Estimation of Inheritance with Fixed and Random Effects

Patrick Carter Washington State University Evolutionary Quantitative Genetics Workshop 2025

Estimating Variance Components

 Many ways to do it - ANOVA Regression (developed for estimating h²!) For large unpalanced data sets with complex pedigrees: Linear Mixed Models Fixed - Experimental/population specific effects Random -Variables randomly sampled, e.g., individuals randomly sampled from a population

The "Animal Model"

- **y** = Xβ + Za + **e**
 - **y** = (nx1) vector of phenotypes (n = sample size)
 - β = (px1) vector of fixed effect regression coefficients (p = number of fixed effects) (FIXED)
 - **X** = (nxp) design matrix relating **y** to β (FIXED)
 - a = (qx1) vector of additive effects (q = number of individuals in the pedigree) (RANDOM)
 - **Z** = (nxq) design matrix relating **y** to **a** (RANDOM)
 - **e** = (nx1) vector of errors
- Solve for β and a
- Assume

Var(e) = $I\sigma_e^2$ (errors are independent) Var(a) = $A\sigma_a^2$ (var of a depends on relationship matrix A) cov(a,e) = 0 $\alpha = \sigma_e^2 / \sigma_a^2$ is known (!!!!) (need a starting point)

 $\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z+A^{-1}\alpha \end{bmatrix} \begin{bmatrix} \beta \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$

y = (nx1) vector of phenotypic measures = KNOWN

 β = (px1) vector of fixed effect regression coefficients (FIXED) = UNKNOWN

X = (nxp) design matrix relating **y** to β (FIXED) = KNOWN

a = (qx1) vector of additive effects (q = number of individuals in the pedigree) (RANDOM) = UNKNOWN

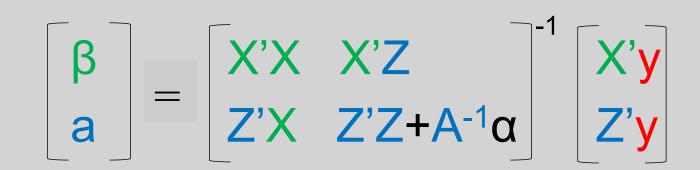
Z = (nxq) design matrix relating y to a (RANDOM) = KNOWN

A relationship matrix = KNOWN = (q x q) matrix where q = number of individuals in the pedigree

 $\alpha = \sigma_e^2 / \sigma_a^2 = \text{ESTIMATED}$

 $\begin{array}{c|c} X'X & X'Z & \beta \\ Z'X & Z'Z+A^{-1}\alpha & a \end{array} = \begin{array}{c} X'y \\ Z'y \end{array}$

SO



Ex: Data and System of Linear Equations

id	Sire	Dam	Herd	Ptype
1	-	-	1	78
2	-	-	2	83
3	-	-	2	70
4	2	1	1	86
5	2	3	2	77

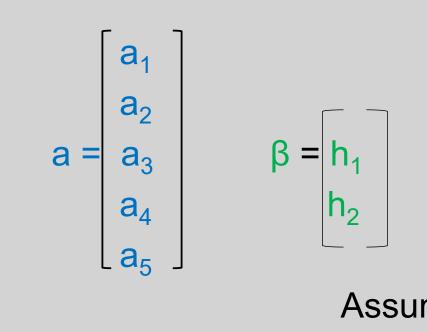
 $78 = herd_1 + animal_1 + error_1$ $83 = herd_2 + animal_2 + error_2$ $70 = herd_2 + animal_3 + error_3$ $86 = herd_1 + animal_4 + error_4$ $77 = herd_2 + animal_5 + error_5$

Ex: Data and Knowns

id	Si	ire		Dam	He	rd Pty	pe
1	-			-	1	78	
2	-			-	2	83	
3	-			-	2	70	
4	2			1	1	86	
5	2			3	2	77	
	78		[10]		10000		
	83		01		01000		
y =	70	X =	0 1	Z =	00100		
	86		10		00010		
	77		01		00001	Note: Z = I	

Ex: Data and Unknowns

id	Sire	Dam	Herd	Ptype
1	-	-	1	78
2	-	-	2	83
3	-	-	2	70
4	2	1	1	86
5	2	3	2	77



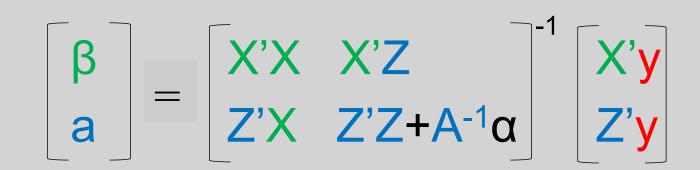
Assume h² = .33, so $\alpha = \sigma_e^2 / \sigma_a^2 = 2.0$

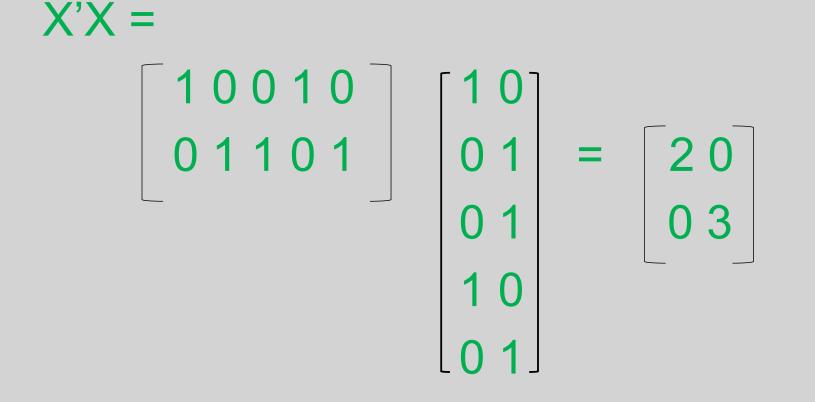
Example: Data and "A" Matrix

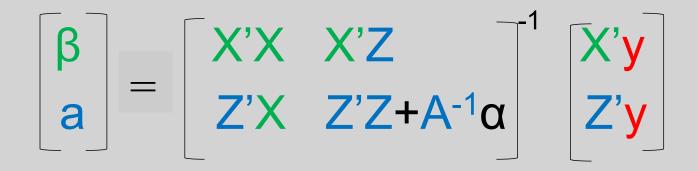
id	Sire)	Dam	า	Hero	t	Ptype
1	-		-		1		78
2	-		-		2		83
3	-		-		2		70
4	2		1		1		86
5	2		3		2		77
		1	2	3	4	5	
	1	1					
	2	0	1				
A =	3	0	0	1			
	4	1/2	1/2	0	1		
	5	0	1/2	1/2	1/4	1	

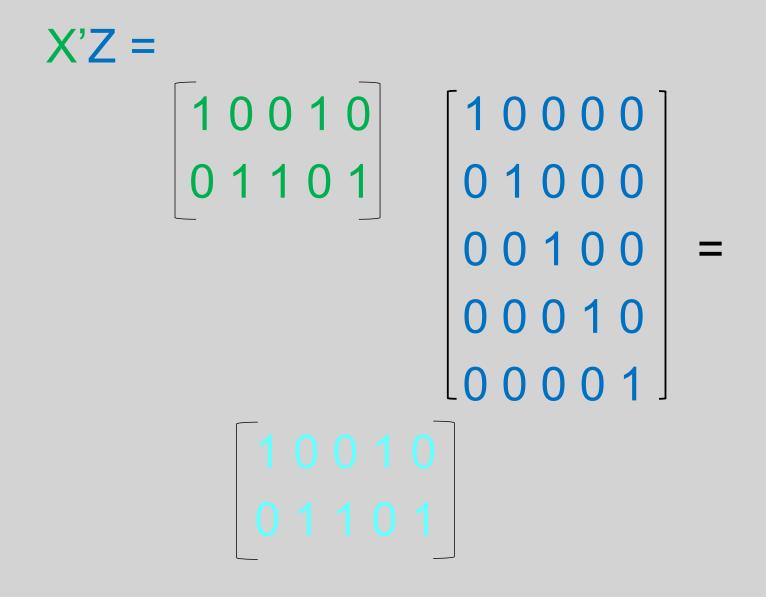
 $\begin{array}{c|c} X'X & X'Z & \beta \\ Z'X & Z'Z+A^{-1}\alpha & a \end{array} = \begin{array}{c} X'y \\ Z'y \end{array}$

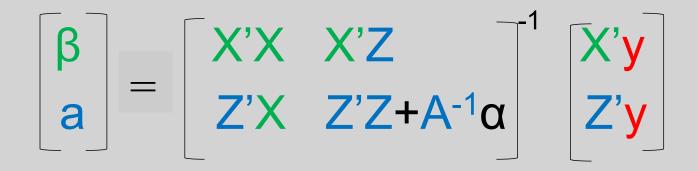
SO

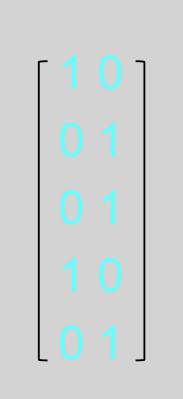




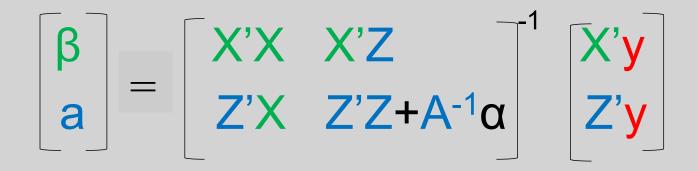






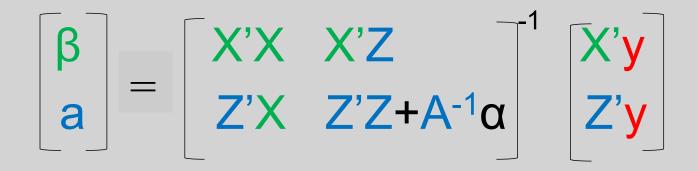


Z'X = |X =



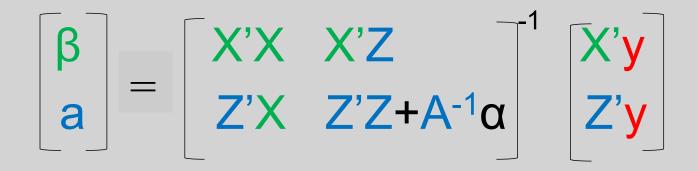
$Z'Z+A^{-1}\alpha =$

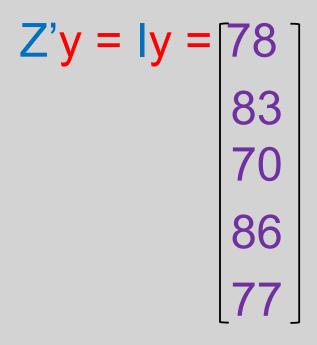
[10000]	[1.5 0.5 0 -1 0]	4 1 0 -2 0
01000	0.5 2 0.5 -1 -1	151-2-2
00100	+2.0 * 0 0.5 1.5 0 -1 =	0140-2
00010	-1 -1 0 2 0	-2 -2 0 5 0
00001	0 -1 -1 0 2	0 -2 -2 0 5



X'y =

86 77





Ex: Solving the Mixed Model Equation $\begin{array}{c} \beta \\ a \end{array} = \begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\alpha \end{bmatrix} \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$ $\begin{bmatrix} h_1 \\ h_2 \end{bmatrix} \begin{bmatrix} 2 & 0 & 1 & 1 & 0 & 0 \\ 0 & 3 & 0 & 0 & 1 & 1 \\ 1 & 0 & 4 & 1 & 0 & -2 & 0 \end{bmatrix} \begin{bmatrix} -1 \\ 164 \\ 230 \\ 78 \end{bmatrix}$

		. •
a ₂ =	10151-2-2	83
a ₃	010140-2	70
a ₄	01-2-2050	86
a ₅	0 1 0 -2 -2 0 5	77

Ex: Solutions

 $h_1 = 79.17$ $h_2 = 77.77$ $a_1 = 0.53$ $a_2 = 2.13$ $a_3 = -2.66$ $a_4 = 2.71$ $a_5 = -0.37$

Additional Effects

- More fixed effects: Just increases the length of Beta = very easy
- More random effects: each one adds a new term consisting of a vector of random effects times a design matrix

- Example: add maternal environmental effects

"Animal Model" with Maternal Effects

• $y = X\beta + Za + Wm + e$

- **y** = (nx1) vector of phenotypic measures
- β = (px1) vector of fixed effect regression coefficients (FIXED)
- **X** = (nxp) design matrix relating **y** to β (FIXED)
- **Z** = (nxq) design matrix relating **y** to **a** (RANDOM)
- **W** = (nxf) design matrix relating **y** to **m** (RANDOM)
- **e** = (nx1) vector of errors
- Solve for β and a and m
- Assume

Var(e) = $I\sigma_e^2$ (errors are independent) Var(a) = $A\sigma_a^2$ (var of a depends on relationship matrix A) Var(m) = $I \sigma_m^2$ (maternal effects are independent) cov(a,m) and cov (e,m) are both 0 (a, m, e independent of each other) σ_e^2 / σ_a^2 and σ_e^2 / σ_m^2 are known (need starting points)

XX XZ XW
Z'X Z'Z +
$$A^{-1}\alpha_a$$
 Z'W
W'X W'Z W'W + $I\alpha_m$

X'y Z'y

y = (nx1) vector of phenotypic measures = KNOWN

- β = (px1) vector of fixed effect regression coefficients (FIXED) = UNKNOWN
- **X** = (nxp) design matrix relating **y** to β (FIXED) = KNOWN
- **a** = (qx1) vector of additive effects (q = number of individuals in the pedigree) (RANDOM) = UNKNOWN
- **Z** = (nxq) design matrix relating **y** to **a** (RANDOM) = KNOWN
- A relationship matrix = KNOWN
- **W** = (nxf) design matrix relating **y** to **m** (RANDOM)
- I = identity matrix

 $\alpha_{a} = \sigma_{e}^{2} / \sigma_{a}^{2}$ = ESTIMATED; $\alpha_{m} = \sigma_{e}^{2} / \sigma_{m}^{2}$ = ESTIMATED

Likelihood Approach

- Likelihood = Pr(y|μ, σ²) = conditional probability of the data (y) given the parameters:
 - $\mu = X\beta$ $\sigma^{2} = Z(A\sigma_{a}^{2})Z' + I\sigma_{e}^{2}$ genetic variance + error variance
- Iterations:

$$\begin{array}{l} (\sigma_{e}{}^{2}\!/\,\sigma_{a}{}^{2})_{sv} \rightarrow \mathbf{a_{i}} \rightarrow (\sigma_{e}{}^{2}\!/\,\sigma_{a}{}^{2})_{i} \\ (\sigma_{e}{}^{2}\!/\,\sigma_{a}{}^{2})_{i} \rightarrow \mathbf{a_{j}} \rightarrow (\sigma_{e}{}^{2}\!/\,\sigma_{a}{}^{2})_{j} \\ (\sigma_{e}{}^{2}\!/\,\sigma_{a}{}^{2})_{j} \rightarrow \mathbf{a_{k}} \rightarrow (\sigma_{e}{}^{2}\!/\,\sigma_{a}{}^{2})_{k} \end{array}$$

Rinse & Repeat until parameters stabilize

Bayesian Approach

- Pr(μ, σ²|y) = conditional probability of the parameters given the data
 - Yay! More intuitive than Likelihood
- Except that it is proportional to:

 $Pr(y|\mu, \sigma^2)Pr(\mu, \sigma^2)$

(Likelihood)(Prior belief in possible parameter values)

- Produces a posterior distribution = probabilistic distribution associating each value of a parameter to a probability
- Need iterative process to solve: MCMC

Markov Chain Monte Carlo

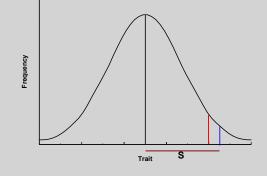
- Algorithm based on the proposal of a new value for a parameter, as a function of the value of the other parameters, at each iterative step.
- Saving the value of the parameter at each iteration, we ultimately get a series of values, which is the posterior distribution of interest, i.e., a posterior probability distribution for each parameter.

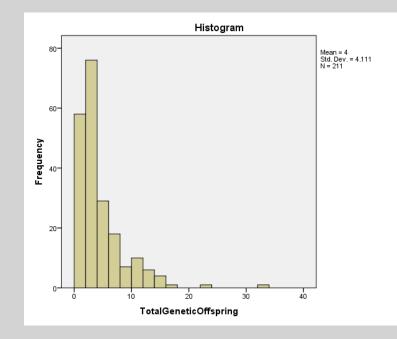
Non-Gaussian Traits

 For a continuous trait, if family relationships in the population are known, and assuming many loci of small effect, the phenotypic variance can be partitioned:

$$-V_{P} = V_{G} + V_{E}$$

 But what if the trait of interest is not continuous or is non-Gaussian? How can we estimate variance components?





Generalized Linear Mixed Model (GLMM)

- Combination of Generalized Linear Models and Linear Mixed Models
- Can handle non-Gaussian traits
 - Requires use of a link function (e.g., probability density function for binary outcomes) otherwise still...
- An "Animal Model"

• **y** = Xβ + Za + e

Requires Bayesian approaches

MCMCglmm

Can estimate variance components for any Gaussian or non-Gaussian trait Can have any number of fixed or random effects Can handle complex pedigrees Very flexible

Need priors (usually choose uninformative) Long runs Difficult assessment of runs