

Increase in accuracy using multi-trait genomic breeding value estimation

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Introduction

- Genomic breeding value estimation yields accurate breeding values for juvenile animals
 - Increased accuracy due to use SNPs
- Multi-trait was a major development in breeding value estimation
 - Increased accuracy due correlation between traits (e.g. across country evaluations)

=> Can we combine both approaches?

Four different MT models¹ were applied

Name	Model	SNP variances
A	Polygenic - pedigree relationship matrix	SNP not included
G	Polygenic - marker relationship matrix	Equal for all SNP
BA	BayesA: effects estimated per SNP	Drawn from 1 distribution
BC	BayesC: effects estimated per SNP	Drawn from 2 distributions

¹ Variances are estimated in all models simultaneously with the effects
=> Single (ST) and multitrait (MT) analyses with all models

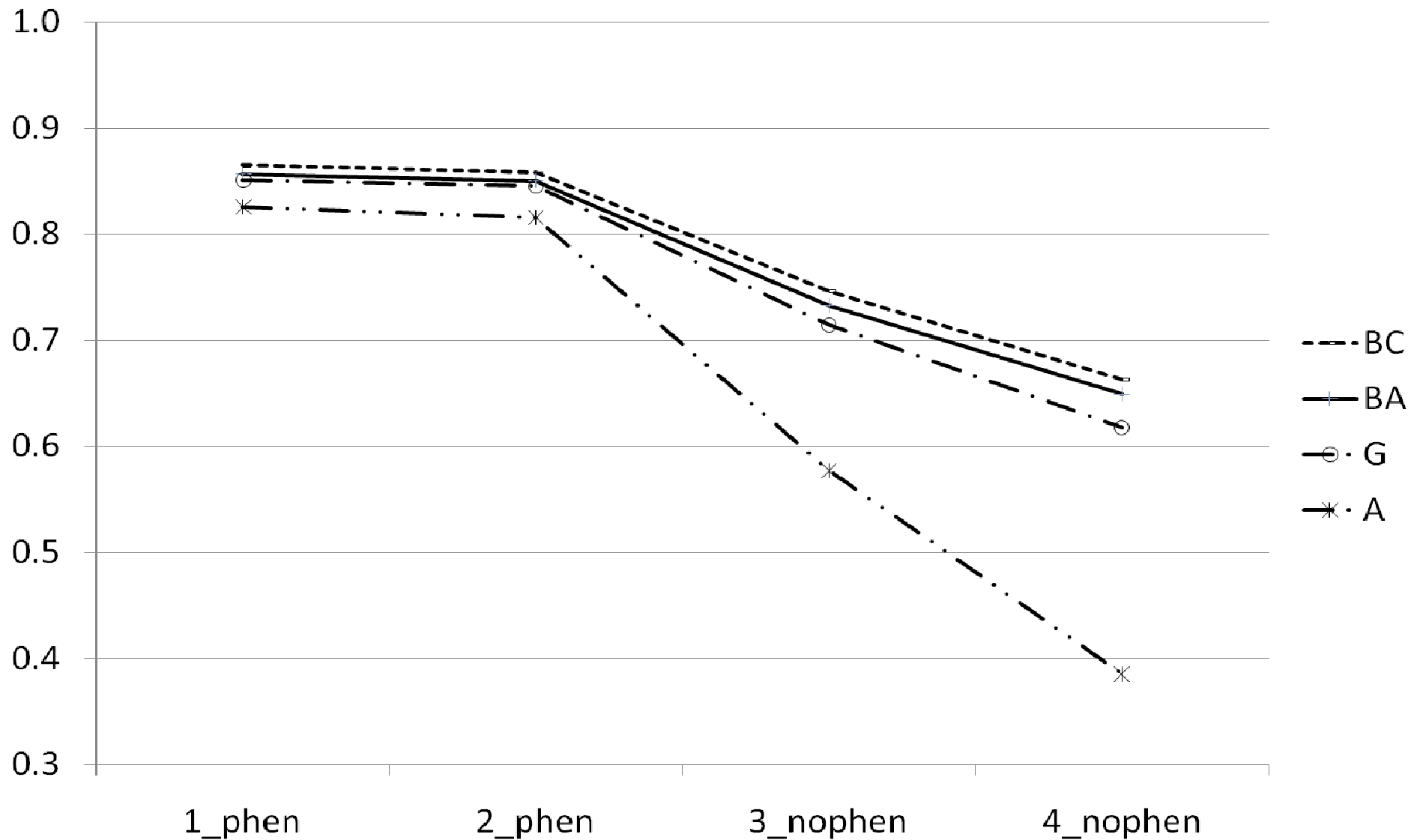
Simulation

- $N_e = 500$
- Genome size: 5 M
- 5.655 SNPs
- 200 QTL equally distributed across genome
- QTL effects normally distributed
- Two traits; $h^2(\text{tr. 1}) = 0.9$ & $h^2(\text{tr. 2}) = 0.6$
- 3 genetic correlations: 0.2, 0.5 & 0.8

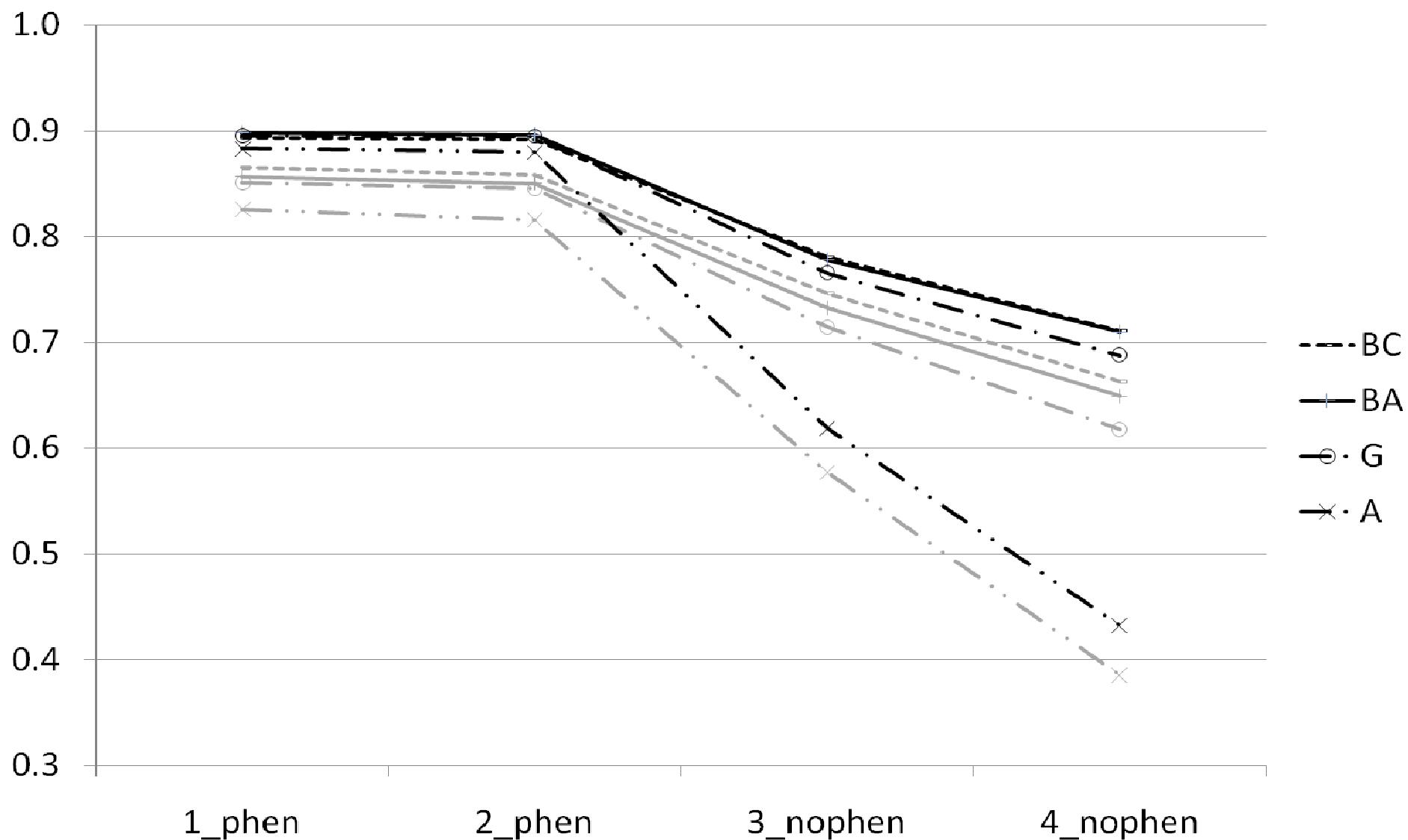
Simulated data

Generation	# animals	Phenotype ?	
		trait 1	trait 2
1	500	Yes	Yes
2	500	Yes	Yes
3	500	No	No
4	500	No	No

Trait 2; $r_g=0.2$ (MT)



Trait 2; $r_g=0.2$; $r_g=0.8$ (MT)



Results summarized

Single trait (not shown):

- Accuracy of G, BayesA & BayesC very similar

Multi-trait:

- Accuracy BayesC > BayesA > G (small differences)

=> How much is the accuracy increased by MT?

Results: accuracy MT – accuracy ST

- ❑ Accuracy of trait 1 did not improve with MT
- ❑ Accuracy of trait 2 juvenile animals (gen. 3):

Model	Genetic correlation		
	0.2	0.5	0.8
A	0.000	0.009	0.034
G	0.004	0.017	0.052
BayesA	0.015	0.024	0.056
BayesC	0.030	0.040	0.071

Conclusions

- MT: Accuracy $BC > BA > G$ (small differences)
 - Difference may increase with more extreme QTL effects
- For juvenile animals, MT yielded a maximum increase in accuracy of 0.07

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