BLUP properties

- Correction for mates and selection over generations.
- Allows estimation of genetic trend
- Selection across age classes
- Accuracy and linkage between herds/CGs
- BLUP and inbreeding

Properties of BLUP solutions

Solutions	Accuracy
311.94	
-9.15	
-8.90	
28.26	0.54
-28.85	0.56
18.34	0.56
18.77	0.56
-0.87	0.50
-22.40	0.58
0.00	0.00

EBV of animals 1 and 2 are zero – on average

EBV of animals 3-6 are above zero – on average   Why?

BLUP provides genetic trend

Possible bias in genetic evaluation:
Some sires have better mates

Sire 1 Dam 1 Sire 2 Dam2

300 200 300 300

250 275

Blup accounts for this (see next)

Need to evaluate all animals jointly

Possible bias in genetic evaluation: Animals are from selected parents

year		sire 1	sire 2	sire 3
1		350	300	250
	offspr. 1	offspr. 2		offspr. 3
2	365	325		310

as years/generations go by, the genetic mean changes

Blup accounts for this (see next)

- need to account for selection (evaluate jointly)
- calculate genetic trend from increase in EBV over years

Properties of BLUP
how are individual EBV's estimated?

- Look at equations for individual animals

$$
\begin{pmatrix}
7 & 1 & 3 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\
1 & 3 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & -1 \\
3 & 1 & 5 & 0 & 0 & 1 & 1 & 1 & 1 & -1 \\
1 & 1 & 5 & \frac{19}{6} & \frac{1}{2} & -\frac{2}{3} & -\frac{2}{3} & -1 & 0 & 0 \\
1 & 1 & 0 & \frac{1}{2} & \frac{17}{6} & 0 & 0 & 0 & -\frac{2}{3} & 0 \\
1 & 0 & 0 & -\frac{2}{3} & 0 & \frac{7}{3} & 0 & 0 & 0 & 0 \\
1 & 0 & 1 & -\frac{2}{3} & 0 & 0 & \frac{7}{3} & 0 & 0 & 0 \\
1 & 0 & 1 & -1 & 1 & 0 & 0 & 3 & 0 & 0 \\
\boxed{1 \quad 0 \quad 1 \quad 0 \quad -\frac{2}{3} \quad 0 \quad 0 \quad 0 \quad \frac{7}{3} \quad 0} \\
1 & -1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 2
\end{pmatrix}
\begin{pmatrix}
\mu \\ b_{1990} \\ b_{1991} \\ \hat{u}_1 \\ \hat{u}_2 \\ \hat{u}_3 \\ \hat{u}_4 \\ \hat{u}_5 \\ \hat{u}_6 \\ \hat{u}_7
\end{pmatrix}
=
\begin{pmatrix}
2161 \\ 275 \\ 896 \\ 354 \\ 251 \\ 327 \\ 328 \\ 301 \\ 270 \\ 330
\end{pmatrix}
$$

Look at animal 6

$$
\mu + b_{1991} - \tfrac{2}{3}\hat{u}_2 + \tfrac{7}{3}\hat{u}_6 = 270
$$

Look at animal 6

$$\mu + b_{1991} - \tfrac{2}{3}\hat{u}_2 + \tfrac{7}{3}\hat{u}_6 = 270$$

$$\hat{u}_6 = \tfrac{3}{7}(270 - \mu - b_{1991}) + \tfrac{2}{7}\hat{u}_2$$

$$\hat{u}_6 = \tfrac{3}{7}\underbrace{(270 - \mu - b_{1991} - \tfrac{1}{2}\hat{u}_2)}_{\text{This is own performance as deviation from expected, given its sire}} + \underbrace{\tfrac{1}{2}\hat{u}_2}_{\text{This comes from sire}}$$

Selection index weight:

¾ VA / (¾VA+VE)

This is own performance as deviation from expected, given its sire

This comes from sire

$$\begin{pmatrix} 7 & 1 & 3 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\ 1 & 3 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & -1 \\ 3 & 1 & 5 & 0 & 0 & 1 & 1 & 1 & 1 & -1 \\ 1 & 1 & 5 & \frac{19}{6} & \frac{1}{2} & -\frac{2}{3} & -\frac{2}{3} & -1 & 0 & 0 \\ 1 & 1 & 0 & \frac{1}{2} & \frac{17}{6} & 0 & 0 & 0 & -\frac{2}{3} & 0 \\ 1 & 0 & 0 & -\frac{2}{3} & 0 & \frac{7}{3} & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & -\frac{2}{3} & 0 & 0 & \frac{7}{3} & 0 & 0 & 0 \\ \boxed{1} & \boxed{0} & \boxed{1} & \boxed{-1} & \boxed{1} & \boxed{0} & \boxed{0} & \boxed{3} & \boxed{0} & \boxed{0} \\ 1 & 0 & 1 & 0 & -\frac{2}{3} & 0 & 0 & 0 & \frac{7}{3} & 0 \\ 1 & -1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 2 \end{pmatrix} \begin{pmatrix} \mu \\ b_{1990} \\ b_{1991} \\ \hat{u}_1 \\ \hat{u}_2 \\ \hat{u}_3 \\ \hat{u}_4 \\ \hat{u}_5 \\ \hat{u}_6 \\ \hat{u}_7 \end{pmatrix} = \begin{pmatrix} 2161 \\ 275 \\ 896 \\ 354 \\ 251 \\ 327 \\ 328 \\ \boxed{301} \\ 270 \\ 330 \end{pmatrix}$$

Look at animal 5

$$\mu + b_{1991} - \hat{u}_1 - \hat{u}_2 + 3\hat{u}_5 = 301$$

For animal 5

$$\mu + b_{1991} - \hat{u}_1 - \hat{u}_2 + 3\hat{u}_5 = 301$$

$$\hat{u}_5 = \tfrac{1}{3}\underbrace{(301 - \mu - b_{1991} - \tfrac{1}{2}(\hat{u}_1 + \hat{u}_2))}_{\substack{\text{This is own performance as} \\ \text{deviation from expected,} \\ \text{given its sire and dam}}} + \tfrac{1}{2}\underbrace{(\hat{u}_1 + \hat{u}_2)}_{\substack{\text{Mean of} \\ \text{parents}}}$$

Selection index weight:

½ VA /(½VA+VE)

$$
\begin{pmatrix}
7 & 1 & 3 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\
1 & 3 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & -1 \\
3 & 1 & 5 & 0 & 0 & 1 & 1 & 1 & 1 & -1 \\
1 & 1 & 5 & \frac{19}{6} & \frac{1}{2} & -\frac{2}{3} & -\frac{2}{3} & -1 & 0 & 0 \\
\boxed{1} & \boxed{1} & \boxed{0} & \boxed{\frac{1}{2}} & \boxed{\frac{17}{6}} & \boxed{0} & \boxed{0} & \boxed{0} & \boxed{-\frac{2}{3}} & \boxed{0} \\
1 & 0 & 0 & -\frac{2}{3} & 0 & \frac{7}{3} & 0 & 0 & 0 & 0 \\
1 & 0 & 1 & -\frac{2}{3} & 0 & 0 & \frac{7}{3} & 0 & 0 & 0 \\
1 & 0 & 1 & -1 & 1 & 0 & 0 & 3 & 0 & 0 \\
1 & 0 & 1 & 0 & -\frac{2}{3} & 0 & 0 & 0 & \frac{7}{3} & 0 \\
1 & -1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 2
\end{pmatrix}
\begin{pmatrix}
\mu \\ b_{1990} \\ b_{1991} \\ \hat{u}_1 \\ \hat{u}_2 \\ \hat{u}_3 \\ \hat{u}_4 \\ \hat{u}_5 \\ \hat{u}_6 \\ \hat{u}_7
\end{pmatrix}
=
\begin{pmatrix}
2161 \\ 275 \\ 896 \\ 354 \\ \boxed{251} \\ 327 \\ 328 \\ 301 \\ 270 \\ 330
\end{pmatrix}
$$

Look at animal 2

$$
\mu + b_{1990} + \tfrac{1}{2}\hat{u}_1 + \tfrac{17}{6}\hat{u}_2 - \hat{u}_5 - \tfrac{2}{3}\hat{u}_6 = 251
$$

For animal 2

$$\mu + b_{1990} + \tfrac{1}{2}\hat{u}_1 + \tfrac{17}{6}\hat{u}_2 - \hat{u}_5 - \tfrac{2}{3}\hat{u}_6 = 251$$

$$\hat{u}_2 = \underbrace{\tfrac{6}{17}(251 - \mu - b_{1990})}_{\text{This is own performance as deviation from expected,}} - \underbrace{\tfrac{6}{17}(\hat{u}_5 - \tfrac{1}{2}\hat{u}_1)}_{\text{Prog 1, corrected for dam}} + \underbrace{\tfrac{4}{17}\hat{u}_6}_{\text{Prog 2, no dam}}$$

Parents themselves estimated based on:

- •own record
- •progeny records
- •correction for mates

Weights are same as in selection indexBLUP accounts for selection!!

Possible bias in genetic evaluation: Animals are from selected parents

year	sire 1	sire 2	sire 3
1	350	300	250

	offspr. 1	offspr. 2	offspr. 3
2	365	325	310

as years/generations go by, the genetic mean changes

- need to account for selection (evaluate jointly)
- calculate genetic trend from increase in EBV over years

EBV's without BLUP (within year)

year		sire 1	sire 2	sire 3
1	300	350	300	250
		13	**0**	**-13**

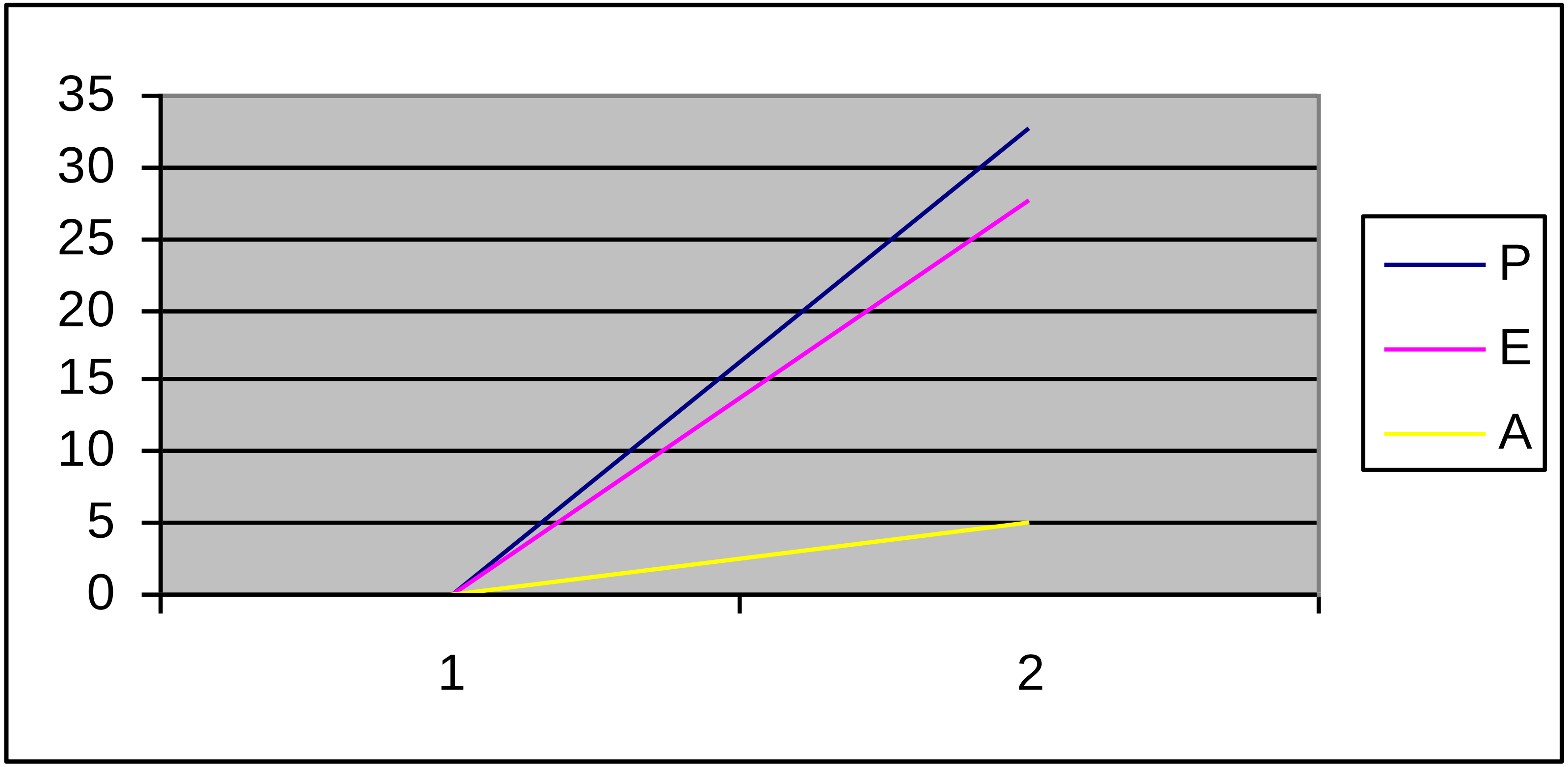
		offspr. 1	offspr. 2	offspr. 3
2	333	365	325	310
		8	**-2**	**-6**

EBV's with BLUP (across year)

year						
			sire 1	sire 2		sire 3
1	300		350	300		250
			14	**-2**		**-13**
		offspr. 1	offspr. 2		offspr. 3	
2	329	365	325		310	
		13	**5**		**-4**	

as years/generations go by, the genetic mean changes

- need to account for selection (evaluate jointly)
- calculate genetic trend from increase in EBV over years



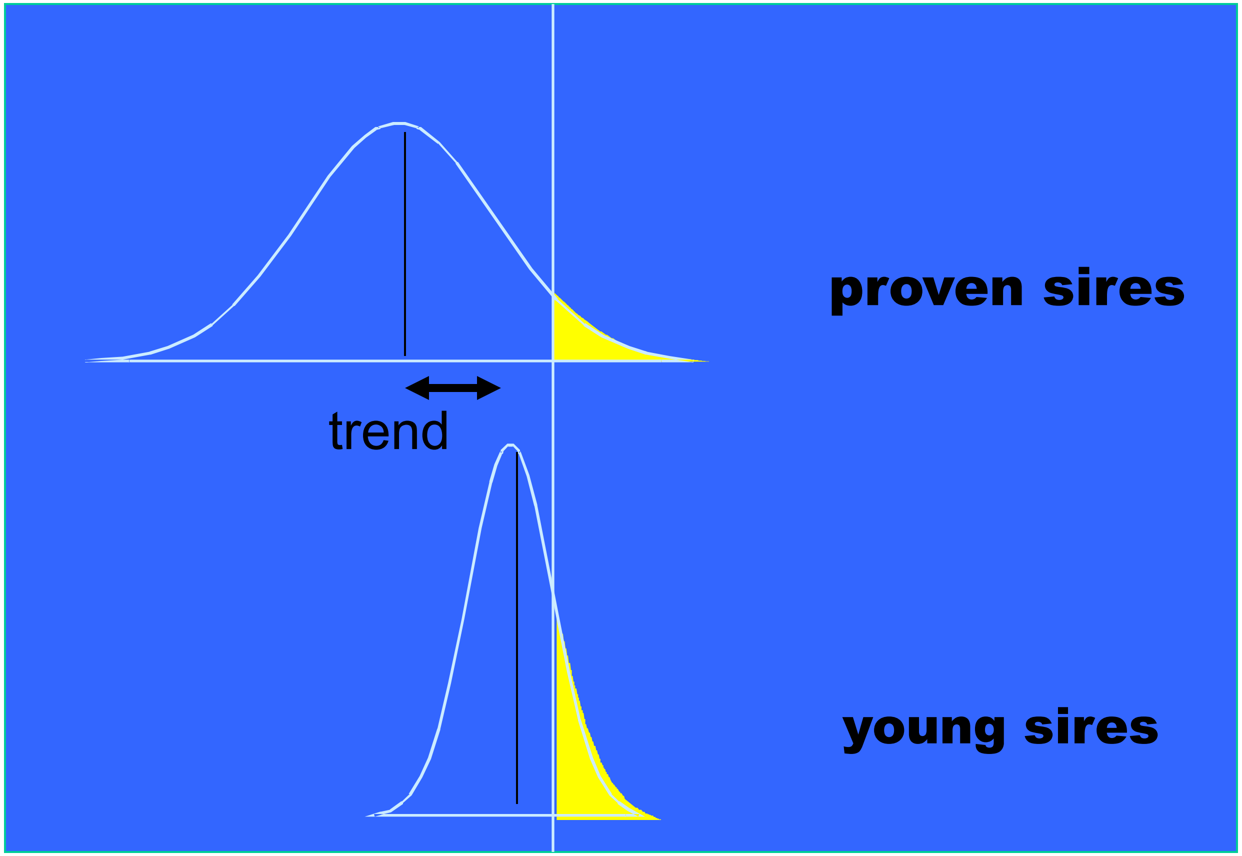
BLUP allows to separate between environmental and

<u>Genetic Trend</u>

Simply as mean EBV's per year of birth

Optimizing Generation Interval

- Dilemma between young and old sires

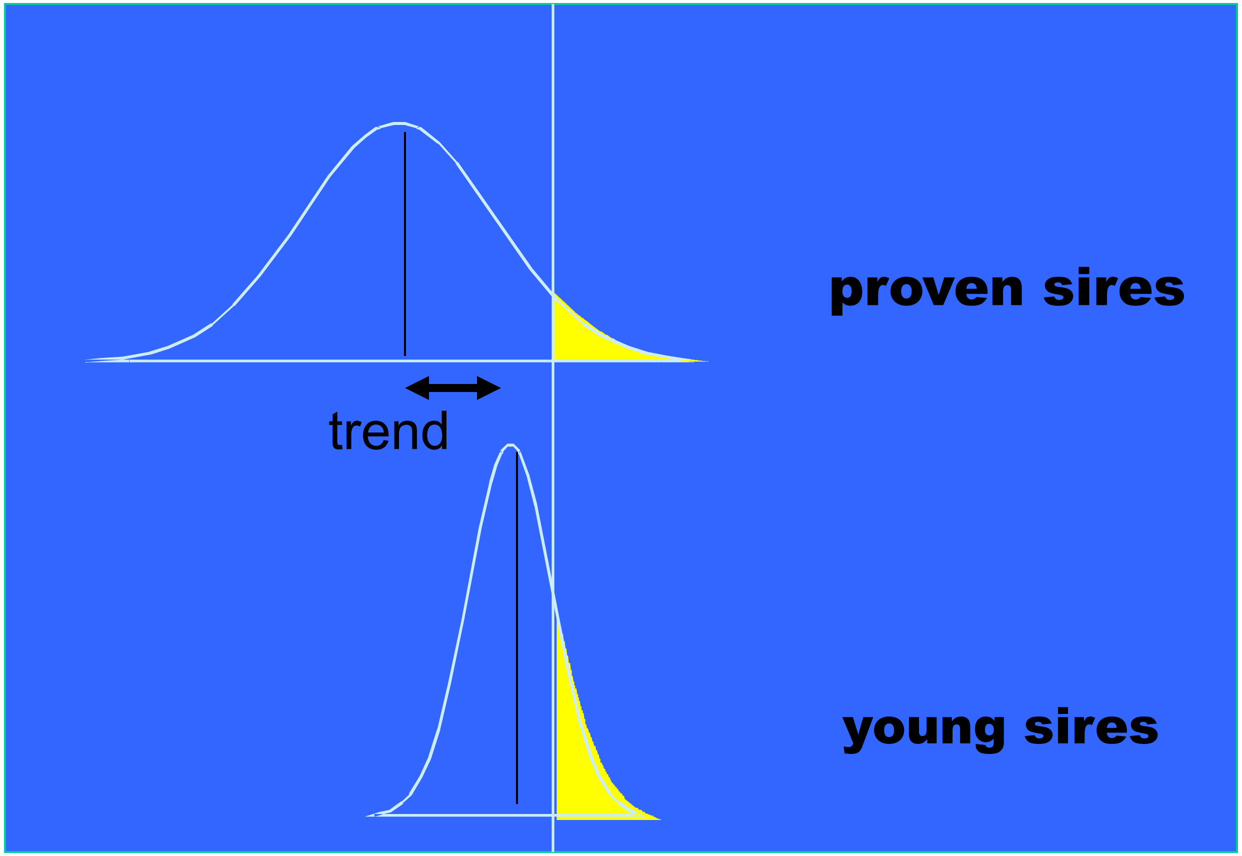


Truncation Point

Genetic Evaluation helps

BLUP EBV Optimizes generation interval

- Dilemma between young and old sires



Truncation Point

BLUP and Inbreeding

BLUP uses family information

→ co-selection of relatives

→ more inbreeding

loss of variance

and inbreeding depression

- Does it balance out increased accuracy?

Simulation:

Selection on INDividual performance vs selection on BLUP

		Merit genetic merit			Inbreeding	
Heritability	Year	IND	BLUP	BLUP/IND	IND	BLUP
0.1	5	0.38	0.63	1.66	0.067	0.167
	10	0.78	1.41	1.81	0.174	0.383
0.3	5	1.1	1.41	1.28	0.078	0.141
	10	2.4	3.14	1.31	0.193	0.332
0.6	5	2.25	2.29	1.02	0.087	0.13
	10	5.16	5.31	1.03	0.205	0.293

1. BLUP more response than phenotypic selection (IND)

   Difference is larger for smaller heritability.

2. BLUP more inbreeding

   Especially for low heritabilities

3. BLUP still better after 10 years (???)

Advantages BLUP EBVs

- Optimal weights for all information sources
- Flexible: Lots of different sets exist of optimal weighting factors, BLUP does it automatically
- Allows comparisons of EBV's of animals in different herd (possibly with different genetic means)
  - *But links need to exist in the data!*
- Accounts for culling and selection, non-random mating
  - *But non selected animals need to be included in analysis!*
- Allows selection across age classes
- Provides an estimate of genetic trend

Consequences of BLUP selection

- Maximize genetic response in next generation

- Can compare animals over age classes
  → BLUP optimises generation interval

- Tend to select more related animals
  the more so with lower heritability
  → BLUP leads to more inbreeding

- Optimal selection uses BLUP + restricted inbreeding (but by how much?)

- BLUP only optimises next generation merit!

Accuracy of BLUP EBV's

The accuracy of an EBV depends on:

'the amount of information used'

own info / relatives

The value of information (say a phenotype) depends on

1) **the heritability,**
2) **the additive genetic relationship**
3) **the genetic correlation**
4) **the <u>effective number</u> of records.**

How is Accuracy (r) of BLUP-EBV's calculated?

- Use *inverse* of coefficient matrix of mixed model equations

$$\begin{pmatrix} \mathbf{X'X} & \mathbf{X'Z} \\ \mathbf{Z'X} & \mathbf{Z'Z} + \lambda\mathbf{A}^{-1} \end{pmatrix}^{-1}$$

independent of data values !!!!

Diagonal of Coeff. Matrix is basically the number of records per class/animal (N)

Inverse of Coeff. Matrix is basically 1/n

- Use diagonal for animal i: C^{ii}
- Prediction Error Variance: PEV = C^{ii}.var(e) (~ "σ^2/N")

Remember PEV = $(1-r^2_{IA}).V_A$

$$\rightarrow \quad r^2_{IA} = (V_A - PEV)/V_A$$

$$r^2_{IA} = 1 - \lambda C^{ii}$$

$$\text{Accuracy} = r_{IA} = \sqrt{(1 - \lambda C^{ii})}$$

C^{ii} is diagonal of MME

Effective number of records

a record has less value when in a small contemporary group

- A single observation is effectively worth

$$n_e = 1 - (1/N)$$

where N is the number of animals
in the contemporary group

- Sire with n progeny in CG of N:

$$n_e = \frac{n*(N-n)}{N}$$

Examples effective number of records

Contemporary group size	1 record is effectively
1	0
2	0.5
4	0.75
20	0.95

Contemporary group size	# sire A	effective # sire A
1	1	0
10	10	0
10	9	0.9
10	1	0.9
10	5	2.5

BLUP accuracy depends on the model used!

animal	model 1	2	3	4
1	0.7683	0.6082	0.5404	0.3809
2	0.7516	0.6264	0.5561	0.5181
3	0.7335	0.609	0.5647	0.4164
4	0.7335	0.609	0.5647	0.5554
5	0.7612	0.5664	0.504	0.4243
6	0.7321	0.6175	0.5788	0.5124
7	0.7071	0.6304	0	0

model 1 y = animal (mean is known)

m2: y = mean + animal

m3: y = mean + year + animal

m4: y = mean + year + sex + animal

Need to find a balance

Conclusion

Need to find a balance between

unbiasedness > many (i.e. small) fixed effect classes

and

accuracy > few large fixed effect classes

An observation is mor worth when comapred with many others

I progeny testing designs, we don’t need necessarily many progeny of the same sire tested in same flock/herd, in fact better spread across as many flocks as possible