

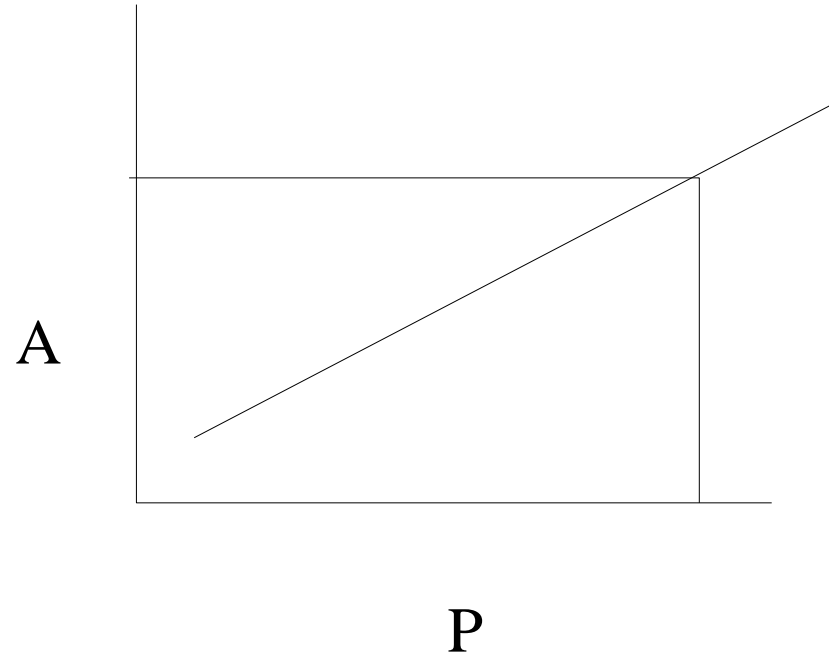
How to combine information from relatives?

Animal	X1	X2	EBV
	own perform.	sire's perform.	Index
1	3.6	9.2	?
2	-8.3	3.2	?
3	3.5	-15.4	?
4	16.7	7.1	?
5	-14.4	-4.9	?
6	6.6	16.1	?
7	-1.4	-12.2	?
8	-6.2	8.7	?
9	6.2	7.4	?
10	15.0	-4.0	?

Who should we select, animal 10 or animal 6?

Principle of EBV estimation

- Regression of breeding value on phenotype



How much do we expect the BV to be better if we know that P is one unit better

$$\text{Slope} = \text{cov}(A,P)/\text{var}(P)$$

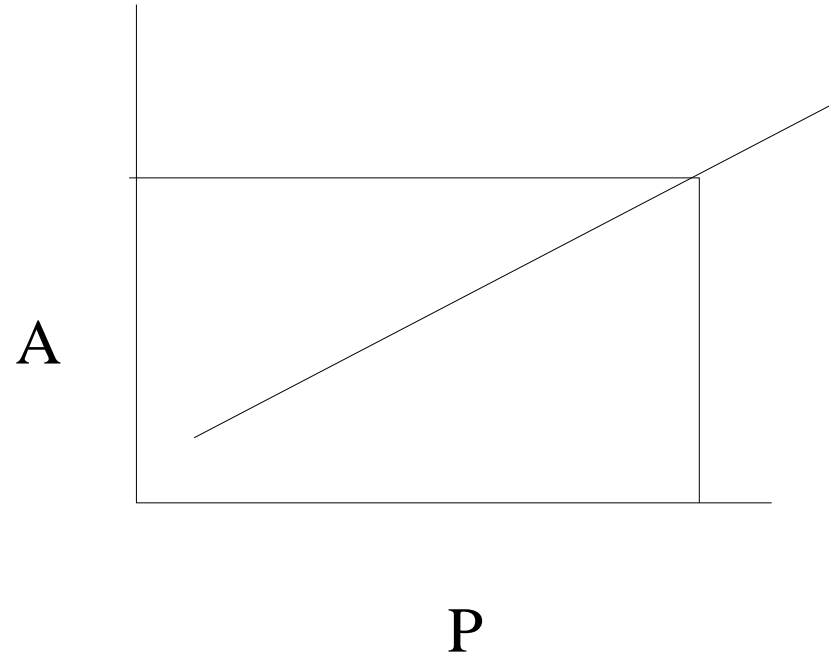
EBV estimation: regression

- If $P = \text{Own Performance}$

$$\text{Slope} = \text{cov}(A, P) / \text{var}(P)$$

$$= V_A / V_P$$

$$= h^2$$



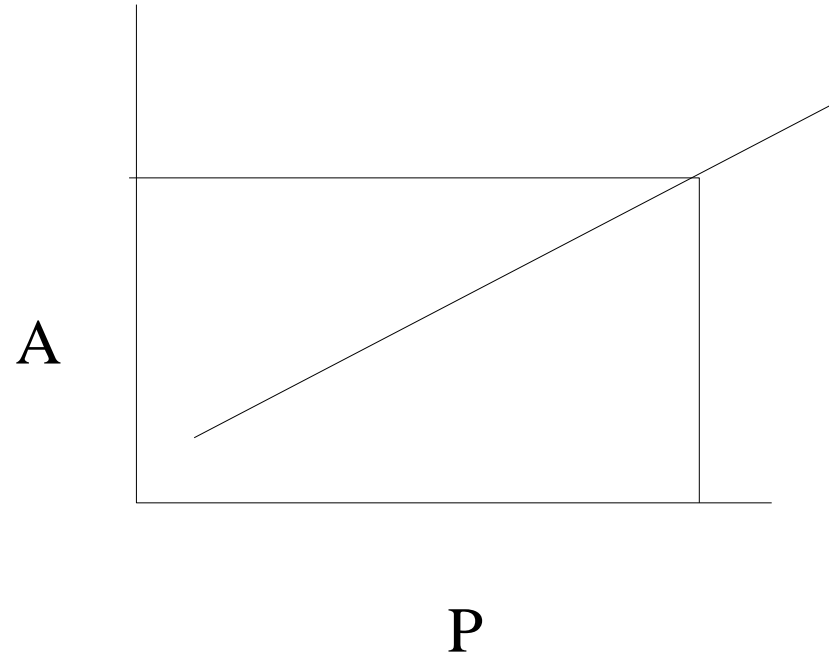
EBV estimation: regression

- If P = Performance of Sire

$$\text{Slope} = \text{cov}(A, P_{\text{sire}}) / \text{var}(P_{\text{sire}})$$

$$= 1/2 V_A / V_P$$

$$= 1/2 h^2$$



Now we need some basic Quantitative Genetic theory

$$P = A + E$$

→ General Model

$$\text{Var}(P) = \text{var}(A) + \text{var}(E) = V_A + V_E$$

no cov. between A and E

$$\text{cov}(A_i, P_i) = \text{cov}(A_i, A_i) + \text{cov}(A_i, E_i) = V_A$$

if A same animal as P

$$\text{cov}(A_i, P_j) = \text{cov}(A_j, A_i) + \text{cov}(A_j, E_i) = a_{ij} V_A$$

a_{ij} = additive genetic
relationship between i and j

$$\text{cov}(P_i, P_j) = a_{ij} V_A$$

as E's are uncorrelated if not same animal

Finding the optimal index weights $EBV = b \cdot P$

Regression of A on P_i

$$\text{Regression coefficient} = \frac{\text{cov}(P_i, A)}{\text{var}(P_i)}$$

Examples:

if P = Own Performance

$$b = \frac{V_A}{V_A + V_E} = h^2$$

if P = Sire Performance

$$b = \frac{\frac{1}{2} V_A}{V_A + V_E} = \frac{1}{2} h^2$$

What does this all mean?

Regression of x on y :

- If we know x, what does that tell us about y?

if we know an animal performed well, what does that tell us about his breeding value?

A: Depends on heritability

$$b = h^2$$

if we know an animal's sire performed well, what does that tell us about his breeding value?

A: It carries only half of Sire's genes + it depends on heritability

$$b = \frac{1}{2} h^2$$

if we know an animal's great granddam performed well, what does that tell us about his breeding value?

A: It carries even less of great grandma's genes

$$b = \frac{1}{8} h^2$$

Some more basic Quantitative Genetics theory

$$\text{var}(\text{mean}) = \text{common variance} + \text{specific}/n$$

equal to all *Specific bit is averaged out*

e.g.: Performance of one progeny:

$$P = \frac{1}{2} A_{\text{sire}} + \frac{1}{2} A_{\text{dam}} + \text{Mendelian Sampling term} + \text{Residual}$$

breeding value

e.g.: Mean performance of n progeny (= HS mean):

$$P_{HS} = \frac{1}{2} A_{\text{sire}} + \{ \frac{1}{2} A_{\text{dam}} + \text{Mendelian Sampling term} + \text{Residual} \} / n$$

$$\text{Var}(P_{HS}) = \frac{1}{4} V_A + (\frac{3}{4} V_A + V_E) / n$$

Weight for Mean of n Half Sibs	$\frac{\frac{1}{4} V_A}{\frac{1}{4} V_A + (\frac{3}{4} V_A + V_E) / n}$	$\frac{\text{Cov}}{\text{Var}}$
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Progeny Testing

$$\hat{A}_{\text{sire}} = b_{\text{PM}} \quad \text{PM} = \text{Mean of } n \text{ progeny}$$

b = Index Weight

= "heritability of progeny test

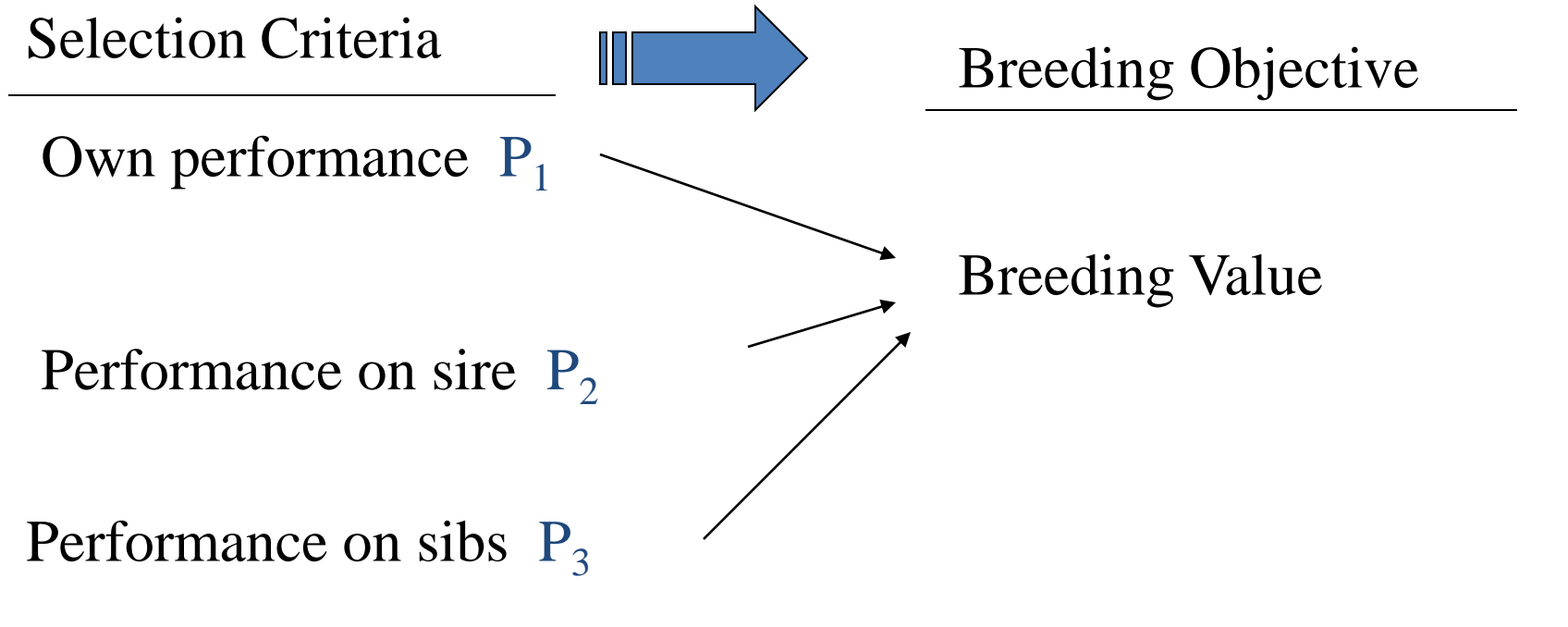
b_1 depends on the number of progeny and on the heritability

$$\begin{aligned} \mathbf{b}_1 &= \frac{\frac{1}{2} \mathbf{V}_A}{\frac{1}{4} \mathbf{V}_A + (\mathbf{V}_P - \frac{1}{4} \mathbf{V}_A) / \mathbf{n}} && \frac{\text{Cov}(A_{\text{sire}}, \text{PM})}{\text{Var}(\text{PM})} \\ &= \frac{2\mathbf{n}}{\mathbf{n} + 4/\mathbf{h}^2 - 1} && = \frac{2\mathbf{n}}{\mathbf{n} + \frac{4 - \mathbf{h}^2}{\mathbf{h}^2}} = \frac{2\mathbf{n}}{\mathbf{n} + \alpha} \end{aligned}$$

You can work these through with examples (in Excel), see below

						Index Weight b
Vp	100	nr of FS	4	cov	12.5	0.308
h2	0.25					
c2	1.5			var	40.625	
VA	25	nr of HS	20	cov	6.25	0.629
VE-common	15					
VE-specific	40			var	9.9375	
		nr of Prog	20	cov	12.5	1.258
				var	9.9375	

Combining different sources of information



Selection Index (multiple regression)

$$EBV = \text{Index} = b_1P_1 + b_2P_2 + b_3P_3 + \dots + b_nP_n$$

Selection index with more information sources (multiple regression: $\text{Index} = b_1 X_1 + b_2 X_2$)

Need to account for covariance between various sources of information

X = vector with information sources

(phenotypic deviation, or P_i = Sel. Criteria, we call these now $X = [X_1 \ X_2]$)

A = True breeding Value

$$\text{var}(X) = P \text{ - matrix} = P = \begin{bmatrix} \text{var}(X_1) & \text{cov}(X_1, X_2) \\ \text{cov}(X_2, X_1) & \text{var}(X_2) \end{bmatrix}$$


$$\text{cov}(X, A) = G \text{ - vector} = G = \begin{bmatrix} \text{cov}(X_1, A) \\ \text{cov}(X_2, A) \end{bmatrix}$$

$$\text{Index weights} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} = P^{-1}G \quad \text{is like "cov}(X,A)/\text{var}_X"$$

How do we use such weights?

Animal	X1	X2	EBV Index
	own perform.	sire's perform.	
1	3.6	9.2	2.00
2	-8.3	3.2	-2.01
3	3.5	-15.4	-0.67
4	16.7	7.1	5.50
5	-14.4	-4.9	-4.63
6	6.6	16.1	3.60
7	-1.4	-12.2	-1.72
8	-6.2	8.7	-0.82
9	6.2	7.4	2.54
10	15.0	-4.0	3.83

98	17
	104

Var-covar of actual x1 and x2

This is like the P-matrix but based on realized values

Another example of weights

h^2	Own Performance b_1	Mean of 3 FS b_2	Own Performance b_1	Mean of 3 FS b_2
0.10	0.09	0.12	0.08	0.32
0.30	0.26	0.26	0.22	0.49
0.50	0.43	0.29	0.38	0.48
0.70	0.62	0.24	0.57	0.36

- **Own performance more important with high heritability
.....and smaller amount of family info**
- **Otherwise, family information more important**

Can use STSELIND

Single Trait selection index calculation

Parameters				
	Heritability	0.1		
	Repeatability of subsequent records	0		
	c-squared (among full sibs)	0.15		
			0.732	Accuracy
Information used	Nr.Records	Index weight	value of	percent decrease of accuracy by o
nr of own records	1	0.000	0.000	
nr. of records on dam	1	0.000	0.000	
nr of records on sire	1	0.000	0.000	
nr of fulls sib records	0	0.000	0.000	
nr. of half sib records (excl. full sibs)	20	0.000	0.000	
nr. of progeny	45	1.071	1.000	

Run

Accuracy of selection index

r_{IA} = correlation between Index (=EBV) and A

$$= \frac{\text{cov}(I,A)}{\sigma_I \sigma_A} = \frac{\sigma_I^2}{\sigma_I \sigma_A} = \frac{\sigma_I}{\sigma_A} = \sqrt{(b'Pb/V_A)}$$

$$\text{cov}(I,A) = \text{cov}(bX,A) = b'\text{cov}(X,A)$$

$$= b'G = b'Pb = b'\text{var}(X) = \text{var}(bX) = \text{var}(I)$$

$$b = P^{-1}G$$

$$\text{or: } Pb = G$$

remember from Lecture 2:

Note: $I = \text{EBV}$

$$A = \text{BV}$$

→ $r_{IA} = \text{sqrt}(\text{var}(\text{EBV}) / V_A) = \text{accuracy}$

This is reference only, not to memorize

Summary of this lecture

- Selection Index Theory can be used to work out weights and accuracy for a given set of information about an particular EBV
- Quantitative Genetic Theory and matrices (P, G) are used to work out such index weights (b) and accuracies
- In Genetic Evaluation we use BLUP where this all occurs 'automatically'
- Selection Index Theory still useful to predict what happens
 - Accuracy for a given amount of information
 - Accuracy if using genetic marker information
 - Importance of own vs family information for given situations