Genomic breeding value estimation and QTL detection using univariate and bivariate models

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Introduction

- Genomic breeding value estimation yields accurate breeding values for juvenile animals
  - Increased accuracy due to use of SNPs

- Multiple 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?

Objectives

1. Estimate genomic breeding values with SNP based univariate and bivariate models

2. Detect QTL with univariate and bivariate models

Four different models[1] were applied

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

[1] Variances are estimated in all models simultaneously with the effects

[2] BA and BC include a polygenic effect

=> Univariate and bivariate analyses with all models

BayesC; QTL-mapping

- Univariate: for each trait separately

- Bivariate: QTL probability inferred for both traits simultaneously

=> no distinction in QTL that affect one or both traits

- Significance thresholds were derived for the bivariate model using 2,000 permutations
  - Genotypes permuted against phenotypes & pedigree

Correlation reference population phenotypes & EBV

		Model			
Model	Trait	A	G	BA	BC
Univariate	Quantitative	0.892	0.741	0.824	0.824
	Binary	0.671	0.602	0.637	0.631
Bivariate	Quantitative	0.878	0.740	0.744	0.746
	Binary	0.618	0.591	0.592	0.583

Correlations EBV juveniles quantitative (binary) trait

		Univariate				Bivariate			
		A	G	BA	BC	A	G	BA	BC
Univariate	A		0.60	0.67	0.63	0.99	0.62	0.61	0.58
	G	0.60		0.98	0.94	0.60	0.99	0.99	0.94
	BA	0.62	1.00		0.98	0.66	0.98	0.99	0.96
	BC	0.56	0.95	0.96		0.63	0.94	0.96	0.98
Bivariate	A	0.93	0.62	0.64	0.60		0.63	0.61	0.58
	G	0.60	0.95	0.95	0.94	0.64		0.99	0.95
	BA	0.58	0.94	0.95	0.96	0.63	0.99		0.98
	BC	0.50	0.88	0.88	0.95	0.57	0.94	0.96	

Correlations EBV juveniles quantitative (binary) trait

		Univariate				Bivariate			
		A	G	BA	BC	A	G	BA	BC
Univariate	A		0.60	0.67	0.63	0.99	0.62	0.61	0.58
	G	0.60		**0.98**	**0.94**	0.60	0.99	0.99	0.94
	BA	0.62	**1.00**		**0.98**	0.66	0.98	0.99	0.96
	BC	0.56	**0.95**	**0.96**		0.63	0.94	0.96	0.98
Bivariate	A	0.93	0.62	0.64	0.60		0.63	0.61	0.58
	G	0.60	0.95	0.95	0.94	0.64		**0.99**	**0.95**
	BA	0.58	0.94	0.95	0.96	0.63	**0.99**		**0.98**
	BC	0.50	0.88	0.88	0.95	0.57	**0.94**	**0.96**	

Correlations EBV juveniles quantitative (binary) trait

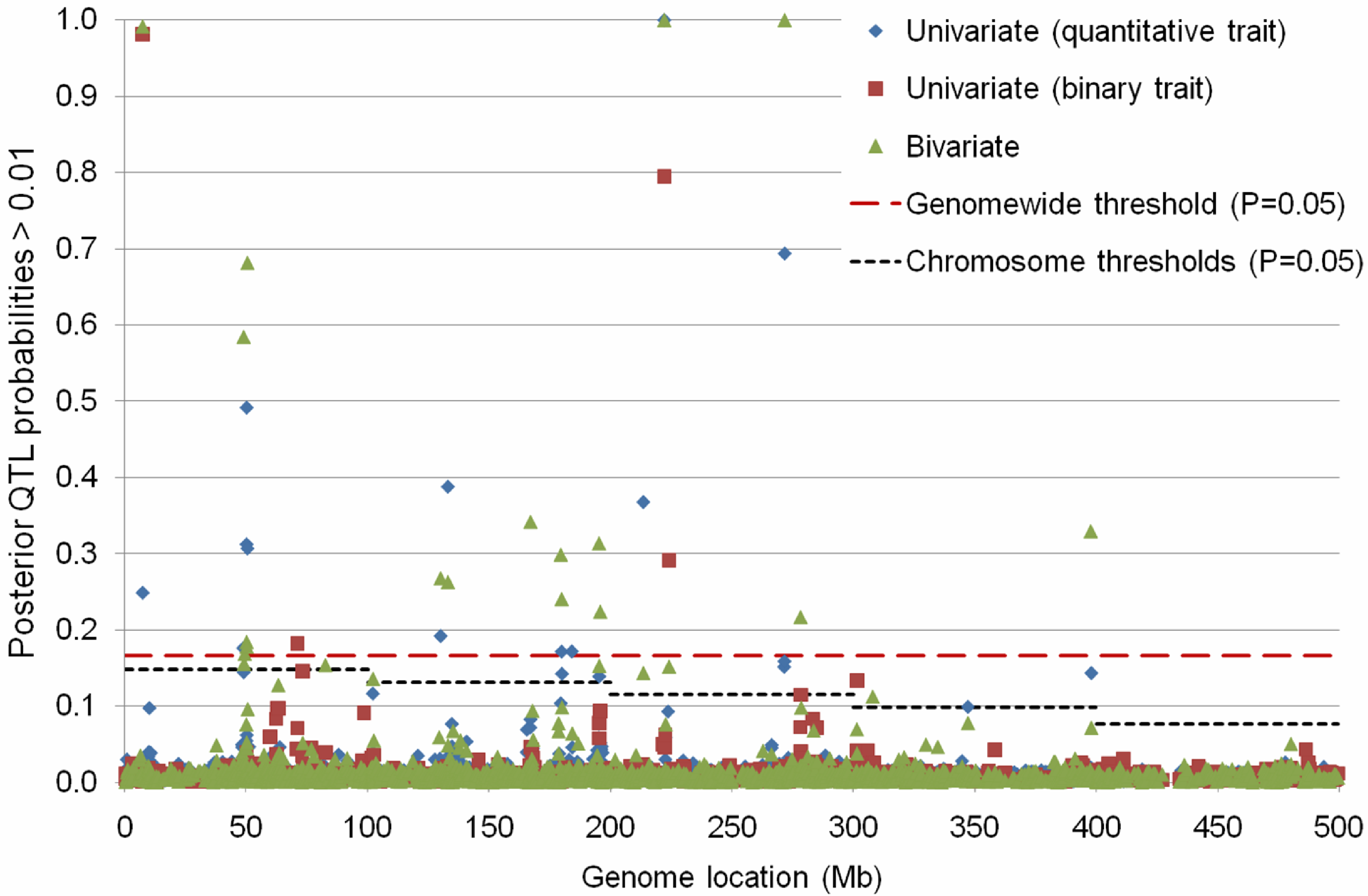
		Univariate				Bivariate			
		A	G	BA	BC	A	G	BA	BC
Univariate	A		0.60	0.67	0.63	**0.99**	0.62	0.61	0.58
	G	0.60		0.98	0.94	0.60	**0.99**	0.99	0.94
	BA	0.62	1.00		0.98	0.66	0.98	**0.99**	0.96
	BC	0.56	0.95	0.96		0.63	0.94	0.96	**0.98**
Bivariate	A	**0.93**	0.62	0.64	0.60		0.63	0.61	0.58
	G	0.60	**0.95**	0.95	0.94	0.64		0.99	0.95
	BA	0.58	0.94	**0.95**	0.96	0.63	0.99		0.98
	BC	0.50	0.88	0.88	**0.95**	0.57	0.94	0.96	

Results summarized - EBV

- Correlation phenotype & EBV:
  - Lower for SNP based models
  - Lower for bivariate models

- Correlations among predicted EBV:
  - High between univariate and bivariate runs
  - EBV of SNP based models with most extreme assumptions (G vs. BC) are least related

Posterior QTL probabilities



Results summarized – QTL detection

- 14 regions of < 2Mb with significant SNP effects, each explained:
  - 0.001 to 13.2% of genetic variance quantitative trait
  - 0.017 to 11.9% of genetic variance binary trait
- Bivariate analysis detects QTL with higher posterior probability compared to univariate analysis
- 3 out of 4 major QTL affect both traits
- No QTL identified on chromosome 5

Conclusions

- Estimated breeding values:
  - G and BayesA very similar
  - BayesC is different from G and BayesA
- QTL mapping:
  - Bivariate analysis detects QTL with higher posterior probability

Acknowledgements

- RobustMilk (www.robustmilk.eu)