Accuracy of MEBV

Effect of number of QTL and distribution of QTL variance

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Introduction

- Breeding values estimated with markers: MEBV.
  - Accurate estimated of BV without progeny testing.

This study:

1. Assess effect of QTL distribution on accuracy of MEBV.
2. Assess effect of method for calculating MEBV on accuracy of MEBV.

QTL distribution

Simulation studies assessing accuracy of MEBV:

- Simulated QTL according to Hayes and Goddard [2001]:
  - Few large QTL and many small QTL
- Genetics underlying traits differ:
  - Many genes involved in growth (*e.g.* human length, [Weedon et al., 2008]).
  - Single gene responsible for large proportion of genetic variation of milk fat composition, [Grisart et al., 2002].

- Need to identify effect of QTL distribution on accuracy of MEBV.

Methods for calculating MEBV

- Bayesian method of Meuwissen et al. [2001], BM;
- Least Angle Regression (LARS);
- Partial least square regression (PLSR);

- Do methods perform differently depending on distribution of QTL?

This study

- Effect of QTL distribution:
  - Number of QTL: low, intermediate, high.
  - QTL variance: all QTL equal; few large, many small.

Number of QTL	**QTL variance**
Low nQTL	unequal
Int. nQTL	unequal
High nQTL	unequal
Low nQTL	equal
Int. nQTL	equal
High nQTL	equal

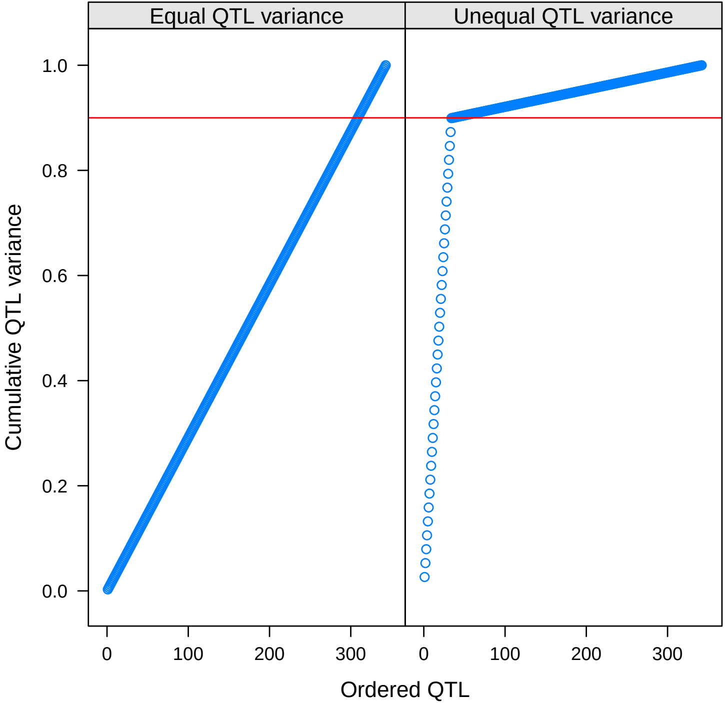
- Effect of method:
  - BM, LARS, PLSR.

Simulations

- Population of size 100 in mutation drift equilibrium.
  - Simulated for 5000 generations.
- Population of size 500 used for training.
- Offspring population of size 500 for evaluating MEBV.
- 5 chromosomes of 1 Morgan each.
- Average of 1431 SNP.
- 60 replicates.
- Heritability equal to 0.5.
- Simulations performed using package `HaploSim` in R.

Simulated data

variable	low nQTL	int. nQTL	high nQTL
nSNP	1431	1431	1431
LD SNP (r^2)	0.048	0.048	0.048
nQTL	35	172	343


Equal QTL variance
Unequal QTL variance
Cumulative QTL variance
1.0
0.8
0.6
0.4
0.2
0.0
0
100
200
300
0
100
200
300
Ordered QTL

Accuracies of MEBV

Method	**unequal QTL variance**		
	low nQTL	int. nQTL	high nQTL
BM	0.77	0.67	0.60
LARS	0.75	0.67	0.65
PLSR	0.66	0.66	0.67

Method	**equal QTL variance**		
	low nQTL	int. nQTL	high nQTL
BM	0.71	0.67	0.67
LARS	0.65	0.63	0.63
PLSR	0.68	0.67	0.66

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Genetic variances

Method	**unequal QTL variance**		
	low nQTL	int. nQTL	high nQTL
BM	55%	35%	14%
LARS	56%	55%	49%
PLSR	77%	73%	76%

Method	**equal QTL variance**		
	low nQTL	int. nQTL	high nQTL
BM	51%	43%	37%
LARS	48%	45%	46%
PLSR	81%	81%	75%

Table: Variance of MEBV estimated by each method as percentage of simulated genetic variance.

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Conclusions

- Number and distribution of genes is an important factor for accuracy of MEBV.
- In general: accuracies decreased when number of genes increased.
- Accuracies obtained with PLSR almost not affected by QTL scenario.

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