

# Multi-breed genomic prediction using biological information

Breed4Food seminar, 12th July, 2018

Biaty Raymond



## ACKNOWLEDGEMENT

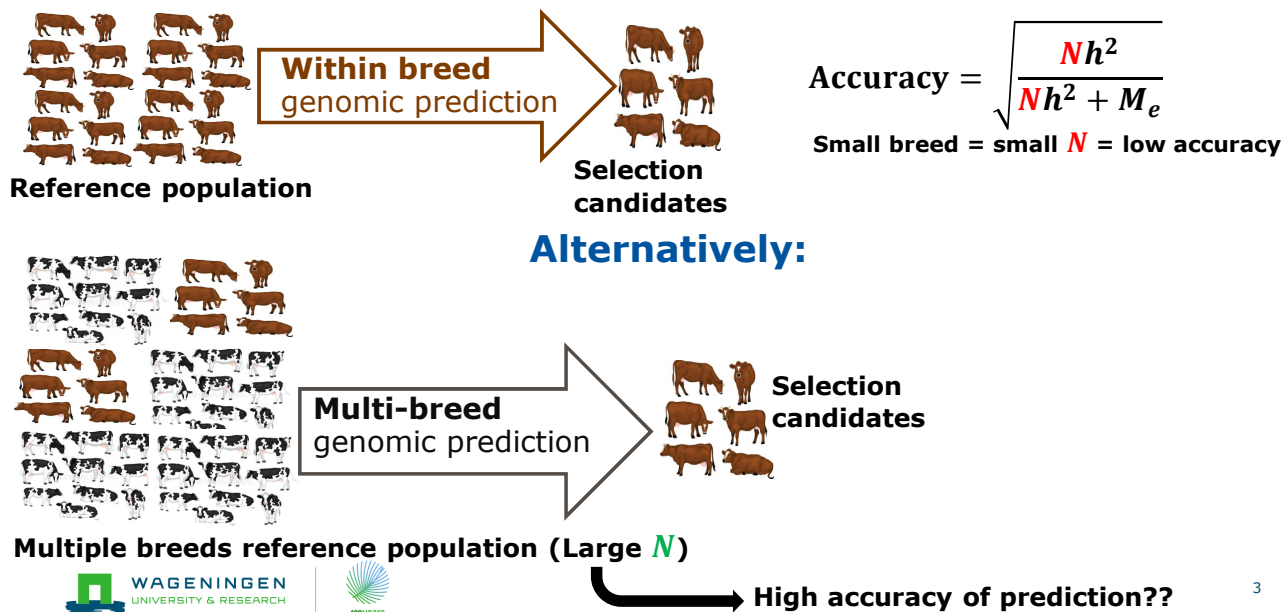


LEIDEN UNIVERSITY  
MEDICAL CENTER



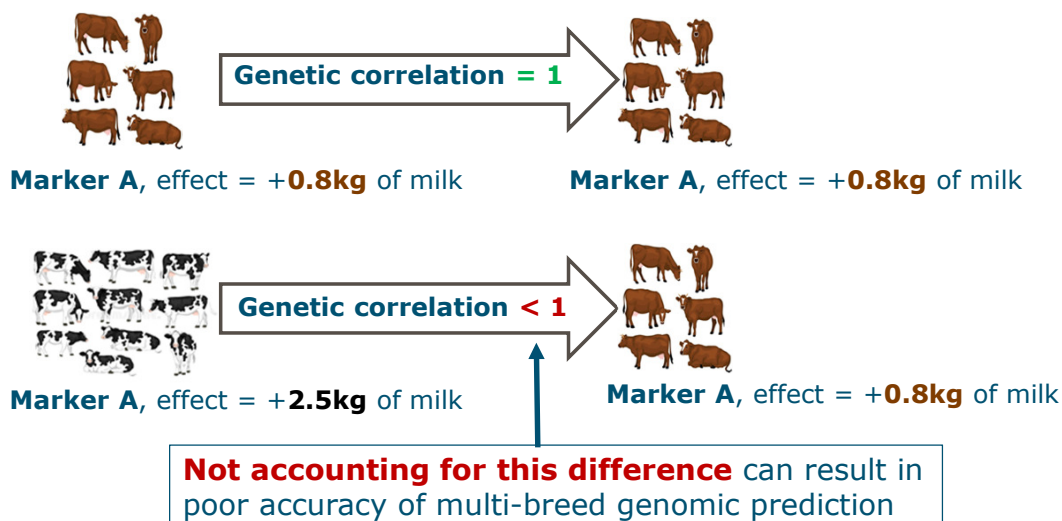
Applied and  
Engineering Sciences

# Multi-breed genomic prediction



3

# Challenges with multi-breed genomic prediction (1)



4

## Challenges with multi-breed genomic prediction (2)



Genetic correlation = 0.8

Does not depend on LD patterns across breeds



Effect of causal variants

Effect of causal variants



Genetic correlation = 0.2

Depends on LD patterns across breeds



Effect of non-causal variants

Effect of non-causal variants

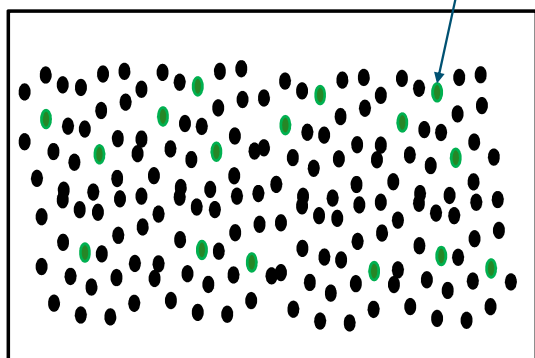
Difference in covariance structure of variants effects across breeds

❖ This difference must be accounted for



## Challenges with multi-breed genomic prediction (3)

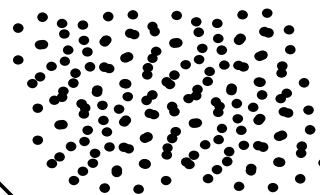
.....the use of whole genome sequence data



All markers in WGS

Pre-select the most important markers and model them differently

Non-causal markers in WGS



Causal markers in WGS

There is need for an efficient marker pre-selection strategy



## Objective



Develop and evaluate a multi-breed genomic prediction model that:

- ❖ Appropriately **utilise information on pre-selected functional markers**
- ❖ Capture **residual genetic variance** missed by pre-selected functional markers
- ❖ Weigh reference breeds information by their **genetic correlation** with validation breed

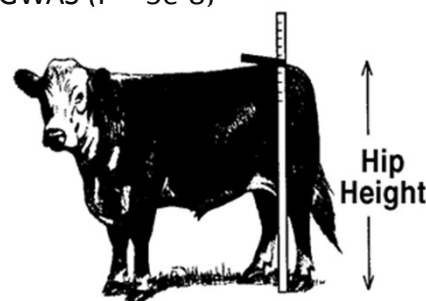
## Material & Methods

**Phenotype:** Stature on **5503** Dutch Holsteins & **595** New Zealand Jerseys

**Summary level results from a meta-GWAS** on stature (58,265 Individuals)

**Sets of DNA markers used in this study:**

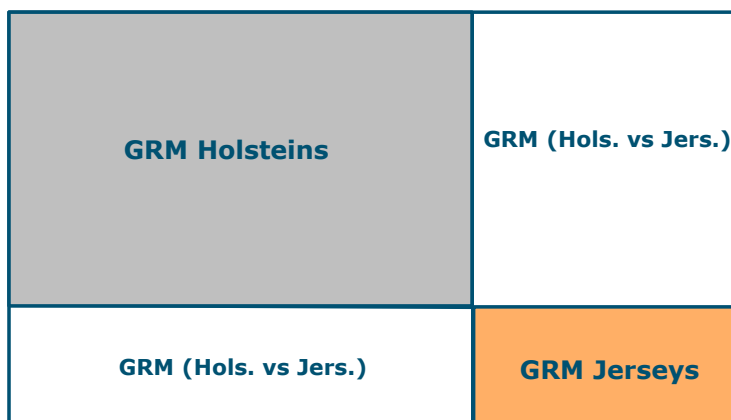
- **COJO8:** Independently significant markers from the meta-GWAS ( $P = 5e-8$ )
- **50K:** traditional 50k markers excluding COJO8 markers
- **50K+COJO8 :** COJO8 markers added to 50K



## Statistical analyses (model 1)

- Individuals across breeds are related at all markers

A **single GRM** fitted in a bivariate model

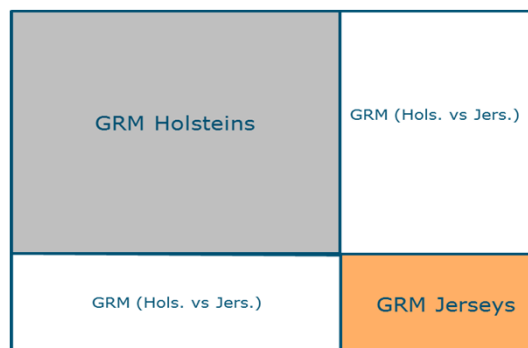


## Statistical analyses (model 2)

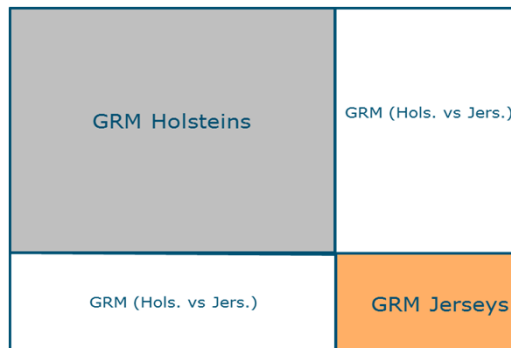
- Individuals across breeds are related at all markers
- **Differences in effect size variance** between **functional** and **non-functional** markers

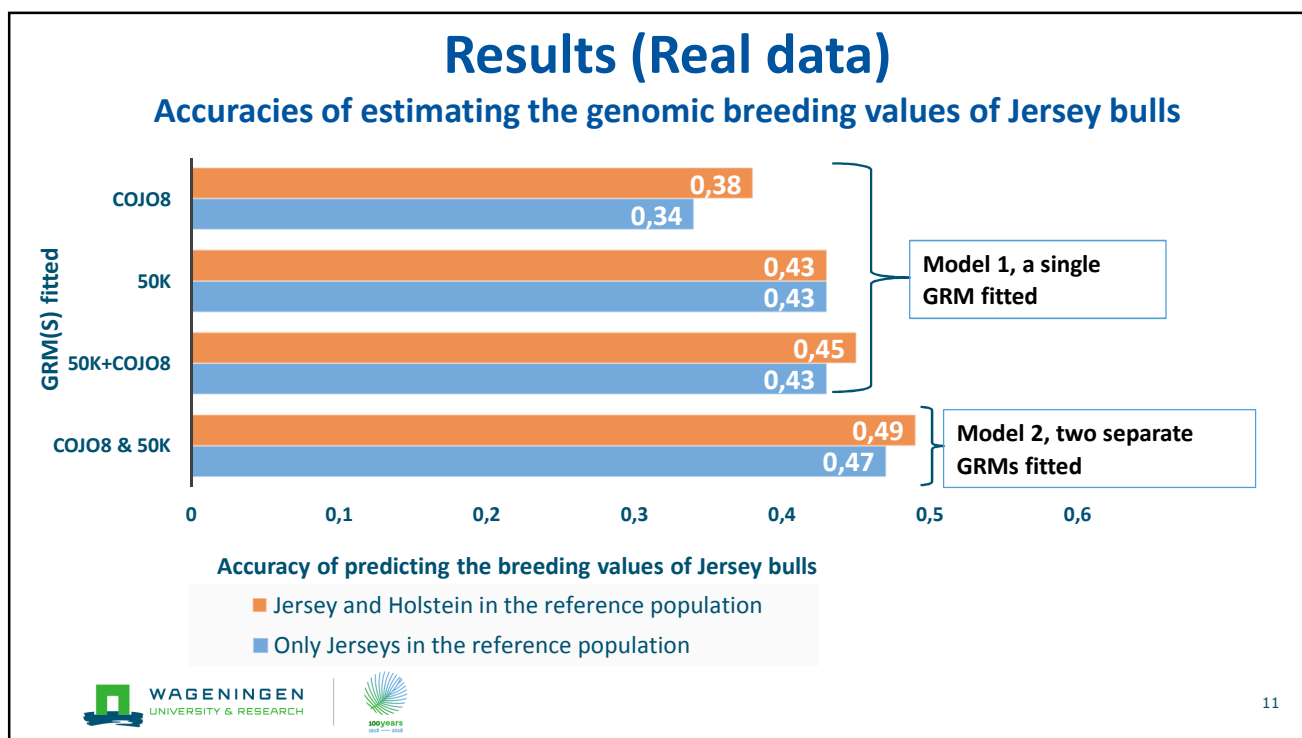
**2 different GRMs** fitted in a bivariate model

**GRM1 (functional markers)**



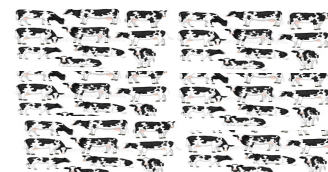
**GRM2 (remaining markers)**





## Conclusion: Recipe for multi-breed Genomic prediction

- ❖ **Pre-select functional markers** from whole genome sequence
  - Weigh the pre-selected markers differently from others
- ❖ Use the remaining markers to **capture residual genetic variance**
- ❖ Weigh the information of breeds in the reference population by **their genetic correlation** with the validation breed



biaty.raymond@wur.nl