Weight vs Feed Intake
Sensitivity to economic weights

Econ wght	Resp	$Resp	σI	acc
1	7.203	7.20	5.657	0.6071
-5	0.309	-1.55		
1	6.536	6.54	4.296	0.4132
-10	0.224	-2.24		
1	0.705	0.71	3.865	0.2229
-20	-0.158	3.16		

Weight vs Feed Intake
Sensitivity to economic weights

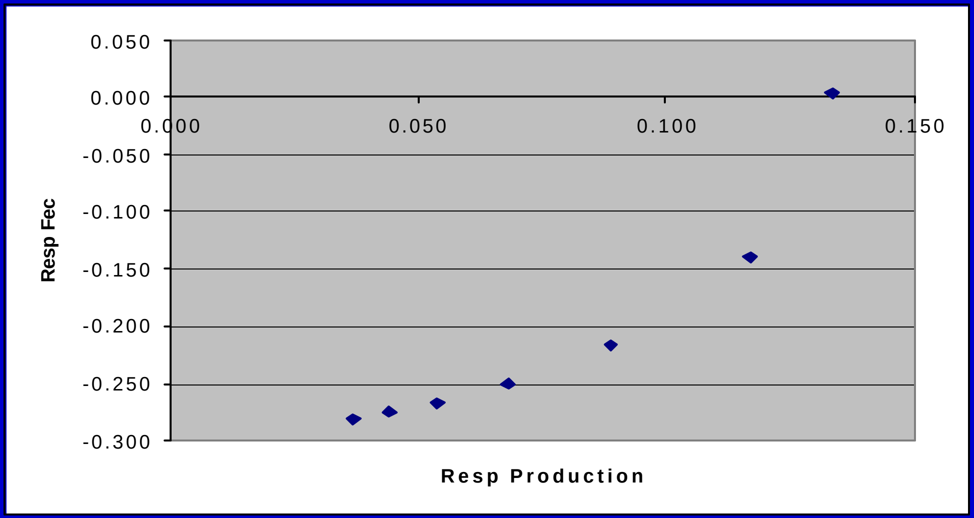
Econ wght	Resp	$Resp	σI	acc	σH
1	7.203	7.20	5.657	0.6071	9.318867
-5	0.309	-1.55			
1	6.536	6.54	4.296	0.4132	10.39628
-10	0.224	-2.24			
1	0.705	0.71	3.865	0.2229	17.33681
-20	-0.158	3.16			

Weight vs Feed Intake
Sensitivity to correlation

Gen.corr	Resp	$Resp	σI	acc	σH
0.25	6.719	7.20	6.10	0.48	12.72
	0.062	-1.55			
0.5	6.54	6.54	4.30	0.41	10.40
	0.224	-2.24			
0.75	6.459	6.46	2.42	0.33	7.37
	0.404	-4.04			

Fleece Weight vs Faecal Egg Count “Unknown” Economic Weight

			Mean	Observed
ew_FEC	Resp_P	Resp_FEC	10	1000
0	0.134	0.004	10.004	1001
-0.25	0.117	-0.139	9.861	959
-0.5	0.089	-0.216	9.784	937
-0.75	0.068	-0.251	9.749	927
-1	0.054	-0.267	9.733	922
-1.25	0.044	-0.276	9.724	919
-1.50	0.037	-0.281	9.719	918



Extra Response due to IGF1

	Response		$Response	Accc	
No IGF!, FI on sire					
Weight	6.536	kg	4.296	0.4132	
Feed Intake	0.224	kg			
IGF1	0.176	ng/ml			
IGF! On sire, FI on sire					
Weight	6.417	kg	4.376	0.4209	
Feed Intake	0.204	kg			
IGF1	-0.01	ng/ml	with FI on sire, dG =		0.080 extra
No IGF1. no FI					
Weight	7.304	kg	3.908	0.3759	
Feed Intake	0.340	kg			
IGF1	0.391	ng/ml			
IGF1. no FI					
Weight	6.997	kg	4.073	0.3918	
Feed Intake	0.292	kg			
IGF1	0.08	ng/ml	with no FI on sire		0.165 extra

Extra Response due to IGF1

Note that also

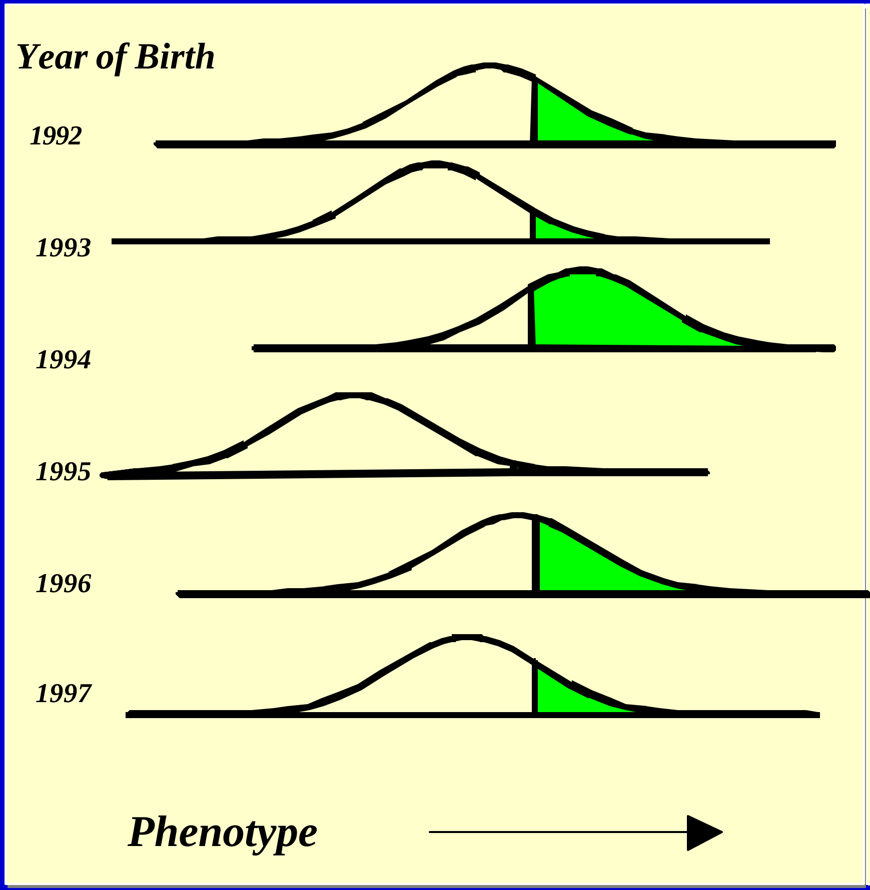
the generation interval can be shortened!

Truncsel.xls

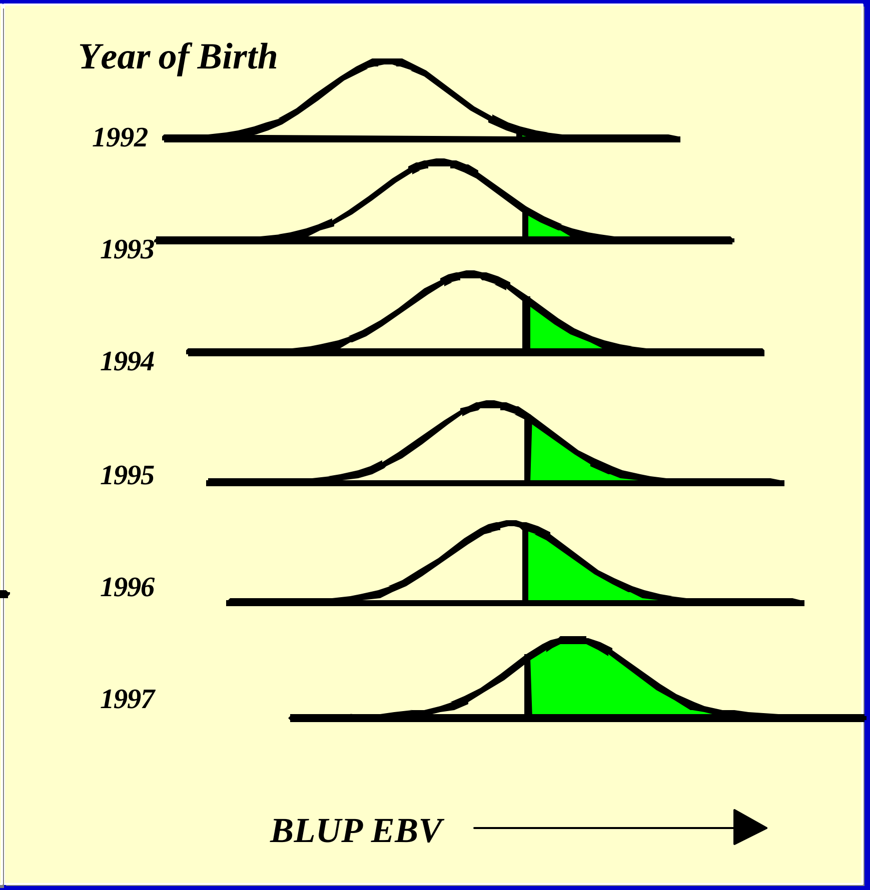
What if no info in Feed Intake?

A genetic evaluation system helps to design breeding programs.

Select on phenotype



Select on EBV



What if no info in Feed Intake?

$EBV_{FI} = cov(A_{FI},A_W)/var(A_w).\ EBV_W$

$= b.EBV_W$

$Index = v_1 EBV_W + v_2\ EBV_{FI}$

$= v_1 EBV_W + v_2\ .b.EBV_W$

$= (v_1 + v_2.b).\ EBV_W$

What if no info in Feed Intake?

Can just as well adapt economic weight

- Beef case
- Wool case

Increased accuracy from using info from correlated traits

(derive with selection index theory)

depends on

- **heritability of the trait considered**
- **correlations**
- **difference between re and rg!**
- **information already available for each trait**

Relative accuracy of MT selection vs ST selection: Accuracy of Trait 1 (with h_1^2) using information from Trait 1 and correlated Trait 2 (with h_2^2)

Selection on phenotype only

	h^2_2	h^2_1 0.1	0.3	0.5
$r_g = r_e = 0.5$	0.1	1.00	1.02	1.03
	0.3	1.09	1.00	1.01
	0.5	1.25	1.02	1.00
$r_g = -r_e = 0.5$	0.1	1.40	1.18	1.10
	0.3	1.59	1.23	1.11
	0.5	1.70	1.25	1.12

Using relatives information for each trait

	h^2_2	0.1	0.3	0.5
$r_g = r_e = 0.5$	0.1	1.00	1.01	1.02
	0.3	1.03	1.00	1.00
	0.5	1.08	1.01	1.00
$r_g = -r_e = 0.5$	0.1	1.18	1.08	1.05
	0.3	1.22	1.10	1.06
	0.5	1.25	1.11	1.07

Effect of using incorrect parameters in genetic evaluation

the optimum response is (in units of i)

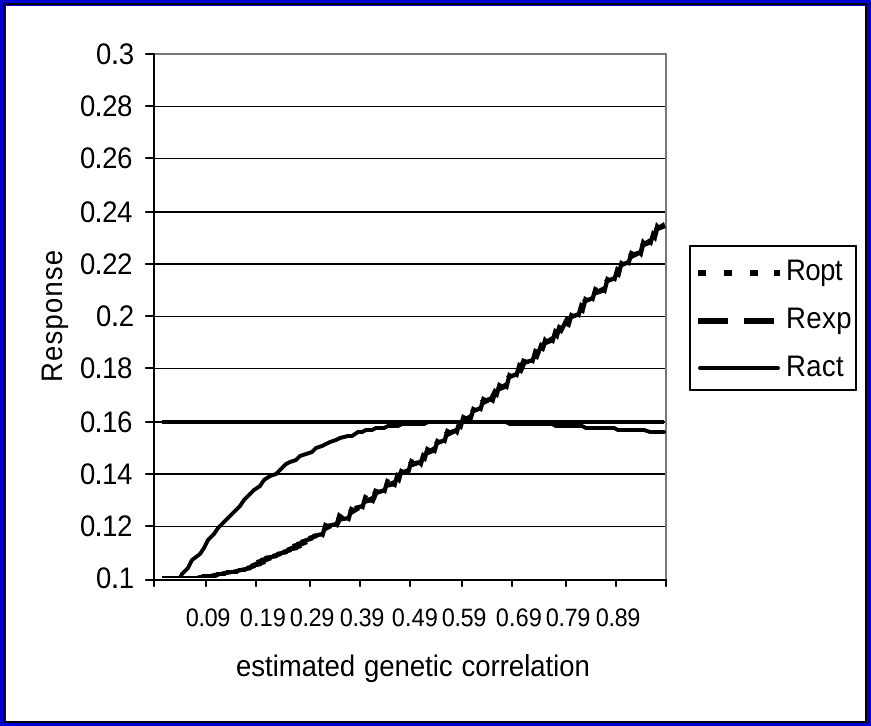
$$R_{opt} = \sqrt{G' P^{-1} G}$$

the expected response is

$$R_{\exp} = \sqrt{\hat{G}' \hat{P}^{-1} \hat{G}}$$

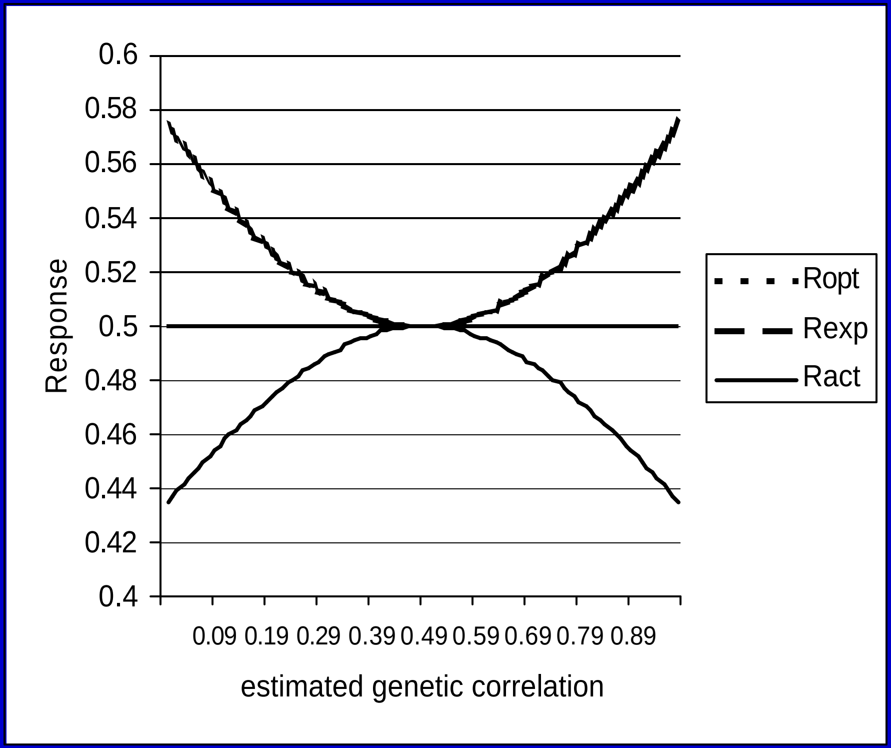
and the actual realized response is

$$R_{act} = \frac{\hat{G}' \hat{P}^{-1} G}{\sqrt{\hat{G}' \hat{P}^{-1} P \hat{P}^{-1} \hat{G}}}$$



h21= 0.1; h22=0.5;

rg = 0.6; rp = 0.1



h21=h22=0.5; rg = rp = 0.5

Schaeffer (1984) used Absolute Difference

$$AD = ½(r\hat{}_e - r_e) - (r\hat{}_g - r_g)½$$

to predict increase in PEV

g	e		AD	h^2_1=0.3, h^2_2=0.3 MT/ST	h^2_1= .1, h^2_2= .5 MT/ST
.5	.5	true values	0	1.00	1.08
.2	.2		0	1.00	1.04
-.2	-.2		0	.97	.84
.7	.3		.4	.98	1.05
.3	.7		.4	.97	1.03
-.2	.2		.4	.94	.74
-.5	.5		1	.93	1.04
.5	-.5	true values	0	1.10	1.25
.7	-.3		0	1.10	1.23
.2	-.2		.6	1.06	1.17
-.2	.2		1.4	.84	.64

Testing trial and error values is not very practical

Sales and Hill looked at proportional loss in response when estimated parameters are used, in relation to the size of the experiment

For single trait selection

loss of efficiency from using incorrect heritability is very low

Multiple Traits

proportional loss for trait 1 depends critically on its h2, less on correlations and h2 of correlated trait

h_1^2	h_2^2	R_g	R_e	R_p	R/R_{ST}	T (n=4)	T (n=16)
0.2	0.5	0.0	0.16	0.10	1.005	17800	11632
		0.0	0.50	0.32	1.054	1696	105
		0.5	-0.5	-0.16	1.386	208	80
		0.5	0.0	0.16	1.187	456	208
		0.5	0.5	0.47	1.062	1432	832
0.5	0.5	0.0	0.2	0.10	1.005	3080	2672
		0.0	0.5	0.25	1.035	476	400
		0.5	-0.5	0.0	1.118	124	80
		0.5	0.0	0.25	1.035	456	336
		0.5	0.5	0.5	1.000	-	-

Conclusion Sales & Hill

larger experiments needed when true parameters are such that correlated trait does not add much

‘infinite size’ if nothing added at all

Further:

incorrect parameters ‘no effect on bias’

provided that there is no selection!