Accounting for breed origin of alleles increase accuracy of genomic prediction in admixed populations

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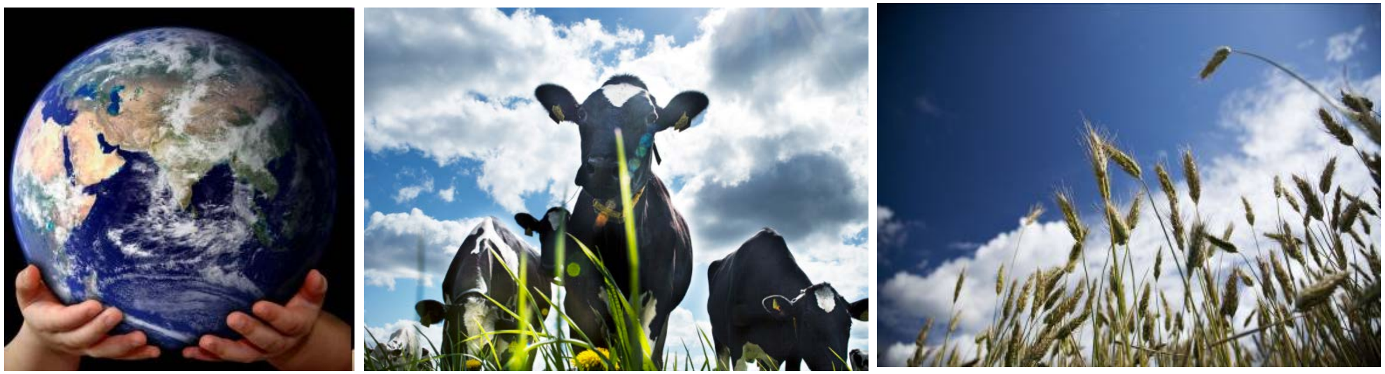


Introduction

- Genomic prediction in admixed population context is challenging
  - Differences in linkage disequilibrium
  - Specific QTL effects across breeds

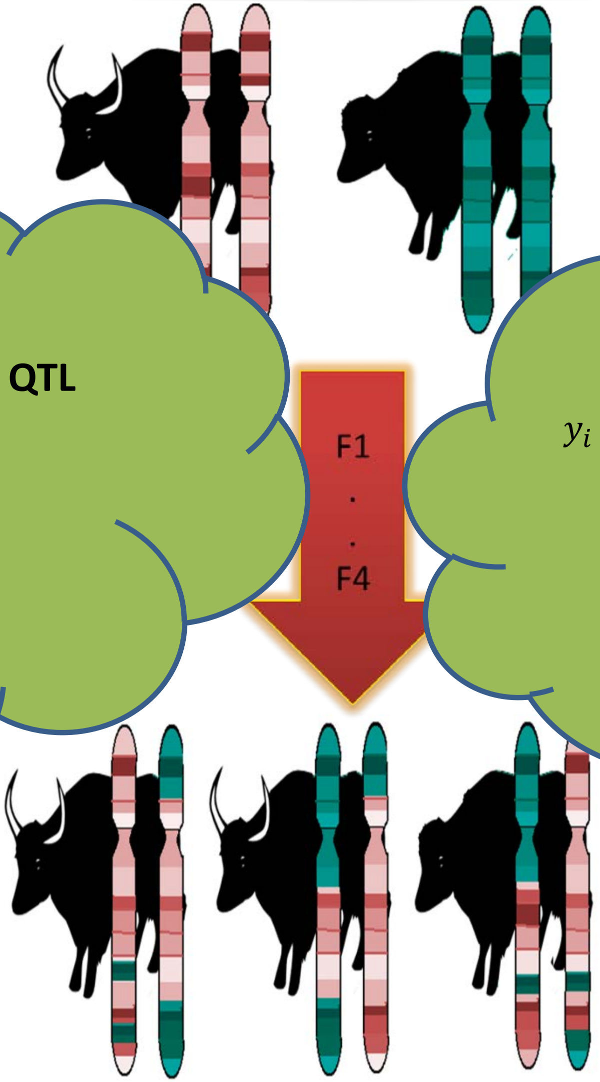
☐ Objective

Breed Origin of alleles Genomic Model (BOGM)

vs

Traditional Genomic Model (TGM)

Material & Methods



Single trait, h2=0.25, 100 QTL

QTL effects of two breeds:
Identical,
correlation of 0.5, or
correlation of 0.1

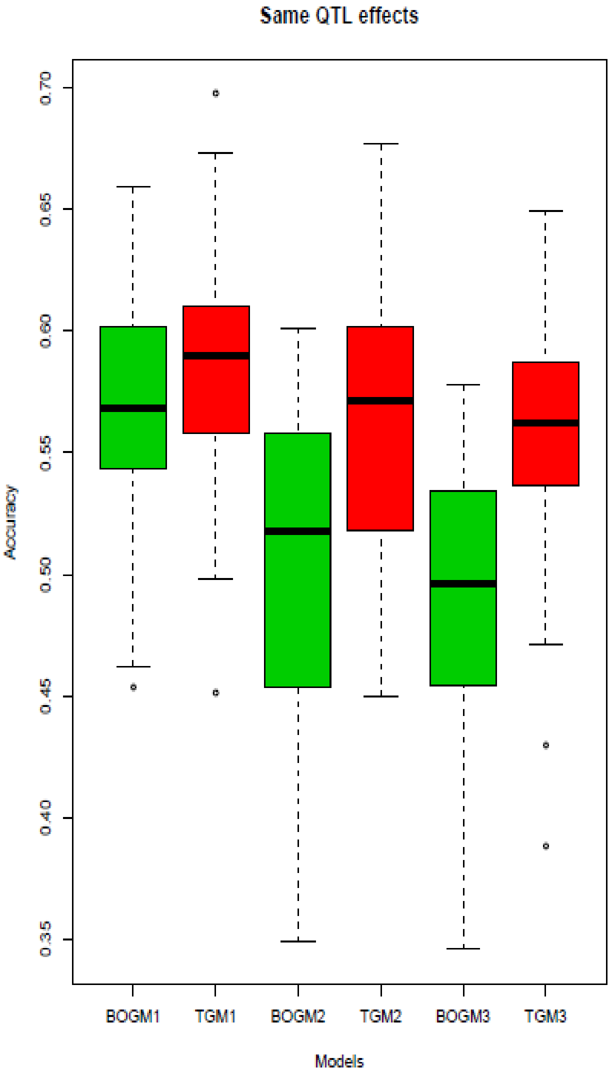
BOGM:

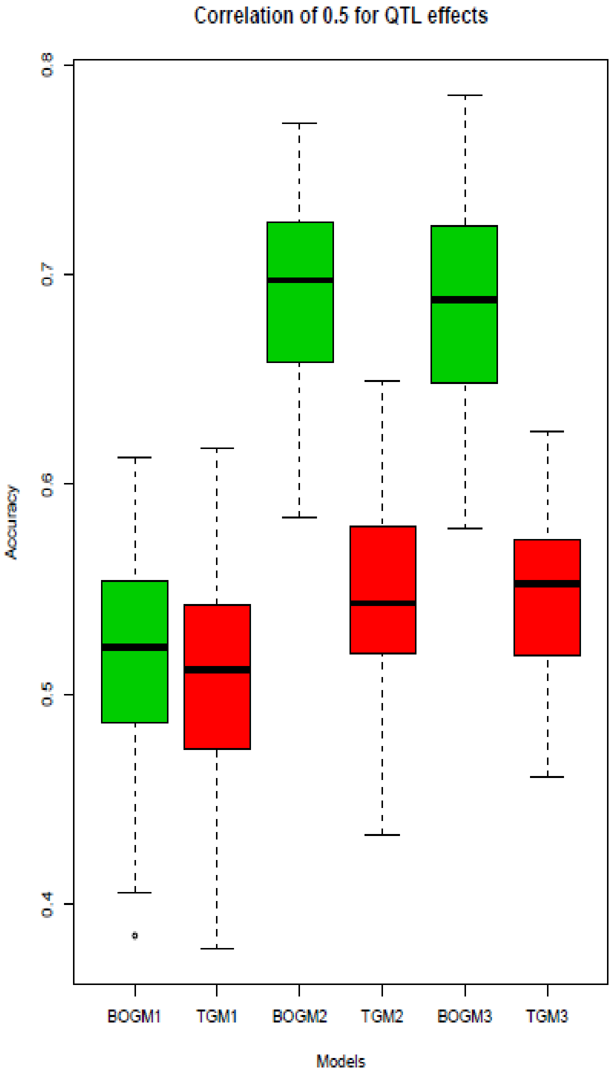
$$y_i = \mu + \sum_{b=1}^{breeds} \left(\sum_{j=1}^{m} \boldsymbol{U}_{ijb} \boldsymbol{\beta}_{jb} \zeta_{jb}\right) + e_i$$

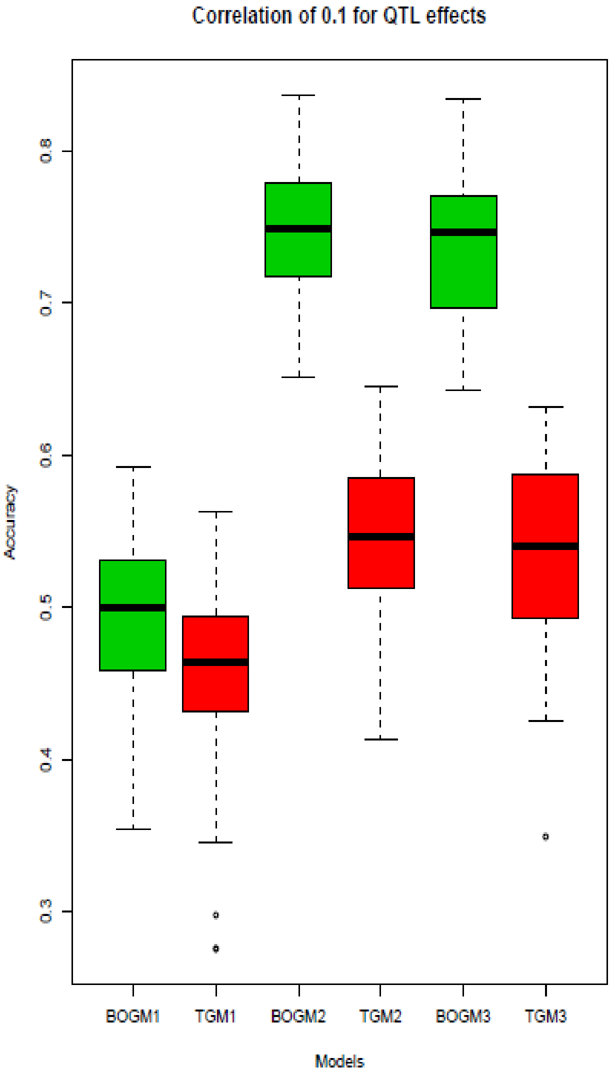
TGM:

$$y_i = \mu + \sum_{j=1}^{m} X_{ij} \beta_j \zeta_j + e_i$$

Results


Same QTL effects
Accuracy
0.35
0.40
0.45
0.50
0.55
0.60
0.65
0.70
BOGM1
TGM1
BOGM2
TGM2
BOGM3
TGM3
Models


Correlation of 0.5 for QTL effects
Accuracy
0.4
0.5
0.6
0.7
0.8
BOGM1
TGM1
BOGM2
TGM2
BOGM3
TGM3
Models


Correlation of 0.1 for QTL effects
Accuracy
0.3
0.4
0.5
0.6
0.7
0.8
BOGM1
TGM1
BOGM2
TGM2
BOGM3
TGM3
Models

Results

Accuracy and bias in subsequent generation

Scenarios		1				0.5				0.1			
Populations		Accuracy		Bias		Accuracy		Bias		Accuracy		Bias	
TrG	TeG	BOGM	TGM	BOGM	TGM	BOGM	TGM	BOGM	TGM	BOGM	TGM	BOGM	TGM
1	2	0.476	0.610	0.823	0.922	0.504	0.339	1.104	0.831	0.460	0.208	1.191	0.643
1	3	0.456	0.548	0.793	0.898	0.455	0.285	1.093	0.764	0.419	0.172	1.179	0.567
2	3	0.557	0.608	0.980	1.010	0.719	0.594	1.010	1.033	0.749	0.576	0.993	1.018
2	4	0.494	0.563	0.907	0.985	0.685	0.535	1.009	0.988	0.714	0.510	0.982	0.960
3	4	0.541	0.607	0.977	0.988	0.713	0.588	1.004	1.020	0.748	0.569	0.986	1.012
3	5	0.480	0.561	0.918	0.971	0.675	0.527	0.990	0.975	0.723	0.516	0.992	0.988

TrG: Training generation, TeG: Test generation, BOGM: Breed of Origin Genomic Model, TGM: Traditional Genomic Model

Conclusions

- BOGM outperformed TGM when the correlation between QTL effects was <1.
- Accuracy of TGM was higher than BOGM when QTL effects were identical.
- Prediction bias was only observed when the first generation was used for training.

Accuracy of genomic prediction in an admixed population can be increased by taking into account the breed of origin of alleles.

Thank you for your attention