

# Increasing accuracy of genomic prediction combining cow and bull reference populations

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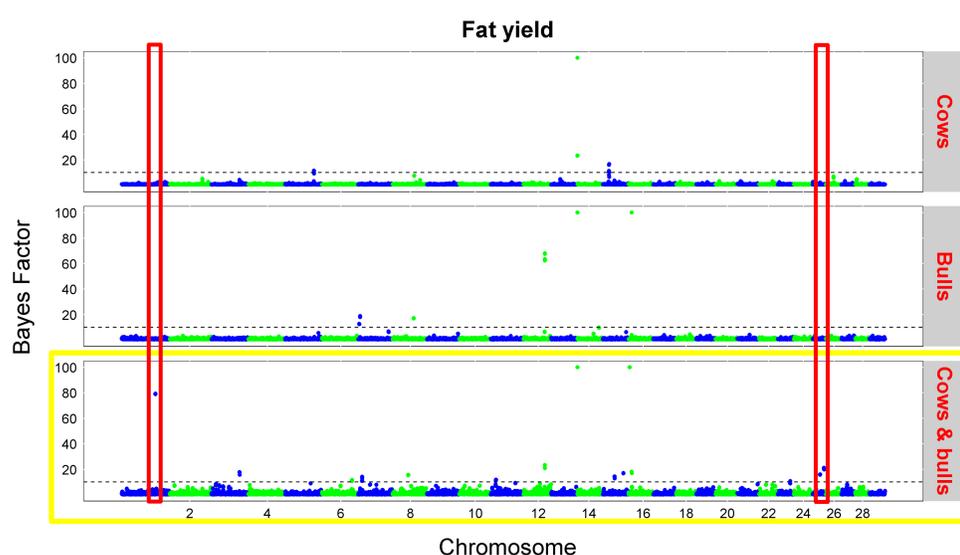
## Objective

Combine cow and bull reference population information in a Bayesian genomic prediction model, to increase accuracy of genomic breeding values.

**Table 1.** Accuracy of genomic prediction for fat and protein yield, for various reference populations. Accuracy =  $r(\text{genomic breeding values ; cow phenotypes}) / \sqrt{h^2}$ .

Reference population	Cow trait			
	Fat		Protein	
	Accuracy	SE	Accuracy	SE
Cows <sup>1</sup>	0.328	0.068	0.189	0.050
Bulls (fat)	0.238	0.053	-0.004	0.060
Bulls (protein)	-0.069	0.055	0.146	0.050
Bulls (fat) & cows	0.347	0.063	0.192	0.053
Bulls (protein) & cows	0.271	0.048	0.206	0.055

<sup>1</sup>For cows, always the evaluated trait was included.

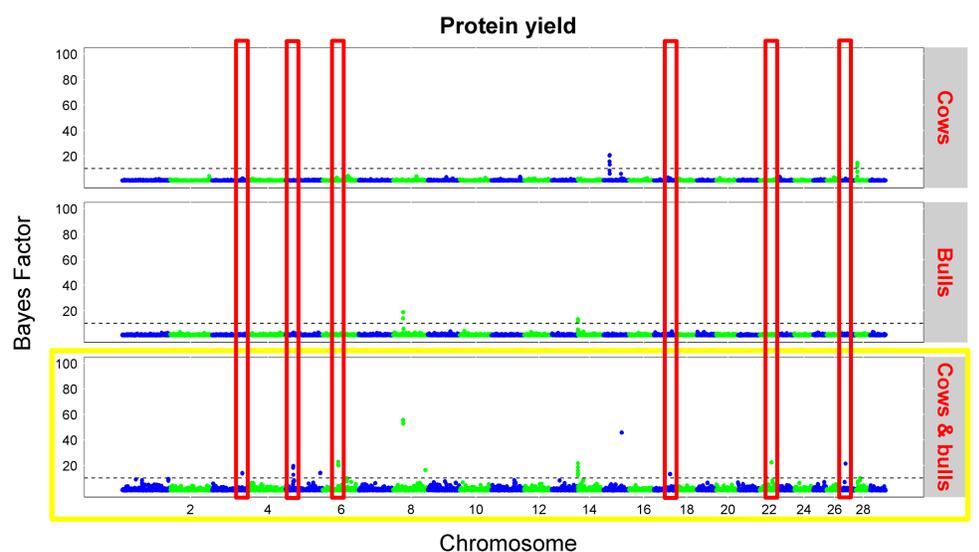


**Figure 1.** Bayes Factors (BF) across the genome for fat yield, using cow, bull, or cow & bull data (BF > 100 are set to 100).

## Conclusions

The bivariate Bayes-SSVS model:

- Showed a marginal increase in accuracy for the cow traits (0.02); a higher increase is expected when adding more bulls
- Revealed several QTL peaks not found in the separate analyses (indicated in red)



**Figure 2.** Bayes Factors across the genome for protein yield, using cow, bull, or cow & bull data.

## Background

Genomic selection enables selection for difficult to measure traits, like feed efficiency and methane emission in dairy cattle, for which only a few thousand phenotypic records may be collected.

### Data

- 1,609 cows with phenotypes for fat and protein yield
- 296 bulls had highly accurate daughter yield deviations (DYD) for fat and protein yield from the Irish national evaluations
- Genotypes for 36,346 SNPs were available for all animals

### Model

- Bayesian stochastic search variable selection (Bayes-SSVS)
- Univariate: 1 cow *or* 1 bull trait
- Bivariate: 1 cow *and* 1 bull trait
- One QTL-indicator sampled for both traits per locus
- Zero residual correlation between (cow & bull) traits

**Table 2.** Estimated **heritabilities** of fat and protein yield measured on cows and based on bull DYD's on the diagonal. Estimated genetic correlations (SEs) above the diagonal, and estimated residual correlations (SEs) below the diagonal. Parameters were estimated with a 4-trait model using a G-matrix in ASReml.

		Cows		Bulls	
		Fat	Protein	Fat	Protein
Cows	Fat	<b>0.368</b> (0.042)	0.711 (0.047)	0.654 (0.093)	0.189 (0.115)
	Protein	0.871 (0.012)	<b>0.286</b> (0.041)	0.307 (0.115)	0.547 (0.114)
Bulls	Fat			<b>0.995</b> (0.002)	0.423 (0.055)
	Protein			0.823 (0.131)	<b>0.991</b> (0.004)

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