



Centre for
Tropical Livestock
Genetics and Health

Introduction to genetic evaluation (intuition & simple cases)

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Slides adapted from Gregor Gorjanc and Gabriela Mafra Fortuna





Learning objectives

Understand forward and backward/inverse views of working with models

Familiarise yourself with simple cases of inferring breeding values from the data

Practice inference of breeding values for simple cases



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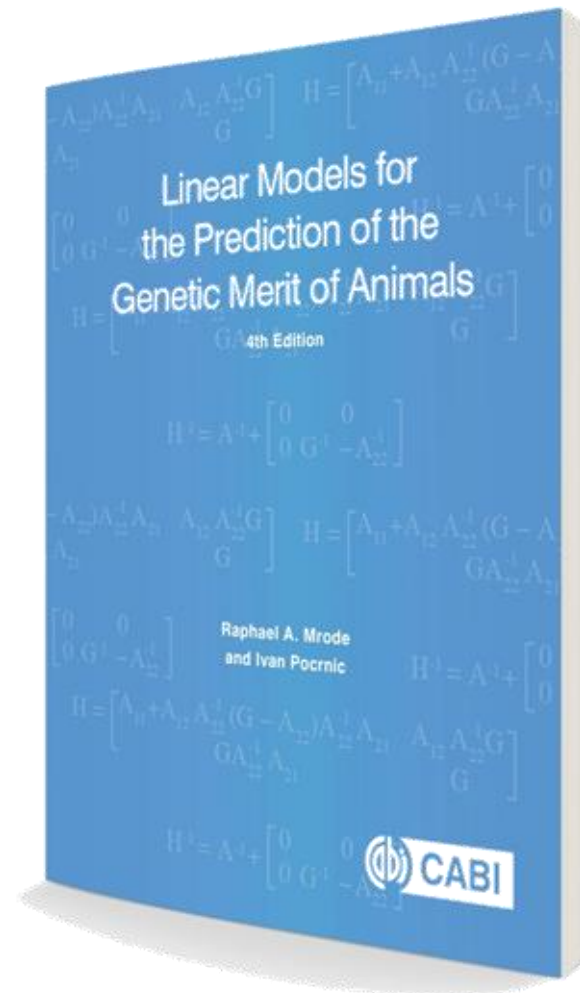
Linear models for the prediction of the genetic merit of animals

CABI Biotechnology Series

September 2023 | 412pp

Raphael A Mrode
Ivan Pocrnic

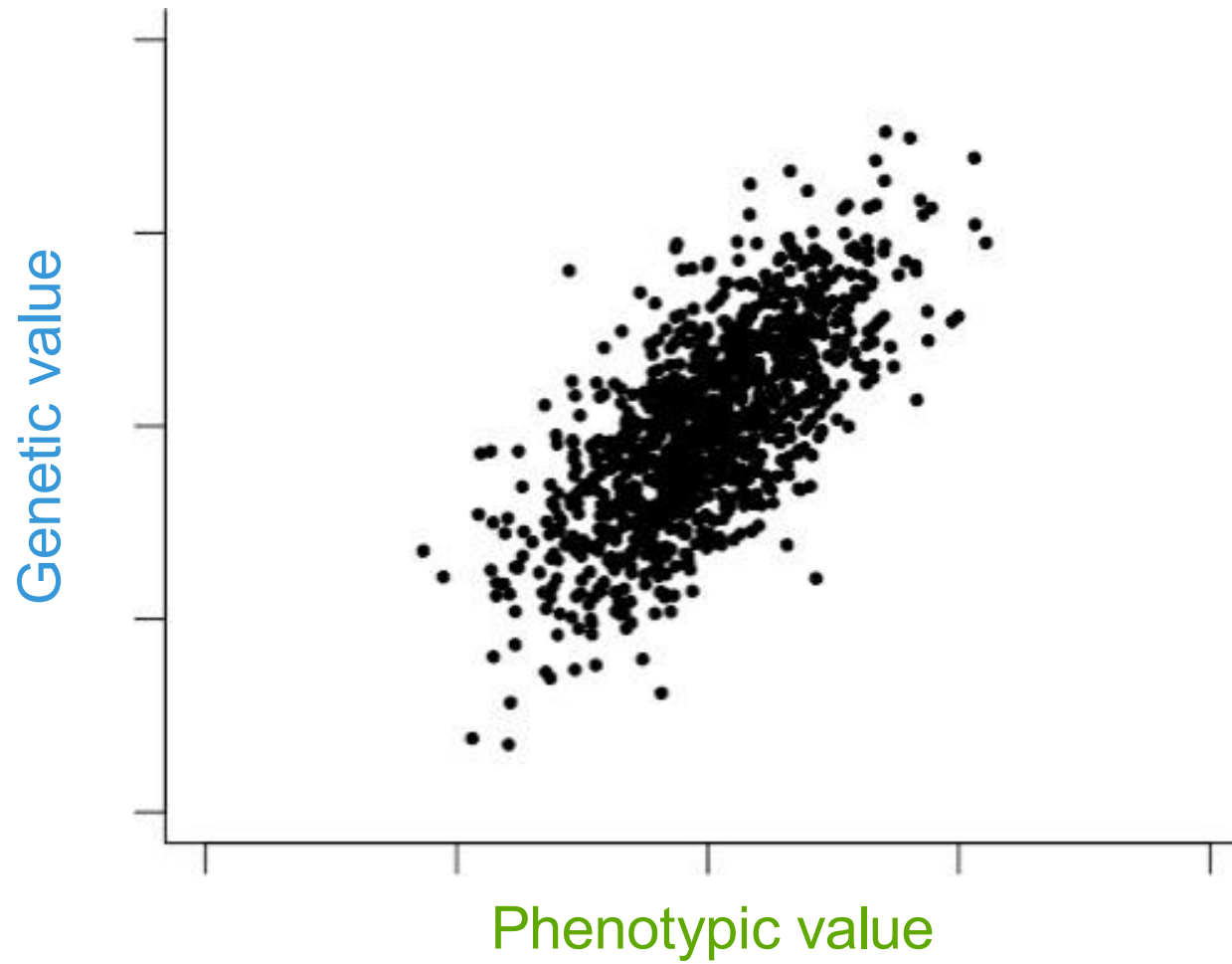
Robin Thompson
Gregor Gorjanc



See chapter 2!

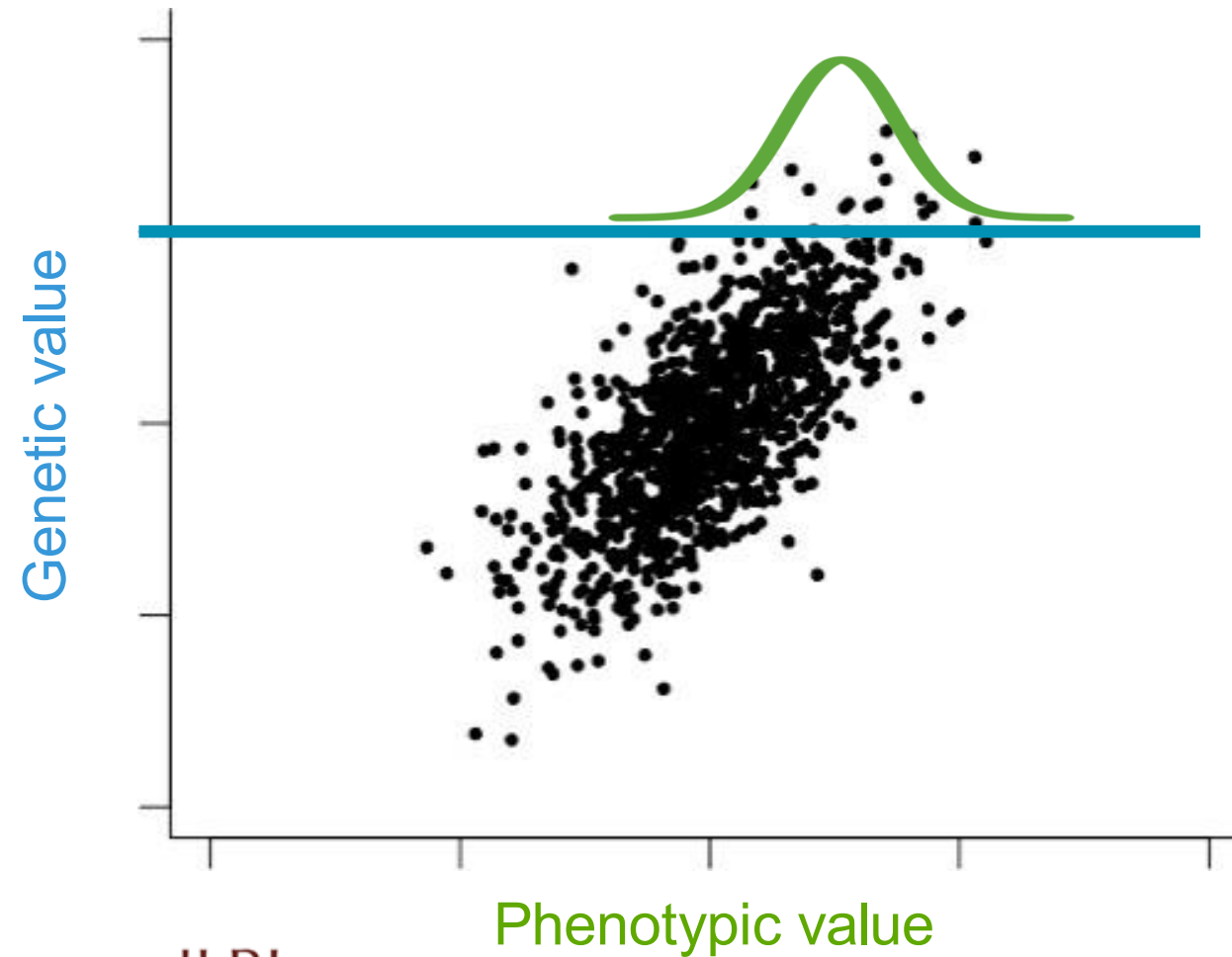


Phenotypic and genetic values





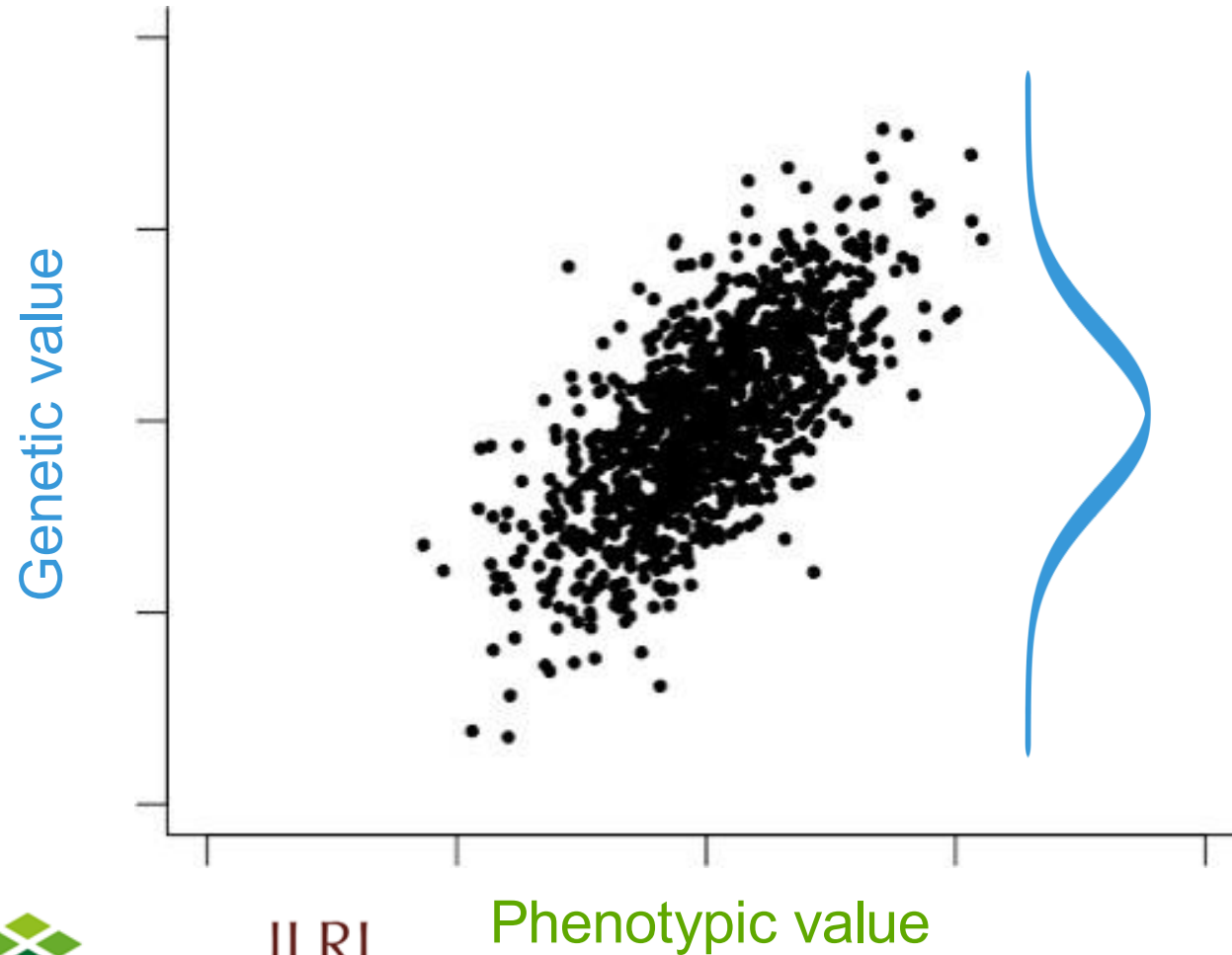
Forward (DATA GENERATION) view





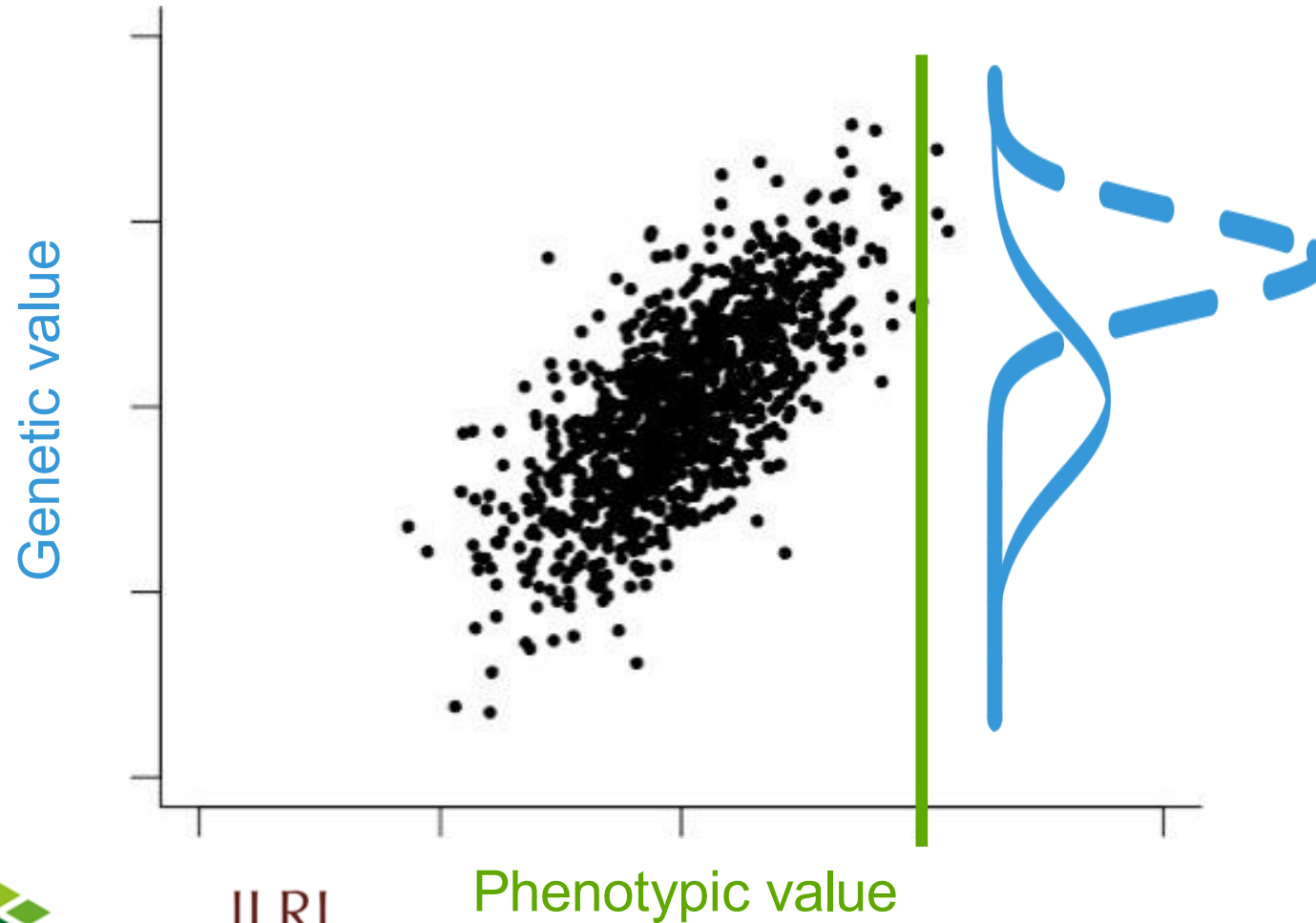
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Backward/inverse (INFERENCE) view – no info





Backward/inverse (INFERENCE) view – pheno info





Forward and backward/inverse views

Forward (DATA GENERATION) view

- parameters \rightarrow data
- the true process (unknown!!!)
- a simulation model (assumptions!!!)
- a data analysis model (assumptions!!!)

Backward/Inverse (INFERENCE) view

- data \rightarrow parameters
- inferring parameters of the data analysis model



Estimand, estimator, estimate!

Estimand

→ The quantity that we want to infer from the data

Estimator

→ The inference procedure based on some assumptions (an assumed model)

Estimate

→ The value obtained from the inference procedure applied to your data





Fisher's 1918 model

Observe: Phenotypic value, y_i

Estimand: Genotypic/Genetic value, g_i (or its components)

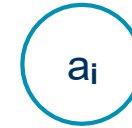
Assume:

- Phenotype = Genotype + Environment
 - $y_i = \mu + g_i + e_i$
- Genotype = Additive + Dominance + Epistasis
 - $g_i = a_i + d_i + x_i$
 - $y_i \approx \mu + a_i + e_i$



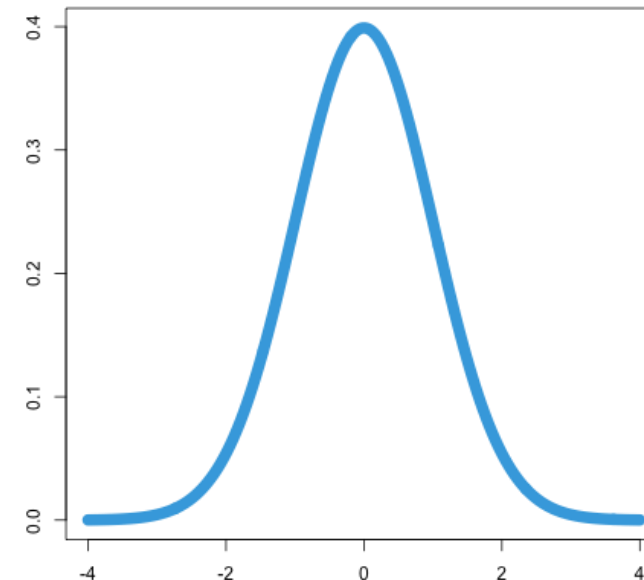
Case with no information

Assume: $a_i \sim N(0, \sigma_a^2)$



Having no information about an individual, what can we say about its breeding value?

Let's follow the above assumptions!



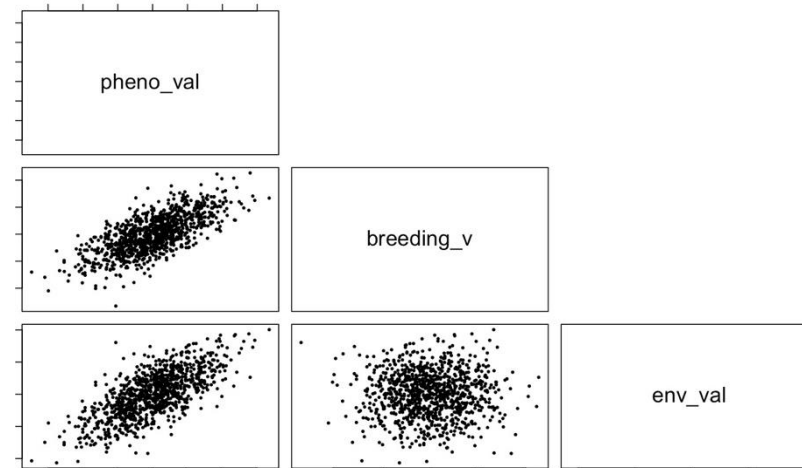
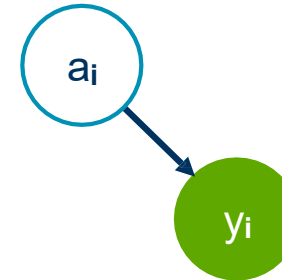


Case with own phenotype

Assume:

$$y_i \approx \mu + a_i + e_i$$

$$\begin{pmatrix} y_i \\ a_i \\ e_i \end{pmatrix} \sim N \left(\begin{pmatrix} \mu \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_y^2 & & \\ \sigma_a^2 & \sigma_a^2 & \\ \sigma_e^2 & 0 & \sigma_e^2 \end{pmatrix} \text{ sym.} \right)$$



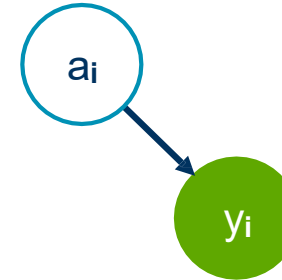


Case with own phenotype

Assume:

$$y_i \approx \mu + a_i + e_i$$

$$\begin{pmatrix} y_i \\ a_i \\ e_i \end{pmatrix} \sim N \left(\begin{pmatrix} \mu \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_y^2 & & \\ \sigma_a^2 & \sigma_a^2 & \\ \sigma_e^2 & 0 & \sigma_e^2 \end{pmatrix} \begin{matrix} sym. \\ \\ \end{matrix} \right)$$



Observing phenotypic value of an individual, what can we say about its breeding value?

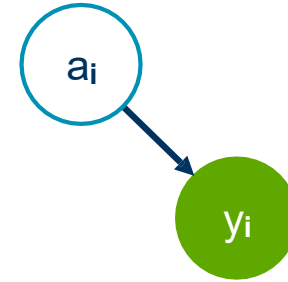
Given the above assumptions and observed phenotype we can calculate conditional distribution $p(a_i|y_i)$



Case with own phenotype

Assume:

$$y_i \approx \mu + a_i + e_i$$



$$\begin{pmatrix} y_i \\ a_i \\ e_i \end{pmatrix} \sim N \left(\begin{pmatrix} \mu \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_y^2 & & \\ \sigma_a^2 & \sigma_a^2 & \\ \sigma_e^2 & 0 & \sigma_e^2 \end{pmatrix} \begin{matrix} \\ \text{sym.} \\ \end{matrix} \right)$$

Estimator (summarising the conditional distribution):

$$E(a_i | y_i) = \hat{a}_i = E(a_i) + \text{Cov}(a_i, y_i) \text{Var}(y_i)^{-1} (y_i - E(y_i))$$

$$\text{Var}(a_i | y_i) = \text{Var}(a_i) - \text{Cov}(a_i, y_i) \text{Var}(y_i)^{-1} \text{Cov}(y_i, a_i)$$

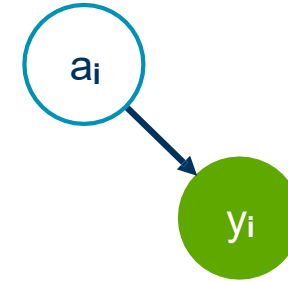
$$\text{Cor}(a_i, y_i)^2 = 1 - \text{Var}(a_i | y_i) / \text{Var}(a_i)$$



Case with own phenotype

Assume:

$$y_i \approx \mu + a_i + e_i$$



$$\begin{pmatrix} y_i \\ a_i \\ e_i \end{pmatrix} \sim N \left(\begin{pmatrix} \mu \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_y^2 & & \\ \sigma_a^2 & \sigma_a^2 & \\ \sigma_e^2 & 0 & \sigma_e^2 \end{pmatrix} \begin{matrix} sym. \\ \\ \end{matrix} \right)$$

Estimator (summarising the conditional distribution):

$$E(a_i | y_i) = \sigma_a^2 \sigma_y^{-2} (y_i - \mu) = h^2 (y_i - \mu)$$

$$Var(a_i | y_i) = \sigma_a^2 - \sigma_a^2 \sigma_y^{-2} \sigma_a^2 = \sigma_a^2 (1 - h^2)$$

$$Cor(a_i, y_i) = h \qquad Cor(a_i, y_i)^2 = h^2$$



Case with own phenotype - example

Observe: CR's height is 170 cm

Assume (from literature):

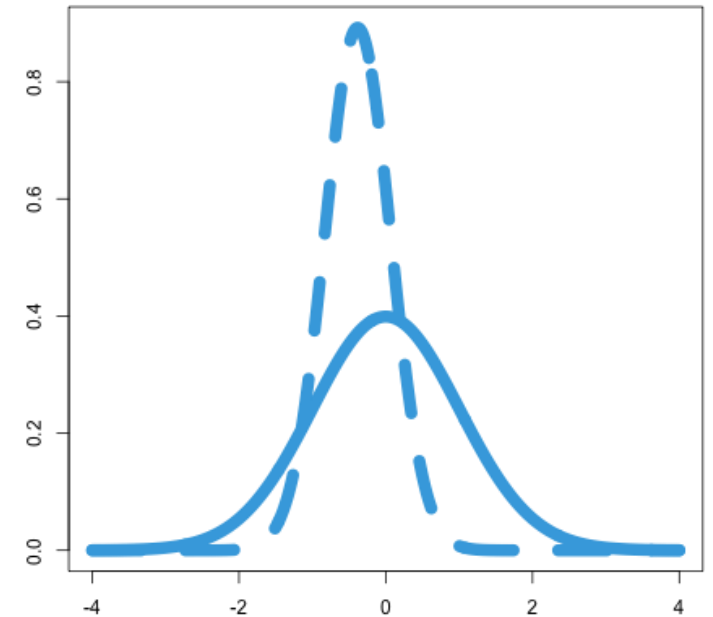
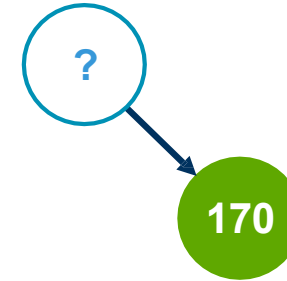
- mean height in females is ~165 cm
- heritability for height is ~0.8
- phenotypic standard deviation is ~7 cm
- genetic variance is $7^2 \times 0.8 = 39 \text{ cm}^2 = 6.2^2 \text{ cm}^2$

Estimator & Estimate:

$$E(a_i | y_i = 170) = 0.8(170 - 165) = 5 \text{ cm}$$

$$\text{Var}(a_i | y_i) = 7^2 \times 0.8(1 - 0.8) = 7.84 \text{ cm}^2 = 2.8^2 \text{ cm}^2$$

$$\text{Cor}(a_i, y_i) = \sim 0.9, \text{Cor}(a_i, y_i)^2 = 0.8$$





Case with own phenotype - example

Observe: Your height is ??? cm

Assume (from literature):

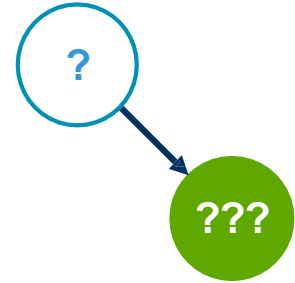
- mean height in females is ~165 cm / in males is ~175 cm
- heritability for height is ~0.8
- phenotypic standard deviation is ~7 cm
- genetic variance is $7^2 \times 0.8 = 39 \text{ cm}^2 = 6.2^2 \text{ cm}^2$

Estimator & Estimate:

$$E(a_i | y_i = ???) = 0.8(??? - ???) = ??? \text{ cm}$$

$$\text{Var}(a_i | y_i) = 7^2 0.8(1 - 0.8) = 7.84 \text{ cm}^2 = 2.8^2 \text{ cm}^2$$

$$\text{Cor}(a_i, y_i) = \sim 0.9, \text{Cor}(a_i, y_i)^2 = 0.8$$

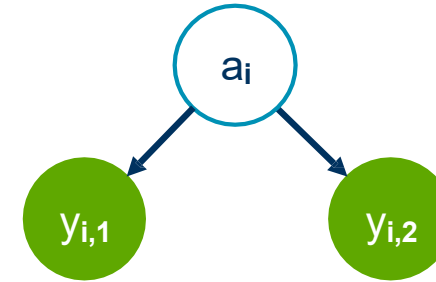




Case with repeated own phenotypes

Assume:

$$y_{i,j} \approx \mu + a_i + p_i + e_{i,j}$$



Estimator:

$$E(a_i | y_i) = \hat{a}_i = k(\bar{y}_i - \mu)$$

$$\text{Cov}(a_i, \bar{y}_i)^2 = k$$

$$k = \frac{nh^2}{1 + (n-1)(h^2 + p^2)}$$

$$p^2 = \sigma_p^2 \sigma_y^{-2}$$



Case with repeated own phenotypes

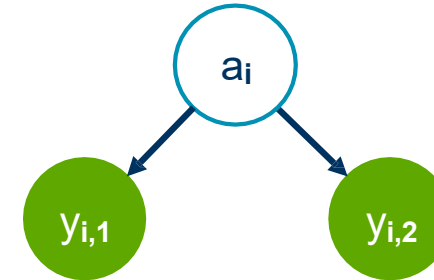


Table 1.1. Percentage increase in accuracy of prediction with repeated records compared with single records at a heritability of 0.35.

<i>t</i> values	Number of records				
	2	4	6	8	10
0.2	29	58	73	83	89
0.5	15	26	31	33	35
0.8	5	8	10	10	10

$$t = h^2 + p^2$$

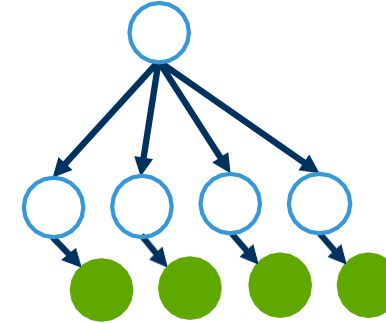
See chapter 2 in
Mrode et al. (2023)



Case with progeny phenotypes

Assume:

$$y_{i,j} \approx \mu + \frac{1}{2}a_i + e_{i,j}$$



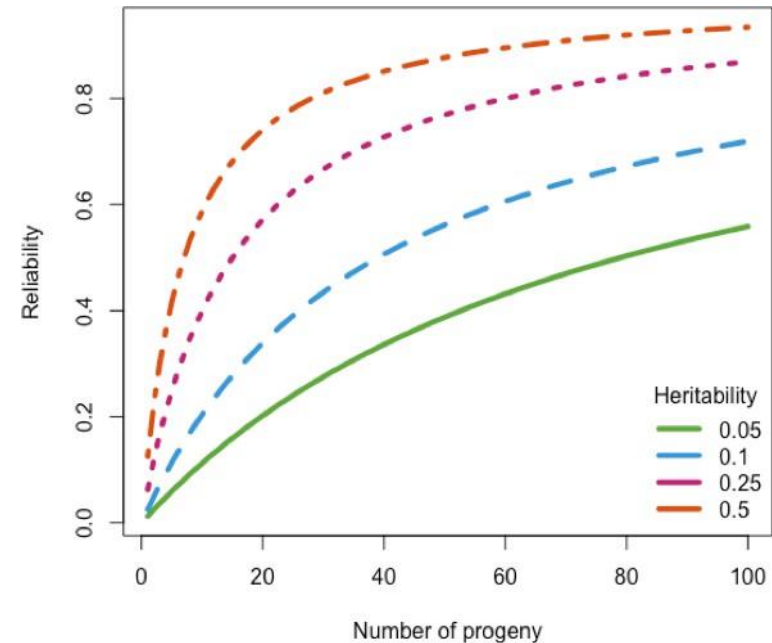
Estimator:

$$E(a_i | y_i) = \hat{a}_i = 2k(\bar{y}_i - \mu)$$

$$\text{Cov}(a_i, \bar{y}_i)^2 = k$$

$$k = \frac{n}{n + (4 - h^2)/h^2}$$

See chapter 2 in
Mrode et al. (2023)





Case with progeny prediction (a pedigree detour)

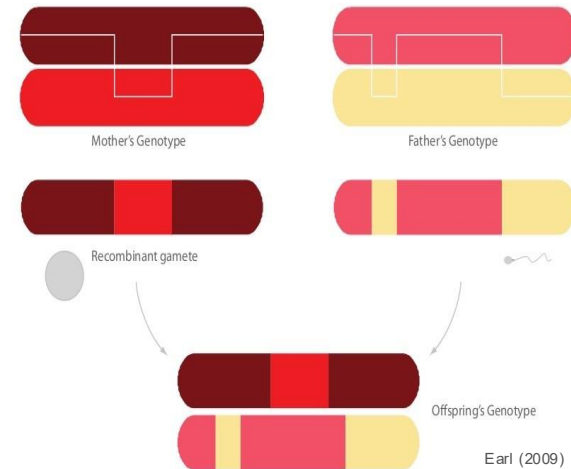
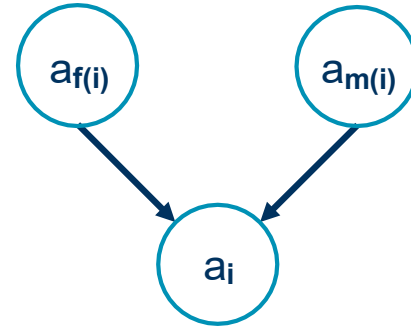
Assume:

$$a_i = a_{i,1} + a_{i,2}$$

Variance between breeding values?

Key rules:

- $\text{Var}(x \pm y) = \text{Var}(x) + \text{Var}(y) \pm 2\text{Cov}(x, y)$
- $\text{Var}(ax) = a^2 \text{Var}(x)$





Case with progeny prediction (a pedigree detour)

Assume:

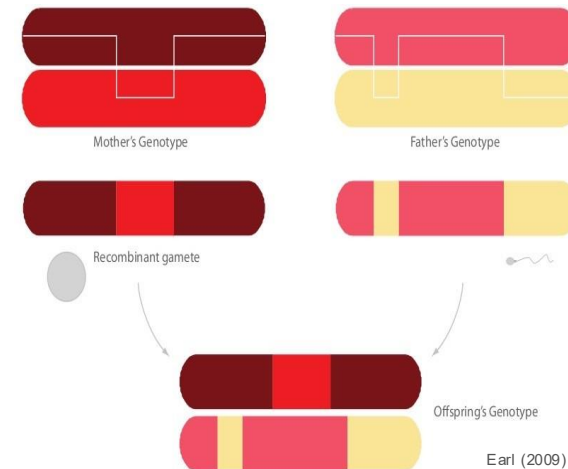
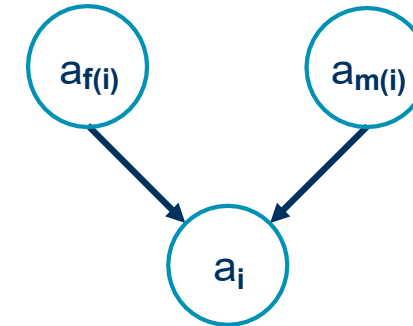
$$a_i = a_{i,1} + a_{i,2}$$

$$\begin{aligned} \text{Var}(a_i) &= \text{Var}(a_{i,1} + a_{i,2}) = \frac{1}{2}\sigma_a^2 + \frac{1}{2}\sigma_a^2 + F_i\sigma_a^2 \\ &= (1 + F_i)\sigma_a^2 \end{aligned}$$

$$a_i \sim N(0, (1 + F_i)\sigma_a^2)$$

Some cases:

- Non-inbred individuals $a_i \sim N(0, \sigma_a^2)$
- Fully-inbred individuals $a_i \sim N(0, 2\sigma_a^2)$





Case with progeny prediction (a pedigree detour)

Assume:

$$a_i = a_{i,1} + a_{i,2}$$

$$\begin{aligned} \text{Var}(a_i) &= \text{Var}(a_{i,1} + a_{i,2}) = \frac{1}{2}\sigma_a^2 + \frac{1}{2}\sigma_a^2 + F_i\sigma_a^2 \\ &= (1 + F_i)\sigma_a^2 \end{aligned}$$

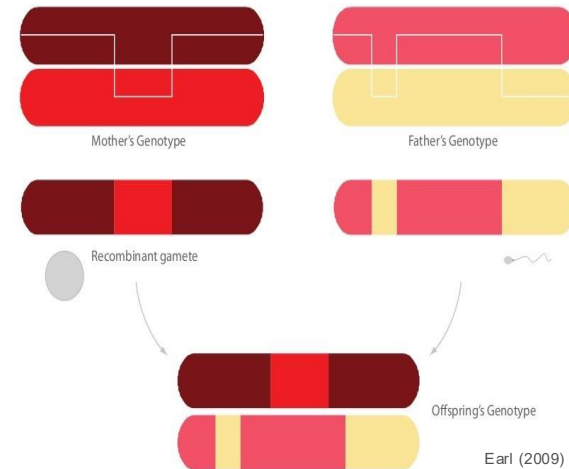
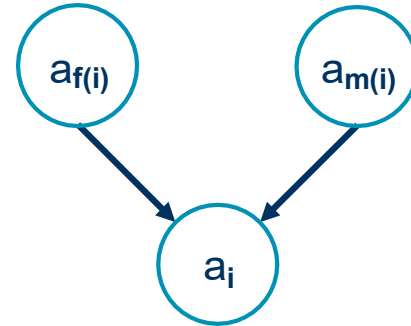
$$a_i \sim N(0, (1 + F_i)\sigma_a^2)$$

$$a_{i,1} = \frac{1}{2}a_{f(i),1} + \frac{1}{2}a_{f(i),2} + r_{i,1}$$

$$a_{i,2} = \frac{1}{2}a_{m(i),1} + \frac{1}{2}a_{m(i),2} + r_{i,2}$$

$$a_i = \frac{1}{2}a_{f(i)} + \frac{1}{2}a_{m(i)} + r_i$$

$$a_i | a_{f(i)}, a_{m(i)} \sim N\left(\frac{1}{2}a_{f(i)} + \frac{1}{2}a_{m(i)}, k\sigma_a^2\right)$$





Case with progeny prediction (a pedigree detour)

Assume:

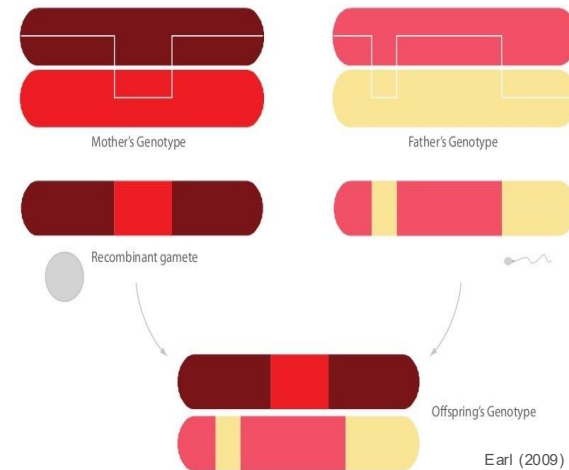
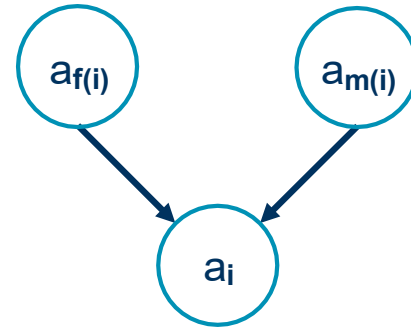
$$a_i = \frac{1}{2} a_{f(i)} + \frac{1}{2} a_{m(i)} + r_i$$

$$a_i | a_{f(i)}, a_{m(i)} \sim N\left(\frac{1}{2} a_{f(i)} + \frac{1}{2} a_{m(i)}, k\sigma_a^2\right)$$

- Parent average (expectation)
- Mendelian sampling (deviation from the expectation due to recombination, segregation, and an odd mutation)

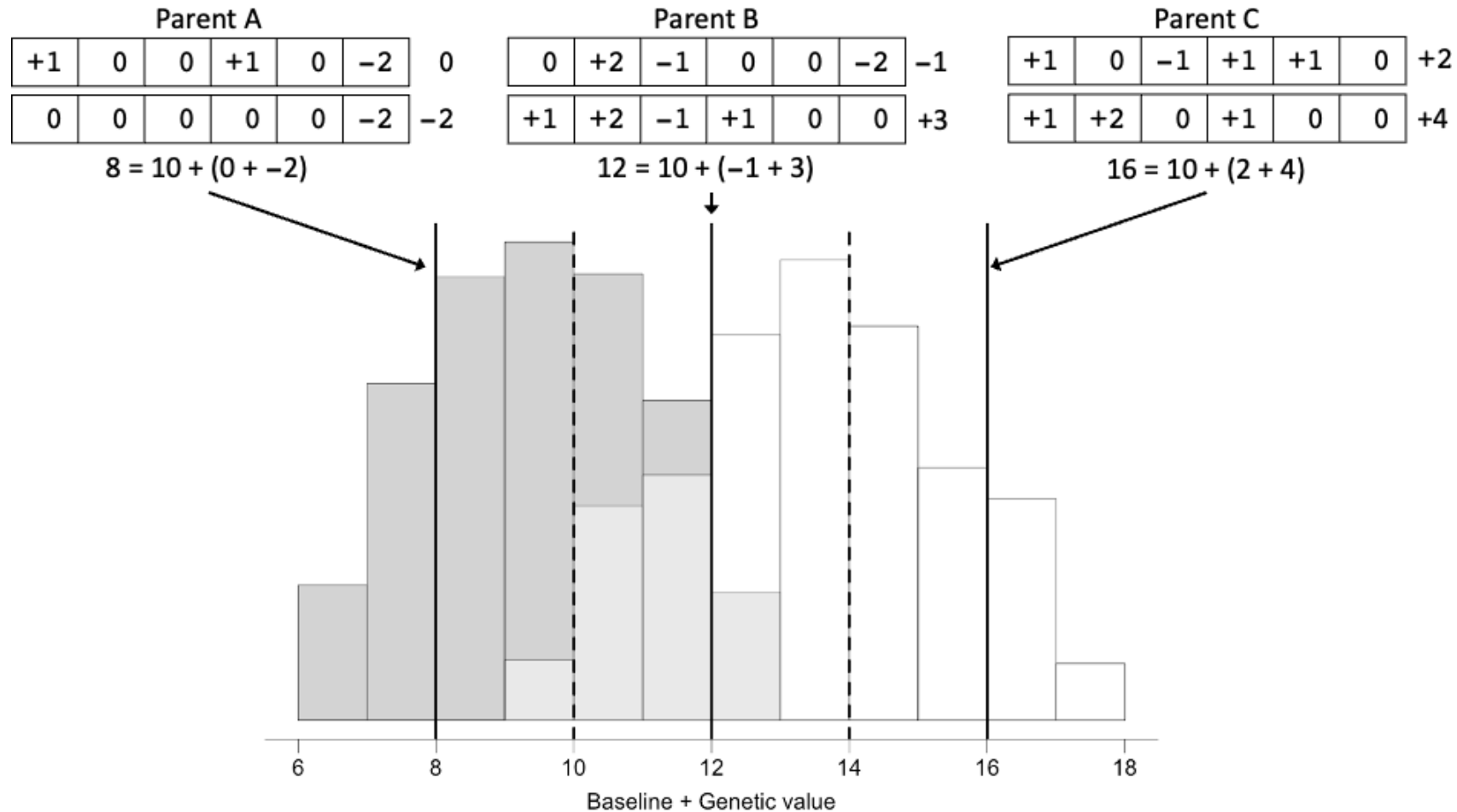
$$\frac{1}{2} a_{f(i)} + \frac{1}{2} a_{m(i)}$$

r_i





Between and within family genetic variation





Case with progeny prediction (a pedigree detour)

Assume:

$$a_i = \frac{1}{2}a_{f(i)} + \frac{1}{2}a_{m(i)} + r_i$$

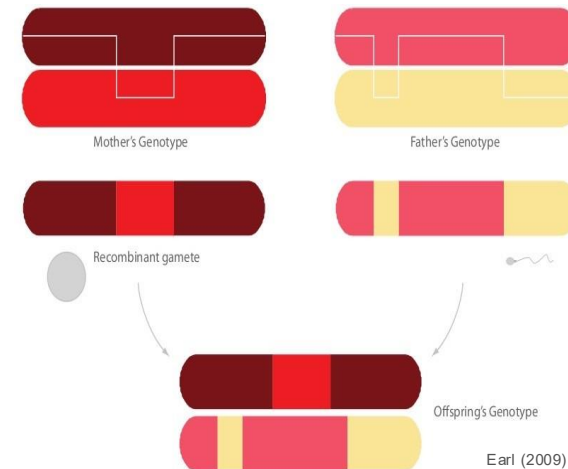
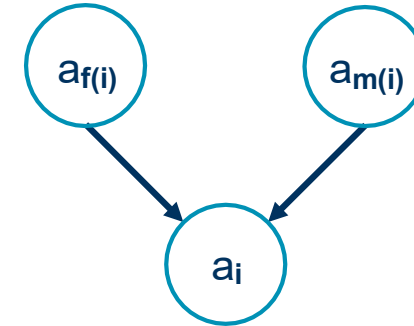
$$a_i | a_{f(i)}, a_{m(i)} \sim N\left(\frac{1}{2}a_{f(i)} + \frac{1}{2}a_{m(i)}, k\sigma_a^2\right)$$

$$r_i \sim N(0, k\sigma_a^2)$$

$$k = \frac{1}{2} - \frac{1}{4}(F_{f(i)} + F_{m(i)})$$

Some cases:

- Non-inbred parents $k = \frac{1}{2}$
- Fully-inbred parents $k = 0$





Case with progeny prediction

Assume:

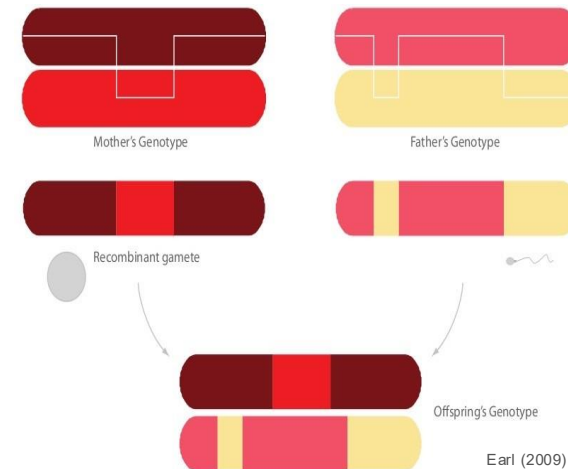
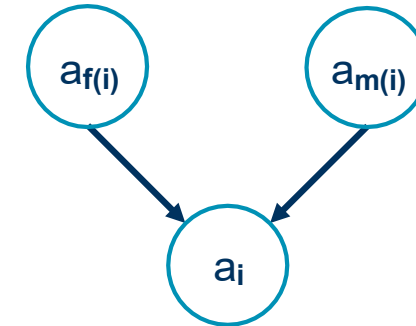
$$a_i = \frac{1}{2}a_{f(i)} + \frac{1}{2}a_{m(i)} + r_i$$

$$a_i | a_{f(i)}, a_{m(i)} \sim N\left(\frac{1}{2}a_{f(i)} + \frac{1}{2}a_{m(i)}, k\sigma_a^2\right)$$

Estimator/predictor:

$$E(a_i | \hat{a}_{f(i)}, \hat{a}_{m(i)}) = \hat{a}_i = \frac{1}{2}\hat{a}_{f(i)} + \frac{1}{2}\hat{a}_{m(i)}$$

$$\text{Cov}\left(a_i, \frac{1}{2}\hat{a}_{f(i)} + \frac{1}{2}\hat{a}_{m(i)}\right)^2 = \frac{1}{4}(R_{f(i)}^2 + R_{m(i)}^2)$$



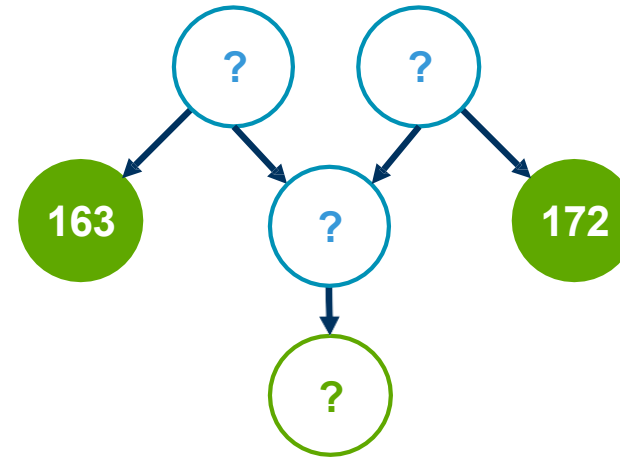


Case with progeny prediction - example

Assume:

- average height
 - males ~175 cm
 - females ~165 cm
- heritability ~0.8

Calculate



$$E(a_{f(i)} | y_{f(i)} = 172) = 0.8(172 - 175) = -2.4cm \quad R^2 = 0.80$$

$$E(a_{m(i)} | y_{m(i)} = 163) = 0.8(163 - 165) = -1.6cm \quad R^2 = 0.80$$

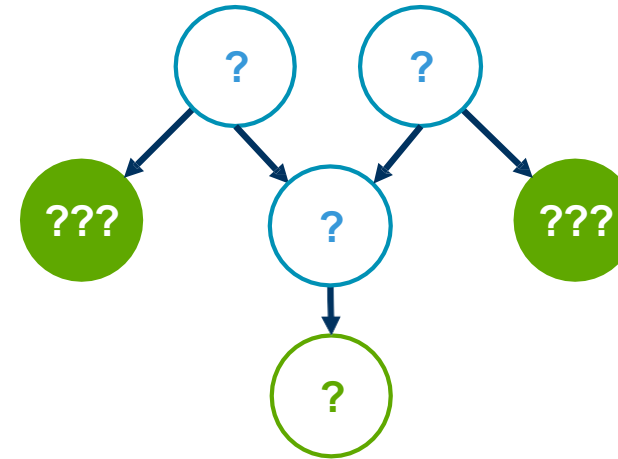
$$E(a_i | \hat{a}_{f(i)}, \hat{a}_{m(i)}) = \frac{1}{2}(-2.4 - 1.6) = -2cm \quad R^2 = 0.40$$

$$E(y_i | \hat{a}_i) = 165 - 2mc163 = \quad R^2 = 0.32$$



Case with progeny prediction - example

- Assume:
 - average height
 - males ~175 cm
 - females ~165 cm
 - heritability ~0.8
- Calculate



$$E(a_{f(i)} | y_{f(i)} = \quad) =$$

$$R^2 = 0.80$$

$$E(a_{m(i)} | y_{m(i)} = \quad) =$$

$$R^2 = 0.80$$

$$E(a_i | \hat{a}_{f(i)}, \hat{a}_{m(i)}) =$$

$$R^2 = 0.40$$

$$E(y_i | \hat{a}_i) =$$

$$R^2 = 0.32$$



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Careful with selection based on progeny predictions

Low reliability (halves with every generation)

→ very quickly ~random selection

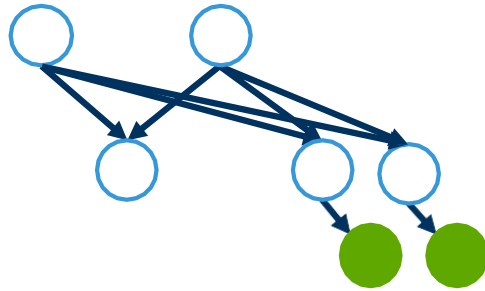
Parent average captures only between-family genetic variance
(=half of genetic variance)

→ selection on it erodes diversity quickly

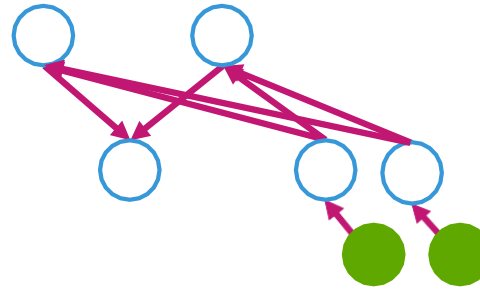


Case with sib phenotypes

Gene flow



Information flow



Sib test = Progeny test of parents &
Progeny prediction

Without genomic data sibs don't give direct information
about other sibs



Learning objectives

Understand forward and backward/inverse views of working with models

Familiarise yourself with simple cases of inferring breeding values from the data

Practice inference of breeding values for simple cases