University of New England

Estimating breeding value

Key terms

- Estimated breeding value (EBV)
- Heritability
- Contemporary groups

- Using information from relatives
- Accuracy

Which animal to select ?

	P1	P2	EBV
Animal	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	?

$$EBV = 0.284\ P_{own} + 0.107\ P_{sire}$$

	P1	P2	EBV
Animal	own perform.	sire's perform.	Index
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

Information sources

- There can be many information sources
  - own performance
  - mean performance of full sibs
  - mean performance of half sibs
  - performance of sire and / or dam
  - performance of progeny

See STINDEX.xls

$$EBV = b_1P + b_2P_2 + b_3P_3 + \ldots\ldots\ldots b_nP_n$$

These weights are derived from selection index theory, they are applied in BLUP

Note that

- Index weights are higher with higher heritability
  - More of what we see is 'counted'
- Higher heritability → more weight on own information
- Low h^2 → more weight on family information

And note that ...

- Under high heritability selection on such an index is similar to phenotypic selection
- Under low heritability selection on such an index is more like family selection, which leads to higher inbreeding
- The best estimate is based on many progeny

Accuracy of predicting a breeding value

Info used. h2 = 0.25	Accuracy of EBV
Sire + Dam	0.35
Prog Tested Sire + Dam	0.49
… ……. + Own Record	0.63
..... + DNA markers	0.71
..... . + 30 progeny	0.85
..... + 1000 progeny	0.99

Features of EBVs

High accuracy, for high response *'best'*

- *highest correlation between true and estimated breeding value*

Lack of any bias, for fair comparison *'unbiased'*

- *Comparisons between animals should not be affected by non-genetic effects → correct for contemporary groups, age etc*

Example of contemporary groups

Bull	YW	Herd Ave	P	EBV h^2=40%
Bert	330	300	+30	+12
Flossy	300	260	+40	+16

Note that this assumes that herds have the same *genetic* mean

Correcting for age differences

These are cows!

	Age (mo)	Weaning Weight Kg.
Aelfy	11	280
Betty	13	295

Population mean
at 12 mo = 285kg

Correcting for age differences

	Age (mo)	Weaning Weight Kg.
Alfy	11	280
Betty	13	295

Population mean at 12 mo = 285kg

Correct phenotypes to a 'constant' age

If growth per month is 9 kg/mo) →

Corrected weights

A: 280 – 9.(11 - 12) = 289 kg → P = +4

B: 295 – 9.(13 - 12) = 286 kg → P = +1

Can not always take simple deviation from herd averages

	Herd A	Herd B
Progeny of Sire 1	320	
Progeny of Sire 2	300	
Progeny of Sire 3	-	310
Progeny of Sire 4	-	330

Can not always take simple deviation from herd averages

	Herd A	Herd B
Progeny of Sire 1	320	
Progeny of Sire 2	300	
Progeny of Sire 3	-	310
Progeny of Sire 4	-	330
Progeny of Sire 5	290	340

Link sire

A linear model is used to correct for unbalanced data

In most genetic evaluation programs:

- Linkage between flocks/herd is now substantial
- This allows across-flock and even across-breed analysis

Possible causes of bias
'unequal merit of mates'

- Problem: Some sires have better mates

Sire 1: +300	Dam 1: +200	Progeny: +250
Sire 2: +300	Dam 2: +300	Progeny: +300

Without information on the dams, sire 2 would 'look better' due to a higher progeny mean

- Solution: Account for mates by evaluating all animals jointly

A feature of BLUP

Possible causes of bias ‘selection bias’

– Problem: There is culling and selection

- worst sires have more progeny culled ‘culling bias’
- animals are from selected parents

Culling bias

ID	*Sire*	*Weaning Weight*	*Progeny mean*	*Yearling Weight*	*Progeny mean*
101	1	160		300	
102	1	140	140	280	280
103	1	120		260	
104	2	140		280	
105	2	120	120	260	270
106	2	100		no record as culled	

Sire 2 gets an unfair 'lift' in progeny mean of yearling weight, due to culling at weaning.

Animals are from selected parents

Year 1

Mean = 300

350 300 250

Year 2

325 315 285

Mean = 308

Estimating genetic trend

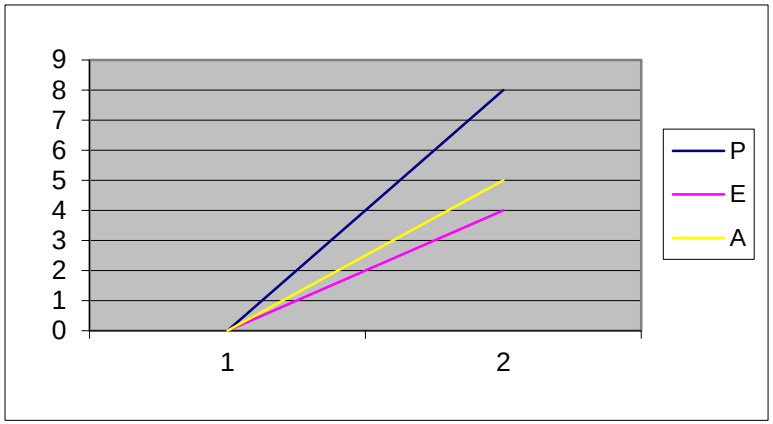
	Ave EBV	Year Effect
Year 1 Mean = 300	0	300
Year 2 Mean = 308	5	304

Year 1 Mean = 300

350 (EBV: 14) 300 (-2) 250 (-13)

Year 2 Mean = 308

325 (EBV: 10) 315 (8) 285 (-4)

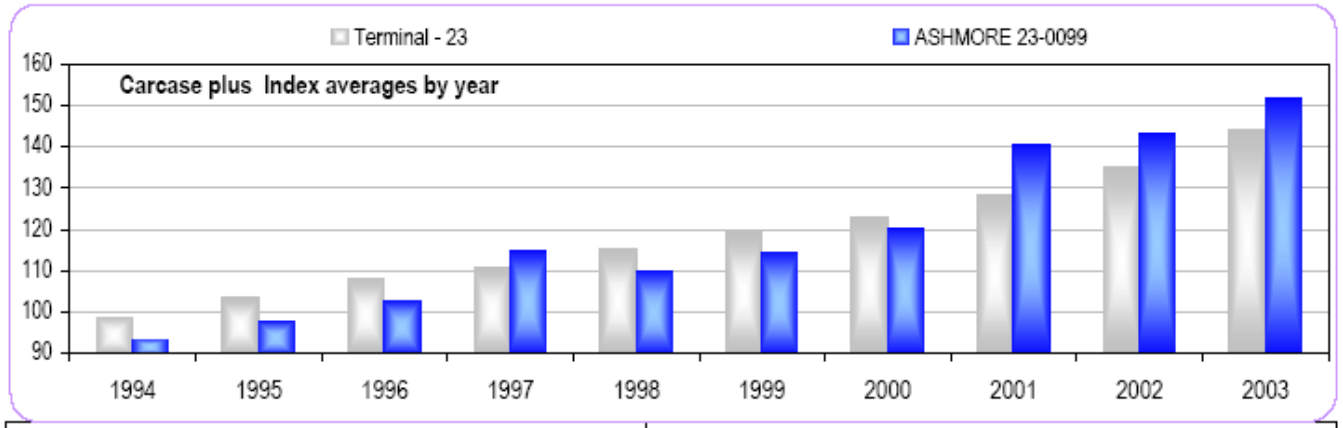


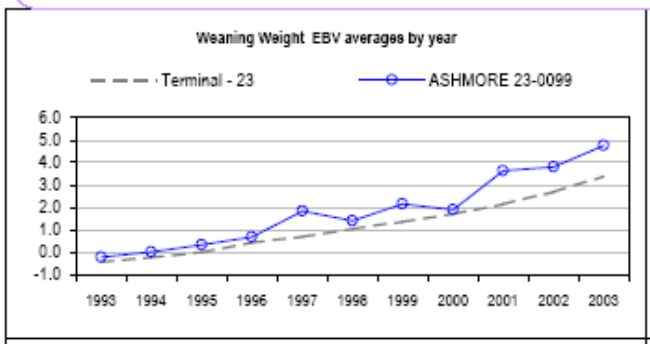
A feature of BLUP

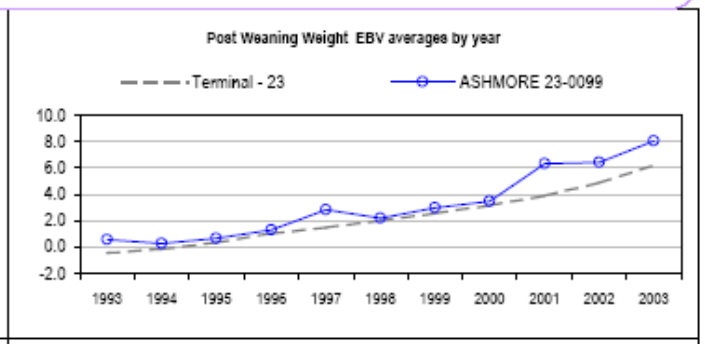
ASHMORE
BRIAN & TROY FISCHER
23-0099

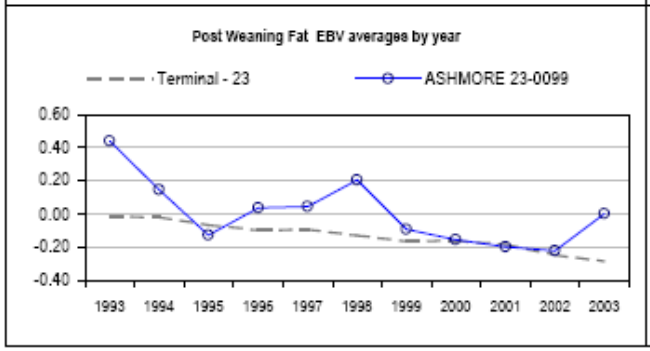
Analysis : ***Terminal - 23***

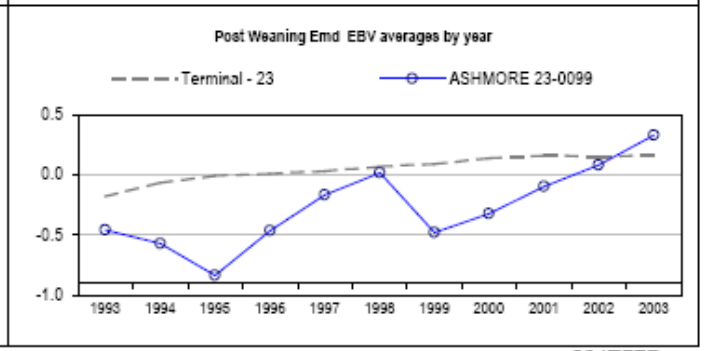
Dated : 1/11/03











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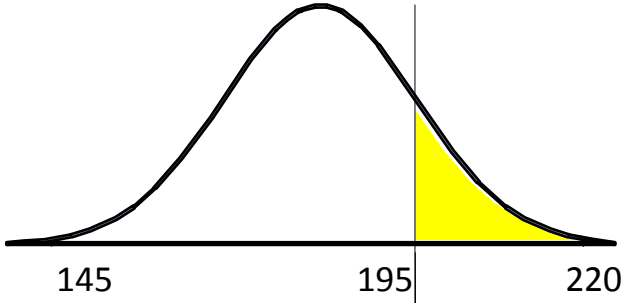
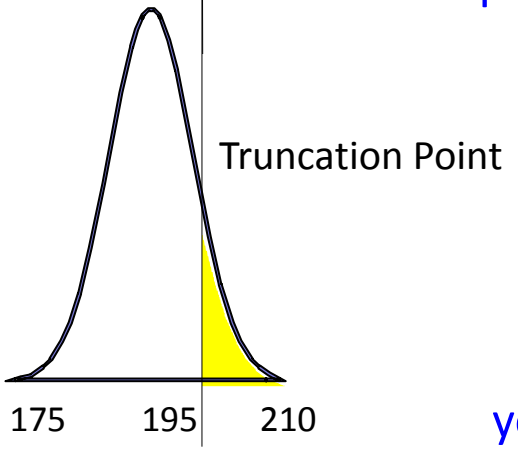
BLUP helps selecting between old and young bulls

- EBVs can be compared directly over age classes
- Selection on BLUP EBVs optimizes generation interval



proven sires



young sires

Example of BLUP selection (truncation)

Terminals - Top 150

Analysis Date Friday, 15 June 2001

LAMBPLAN

Sires

ID	Stud of breeding	Wwt	Pwwt	Ywt	Pfat	Pemd	Carcase +	Progeny	Inbreeding & Accuracies Coeff	Weight	Carcase	Sire	Sire of Dam
161972-1999-990196	HILLCROFT FARMS	5.46	14.95	14.94	-1.19	1.62	226.64	38	0.133	83	70	1619721998980093	1630001993930134
162368-1998-980211	KURRALEA	6.60	12.39	12.69	-0.89	2.50	215.20	1148		97	96	1623681994940260	8600401992920175
162204-1999-990453	BETHELREI	8.52	13.38	15.87	-1.18	1.11	211.75	224		93	89	8601221993930205	1619721995950289
161972-1998-980093	HILLCROFT FARMS	5.15	14.40	16.00	-1.08	0.25	207.51	12		80	74	1630001993930134	1603361992920349
161972-1998-980527	HILLCROFT FARMS	8.46	13.45	10.97	-1.66	-0.47	204.10	25		85	76	1619721996960091	1630001993930134
860122-1993-930205	OHIO	6.95	11.94	13.72	-1.60	0.49	203.76	1522		98	97	8601221992920200	8601221987870073
161143-1999-990204	DERRYNOCK	8.39	12.10	12.19	-0.49	2.19	203.60	38		82	76	1623681998980211	1640001993930411
160060-1996-960004	ANNA VILLA	8.56	14.90	16.18	-0.48	0.24	200.47	151		93	87	1632801992920016	1623541990900584
161143-1999-990201	DERRYNOCK	5.43	11.83	11.14	-1.19	0.83	199.83	39		83	77	1623681998980211	1613151995950042
230034-1997-970904	BURWOOD	4.98	11.01	8.82	-2.27	-0.55	198.82	380	0.003	96	92	2300091994940171	2300341994940314
163677-2000-000140	FELIX	6.69	13.56	13.36	-0.59	0.61	197.98	56		70	63	1619721995950289	1600341994940020
160060-1997-970115	ANNA VILLA	6.30	14.47	11.69	-0.42	0.24	196.90	118		90	83	1600601996960004	1600601992920057
162204-1999-990394	BETHELREI	7.42	12.97	14.27	-1.03	0.14	196.85	24		82	74	8601221993930205	1622041996960579
161143-1999-990064	DERRYNOCK	5.10	11.20	10.10	-0.72	1.60	196.01	18		80	74	1623681998980211	1640001994940317
161972-1996-960020	HILLCROFT FARMS	5.32	12.96	10.66	-0.80	0.36	195.20	83		88	75	1630001993930134	
160185-1996-960001	JOLMA	6.19	10.29	10.42	-1.56	0.63	194.57	101		90	83	1630001993930134	1613151991910870
161235-1997-970830	POLLAMBI	7.10	10.69	10.35	-0.88	1.50	194.54	34		87	79	1700991993930002	1612351991910691
163677-1999-990307	FELIX	7.09	12.52	11.59	-1.29	-0.47	192.45	54		83	74	8601221993930205	1636771994940008
162368-1999-990290	KURRALEA	5.53	10.84	10.58	-0.62	1.59	192.11	68		69	62	1623681998980211	1630001993930160
860074-1995-950044	ADELONG	7.17	14.47	13.22	-0.80	-0.94	191.15	448		96	94	8600741993930189	
163000-1998-980575	RENE	7.59	12.01	13.06	-0.50	0.99	190.92	12		71	60	1623681994940260	8600371992920165
162368-1997-970443	KURRALEA	6.58	12.13	7.96	-1.00	0.08	190.69	178		88	83	1640001993930411	8600401992920175
160034-1999-991208	MOSSLEY	5.52	13.45	10.27	-0.53	0.04	190.41	17	0.003	78	70	1621001998980130	1600341994940171
161437-1999-990006	WARBURN	5.41	10.97	10.93	-1.21	0.37	190.26	14		73	65	1604621994940012	1640001993930411

Consider top 15 sires, truncation point = 195

Sires in top are from various age classes

Another feature of BLUP

- BLUP uses family information (and more so at lower heritabilities)
- Selection on BLUP EBVs can thus results in higher inbreeding than selection on phenotypes alone
- Best strategy: Balance merit and genetic diversity
  - Start selecting from top, but leave an animal out if sibs have been selected already

Example of BLUP selection

Terminals - Top 150

Analysis Date Friday, 15 June 2001

LAMBPLAN

Sires

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161143-1999-990064	DERRYNOCK	5.10	11.20	10.10	-0.72	1.60	196.01	18		80	74	1623681998980211	1640001994940317
161972-1996-960020	HILLCROFT FARMS	5.32	12.96	10.66	-0.80	0.36	195.20	83		88	75	1630001993930134	
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161437-1999-990006	WARBURN	5.41	10.97	10.93	-1.21	0.37	190.26	14		73	65	1604621994940012	1640001993930411

These are sibs so might not select all of them as flock sire

Good methods need good data

- Accuracy of BLUP EBVs depends on amount and the quality of the data (as well as the trait heritability)
  - Accurate phenotypic measurements
  - Correct pedigree
  - Correct recording of fixed effects & contemporary groups
  - Appropriate data structure (e.g. information on mates, culls)
- Remember, if BLUP doesn't know a piece of information, it cannot account for it

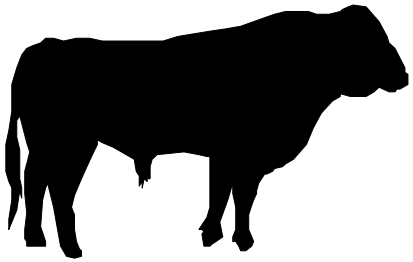
BLUP summary

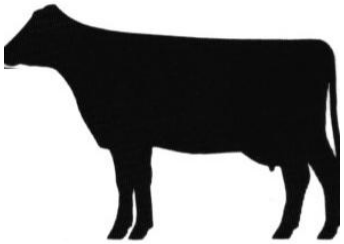
- Uses information on all relatives optimally
- Accounts for fixed effects such as herd, birth type, age
- Accounts for unequal usage of sires in different herds
- Can compare across herd or flocks but need links to exist
- Accounts for culling and selection, non-random mating
  - *but non selected animals and mates need to be included in analysis!*
- Allows selection across age classes
- Provides an estimate of genetic trend

Why is selection on BLUP EBVs better than selecting on an animals' phenotype?

Observed Phenotype (Fleece Weight)	P	A	E	EBV	PE
4.6	0.6	0.20	0.40	0.13	-0.07
4.5	0.5	-0.10	0.60	0.11	0.21
3.85	-0.15	0.25	-0.40	-0.03	-0.28
3.55	-0.45	-0.05	-0.40	-0.09	-0.04
3.6	-0.4	-0.3	-0.20	-0.08	0.22
Standard Deviation	0.498	0.226	0.469	0.105	0.209
Variance	0.248	0.051	0.220	0.011	0.044
Mean	0.020	0.000	0.000	0.004	0.004

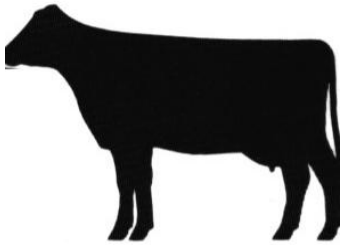
Selection on EBV





50% of dad's genes
1/2 EBV Sire

50% of mum's genes
1/2 EBV Dam



Expected Value of progeny = 1/2 EBV_{sire} + 1/2 EBV_{dam}

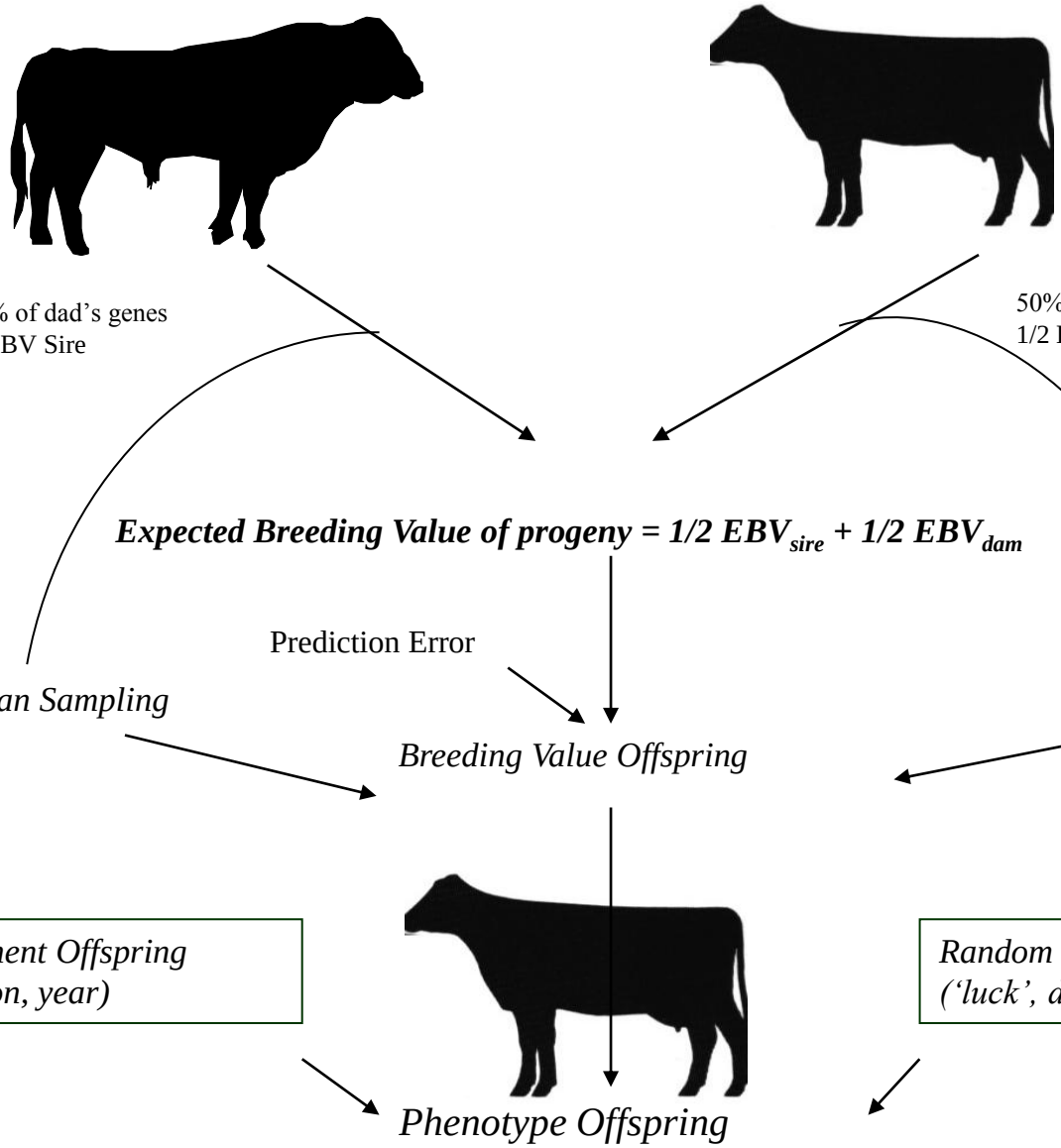


Figure 4.2. Genetic and environmental factors influencing a progeny's genotype

Some things to note

- EBV's on parents are additive
- Predicted performance of offspring does not depend on accuracy of the parents' EBVs
- Suppose

EBV_A	+56	r = 0.50
EBV_B	+56	r = 0.95

select A or B?

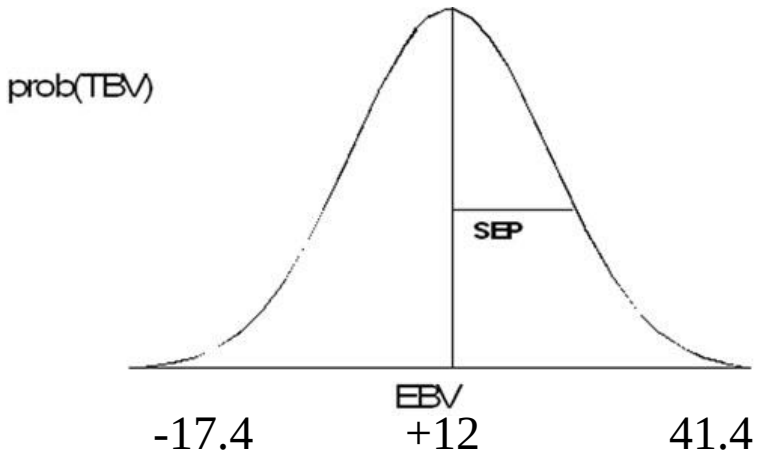
Answer: should not matter (if one is risk neutral)

EBV properties:

- how much they still may change

- $SEP = \sqrt{(1 - accurcy^2)}\sigma_A$ Standard Error of Prediction

Probability density of TBV)



Conf. Interval: EBV± 2.SEP