

Genomic selection in mink yield higher accuracies with a Bayesian approach allowing for heterogeneous variance than a GBLUP model

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Motivation

- **Produce large, high quality skins**
- **Expect genomic selection can increase accuracy of breeding value**
- **Mink genome sequenced in 2017**
 - Bayesian approach with scaffold variance possible

Objectives

- **Is a Bayesian approach superior to GBLUP?**
- **Do we need to take account of heterogeneous (co)variance structure over the genome?**
- **Is a multi-trait model more accurate than a single-trait model?**

Single-trait models

- **GBLUP:** $y_i = \mu + g_i + e_i$, $\text{Var}(\mathbf{g}) = \mathbf{G}\sigma_g^2$
- **BayesA:** $y_i = \mu + \sum_{j=1}^{n_{snp}} w_{ij} a_j + e_i$
- **BayesAS:** $y_i = \mu + \sum_{j=1}^{n_{scaffold}} w_{ij} \mathbf{a}_j + e_i$
 - Elements in \mathbf{a}_j are correlated within scaffold

Phenotypes

- **Brown line at Aarhus University research farm**
- **Live grading:**
 - Body weight, quality, underwool density, silkyness
- **Pelt grading:**
 - Pelt length, pelt quality, pelt density, pelt silkyness
- **Phenotypes corrected for fixed effects (Yc)**
 - Birth year, sex, house after weaning, age at pelting*
 - From BLUP model with all available information

*pelt traits

Genotypes

- **Genotypes from 2,100 mink, born 2010-2014**
- **Genotyping-by-sequencing (GBS)**
 - No chromosome information
- **28,000 markers from 400 scaffolds with 6-800 markers**
 - (mean~70, SD~120)

Compare models

- **Reference model: single-trait GBLUP**
- **Alternative 1: BayesA**
- **Alternative 2: BayesAS**
 - Markers close to each other tend to have correlated effects
- **Multi-trait alternatives**

Predictive ability

- **5-fold cross validation**

- In each fold 1/5 of paternal half sib families born in 2014 were discarded
- Predict GEBV of discarded animals from remaining data ~700 in total

- **Prediction accuracy**

$$Accuracy = cor(Y_c, GEBV) / \sqrt{h^2}$$

- **Compare models: Increase in accuracy and bootstrapping**

- Does accuracy increase in alternative models?
- Does contrast between models correlations include 0 in the 95% confidence interval?

Accuracies, single-trait

				Accuracy, relative to ST-GBLUP	
	Trait	h ² (BLUP)	ST-GBLUP	ST-BayesA	ST-BayesAS
Live grading	Bodyweight	0.53	0.49	+0.05	+0.03
	Quality	0.30	0.69	+0.00	<div style="border: 1px solid red; padding: 5px; text-align: center;"> <p>Avg incr: 5%</p> <p>0 Significant</p> </div>
	Density	0.16	0.39	+0.03	
	Silky	0.30	0.82	+0.02	
Dried skins	Length	0.46	0.48	+0.17	
	Quality	0.33	0.23	+0.04	+0.04
	Density	0.16	0.30	+0.07	+0.06
	Silky	0.18	0.14	+0.06	+0.06

Accuracies, single-trait

				Accuracy, relative to ST-GBLUP	
	Trait	h ² , (BLUP)	ST-GBLUP	ST-BayesA	ST-BayesAS
Live grading	Bodyweight	0.53	0.49	+0.05	+0.03
	Quality	0.30	0.69	Avg incr: 5% 0 Significant	+0.01
	Density	0.16	0.39		+0.06
	Silky	0.30	0.82		+0.02
Dried skins	Length	0.46	0.48		+0.17*
	Quality	0.33	0.23	+0.04	Avg incr: 30% 1 Significant
	Density	0.16	0.30	+0.07	
	Silky	0.18	0.14	+0.06	

Accuracies, single-trait

				Accuracy, relative to ST-GBLUP	
	Trait	h ² , (BLUP)	ST-GBLUP	ST-BayesA	ST-BayesAS
Live grading	Bodyweight	0.53	0.49	+0.05	+0.03
	Quality	0.30	0.69	Avg incr: 5%	+0.01
	Density	0.16	0.39	0 Significant	+0.06
	Silky	0.30	0.82	+0.02	+0.02
Dried skins	Length	0.46	0.48	+0.17*	+0.14
	Quality	0.33	0.23	Avg incr: 30%	+0.04
	Density	0.16	0.30	1 Significant	+0.06
	Silky	0.18	0.14	+0.06	+0.06

Avg incr: 6%

0 Significant

Accuracies, single-trait

				Accuracy, relative to ST-GBLUP	
	Trait	h ² , (BLUP)	ST-GBLUP	ST-BayesA	ST-BayesAS
Live grading	Bodyweight	0.53	0.49	+0.05	+0.03
	Quality	0.30	0.69	Avg incr: 5%	Avg incr: 6%
	Density	0.16	0.39	0 Significant	0 Significant
	Silky	0.30	0.82	+0.02	+0.02
Dried skins	Length	0.46	0.48	+0.17*	+0.14*
	Quality	0.33	0.23	Avg incr: 30%	+0.04
	Density	0.16	0.30	1 Significant	+0.06
	Silky	0.18	0.14	+0.06	+0.06

Avg incr: 27%
1 Significant

Accuracies, ST-GBLUP and multi-trait

				Accuracy, relative to ST-GBLUP		
	Trait	h ² , (BLUP)	ST-GBLUP	MT-GBLUP	MT-BayesA	MT-BayesAS
Live grading	Bodyweight	0.53	0.49	+0.01	+0.05	+0.03
	Quality	0.30	0.69	+0.01	Avg incr: 5% 0 Significant	+0.02
	Density	0.16	0.39	+0.07		+0.07
	Silky	0.30	0.82	+0.00		+0.03
Dried skins	Length	0.46	0.48	+0.01		+0.18
	Quality	0.33	0.23	+0.01	+0.03	+0.03
	Density	0.16	0.30	+0.00	+0.08	+0.06
	Silky	0.18	0.14	+0.00	+0.07	+0.06

Accuracies, ST-GBLUP and multi-trait

				Accuracy, relative to ST-GBLUP		
	Trait	h ² , (BLUP)	ST-GBLUP	MT-GBLUP	MT-BayesA	MT-BayesAS
Live grading	Bodyweight	0.53	0.49	+0.01	+0.05	+0.03
	Quality	0.30	0.69	Avg incr: 5%	+0.01	+0.02
	Density	0.16	0.39		+0.01	+0.07
	Silky	0.30	0.82	+0.00	+0.03	+0.02
Dried skins	Length	0.46	0.48	+0.01	+0.18	+0.14
	Quality	0.33	0.23	+0.01	Avg incr: 1%	+0.03
	Density	0.16	0.30	+0.00		+0.06
	Silky	0.18	0.14	+0.00	+0.07	+0.06

Accuracies, ST-GBLUP and multi-trait

				Accuracy, relative to ST-GBLUP		
	Trait	h ² , (BLUP)	ST-GBLUP	MT-GBLUP	MT-BayesA	MT-BayesAS
Live grading	Bodyweight	0.53	0.49	+0.01	+0.05	+0.03
	Quality	0.30	0.69	Avg incr: 5%	+0.01	Avg incr: 6%
	Density	0.16	0.39	0 Significant	+0.01	0 Significant
	Silky	0.30	0.82	+0.00	+0.03	+0.02
Dried skins	Length	0.46	0.48	+0.01	+0.18	+0.14
	Quality	0.33	0.23	Avg incr: 1%	+0.03	+0.03
	Density	0.16	0.30	0 Significant	+0.08	+0.06
	Silky	0.18	0.14	+0.00	+0.07	+0.06

Accuracies, ST-GBLUP and multi-trait

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	Quality	0.30	0.69	Avg incr: 5%	Avg incr: 6%	+0.02
	Density	0.16	0.39	0 Significant	0 Significant	+0.07
	Silky	0.30	0.82	+0.00	+0.03	+0.02
Dried skins	Length	0.46	0.48	+0.01	+0.18*	+0.14
	Quality	0.33	0.23	Avg incr: 1%	+0.03	Avg incr: 32%
	Density	0.16	0.30	0 Significant	+0.08*	2 Significant
	Silky	0.18	0.14	+0.00	+0.07	+0.00

Accuracies, ST-GBLUP and multi-trait

				Accuracy, relative to ST-GBLUP				
	Trait	h ² , (BLUP)	ST-GBLUP	MT-GBLUP	MT-BayesA	MT-BayesAS		
Live grading	Bodyweight	0.53	0.49	+0.01	+0.05	+0.03	Avg incr: 6%	0 Significant
	Quality	0.30	0.69	Avg incr: 5%	Avg incr: 6%	+0.02		
	Density	0.16	0.39	0 Significant	0 Significant	+0.07		
	Silky	0.30	0.82	+0.00	+0.03	+0.02		
Dried skins	Length	0.46	0.48	+0.01	+0.18*	+0.14		
	Quality	0.33	0.23	Avg incr: 1%	Avg incr: 32%	+0.03		
	Density	0.16	0.30	0 Significant	2 Significant	+0.06		
	Silky	0.18	0.14	+0.00	+0.07	+0.06		

Accuracies, ST-GBLUP and multi-trait

				Accuracy, relative to ST-GBLUP		
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Live grading	Bodyweight	0.53	0.49	+0.01	+0.05	+0.03
	Quality	0.30	0.69	Avg incr: 5%	Avg incr: 6%	Avg incr: 6%
	Density	0.16	0.39	0 Significant	0 Significant	0 Significant
	Silky	0.30	0.82	+0.00	+0.03	+0.02
Dried skins	Length	0.46	0.48	+0.01	+0.18*	+0.14*
	Quality	0.33	0.23	Avg incr: 1%	Avg incr: 32%	+0.03
	Density	0.16	0.30	0 Significant	2 Significant	+0.06
	Silky	0.18	0.14	+0.00	+0.07	+0.06

Avg incr: 26%

1 Significant

Conclusions

- **Bayes models tend to be more accurate than ST-GBLUP models**
 - BayesAS not superior to BayesA
- **Multi-trait models not more accurate than single-trait models**
- **Accuracies increased more for dried skins traits, than traits measured at live grading**

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