Estimation of Breeding Values for Haploid Chromosomes

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Introduction

Extreme methods used to estimate genomic breeding values:

- G-BLUP (genomic relationship matrix)
  - Straightforward implementation (standard software)
  - Effects and variance components estimated per animal
- Models with explicit estimates per SNP locus (e.g. BayesC)
  - Implementation is less straightforward
  - Effects estimated per SNP
  - Variance components are NOT obtained at ‘animal’ level

Introduction

- Can we model effects at an intermediate, biologically more relevant level?

=> Estimate breeding values at chromosome level

- Straightforward implementation
- Effects and variances can easily be translated to ‘animal’ level
- Identical-by-descent information can be used
- Opportunities for mate allocation

Objective

- Estimate genomic breeding values and variances at chromosome level, and compare to established models

Models

- A: animal model with A matrix
- G: animal model with G (genomic relationship) matrix
- BayesC: SNP based
- CHROM:
  - Phase genotype data
  - Calculate average similarity between all pairs of haploid chromosomes => per chromosome a matrix with similarities
  - Estimate breeding values and variances (ASReml):
    - for each chromosome in a separate model
    - for all chromosomes simultaneously

Analysis

Data:

- 516 cows with genotypes and phenotypes for fat%
- 41,272 mapped SNPs after editing
- 121 mother-daughter pairs
- Many animals have paternal half-sibs

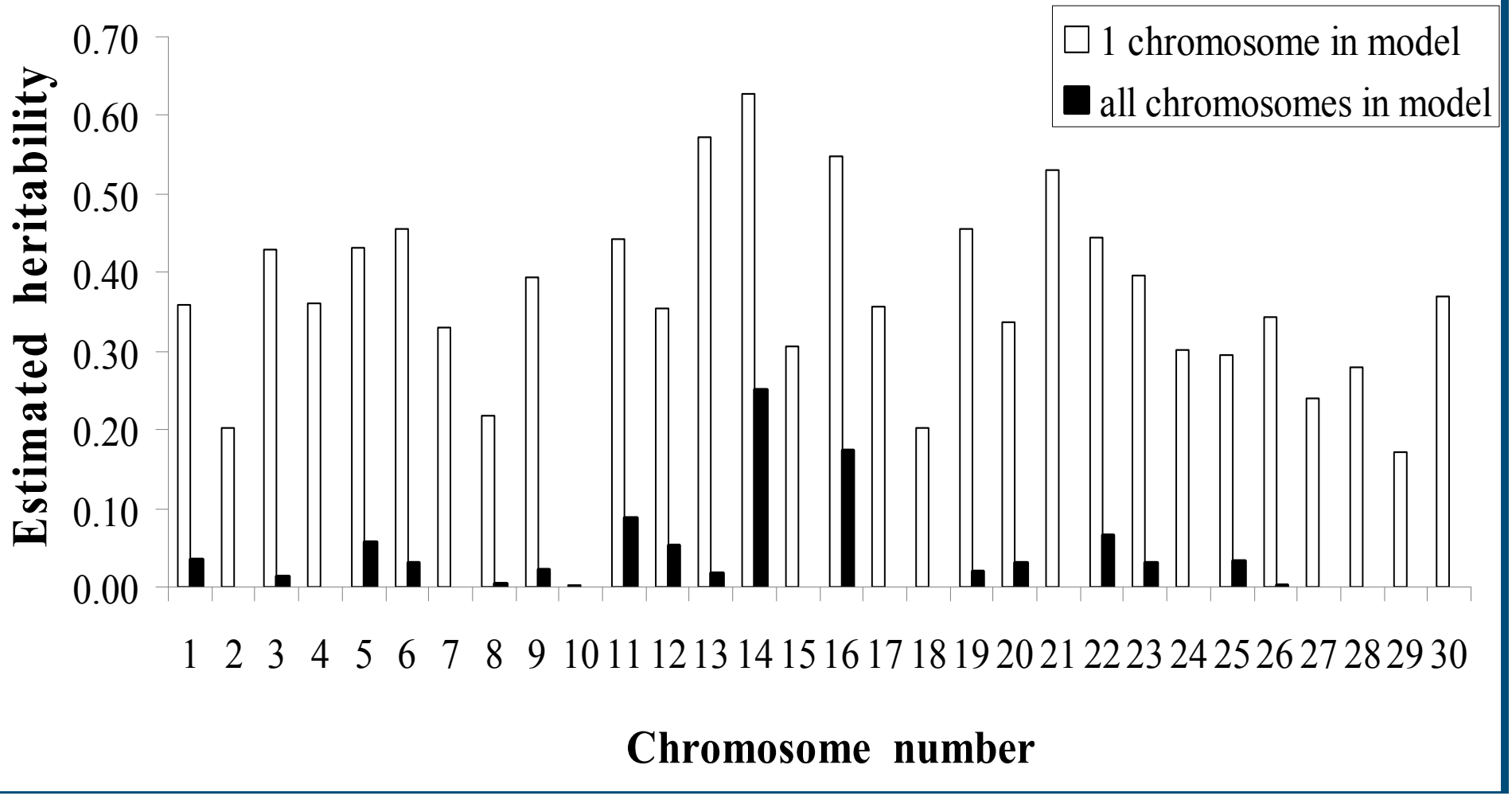
10-fold cross-validation:

- Each animal had its phenotype predicted once

Results

Model	Res. var	Gen. var	h^2	se	Accuracy of predicting phenotype	
					Phenotype included	Phenotype excluded
A	0.019	0.148	0.886	0.096	0.996	0.425
G	0.037	0.120	0.764	0.078	0.984	0.463
CHROM	0.027	0.368	0.933	0.028	0.985	0.597
BayesC	0.019				0.998	0.781

Heritability per chromosome



Differences in variance components

- Variance components BayesC not on animal level

- Differences in variance components is mainly due to differences in base generation
  - CHROM: generation where similarities between chromosomes are 0
  - A: first generation in pedigree
  - G: current generation

=> Chronological order base generations:

- CHROM << A < G

Conclusion

- Estimation of chromosome GEBV is good alternative
- For comparison of variance components, base generations need to be standardized across models
- For a trait with one gene with a large effect, accuracy CHROM is intermediate to G & BayesC

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