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

	$h^2 = 0.1 = r^2$		$h^2 = 0.3 = r^2$	
Trait Measurability	%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 → $V_{qtl} = x^2 V_A$

Lande and Thompson, 1990 Genetics:

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

Models

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

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

Predict from phenotypes pedigree

Predict from DNA markers

Selection Index Approach

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

Without GS:

							P-matrix	G-matrix
Own perf.	Vp							Va
Sire		Vp						Va/2
Dam			Vp					Va/2
FullSibs	etc			{t-(1-t)/n}Vp				Va/2
HalfSibs					{t-(1-t)/n}Vp			Va/4
Progeny						{t-(1-t)/n}Vp		Va/2

With GS:

							P-matrix	G-matrix
Own perf.	Vp-Vq						0	Va-Vq
Sire		Vp-Vq					0	(Va-Vq)/2
Dam			Vp-Vq				0	(Va-Vq)/2
FullSibs	etc			{t-(1-t)/n}(Vp-Vq)			0	(Va-Vq)/2
HalfSibs					{t-(1-t)/n}(Vp-Vq)		0	(Va-Vq)/4
Progeny						{t-(1-t)/n}(Vp-Vq)	0	(Va-Vq)/2
QTL	0	0	0	0	0	0	Vq	Vq

Selection Index Approach

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

Without GS:

Own perf.	Vp						Va
Sire		Vp					Va/2
Dam			Vp				Va/2
FullSibs	etc			{t+(1-t)/n}Vp			Va/2
HalfSibs					{t+(1-t)/n}Vp		Va/4
Progeny						{t+(1-t)/n}Vp	Va/2

With GS:

Own perf.	Vp						Vq	Va
Sire		Vp					Vq/2	(Va)/2
Dam			Vp				Vq/2	(Va)/2
FullSibs	etc			{t+(1-t)/n}(Vp)			Vq/2	(Va)/2
HalfSibs					{t+(1-t)/n}(Vp)		Vq/4	(Va)/4
Progeny						{t+(1-t)/n}(Vp)	Vq/2	(Va)/2
QTL	Vq	Vq/2	Vq/2	Vq/2	Vq/4	Vq/2	Vq	Vq

P-matrix

G-matrix

Selection index: example of 2 approaches

own phenotype + GBV

$h^2 = 0.5$

GBV accuracy = 0.5

	P	G (,BV)		b	varIndex	acc
Phenotype	1	0.5	a	0.5000	0.2500	0.7071

	P		G				
Phenotype	1	0.25	0.5	a	0.3333	0.3333	0.8165
mBV	0.25	0.25	0.25	q	0.6667		

	P		G				
Corrected Phenotype	0.75	0	0.25	u	0.3333	0.3333	0.8165
mBV	0	0.25	0.25	q	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		

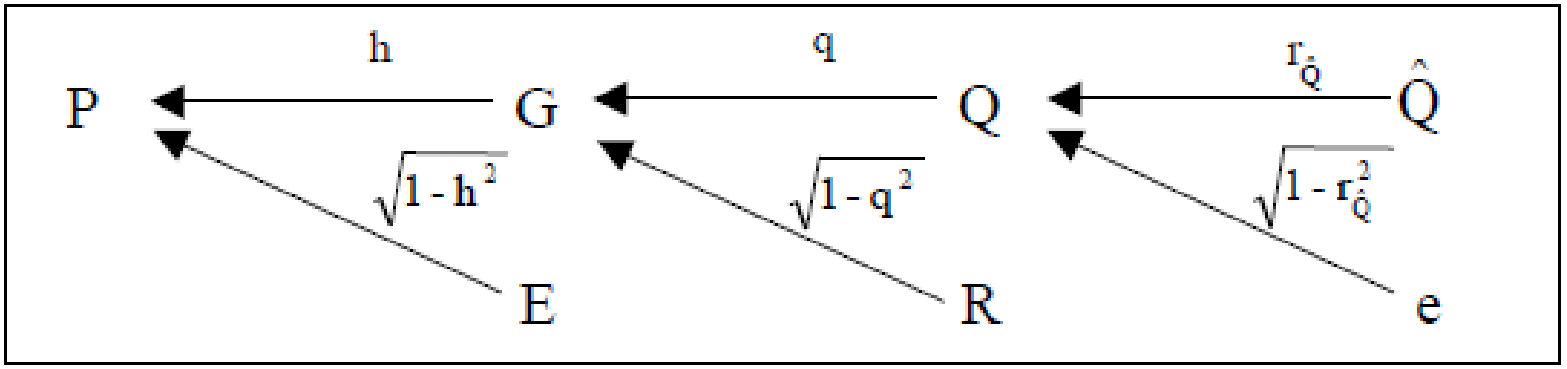
	P			G	b	varIndex	acc
ownPoly	0.75	0	0.125	0.25	0.3182	0.3409	0.8257
ownGBV	0	0.25	0.125	0.25	0.9545		
Sirepheno	0.125	0.125	1	0.25	0.0909		

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" = $q.r_{Qhat}$

Phenotypic correlation: $r_{P,Qhat} = h.x$

Genetic correlation $r_{G,Qhat} = x$

Conclusion: single trait

- Can include GBV as a correlated trait
  - And use standard software for selection index

- r_g = accurcay, same as ‘x’
- r_p = h.x
- econ value for GBV = 0

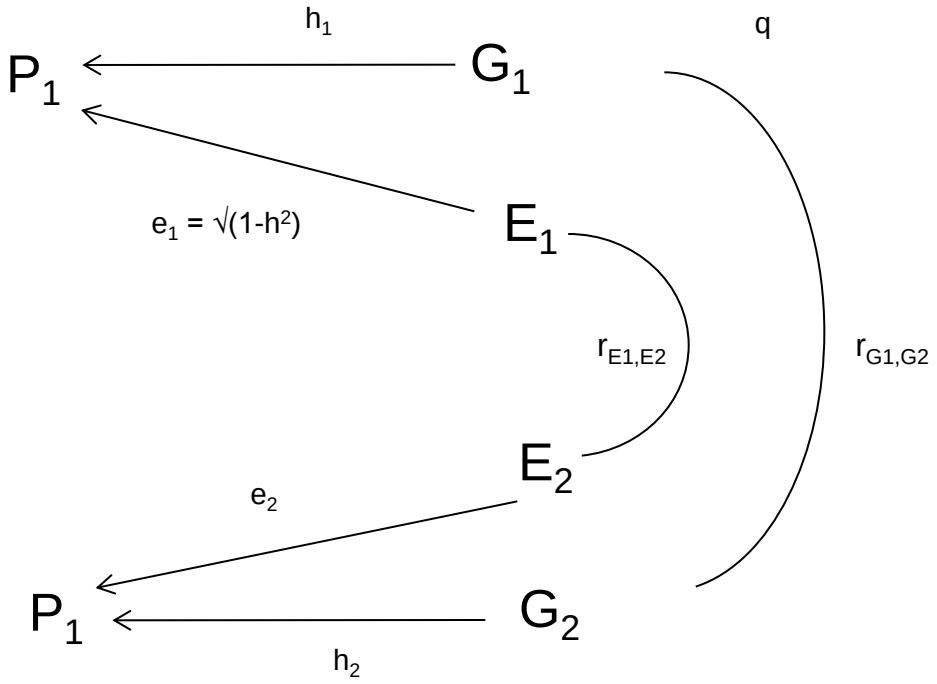
- This is equivalent to treating it as an extra info source in a single trait multiple info sources approach:

  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

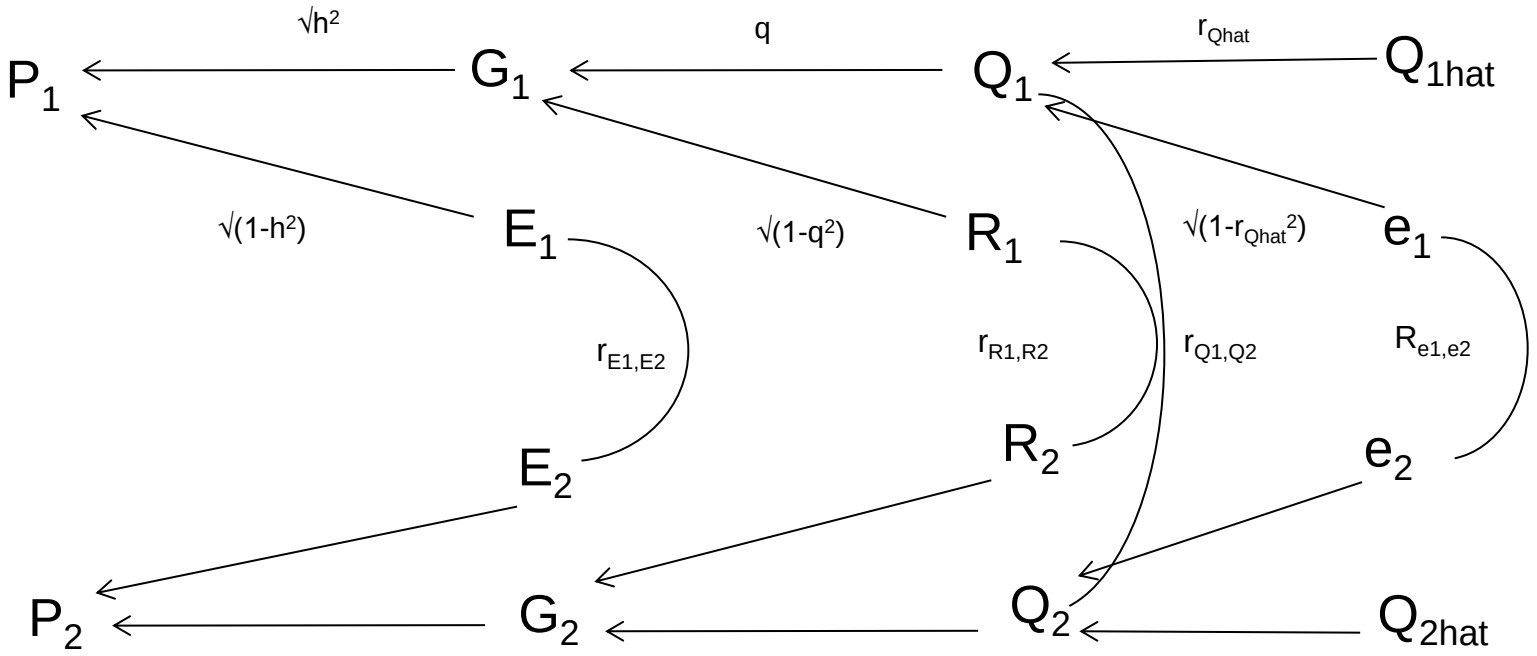
Path coefficient method *Dekkers Dec 2007 JABG*



$r_{P1G2} = h_1 r_{G1,G2}$

$r_{p1p1} = h_1\ h_2\ r_{G1,G2} + e_1\ e_2\ r_{E1,E2}$

Path coefficient method following *Dekkers Dec 2007 JABG*



$r_{Gi,Qhatj} = r_{Q1hat}.r_{Q1,Q2}$

$r_{Pi,Qhatj} = h_i r_{Q1hat}.r_{Q1,Q2}$

$r_{Qhati\ ,Qhatj} = r_{Q1hat}.r_{Q2hat}.r_{Q1,Q2}$

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.x
Econ value of GBV = 0