



Cow genotyping strategies for genomic selection in small dairy cattle population

Janez Jenko

G.R. Wiggans, T.A. Cooper, S.A.E. Eaglen, W.G. De L. Luff, M. Bichard,
R. Pong-Wong and J.A. Woolliams

EAAP 2016

67th Annual Meeting of the European Federation of Animal Science
Belfast UK, 29 Aug – 2 Sept 2016



THE UNIVERSITY *of* EDINBURGH



Overview of the talk



- Guernsey cattle breed
- Genotypes
- Quality check (QC) and imputation
- Phenotypes
- Prediction of genomic breeding values (GEBV)
- Scenarios of cow genotyping
- Conclusions



Guernsey cattle breed

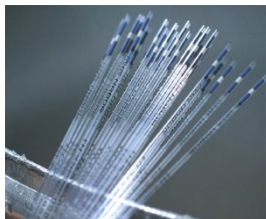
- Small dairy cattle breed population
- Approximately 14,000 recorded individuals worldwide
- Milk from Guernsey cow has unique qualities

GUERNSEY ISLAND ROYAL SHOW 2014
HM QUEEN'S CUP COW



- Small number of bulls with conventional proofs
 - 197 bulls genotyped (born from 1957 to 2013)
 - 168 on 75K
 - 29 on 777K
- Genotyping cows to improve accuracies
 - 1,440 cows (present in herds at the end of 2014)
 - All genotyped on 25K

Sample collection



DNA extraction

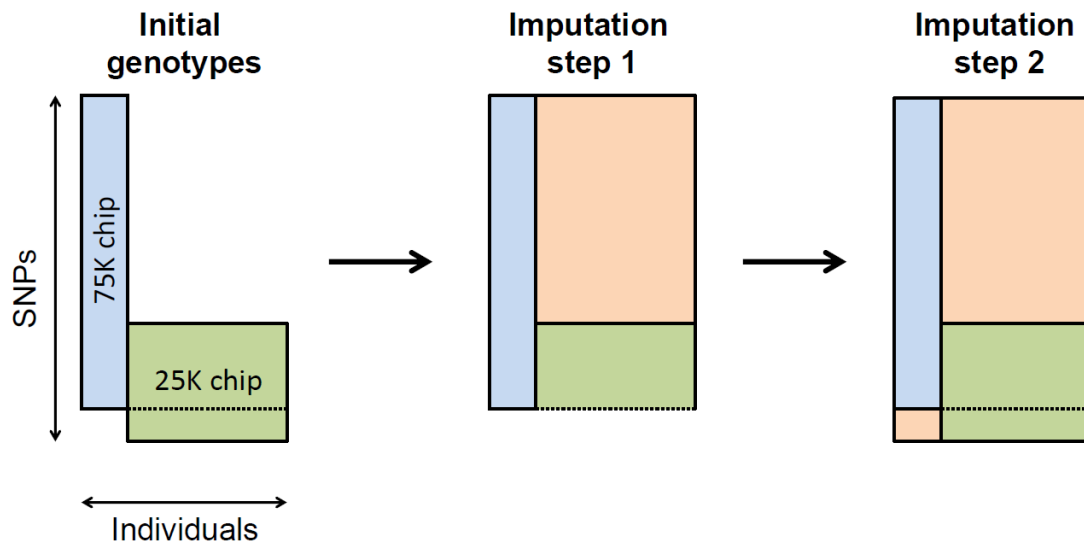
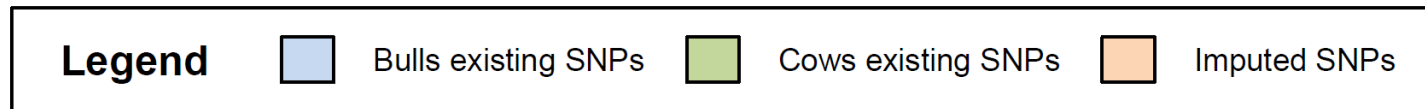


Genotyping



QC & Imputation

- QC for genotypes and SNPs
 - Call rate, minor allele frequency, heterozygosity rate, Hardy-Weinberg equilibrium, Mendelian inconsistencies
- Imputation



Correlation between true and imputed SNP genotypes

using

10-fold cross-validation on:

1,333 cow genotypes with
11,983 SNP existing on both: 75K and 25K chip

Between individuals		Between SNP	
Mean	SD	Mean	SD
0.952	0.033	0.945	0.072

Phenotypes

	Bulls	Cows
• “Phenotypes”	PTA from MACE	Milk records
• Adjustment of “phenotypes”	Deregression	Adjusted lactation records
• No. of milk, fat, and protein yield records	185	1,307

Model

Phenotypes

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

Vector of errors

Mean

Incidence matrix
linking records from
vector \mathbf{y} to vector \mathbf{u}

Vector of random
genetic effects

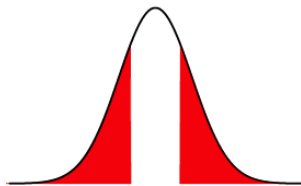
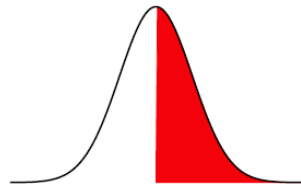
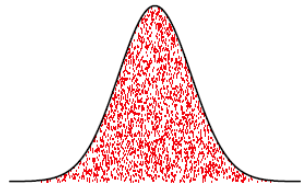
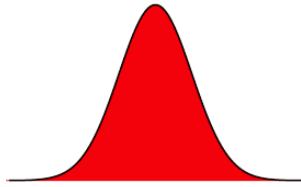
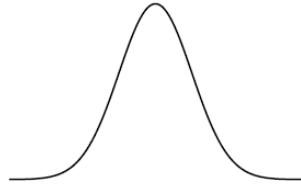
- $\text{Var}(\mathbf{u}) = \mathbf{G}\sigma_g^2$

$$\mathbf{G} = \frac{\mathbf{M}\mathbf{M}'}{2 \sum_j^{N_{\text{snp}}} p_j(1-p_j)}$$

- $\text{Var}(\mathbf{e}) = \sigma_e^2 \mathbf{W}^{-1}$

\mathbf{W}^{-1} - weights the contribution from
each individual

Cow genotyping strategies



- Bull genotypes
- Bull and cow genotypes
- Bull and 50% of cow genotypes selected at random
- Bull and 50% of cow genotypes with top performance
- Bull and 50% of cow genotypes with extreme phenotypes

10-fold cross-validation

Accuracy

Correlation between phenotypes and GEBV

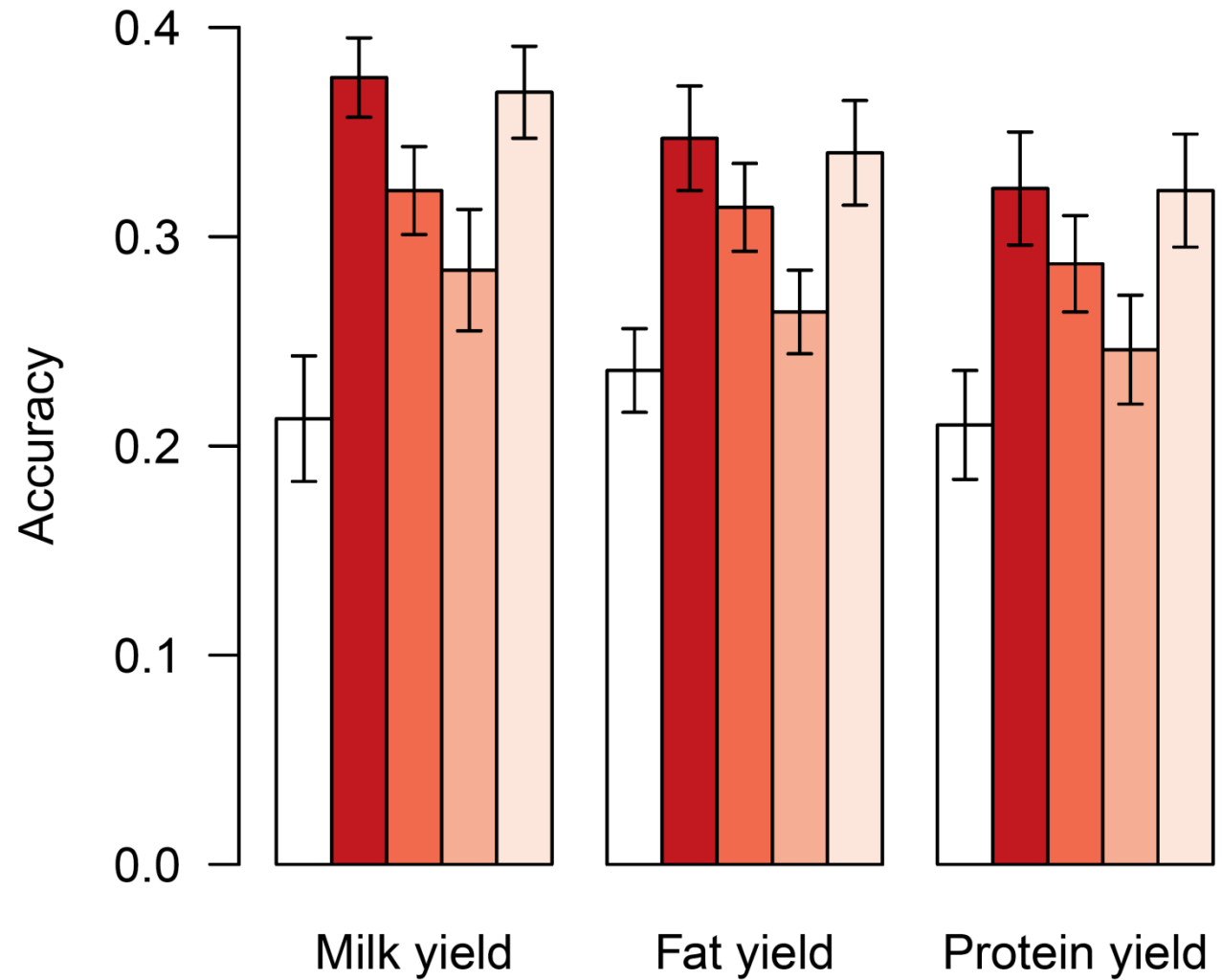
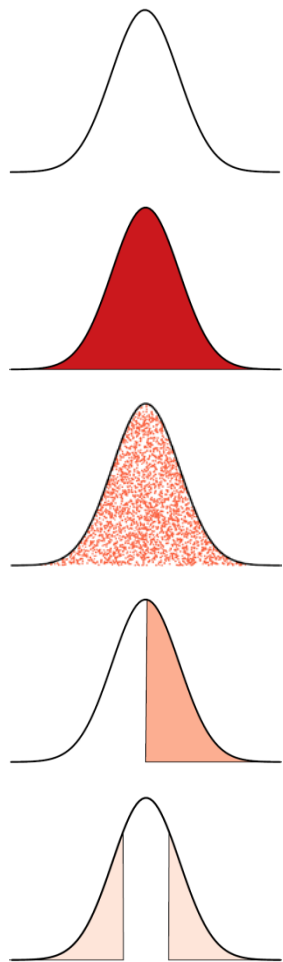
Bias

Slope of the regression of phenotypes on GEBV

- > 1 underestimation
- < 1 overestimation

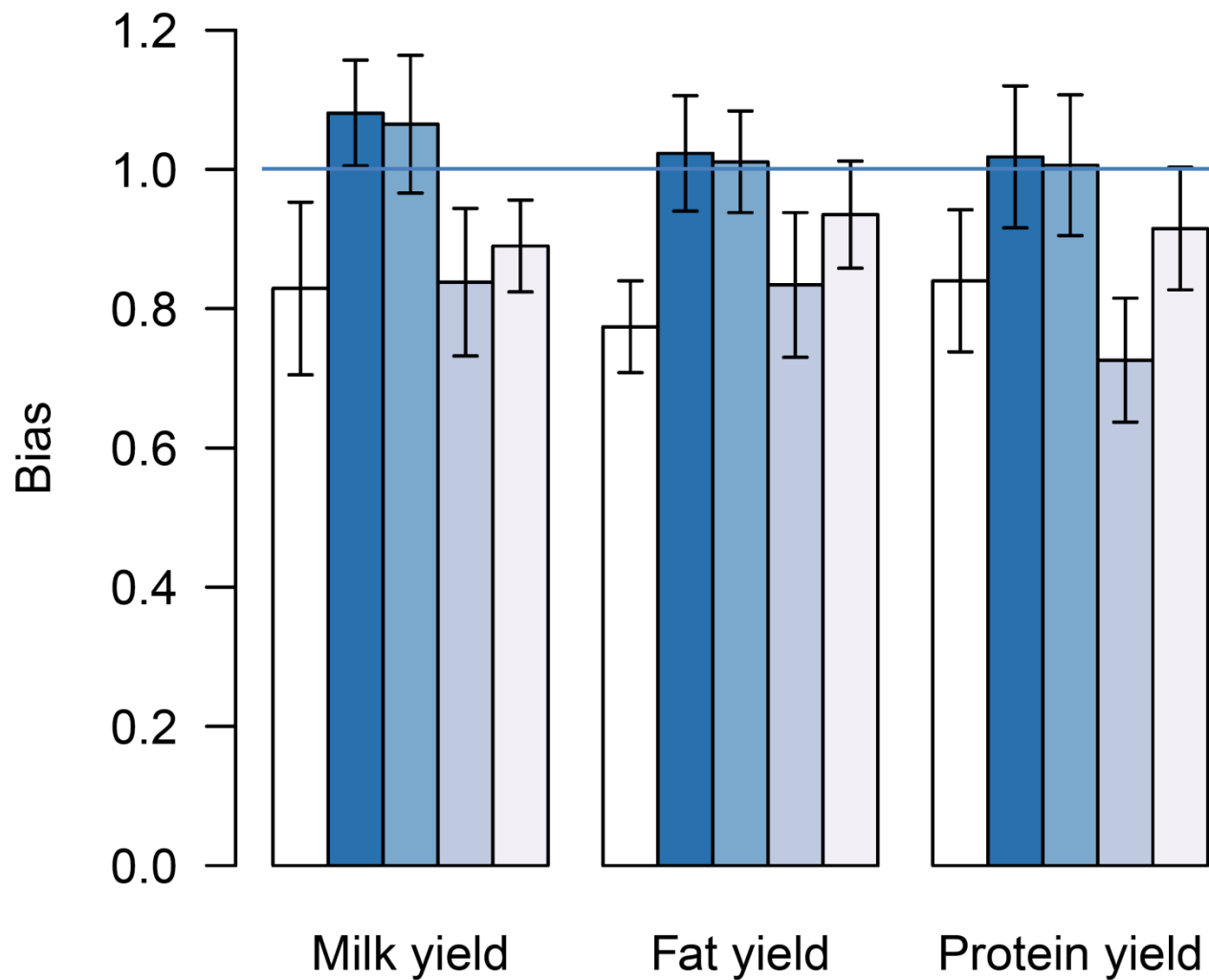
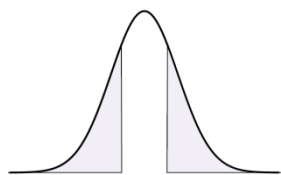
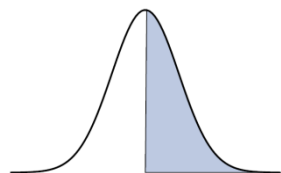
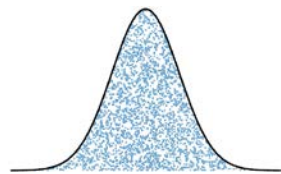
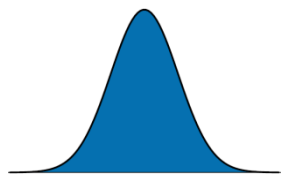
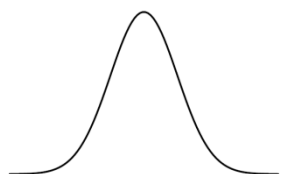
Accuracy

Cow genotyping strategies



Bias

Cow genotyping strategies



Conclusions



- Genotyping cows improves the accuracy of GEBV in small dairy cattle population
- Genotyping half of cows (those with extreme adjusted phenotypes) yields only slightly lower accuracies as compared to the scenario when genotyping all cows
- Selective genotyping introduces bias - GEBV is overestimated



Manuscript in revision



- Results for Calving interval
- Genotyping only 40% or 30% of cows from both tails
- Selection of cow genotypes based on indexes (Profit Lifetime Index, Guernsey Merit Index)
- Predicted model

Acknowledgement



Financial support



This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement n° 289592

Data providers



The Royal Guernsey
Agricultural & Horticultural
Society



Thank you for your attention

