m** is a vector of random maternal genetic (dam) effects, and
- **p** , in this model, is a vector of maternal permanent environmental effects (because dams may have more than one offspring in the data),
- **u** could be other random effects, such as contemporary groups or litter effects (not shown in equation).

# Model

$$Var\begin{pmatrix}\mathbf{a}\\ \mathbf{m}\\ \mathbf{p}\\ \mathbf{e}\end{pmatrix} = \begin{pmatrix}\mathbf{A}\sigma_a^2 & \mathbf{A}\sigma_{am} & \mathbf{0} & \mathbf{0}\\ \mathbf{A}\sigma_{am} & \mathbf{A}\sigma_m^2 & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_p^2 & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma_e^2\end{pmatrix}$$

$$\left(\begin{array}{c|c}\mathbf{a} & \\ & \mathbf{A},\mathbf{G}\\ \mathbf{m} & \end{array}\right) \sim N\left(\begin{pmatrix}\mathbf{0}\\ \mathbf{0}\end{pmatrix},\ \mathbf{G}\otimes\mathbf{A}\right)$$

$$\mathbf{G} = \begin{pmatrix}\sigma_a^2 & \sigma_{am}\\ \sigma_{am} & \sigma_m^2\end{pmatrix}$$

$$\mathbf{p} \mid \mathbf{I},\sigma_p^2 \sim N(\mathbf{0},\mathbf{I}\sigma_p^2)$$

$$\mathbf{e} \sim N(\mathbf{0},\mathbf{I}\sigma_e^2)$$

# Simulation

$$\mathbf{G} = \begin{pmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{pmatrix} = \begin{pmatrix} 49 & -7 \\ -7 & 26 \end{pmatrix}$$

$$\begin{aligned} \mathbf{G} &= \mathbf{L}\mathbf{L}' \\ \mathbf{L} &= \begin{pmatrix} 7 & 0 \\ -1 & 5 \end{pmatrix}. \end{aligned}$$

Let $\sigma_p^2 = 9$ and $\sigma_e^2 = 81$.

# How It Works

Let $\mathbf{G}$ be any positive definite covariance matrix of order $t$, then

$$\mathbf{G} = \mathbf{L}\mathbf{L}'$$

for $\mathbf{L}$ being lower triangular, from Cholesky decomposition.
To generate a vector $\mathbf{v}$ that has $Var(\mathbf{v}) = \mathbf{G}$, then

- Generate a vector $\mathbf{w}$ of $t$ random normal deviates.
- $\mathbf{v} = \mathbf{L}\mathbf{w}$

$$\begin{aligned} Var(\mathbf{L}\mathbf{w}) &= \mathbf{L}\,Var(\mathbf{w})\mathbf{L}' \\ &= \mathbf{L}\ \mathbf{I}\ \mathbf{L}' \\ &= \mathbf{L}\mathbf{L}' = \mathbf{G} \end{aligned}$$

# Genetic Values

**Base animals, unrelated**

$$\begin{aligned}
\mathbf{w}' &= (2.533 \quad -.299) \\
\begin{pmatrix} a_A \\ m_A \end{pmatrix} &= \mathbf{Lw} \\
&= \begin{pmatrix} 7 & 0 \\ -1 & 5 \end{pmatrix} \begin{pmatrix} 2.533 \\ -.299 \end{pmatrix} \\
&= \begin{pmatrix} 17.731 \\ -4.028 \end{pmatrix}
\end{aligned}$$

# Genetic Values

**Parents Known**

$$
\begin{aligned}
\begin{pmatrix} a_i \\ m_i \end{pmatrix} &= \frac{1}{2}\begin{pmatrix} a_s + a_d \\ m_s + m_d \end{pmatrix} + (b_{ii})^{.5}\mathbf{Lw} \\
&= \frac{1}{2}\begin{pmatrix} 17.731 - 7.987 \\ -4.028 + 2.316 \end{pmatrix} + (\frac{1}{2})^{.5}\mathbf{L}\begin{pmatrix} .275 \\ .402 \end{pmatrix} \\
&= \begin{pmatrix} 6.233 \\ .371 \end{pmatrix}
\end{aligned}
$$

All animals have both direct and maternal genetic breeding values.

# Record

$$
\begin{aligned}
y &= \text{Fixed Effects} + a_i + m_d + p_d + \sigma_e * RND \\
&= 140 + 6.233 + 2.316 + (3)(-1.497) + (9)(1.074) \\
&= 153.724 \\
&= 154
\end{aligned}
$$

# Example Data

| Animal | Sire | Dam | CG | Weight |
|---|---|---|---|---|
| 5 | 1 | 3 | 1 | 156 |
| 6 | 2 | 3 | 1 | 124 |
| 7 | 1 | 4 | 1 | 135 |
| 8 | 2 | 4 | 2 | 163 |
| 9 | 1 | 3 | 2 | 149 |
| 10 | 2 | 4 | 2 | 138 |

# MME

$$\begin{pmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z}_1 & \mathbf{X}'\mathbf{Z}_2 & \mathbf{X}'\mathbf{Z}_3 \\ \mathbf{Z}_1'\mathbf{X} & \mathbf{Z}_1'\mathbf{Z}_1 + \mathbf{A}^{-1}k_{11} & \mathbf{Z}_1'\mathbf{Z}_2 + \mathbf{A}^{-1}k_{12} & \mathbf{Z}_1'\mathbf{Z}_3 \\ \mathbf{Z}_2'\mathbf{X} & \mathbf{Z}_2'\mathbf{Z}_1 + \mathbf{A}^{-1}k_{12} & \mathbf{Z}_2'\mathbf{Z}_2 + \mathbf{A}^{-1}k_{22} & \mathbf{Z}_2'\mathbf{Z}_3 \\ \mathbf{Z}_3'\mathbf{X} & \mathbf{Z}_3'\mathbf{Z}_1 & \mathbf{Z}_3'\mathbf{Z}_2 & \mathbf{Z}_3'\mathbf{Z}_3 + \mathbf{I}k_{33} \end{pmatrix} \begin{pmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{a}} \\ \hat{\mathbf{m}} \\ \hat{\mathbf{p}} \end{pmatrix} = \begin{pmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}_1'\mathbf{y} \\ \mathbf{Z}_2'\mathbf{y} \\ \mathbf{Z}_3'\mathbf{y} \end{pmatrix},$$

$$\begin{aligned} \begin{pmatrix} k_{11} & k_{12} \\ k_{12} & k_{22} \end{pmatrix} &= \begin{pmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{pmatrix}^{-1} \sigma_e^2, \\ &= \begin{pmatrix} 49 & -7 \\ -7 & 26 \end{pmatrix}^{-1} (81), \\ &= \begin{pmatrix} 1.7192 & .4628 \\ .4628 & 3.2400 \end{pmatrix} \\ k_{33} &= \sigma_e^2/\sigma_p^2 = 81/9 = 9 \end{aligned}$$

# Solutions

$$\hat{\mathbf{b}} = \begin{pmatrix} 137.8469 \\ 150.4864 \end{pmatrix}, \quad \hat{\mathbf{p}} = \begin{pmatrix} .0658 \\ -.0658 \end{pmatrix},$$

$$\hat{\mathbf{a}} = \begin{pmatrix} 2.3295 \\ -2.3295 \\ .1280 \\ -.1280 \\ 5.1055 \\ -4.1143 \\ .2375 \\ 2.0161 \\ .5447 \\ -3.7896 \end{pmatrix}, \quad \text{and} \quad \hat{\mathbf{m}} = \begin{pmatrix} -.3328 \\ .3328 \\ .1646 \\ -.1646 \\ -.6379 \\ .6792 \\ -.1254 \\ -.3795 \\ .0136 \\ .4499 \end{pmatrix}.$$

# VC Estimation

Everything is the same as for any animal model except,

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

has an inverted Wishart distribution. An entire matrix has to be sampled during MCMC to estimate

$$\begin{pmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{pmatrix}$$

# Data Structure

To estimate maternal genetic covariance properly the data must have a good structure.

- Sires must have daughters that are in the data as dams of calves(lambs).
- Females should appear in data as both a calf(lamb) and as a dam of calves(lambs).

Sometimes IDs of female change from calf to dam, which breaks up the structure.

If structure is poor, then $\sigma_{am} = 0$ may be a good option.

# Embryo Transfers

- Cows chosen to provide embryos can produce from 1 to 6 and sometimes more embryos, which are implanted into recipient cows.
- The recipient cow provides the maternal environment for the calf and not the biological mother.
- The maternal effect in the model is assigned to the recipient cow, but the genetic link between the calf and the biological mother is included in $\mathbf{A}$.
- Genetic links of recipients are also included in $\mathbf{A}$ to their parents and biological offspring, if they exist.
- Usually recipient cows are unrelated to all other cows in the herd, and may even be of different breed types.
- Recipient cows often do not have identification or records in the herd, and are just temporary animals.

# Cytoplasmic Effects

- Mitochondrial DNA is inherited from the female parent only through the embryo. There is no mitochondrial DNA in sperm.
- The DNA in mitochondria does not segregate as in meiosis, but is transferred in whole.
- There are a few genes in the mitochondria that may have an effect on animal performance for some traits - the hypothesis of the 1980's.
- Every animal must be traced back (through female parent) to the female origin in the base population, to give a female line of origin effect for the model, which would be a random factor.
- Cytoplasmic effects were found to be ignorable.