



Genomic prediction using haplotypes in Brown Swiss

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Prediction based on haplotypes

Opportunities:

- Reduction of variables
- Increased accuracy
- Higher ability to identify mutations

Challenges – Questions:

- Definition haplotype:
 - Phasing –which algorithm
 - Length (absolute based on LD)
 - Pseudo-SNPs or multiallelic
- Haplotype labelling

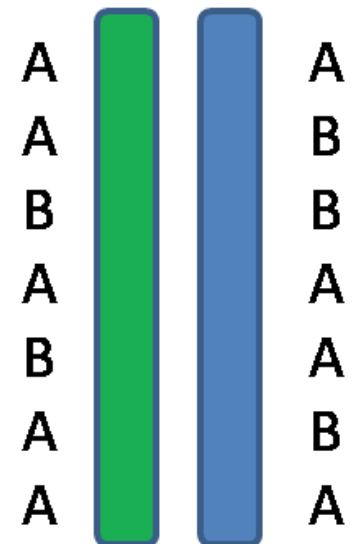
Haplotype labelling

1. Phasing genotypes

a. Unphased Data
(Genotype)



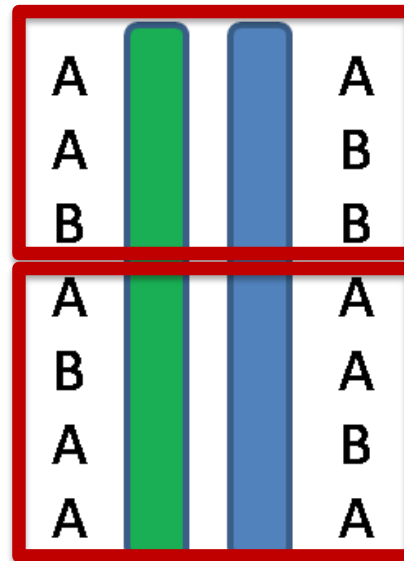
b. Phased Data
(Haplotypes)



Haplotype labelling

1. Phasing genotypes
2. Define length of haplotype blocks

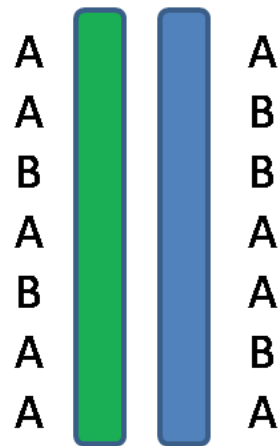
b. Phased Data
(Haplotypes)



Haplotype labelling

1. Phasing genotypes
2. Define length of haplotype blocks
3. Label haplotype alleles

b. Phased Data
(Haplotypes)



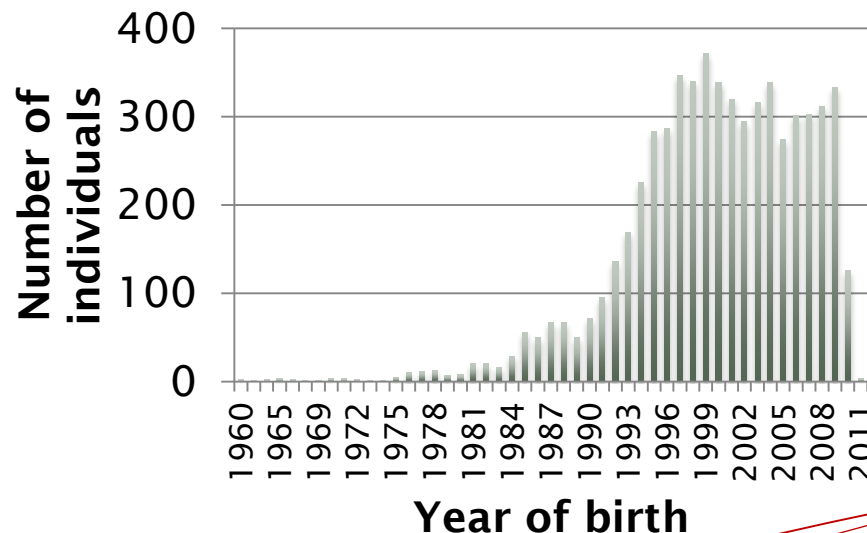
Hap_All1_1	Hap_All1_2	Hap_All2_1	Hap_All2_2
1	1	1	1

Animals and traits

	Non-return rate 56 heifer (NRH)	Somatic cell score (SCS)	Stature (STA)	Protein yield (PY)
Reference	2,018	4,786	5,294	5,128
Validation	240	560	596	596

Phenotypes

- Minimal reliability
- Deregressed BV (Garrick et al., 2009)
- Youngest bulls as validation
- Prediction accuracy: $\text{cor}(\text{deregBV}, \text{GEBV})$



Methods

- 50K genotype data (40,636 SNPs)
- Phasing: Beagle
- Haplotype labelling: Gchap (R-package)
- Prediction: GenSel:

- BayesCpi

- BayesC $y = 1'm + Xb + e$

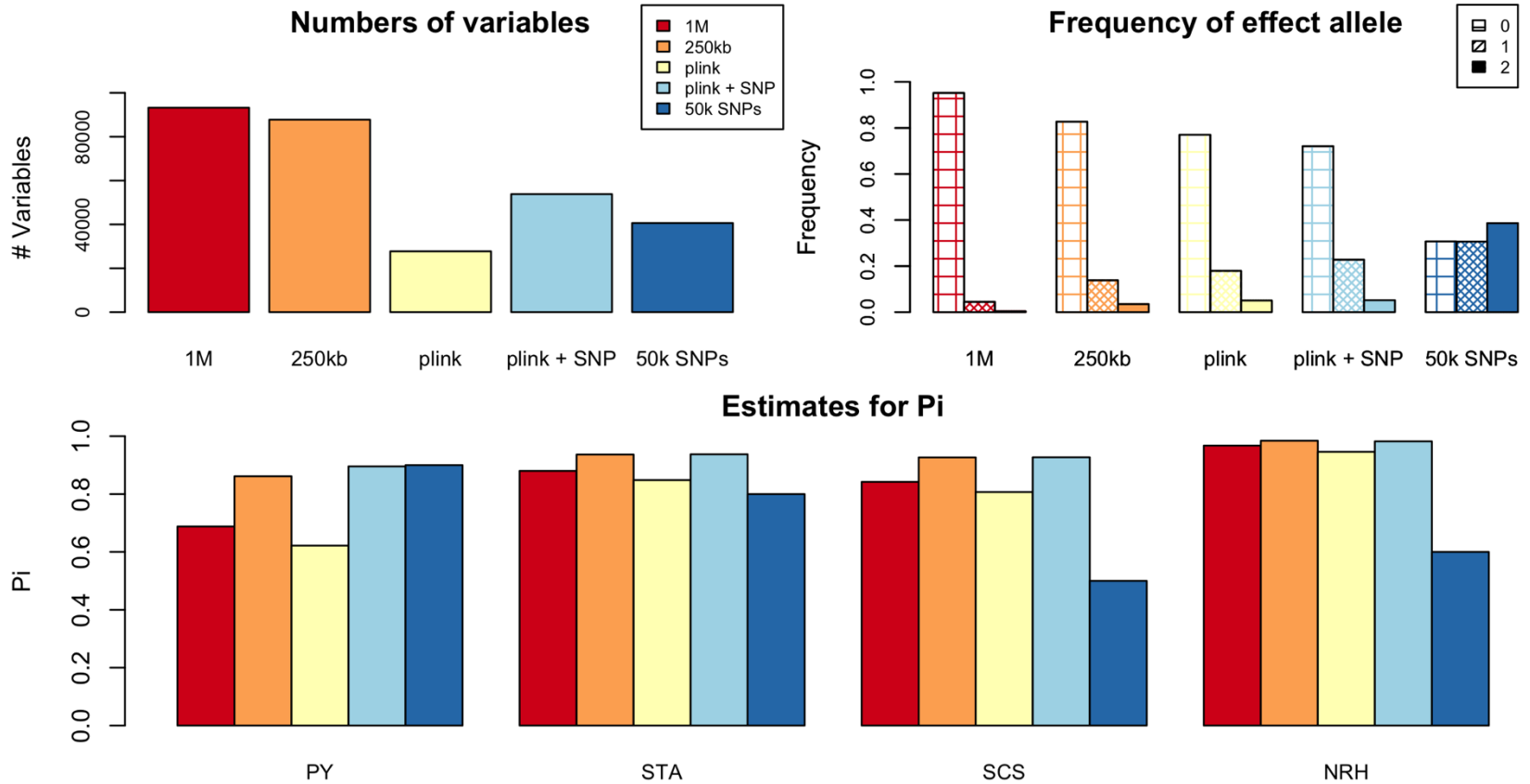
$\hat{b}_i = 0$ with probability p

$\hat{b}_i \sim N(0, S_{SNP}^2)$ with probability $(1 - p)$

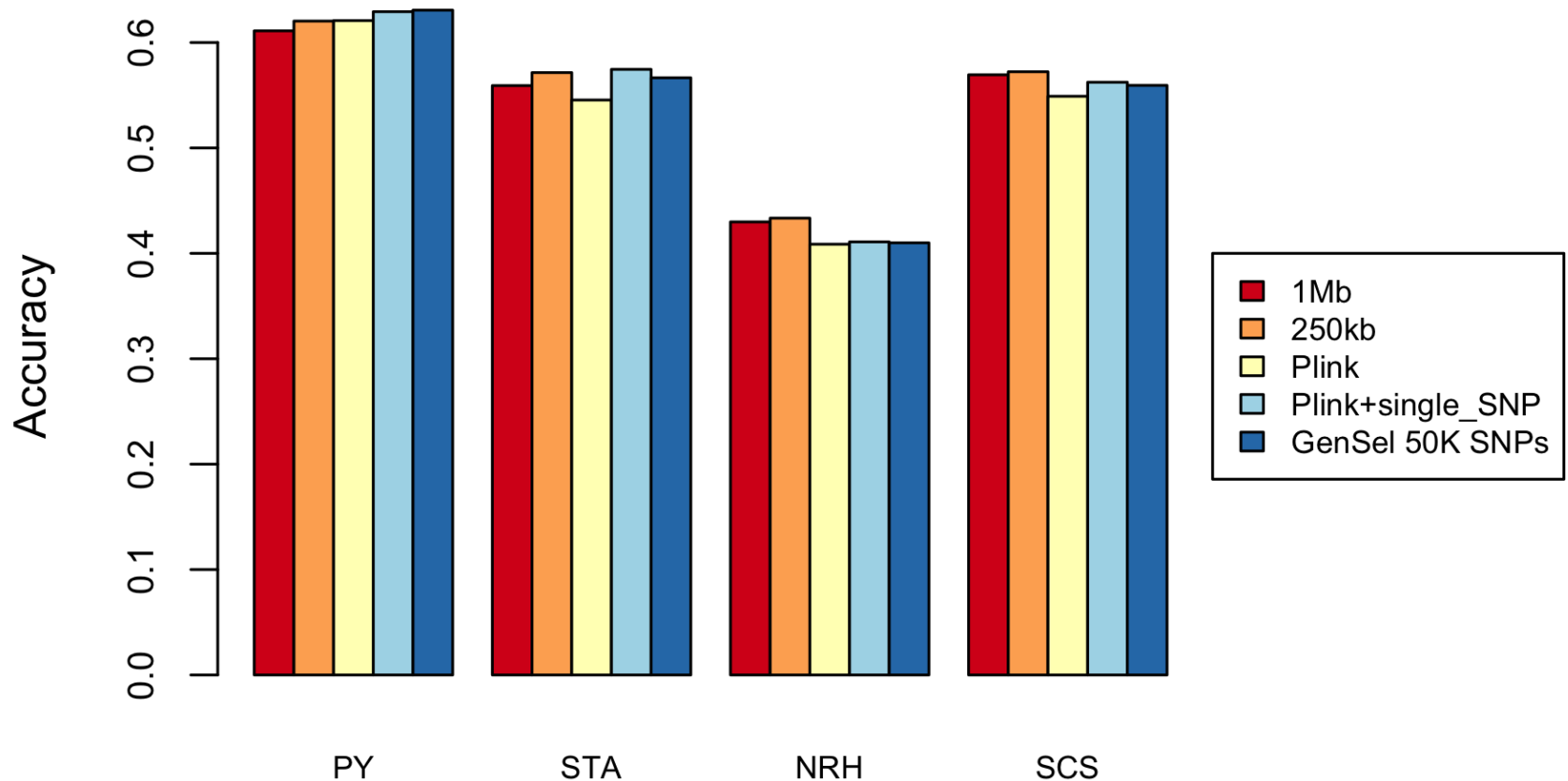
Results

- Haplotype definitions:
 - 1 Mb
 - 250 kb
 - LD blocks from plink
 - LD blocks including single SNP
 - Haplotype alleles with a frequency of less than 0.1% were excluded

Results



Accuracy genomic prediction



Conclusions

- Reduction of variables: No reduction with 50K data
- Little increase in accuracy depending on trait
- Accuracy by trait: Different haplotype labelling method for highest accuracy

Acknowledgement

QUALITAS⁺

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interGenomics

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Thank you for your attention