

Continuing the transformation



Predicting genetic changes with genomic information

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Issues

- We want to combine genotype information with information from phenotypes and pedigree
- Need to know 'additional value' of a genomic test
- Need to predict genetic change when using genomics

Genomic breeding values

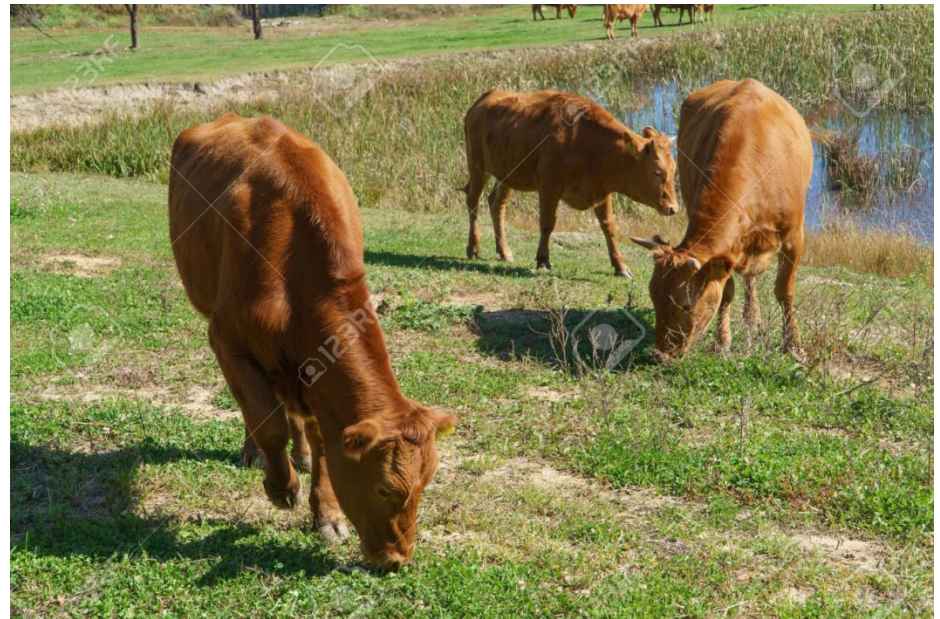
Good for:

Hard to measure, late in life traits HTML

- Lean meat yield, meat quality
- Reproductive Rate
- Adult Weight

But how does it change
selection response?

- Overall
- For each trait



Potential benefits of GS - some principles

% increase in EBV accuracy (male 1yo) and genetic gain

Trait Measurability	$h^2 = 0.1 = r^2$		$h^2 = 0.3 = r^2$	
	%Δ Acc	%Δ Gain	%Δ Acc	%Δ Gain
< 1 year, both sexes	15	7	7	7
> 1 year, both sexes	68	19	59	37
>1 year, females only	119	27	112	52
on Corr. Trait, $r_g = 0.9$	20	12	20	26
on Corr. Trait, $r_g = 0.5$	67	50	76	86

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These effects underestimated due to not accounting for Bulmer effect

How as additional response calculated

■ Selection index theory

- Index weights for various information sources
- Accuracies of EBV -overall index and per trait-
- Response -overall and per trait-

Selection Index Approach

Genomic Selection: Predict TBV with Accuracy = x

→ GS explains x^2 % of V_A → $V_{\text{qtl}} = x^2 V_A$

Lande and Thompson, 1990 Genetics:

$$V_{\text{polygenic}} = (1-x^2)V_A$$

Models

Without GS: $V_{\text{Pheno}} = V_{\text{AddGen}} + V_{\text{error}}$

With GS: $V_{\text{Pheno}} = V_{\text{polygenic}} + V_{\text{qtl}} + V_{\text{error}}$

Predict from
phenotypes pedigree

Predict from DNA markers

Selection Index Approach

use info on various information sources: *below for one trait only*

Without
GS:

Own perf.	V_p						
Sire		V_p					
Dam			V_p				
FullSibs	etc			$\{t-(1-t)/n\}V_p$			
HalfSibs					$\{t-(1-t)/n\}V_p$		
Progeny						$\{t-(1-t)/n\}V_p$	

V_a
$V_a/2$
$V_a/2$
$V_a/2$
$V_a/4$
$V_a/2$

With
GS:

Own perf.	$V_p - V_q$							0
Sire		$V_p - V_q$						0
Dam			$V_p - V_q$					0
FullSibs	etc			$\{t-(1-t)/n\}(V_p - V_q)$				0
HalfSibs					$\{t-(1-t)/n\}(V_p - V_q)$			0
Progeny						$\{t-(1-t)/n\}(V_p - V_q)$		0
QTL	0	0	0	0	0	0	0	V_q

$V_a - V_q$
$(V_a - V_q)/2$
$(V_a - V_q)/2$
$(V_a - V_q)/2$
$(V_a - V_q)/4$
$(V_a - V_q)/2$
V_q

P-matrix

G-matrix

Selection Index Approach

Pseudo BLUP: Genomic Breeding value is an additional trait with $h^2 = 1$

Without
GS:

Own perf.	V_p							V_a
Sire		V_p						$V_a/2$
Dam			V_p					$V_a/2$
FullSibs	etc			$\{t+(1-t)/n\}V_p$				$V_a/2$
HalfSibs					$\{t+(1-t)/n\}V_p$			$V_a/4$
Progeny						$\{t+(1-t)/n\}V_p$		$V_a/2$

With
GS:

Own perf.	V_p						V_q	V_a
Sire		V_p					$V_q/2$	$(V_a)/2$
Dam			V_p				$V_q/2$	$(V_a)/2$
FullSibs	etc			$\{t+(1-t)/n\}(V_p)$			$V_q/2$	$(V_a)/2$
HalfSibs					$\{t+(1-t)/n\}(V_p)$		$V_q/4$	$(V_a)/4$
Progeny						$\{t+(1-t)/n\}(V_p)$	$V_q/2$	$(V_a)/2$
QTL	V_q	$V_q/2$	$V_q/2$	$V_q/2$	$V_q/4$	$V_q/2$	V_q	V_q

P-matrix

G-matrix

Selection index: example of 2 approaches own phenotype + GBV

$h^2 = 0.5$

GBV reliability “ x^2 ” = 0.5

	P		G (,BV)		b	varIndex	acc														
Phenotype	1		0.5	a	0.5000	0.2500	0.7071														
Phenotype	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 5px;">P</td><td style="padding: 5px;">1</td><td style="padding: 5px;">0.25</td></tr> <tr><td style="padding: 5px;">mBV</td><td style="padding: 5px;">0.25</td><td style="padding: 5px;">0.25</td></tr> </table>		P	1	0.25	mBV	0.25	0.25	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 5px;">G</td><td style="padding: 5px;">0.5</td><td style="padding: 5px;">a</td></tr> <tr><td style="padding: 5px;">q</td><td style="padding: 5px;">0.25</td><td style="padding: 5px;">q</td></tr> </table>		G	0.5	a	q	0.25	q	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 5px;">0.3333</td></tr> <tr><td style="padding: 5px;">0.6667</td></tr> </table>	0.3333	0.6667	0.3333	0.8165
P	1	0.25																			
mBV	0.25	0.25																			
G	0.5	a																			
q	0.25	q																			
0.3333																					
0.6667																					
Corrected Phenotype	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 5px;">P</td><td style="padding: 5px;">0.75</td><td style="padding: 5px;">0</td></tr> <tr><td style="padding: 5px;">mBV</td><td style="padding: 5px;">0</td><td style="padding: 5px;">0.25</td></tr> </table>		P	0.75	0	mBV	0	0.25	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 5px;">G</td><td style="padding: 5px;">0.25</td><td style="padding: 5px;">u</td></tr> <tr><td style="padding: 5px;">q</td><td style="padding: 5px;">0.25</td><td style="padding: 5px;">q</td></tr> </table>		G	0.25	u	q	0.25	q	<table style="width: 100%; border-collapse: collapse;"> <tr><td style="padding: 5px;">0.3333</td></tr> <tr><td style="padding: 5px;">1.0000</td></tr> </table>	0.3333	1.0000	0.3333	0.8165
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q	0.25	q																			
0.3333																					
1.0000																					

Note weights on QTL info

MBV = GBV = “QTL”

Selection index: example of 2 approaches

- information from relatives

	P		G		b	VarIndex	accuracy
ownPoly	0.75	0	0.125	0.25	0.3143	0.3429	0.8281
Own GBV	0	0.25	0	0.25	1.0000		
sirepoly	0.125	0	0.75	0.125	0.1143		

Selection index: example of 2 approaches

- information from relatives

	P				G	b	VarIndex	accuracy
ownPoly	0.75	0	0.125	0	0.25	0.3143	0.3429	0.8281
ownGBV	0	0.25	0	0.125	0.25	1		
sirepoly	0.125	0	0.75	0	0.125	0.1143		
sireMBV	0	0.125	0	0.25	0.125	0		

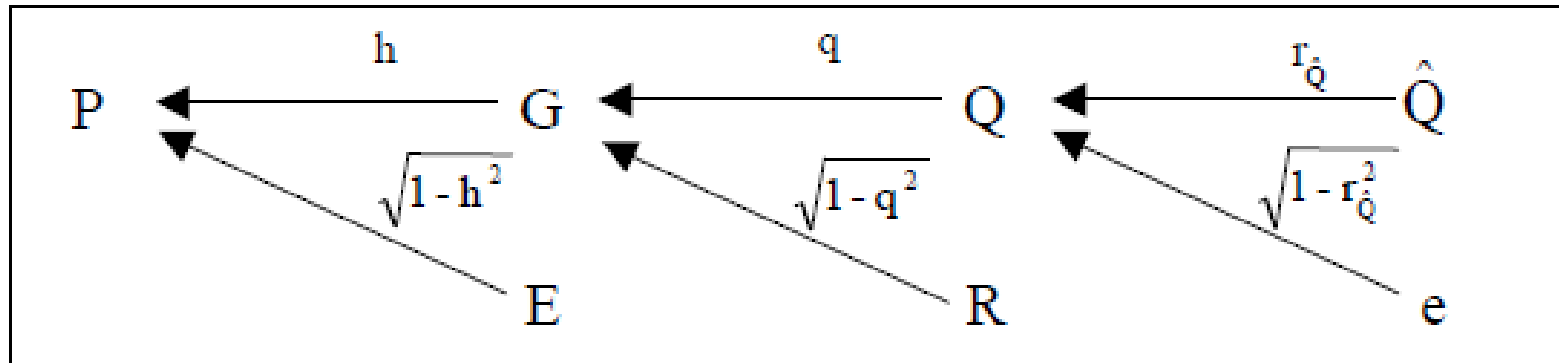
	P				G	b	varIndex	acc
ownPoly	0.75	0	0.125	0.25	0.25	0.3182	0.3409	0.8257
ownGBV	0	0.25	0.125	0.25	0.25	0.9545		
Sirepheno	0.125	0.125	1	0.25	0.25	0.0909		

These models are not equivalent, not same accuracy

Conclusion: Relatives info needs to be 'corrected for markers'

Path coefficient method following

Dekkers Dec 2007 JABG



P = Phenotype

G = Breeding Value

Q = BV component associated with markers (=GBV)

Q_{hat} = estimate of Q

Accuracy GBV = "x" = $q \cdot r_{Q_{\text{hat}}}$

Phenotypic correlation: $r_{P, Q_{\text{hat}}} = h \cdot x$

Genetic correlation $r_{G, Q_{\text{hat}}} = x$

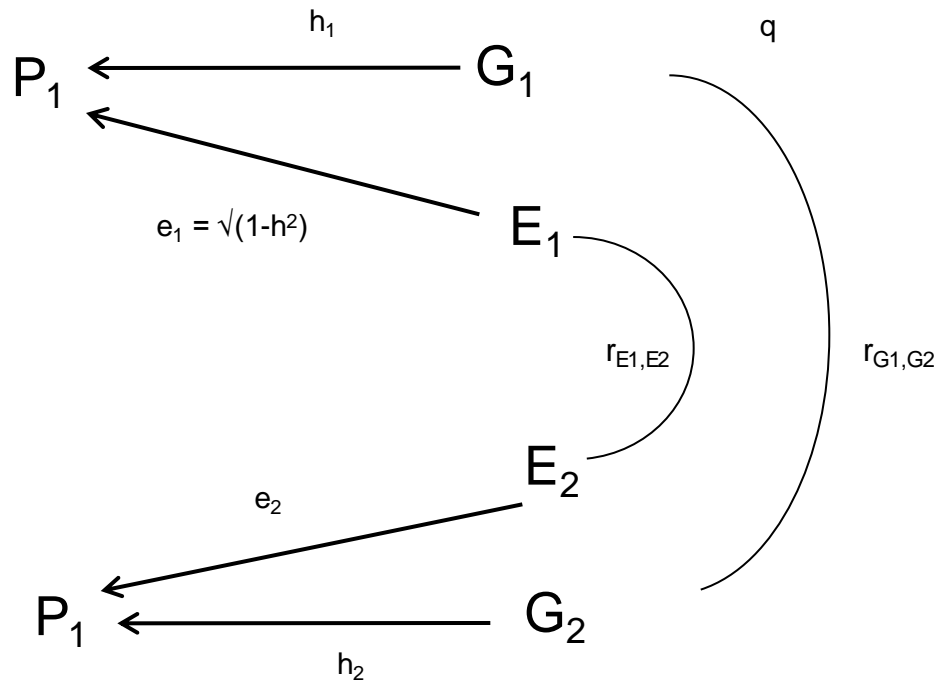
Conclusion: single trait

- Can include GBV as a correlated trait
 - And use standard software for selection index
- $r_g = \text{accuracy}$, same as 'x'
- $r_p = h \cdot x$
- econ value for GBV = 0
- This is equivalent to treating it as an extra info source in a single trait multiple info sources approach:
EBV = f(own perf, dam, sire, sibs, progeny, GBV)

Extension to multiple traits

- The 'polygenic variance option is harder to implement
- Some traits may have GBV, others may not
- Need correlations....
 - between GBV and other trait phenotypes
 - between GBV and other trait genotypes
 - between different GBVs

Path coefficient method Dekkers Dec 2007 JABG

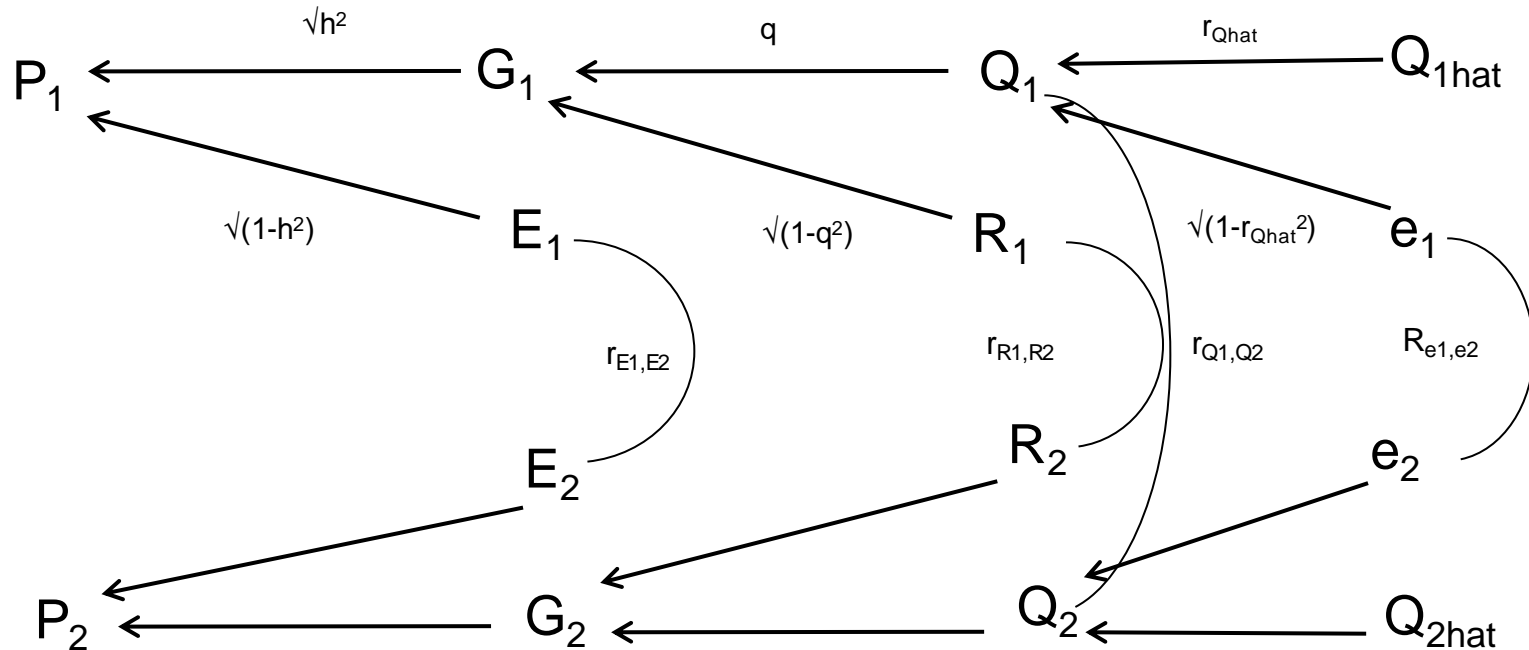


$$r_{P_1 G_2} = h_1 r_{G_1, G_2}$$

$$r_{p_1 p_1} = h_1 h_2 r_{G_1, G_2} + e_1 e_2 r_{E_1, E_2}$$

Path coefficient method following

Dekkers Dec 2007 JABG



$$r_{G_i, Q_{\hat{j}}} = r_{Q_{1\hat{}}, Q_{1,2}} \cdot r_{Q_1, Q_2}$$

$$r_{Q_{\hat{i}}, Q_{\hat{j}}} = r_{Q_{1\hat{}}, Q_{2\hat{}}} \cdot r_{Q_1, Q_2}$$

$$r_{P_i, Q_{\hat{j}}} = h_i \cdot r_{Q_{1\hat{}}, Q_{1,2}} \cdot r_{Q_1, Q_2}$$

Summary



- Can use selection index approach
- GBV + polygenic (no correlation)
- Or: GBV + P, correlation is r^2
- The latter is easier: Genomic BV as a correlated trait.

r_g = accuracy of GBV = 'x'

r_p = $h \cdot x$

Econ value of GBV = 0