SFA2 - Genomic prediction in animals and plants

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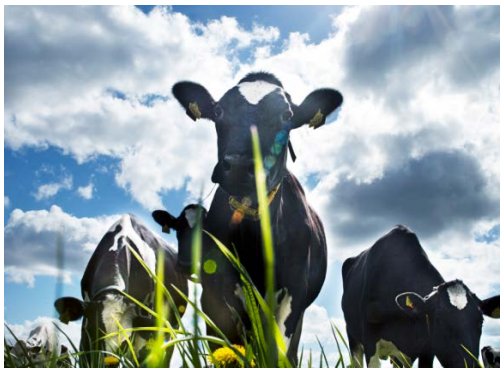
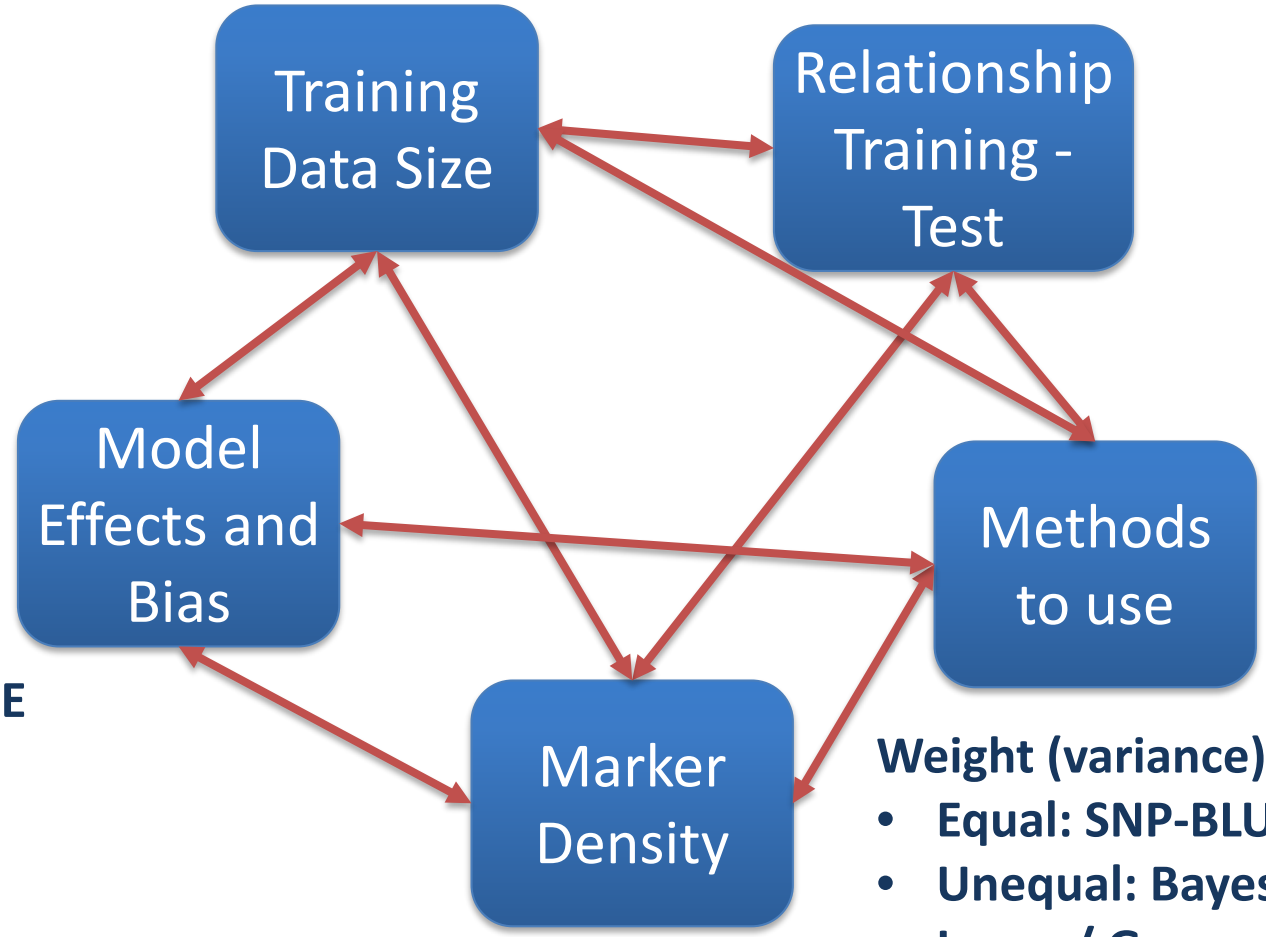


Elements of Genomic Prediction



GxE

Weight (variance) per SNP

- **Equal: SNP-BLUP, GBLUP**
- **Unequal: Bayesian / Machine Learn / Genomic Feature**

Training Size – Relationship – Marker Density

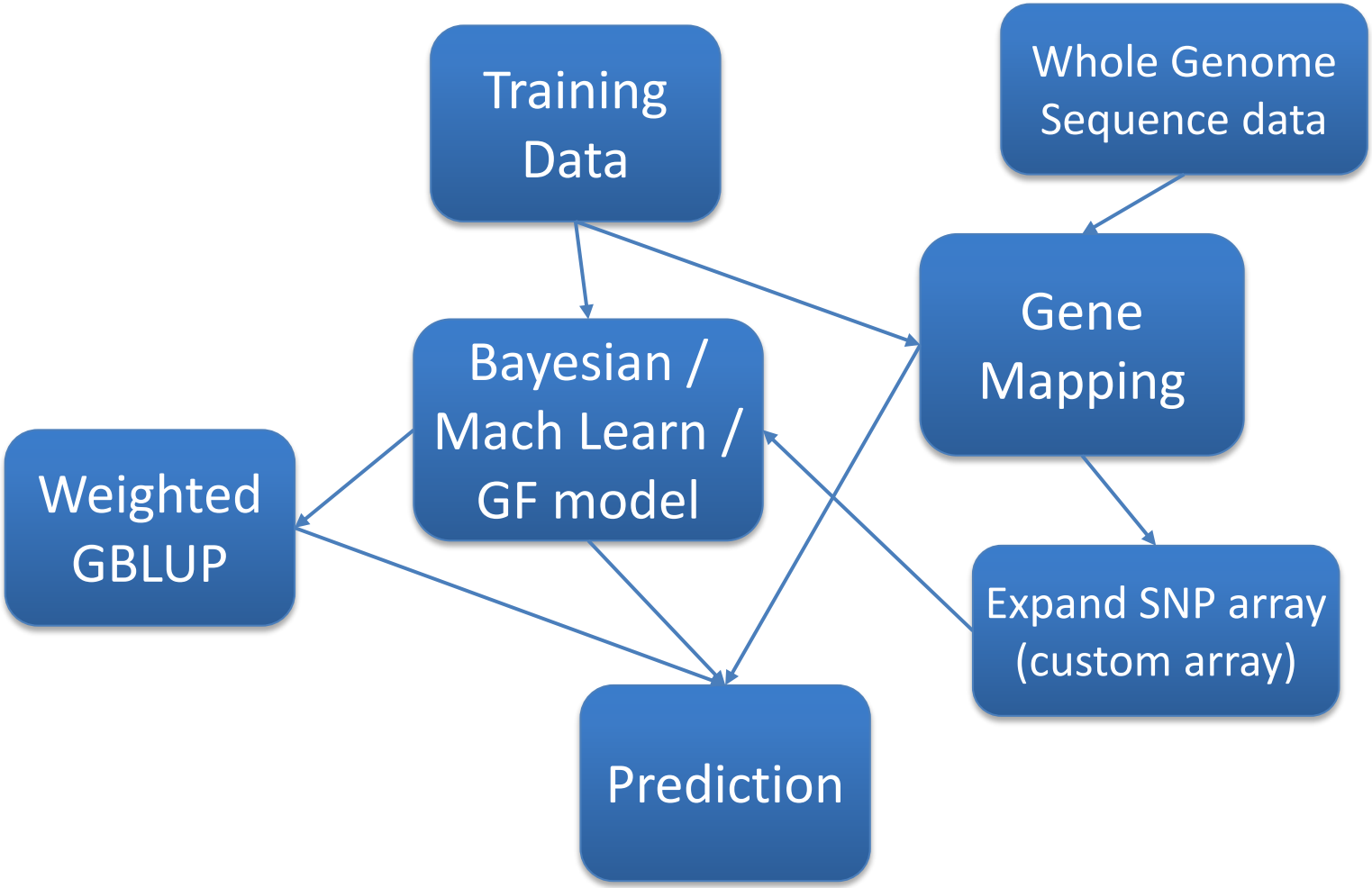
Training Data	Relationship Training - Test	
	Close	Distant
Small	Use GBLUP (Bayes/ML may be worse) Modest marker density	No chance to make accurate predictions
Large	Modest benefits possible from using unequal SNP weights	GBLUP (very) poor, need models with unequal SNP weights
	High marker density needed	

Large Training Data?

- Cow-records behind GS in cattle 50-100M
- Other species need >> 100K – 1M?

- Combining more distant breeds / populations
- Speed breeding (using unphenotyped young individuals)
- Powerful mapping as input for GS

Roads for using unequal-SNP-weight models

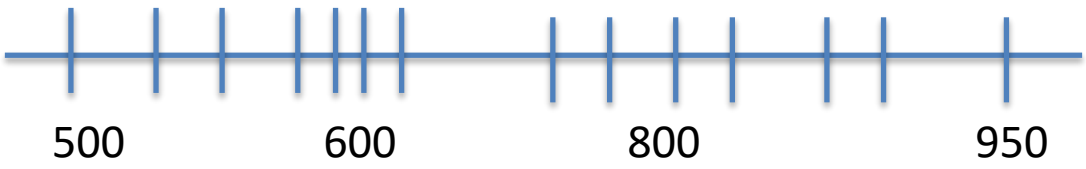


Other Issues

- Multi-trait models
  - Was the standard for breeding value estimation
  - With genomic information not yet in most places
  - Modest to interesting improvements
  - Also work on MT Lasso for ‘unequal correlation’ models
- Other fixed and genetic effects in GS models
  - ‘Incorrect’ model can give ‘bias’ in breeding values
  - Confoundment genetics and environment
  - Insufficient/lacking modelling of GxE

"Bias" in breeding values
Is the scale right?

Existing bulls / varieties ....



Predictions Top young / new

Predictions 'Unbiased' scale

Henderson's Unbiased Predictor (UP in BLUP)

- allows comparison between groups
- optimal selection using overall cut-off
- Saves money

Session Overview

- *Just Jensen*: Use of metabolomics in pig, barley and cattle
- *Mette Dam Madsen*: Adusting for macro-environmental sensitivity in growth rate
- *Mogens Lund*: Use of whole genome sequencing, fine mapping and custom LD chips in cattle
- *Jens Due Jensen*: From project to practice, successful implementation of GS in a commercial barley breeding program