Exercises Day 1
Part 1: EBV accuracy

Exercise 1.1 Effect of using relatives' information on selection accuracy

For single trait prediction of breeding value, write out the P-Matrix and the G-vector for the following cases:

1. One own performance record
2. Information known on own performance and performance of sire (1 record each)
3. Information known on own performance and an EBV of the sire (accuracy = 0.9)
4. Information known on own performance and an EBV of the sire (acc = 0.9) and dam (acc =0.5)
5. Information on own performance, EBV of the sire (acc = 0.9) and the mean of 25 half sibs
6. Information on own performance, mean of 25 half sibs and mean of 50 progeny

Use the symbols V_A for additive genetic variance and V_P for phenotypic variance.
Note that for a single trait prediction you can also substitute these by $V_P = 1$ and $V_A = h^2$

Answers:

1) One own performance record

P-matrix: $\mathrm{var}(X_1) = \sigma^2_P$ is the phenotypic variance

G-vector: $\mathrm{Cov}(X_1, A) = \mathrm{Cov}(A+E, A) = \mathrm{Cov}(A, A) + \mathrm{cov}(E,A) = \sigma^2_A + 0 = \sigma^2_A$

$b = P^{-1}G = (\sigma^2_P)^{-1}\sigma^2_A = h^2$

$\mathrm{accurcay}^2 = \mathrm{Var}(EBV)/\mathrm{Var}(BV) = b'Pb/\sigma^2_A = b'G/\sigma^2_A = h^2 . \sigma^2_{A}/\sigma^2_A = h^2$. Hence, accuracy = equal to h.

Vp	P=matrix		G-vector			index weight		accuracy of EBV	
1	variance of what you measure		Covariance between			is a regression cefficient			
h2			...what you measure						
0.25			....and the breeding value						
				=MMULT(MMULT(TRANSPOSE(H11),B11),H11)					
1	x1=own performance								
	P		G			b	PinvG	accc	
	1		0.25			0.25		sqrt(b'Pb/VA)	
								b'Pb	0.0625
	Pinverse							VA	0.25
	1							acc	0.5

2) **Information known on own performance and performance of sire (1 record each)**

Information sources: X_1 = own performance
   X_2 = performance of sire

- variance and covariance of information sources:

$$\operatorname{var}\begin{pmatrix} X_1 \\ X_2 \end{pmatrix} = P = \begin{pmatrix} \operatorname{var}(X_1) & \operatorname{cov}(X_1, X_2) \\ \operatorname{cov}(X_2, X_1) & \operatorname{var}(X_2) \end{pmatrix}$$

$\operatorname{var}(X_1) = \sigma^2_P$ is the phenotypic variance
$\operatorname{var}(X_2) = \sigma^2_P$ is the phenotypic variance
$\operatorname{Cov}(X_1, X_2)$ $= \operatorname{Cov}(A+E, A_s + E_s)$
   $= \operatorname{Cov}(A, A_s) + \operatorname{cov}(A, E_s) + \operatorname{cov}(E, A_s) + \operatorname{cov}(E, E_s)$
   $= \tfrac{1}{2}\sigma^2_A + 0 + 0 + 0.$

- covariance between information sources and the animal's breeding value

$$\operatorname{cov}\left(\begin{pmatrix} X_1 \\ X_2 \end{pmatrix}, A\right) = G = \begin{pmatrix} \operatorname{cov}(X_1, A) \\ \operatorname{cov}(X_2, A) \end{pmatrix}$$

$\operatorname{Cov}(X_1, A)$ $= \sigma^2_A$
$\operatorname{Cov}(X_2, A)$ $= \operatorname{Cov}(A_s + E_s, A) = \operatorname{Cov}(A_s, A) + \operatorname{cov}(E_s, A) = \tfrac{1}{2}\sigma^2_A + 0 .$

such that index weights obtained by regression = covariance/variance:

$$\begin{pmatrix} b_1 \\ b_2 \end{pmatrix} = P^{-1}G = \begin{pmatrix} \sigma^2_P & \tfrac{1}{2}\sigma^2_A \\ \tfrac{1}{2}\sigma^2_A & \sigma^2_P \end{pmatrix}^{-1} \begin{pmatrix} \sigma^2_A \\ \tfrac{1}{2}\sigma^2_A \end{pmatrix} = \begin{pmatrix} 1 & \tfrac{1}{2}h^2 \\ \tfrac{1}{2}h^2 & 1 \end{pmatrix}^{-1} \begin{pmatrix} h^2 \\ \tfrac{1}{2}h^2 \end{pmatrix}$$

Vp	P=matrix			G-vector			index weight		accuracy of EBV	
1	variance of what you measure			Covariance between			is a regression cefficient			
h2				...what you measure						
0.25				....and the breeding value						
1	x1=own performance, x2=sire performance									
	P			G			b	PinvG	accc	
	1	0.125		0.25			0.238095		sqrt(b'Pb/VA)	
	0.125	1		0.125			0.095238		b'Pb	0.071429
	Pinverse								VA	0.25
	1.015873	-0.12698							acc	0.534522
	-0.12698	1.015873								

3   Information known on own performance and an EBV of the sire (accuracy = 0.9)

- variance and covariance of information sources:

$$\text{var}\begin{pmatrix} X_1 \\ X_2 \end{pmatrix} = P = \begin{pmatrix} \text{var}(X_1) & \text{cov}(X_1, X_2) \\ \text{cov}(X_2, X_1) & \text{var}(X_2) \end{pmatrix}$$

$P(1,1) = \text{var}(X_1) = \sigma^2_P$ is the phenotypic variance
$P(2,2) = \text{var}(X_2) = r^2\sigma^2_A$ where r is accuracy and r^2 is reliability of the sire's EBV
$P(2,1) = P(1,2) = \text{Cov}(X_1,X_2) = \frac{1}{2} r^2 . \sigma^2_A$

- covariance between information sources and the animal's breeding value

$$\text{cov}\begin{pmatrix} X_1 \\ X_2 \end{pmatrix}, A) = G = \begin{pmatrix} \text{cov}(X_1, A) \\ \text{cov}(X_2, A) \end{pmatrix}$$

$G(1,1) = \quad \text{Cov}(X_1, A) \quad = \sigma^2_A$
$G(2,1) = \quad \text{Cov}(X_2, A) \quad = \frac{1}{2} r^2 \sigma^2_A$

Vp	P=matrix		G-vector			index weight		accuracy of EBV	
1	variance of what you measure		Covariance between			is a regression cefficient			
h2			...what you measure						
0.25			....and the breeding value						
1	x1=own performance, x2=sire EBV(acc=			0.9					
	P		G			b	PinvG	accc	
	1	0.10125	0.25			0.210007		sqrt(b'Pb/VA)	
	0.10125	0.2025	0.10125			0.394997		b'Pb	0.092495
	Pinverse							VA	0.25
	1.053325	-0.52666						acc	0.60826
	-0.52666	5.201603							

4) Information known on own performance and an EBV of the sire (acc=0.9) and dam (acc=0.5)

P is a 3 by 3 matrix, G a 3 by 1 vector with elements the same as in the previous (3), and additional elements

$$P(3,3) = \text{var}(X_3) = r^2\sigma^2_A \text{ where r is accuracy and } r^2 \text{ is reliability of the dam's EBV}$$
$$P(1,3) = P(3,1) = \text{Cov}(X_1,X_3) = \tfrac{1}{2} r^2_{dam}. \sigma^2_A$$
$$P(2,3) = P(3,2) = \text{Cov}(X_2,X_3) = 0$$
$$G(3,1) = \text{Cov}(X_3, A) = \tfrac{1}{2} r^2_{dam} \sigma^2_A$$

Vp	P=matrix			G-vector			index weight		accuracy of EBV	
1	variance of what you measure			Covariance between			is a regression cefficient			
h2				...what you measure						
0.25				....and the breeding value						
1	x1=own performance, x2=sire EBV(acc=			0.9		and damEBVacc=	0.5			
	P			G			b	PinvG	accc	
	1	0.10125	0.03125	0.25					sqrt(b'Pb/VA)	
	0.10125	0.2025	0	0.10125						
	0.03125	0	0.0625	0.03125						
	Pinverse						0.196787		b'Pb	0.10241
	1.07095	-0.53548	-0.53548				0.401606		VA	0.25
	-0.53548	5.206009	0.267738				0.401606		acc	0.64003
	-0.53548	0.267738	16.26774							

Note that the EBV of the sire and the dam have the same weights, eventhough the sire is more accurate. The weights are the same because for each EBV, equally much is transferred to the progeny. The sire EBV will still have a lot more influence on the ranking of the progeny, because var(EBV) is higher for the sires than for the dam, Think of an extreme case where the dam accurcay is close to zero. We would still have the same weighting, but since all dams have more or less the same EBV (var(EBV)=0 because acc=0) they would not affect the EBVs of their progny very much.

If there is no own perfrance record (we can mimic this by turning the h2 to zero) then the weights for both parent EBVs will be 0.5. Wih an own performance record on the progeny, some of the parents EBV is also in the own performance record of the animals.so the weight is less than 0.5 to avoid double counting.

5) Information on own performance, EBV of the sire (acc = 0.9) and the mean of 25 half sibs

P is a 3 by 3 matrix, G a 3 by 1 vector with elements the same as in the (3), and additional elements

$P(3,3) = var(X_3) = t_{HS}\sigma^2_P + ((1-t_{HS})/n)\sigma^2_P$ where $t_{HS} = 1/4\ h^2$ is the intra class correlation

$P(1,3) = Cov(X_1,X_3) = t_{HS}$

$P(2,3) = P(3,2) = Cov(X_2,X_3) = ½*r^2*\sigma^2_A$

$G(3,1) = Cov(X_3, A) = t_{HS}$

Vp	P=matrix			G-vector				index weight		accuracy of EBV	
	1	variance of what you measure		Covariance between				is a regression cefficient			
h2				...what you measure							
0.25				....and the breeding value							
1	x1=own performance, x2=sire EBV acc=			0.5		and mean of HS:n=	25				
	P			G				b	PinvG	accc	
	1	0.03125	0.0625	0.25						sqrt(b'Pb/VA)	
	0.03125	0.0625	0.03125	0.03125							
	0.0625	0.03125	0.1	0.0625							
	Pinverse							0.217391		b'Pb	0.086957
	1.043478	-0.23188	-0.57971					0.173913		VA	0.25
	-0.23188	19.01449	-5.7971					0.434783		acc	0.589768
	-0.57971	-5.7971	12.17391								

6) Information on own performance, mean of 25 half sibs and mean of 50 progeny

P is a 3 by 3 matrix, G a 3 by 1 vector with elements the same as in the (3), and additional elements

$var(X_3) = t_{HS}\sigma^2_P + ((1-t_{HS})/n)\sigma^2_P$ where $t_{HS} = 1/4\ h^2$ is the intra class correlation

$Cov(X_1,X_3) = t_{HS}$

$Cov(X_2,X_3) = ½h^2$

And $Cov(X_3, A) = t_{HS}$

P is a 3 by 3 matrix, G a 3 by 1 vector with elements the same as in the (3), and additional elements

$P(3,3) = var(X_3) = t_{HS}\sigma^2_P + ((1-t_{HS})/n)\sigma^2_P$ where $t_{HS} = 1/4\ h^2$ is the intra class correlation

$P(1,3) = Cov(X_1,X_3) = t_{HS}$

$P(2,3) = Cov(X_2,X_3) = ½h^2$

$G(3,1) = Cov(X_3, A) = t_{HS}$

Vp	P=matrix			G-vector				index weight		accuracy of EBV	
	1	variance of what you measure		Covariance between				is a regression cefficient			
h2				...what you measure							
0.25				....and the breeding value							
1	x1=own performance, x2=mean of HS:n=		25			and mean of progeny n=				50	
	P			G				b	PinvG	accc	
	1	0.0625	0.125	0.25						sqrt(b'Pb/VA)	
	0.0625	0.1	0.03125	0.0625							
	0.125	0.03125	0.08125	0.125							
	Pinverse							0.068702		b'Pb	0.198473
	1.24173	-0.20356	-1.83206					0.152672		VA	0.25
	-0.20356	11.39949	-4.07125					1.374046		acc	0.891007
	-1.83206	-4.07125	16.69211								

Exercise 1.2 Correlations between relatives' EBV

Consider the following cases, and for each case, calculate the correlation between EBVs on full sibs and half sibs.
You can use STEBVaccuracy.XLS (using the STSELIND tab) and use the P-matrix and the index weights to work out this problem.
1. Information known on EBV of the sire (acc=0.9) and dam (acc=0.5)
2. One own performance record
3. Information known on own performance and an EBV of the sire (acc=0.9) and dam (acc=0.5)
4. Information on own performance, EBV of the sire (acc=0.9), dam (acc=0.5) and 50 progeny

Answer:

$$Cov(EBV1,EBV2) = cov(bX_1, bX_2) = b'cov(X_1,X_2)b = b'P^*b'$$

and the correlation between these is $b'P^*b'/b'Pb$. The denominator is the variance of the EBV, we assume both sibs have an EBV based on the same information, so $\sigma_{EBV1} = \sigma_{EBV1}$ and $\sigma_{EBV1} . \sigma_{EBV1} = var(EBV) = b'Pb$.

P^* is like the usual P matrix, but rather than variances and covariances of all information sources, it contains all covariances between the information sources of the 2 sibs. Many of these could be in common. For example, for 2 full sibs, the information on the sire, the dam, and the half sib mean will be the same.

1) an index is based on just sire and dam, $P^* = P$ and the correlation between the EBV of 2 FS is 1.

2) If an index is based on an own record, the P=1 whereas $P^* = t_{FS}$, the eight b = h^2 and the accuracy is h (square root of heritability) so the correlation is $h^4.t_{FS}/h^4 = t_{FS}$. You can check this with the STEBVaccuracy.xls (STSELIND tab)

3) For 3 and 4 please check the P^* matrices in STEBVaccuracy.xls (STSELIND tab)

Exercise 1.3 Pseudo BLUP

In real life, parents have not just their own records, but they have an estimated breeding value with certain accuracy, using BLUP. This accuracy is based on ancestor information, their own siblings and perhaps their offspring. Also, BLUP corrects for the records of the mates of sires, when their progeny are evaluated. The amount of ancestral information can be derived from a given population structure.

The STEBVaccuracy.XLS (using the PseudoBLUP tab) program does a full Pseudo-BLUP prediction of EBV accuracy, given genetic parameters, and a certain population structure (Half-sib and full-sib family size). You can follow the steps in more detail in BLUP_EBV.XLS.

For 2 cases:
$h^2=0.25$, $c^2=0.15$ FS family size =3, HS family size = 12   and
$h^2=0.10$, $c^2=0.0$ FS family size =4, HS family size = 80

1) explain the negative weight on EBV of mates;
2) vary h^2 and look at weights on parental EBV
3) compare Pseudo BLUP accuracy with that of a that simple selection index approach assuming just a single record for parents (STEBVaccuracy.XLS; using the STSELIND tab)

Answers
1) BLUP corrects for assortative mating. So if the dams of the half sib group are above average, it would be unfair to us a high HS mean for the prediction of breeding value before correcting that for the contributions of te dams to these half sibs.
2) 1st case: $h^2=0.25$, $c^2=0.15$ FS family size =3, HS family size = 12

Information used	Nr.Records	Index weight		value of variate:
nr of own records	1	0.195	1 own	18%
nr. of dams per sire	4	0.380	EBV dam	7%
nr of progeny per dam	3	0.300	EBV sire	4%
nr. of progeny	0	0.044	2 FS	1%
recorded on	both sexes	0.160	9 HS	2%
		-0.080	4 Mates	0%
		-	-	-

Accuracy of EBV   **0.6241**

correlation EBV FS   0.567
correlation EBV HS   0.340

2nd case: $h^2=0.10$, $c^2=0.0$ FS family size =4, HS family size = 80

Information used	Nr.Records	Index weight		value of variate:
nr of own records	1	0.075	1 own	9%
nr. of dams per sire	20	0.430	EBV dam	9%
nr of progeny per dam	4	0.191	EBV sire	1%
nr. of progeny	0	0.066	3 FS	2%
recorded on	both sexes	0.478	76 HS	11%
		-0.239	20 Mates	0%
		-	-	-

Accuracy of EBV   **0.5737**

correlation EBV FS   0.799
correlation EBV HS   0.561

SO with low heritability: Accuracy is lower, in spite of larger families
The own performance is a lot less valuable, and weight is lower
Correlations between EBV of sibs is a lot higher (also due to larger families)

With Simple STSE LIND:

1) 1st case: h²=0.25, c²=0.15 FS family size =3, HS family size = 12

Information used	Nr.Records
nr of own records	1
nr. of records on dam	1
nr of records on sire	1
nr of full sib records	2
nr. of half sib records (excl. full sibs)	9
nr. of progeny	0

Index weight		value of variate:
0.202	own	22%
0.092	dam	5%
0.070	sire	3%
0.060	FS	1%
0.174	HS	3%
-	-	-

Accuracy of EBV 0.5976

correlation EBV FS 0.766
correlation EBV HS 0.338

2nd case: h²=0.10, c²=0.0   FS family size =4, HS family size = 80

Accuracy of EBV 0.5290

Information used	Nr.Records
nr of own records	1
nr. of records on dam	1
nr of records on sire	1
nr of full sib records	3
nr. of half sib records (excl. full sibs)	76
nr. of progeny	0

Index weight		value of variate:
0.080	own	12%
0.042	dam	3%
0.016	sire	0%
0.082	FS	4%
0.519	HS	18%
-	-	-

correlation EBV FS 0.931
correlation EBV HS 0.606

With simple SELIND, the accuracies are a bit lower than pseudo BLUP, as in BLUP more ancestral information is accounted for

Exercises Day 1

Part 2: Selection response

Exercise 2.1

Consider an ongoing nucleus breeding program for trait with heritability equal to 0.25, a phenotypic standard deviation equal to 20, and a mean of 100. The trait is expressed in females only (sex-limited trait) when they are 1 year of age. Each round 10 sires are mated to 5 dams each, and each dam has 4 male and 4 female progeny.

1. Calculate the accuracy of BLUP EBV of young male and female selection candidates (use STEBVaccuracy.XLS without Bulmer)
2. Predict the genetic superiority of selected males and females, assuming selection of the top 10% of males and the top 50% of females. Use the SELINT.XLS (correlated EBV tab) to account for correlated EBVs.
3. Predict the expected phenotypic performance of the progeny generation (generation 1).

Solutions

First use *STEBVaccuracy.xls* to work out accuracy

Males and female will have different accuracy as females have an own performance info

We need to select 'females only' and in result we see it uses only half the number in each sex,

we get for <u>females</u>:

Parameters						
Heritability	0.25					
Repeatability of subsequent records	0.25	Run without Bulmer Correction				
c-squared (among full sibs)	0	Run *with* Bulmer Correction				
selected proportion males	5%					
selected proportion females	50%	Index			value of	
Information used	Nr.Records	weight			variate:	
nr of own records	1	0.186	1	own	16%	
nr. of dams per sire	5	0.331	1	dam	5%	
nr of progeny per dam	8	0.214	0.001	sire	2%	
nr. of progeny	0	0.152	3.5	FS	3%	
recorded on	females only	0.232	16	HS	2%	
		-0.116	2.5	Mates	0%	

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SD of BV	0.500
Equilibrium Va	0.250
Equilibrium h2	0.250
SD of EBV	0.332
Accuracy of EBV	**0.664**
correlation EBV FS	0.627
correlation EBV HS	0.414

And for |males|

Parameters						
Heritability	0.25					
Repeatability of subsequent records	0.25	Run without Bulmer Correction				
c-squared (among full sibs)	0	Run *with* Bulmer Correction				
selected proportion males	5%					
selected proportion females	50%	Index			value of	
Information used	Nr.Records	weight			variate:	
nr of own records	0	-	-	-	-	
nr. of dams per sire	5	0.406	1	dam	11%	
nr of progeny per dam	8	0.264	0.001	sire	4%	
nr. of progeny	0	0.187	3.5	FS	7%	
recorded on	females only	0.286	16	HS	5%	
		-0.143	2.5	Mates	0%	
		-	-	-	-	

8

SD of BV	0.500
Equilibrium Va	0.250
Equilibrium h2	0.250
SD of EBV	0.280
Accuracy of EBV	**0.559**
correlation EBV FS	0.968
correlation EBV HS	0.623

	prop	selInt	acc	sigma_A	Sup
superiority males	10%	1.755	0.559	10	9.81
superiority females	50%	0.798	0.664	10	5.30
response per generation					7.55
mean of next generation					107.55

Note that there are 200 males and females born every generation, and we need only 10 and 50.
So selected proportions could be 5% and 25%. However, they are 10% and 50%, because we assume only half of the males and females born are available for selection. This is only an assumption. It is quite realistic that breeders discard many of their potential selection candidates, e.g. because i) they cull them for 'other reasons', ii) thy only measure half of all possible candidates.

Exercise 2.2   Selection across age groups

Consider selection of females in dairy cattle for milk yield (heritability = 0.3, genetic SD = 550 kg). Three age groups of females are available, with numbers, ages, trait means, and accuracies of selection as given below. Our aim is to select a total of 50 females for breeding.

Age group	Age when progeny born (yr)	Number available candidates	Age group trait mean (kg)	Accuracy Of selection
1	2	500	12,000	0.55
2	3	300	11,700	0.68
3	4	200	11,400	0.72

Predict the genetic superiority and generation interval for the following two situations:
1. The 50 females are selected by selecting the best 10, 20, and 20 from age groups 1, 2, and 3
2. The 50 females are selected by truncation selection across age groups (use truncsel.xls)

1)   We the predefined age structure

age class	nr	rop selecte	sellnt	acc	sigma_A	superiority	prop (pi)	age	
1	10	0.02	2.42	0.55	550	732.1	0.2	2	
2	20	0.066667	1.95	0.68	550	729.3	0.4	3	
3	20	0.1	1.755	0.72	550	695.0	0.4	4	
						females	males		Resp/year
				weighted a superiority		716.122	0		137.7158
				wighted generation interval		3.2	2		

2)

3)   We can use trncsel.xls

input is

Candidates Age Class	Nr Candidates in age group	mean	SD
1	500	12000	302.50
2	300	11700	374.00
3	200	11400	396.00

and results are

optimize age structure									
age class	nr	rop selecte	sellnt	acc	sigma_A	superiority	prop (pi)	age	
1	41	0.08	1.84	0.55	550	556.8	0.819	2	
2	8	0.03	2.27	0.68	550	850.0	0.161	3	
3	1	0.00	2.71	0.72	550	1072.4	0.020	4	
						females	males		Resp/year
				weighted a superiority		614.368	0		146.2419
				wighted generation interval		2.201038	2		

Note that in both cases we assume the male superiority is zero and male generation interval is 2. This might not be realistic but the difference =between the scenarios (comapring female age structure) is the same.

Exercise 2.3

The response per year can be given by the formula of Rendel and Robertson: Ryr = S/L.
For simplicity assume equal selection intensities in males and females).
We can maximize selection response by truncation section across age classes, (assuming the selection criteria are comparable across age classes). Truncation selection across age classes maximizes the mean of the selected parents.
Show algebraically that maximizing the mean of selected parents results in maximizing the response per year (hence, optimizes selection across age classes)

Answer:
We have

Mean of offspring generation	$\bar{g}_o$
Mean of parents from age class i (with age L_i)	$\bar{g}_o - L_i R_{yr}$
Mean of parents selected from age class i	$\bar{g}_o - L_i R_{yr} + S_i$

   Where S_i = superiority of animals selected within age class i

Proportion of parents originating from age class i p_i with ($\Sigma p_i = 1$)

The mean of all selected parents from n different age classes is $\sum_{i=1}^{n} p_i \overline{(g_o - L_i R_{yr} + S_i)}$.
This is the same as $\bar{g}_o$ because the mean of all selected parents is the same as the mean of the current generation
So maximizing the mean of all selected parents is the same as maximizing the mean of the progeny.
We use the same proportions selected (set of optimal p_i values) in the following

We can rearrange $\bar{g}_o = \sum_{i=1}^{n} p_i(\overline{g_o} - L_i R_{yr} + S_i)$

So $\bar{g}_o = \sum_{i=1}^{n} p_i \overline{g_o} - \sum_{i=1}^{n} p_i L_i R_{yr} + \sum_{i=1}^{n} p_i S_i$

$\qquad = \overline{g_o} - \sum_{i=1}^{n} p_i L_i R_{yr} + \sum_{i=1}^{n} p_i S_i$ because ($\Sigma p_i = 1$)

Therefore $- \sum_{i=1}^{n} p_i L_i R_{yr} + \sum_{i=1}^{n} p_i S_i = 0$

SO that $\sum_{i=1}^{n} p_i S_i = \sum_{i=1}^{n} p_i L_i R_{yr}$

And $R_{yr} = \sum_{i=1}^{n} p_i S_i / \sum_{i=1}^{n} p_i L_i$ so the same optimal proportions are used in optimizing R_{yr}

More intuitive:
Would we pick a young bull that has an EBV of +11 or an old bull that has a +12 EBV?
On one hand we want to select young bulls to keep a low generation interval
But the predicted progeny mean is the same as the mean of the selected bulls, so we should always select the bulls with the highest EBV, the old bull in this instance.
But remember that BLUP EBVs are comparable across age

classes, they correct for genetic trend. On average, we would expect the young bulls to be better. But their EBVs will be less spread out than those of the old bulls, as SD_{EBV} = accuracy x SD_{BV} and older bulls will have more accurate EBVs. So the best old bulls will be competitive with the best young bulls, as illustrated in the pictre (red = young bulls distribution of EBV, blue is old bulls). We would more likely have more young bulls in the top 100 bull list if 10 the genetic trend was higher and 2) if young bulls have more accurate EBVs, e.g. because we use genomic predictions.
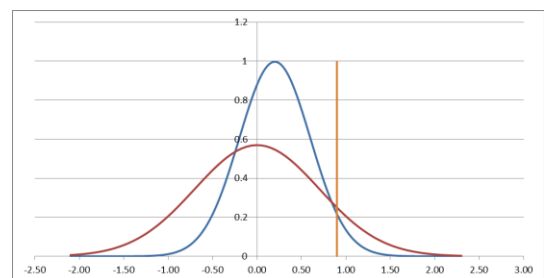
Exercise 2.4

Using the Excel Spreadsheet 'Genetic_gain.xls', evaluate the impact of the percentage of cows inseminated by young bulls and progeny group size on genetic gain. Find the optimal combination of these two variables in order to maximize genetic gain

<div align="center">

NO ANSWER GIVEN

Exercises Day 1
Part 3: Change of Variance

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Exercise 3.1   Response to selection with the Bulmer effect

Consider the problem of Exercise 2.1.

1. Calculate the genetic variance and heritability among the individuals produced in generation 1

2. Calculate accuracy of BLUP EBV of male and female selection candidates from generation 1. For the accuracy of sires and dams, use the accuracies of EBV you obtained in Exercise 2.1 (i.e. from an unselected population).

3. Predict the mean, genetic variance, and heritability of individuals produced in generation 2

4. Derive the asymptotic genetic variance, accuracy, heritability and response to selection for this breeding program.

5. Compare results from 4. to those you get from using the program SelAction.

USE THE BULMER.XLS use the BLUP tab
The initial response of 7.55 is now reduced to5.60

ILLUSTRATING BULMER EFFECT

	Initial			sires	dams	Initial ACCURACY sires	Initial ACCURACY dams	Initial
	Phenotypic	proportion selected		0.1	0.5	sires	dams	Mean
	Variance	threshold x		1.2816	0.0000	0.559	0.664	0
	400	selection intensity i		1.7550	0.7979			
h2	0.25	var reduction k		0.8309	0.6366			

Generation	Phenotypic Variance	Genetic Variance	Mendelian Sampling Variance	Variance among selected sires (% of unselected)	Variance among selected dams (% of unselected)	Heritability	Genetic mean	Response to selection	r sires	r dams
0	400	100.000	50.000	74.037	71.932	0.250	0.000	7.554	0.559	0.664
1	386.492	86.492	50.000	71.752	67.023	0.224	7.554	5.902	0.453	0.595
2	384.694	84.694	50.000	71.448	66.370	0.220	13.456	5.644	0.434	0.583
3	384.455	84.455	50.000	71.408	66.283	0.220	19.100	5.609	0.431	0.581
4	384.423	84.423	50.000	71.402	66.271	0.220	24.709	5.604	0.431	0.581
5	384.418	84.418	50.000	71.402	66.270	0.220	30.313	5.603	0.431	0.581
6	384.418	84.418	50.000	71.402	66.269	0.220	35.916	5.603	0.431	0.581
7	384.418	84.418	50.000	71.402	66.269	0.220	41.519	5.603	0.431	0.581
8	384.418	84.418	50.000	71.402	66.269	0.220	47.122	5.603	0.431	0.581
9	384.418	84.418	50.000	71.402	66.269	0.220	52.725	5.603	0.431	0.581
10	384.418	84.418	50.000	71.402	66.269	0.220	58.329	5.603	0.431	0.581

Exercise 3.2   **Pseudo BLUP EBV with the Bulmer effect**

1. Use STEBVaccuracy.xls and compare accuracy and index weights of females of Exercise 2.1 with and without Bulmer. Do the same for males

2. Change the % selected and see how this changes index weights and accuracy of EBV.

3. Calculate the accuracy of a parental average EBV with and without selection (Bulmer correction) for different proportions selected. Look also at the variance of parental EBV.

   PA = ½ EBVsire + ½ EBVdam
   Var(PA) = ¼Var(EBVsire) + ¼Var(EBVdam)
   Accuracy = sqrt(Var(PA)/V_A)

4. Evaluate reduction in accuracy due to Bulmer with different heritabilities

Matrix calculations using Excel

You can do some basic matrix calculations with MS Excel.

First put in the values of your matrices

To multiply two matrices:
- select an area of the size of the resulting matrix
- type: =**MMULT(**
- select the area of the first matrix
- type a comma (,)
- select area of the second matrix
- type a close bracket)
- on Windows press: Ctrl_Shift_Enter   on Mac press: Cmnd_Shift_Enter

To add or subtract a matrix (vector):
- select an area of the size of the resulting matrix
- type: = (
- select the area of the first matrix
- type a **+** or   **-**
- select area of the second matrix
- type a close bracket)
- press: Ctrl_Shift_Enter

To invert a matrix:
- select an area of the size of the resulting matrix
- type: =**MINVERSE(**
- select the area of the first matrix
- type a close bracket)
- press: Ctrl_Shift_Enter

To transpose a matrix (vector):
- select an area of the size of the resulting matrix
- type: =**TRANSPOSE(**
- select the area of the first matrix
- type a close bracket)
- press: Ctrl_Shift_Enter

A more specialized matrix calculation program is MATLAB. It contains many more matrix functions and mathematical function than excel. MATLAB allows you to make and run programs, draw graphs, and run simulation). A MATLAB student version is very well suitable for animal breeding problems and quite easy to use.