

GxE for age at slaughter in Irish dairy and beef crossbreds using a genomic reaction norm model

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Genomic GxE models

- Multi-trait approach and reaction norm model can be implemented relying on:
 - Genomic relationships (GREML)
 - Random regression on SNP genotypes (RR-REML)
- GREML and RR-REML are equivalent
 - Homogeneous (co)variance assumed for all SNPs
- Certain regions in genome may harbour QTL → assumption of equal (co)variances is violated

Model heterogeneous SNP variances

- Make SNP (co)variances heterogeneous by **weighing**
 - (1) Weights derived from estimated SNP effects
 - (2) Re-compute SNP-effects using those weights
- Issue: computing (1) & (2) from the same data may inflate large SNP-effects

Proposed solution: split data in two



- Estimate SNP-effects assuming equal (co)variances for all SNP
- Calculate SNP specific weights within environment



- Estimate GEBV using the 2nd subset, applying weights on SNP (co)variance matrix within environment

Proposed solution: split data in two



Approach has been tested in simulated data
resulting in slightly higher accuracies of GEBV

(Gredler-Grandl and Calus, 2021)

- Calculate SNP specific weights within environment

matrix within environment

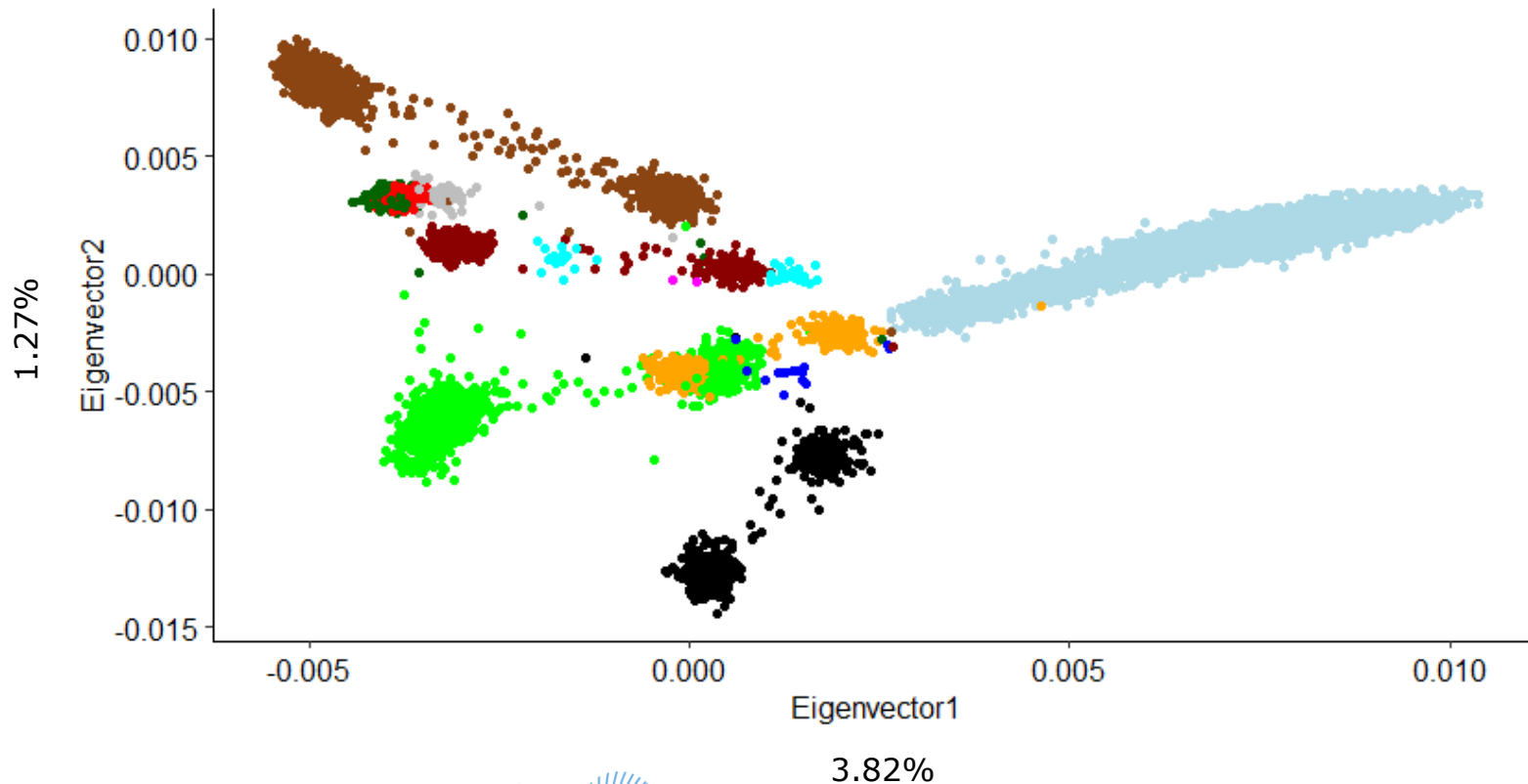
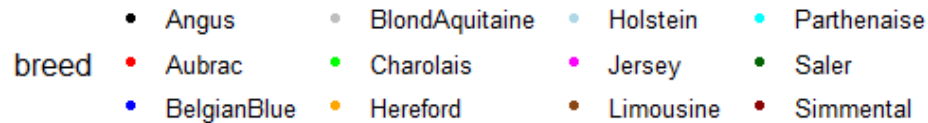
Objective

Estimate GxE for age at slaughter in an Irish dairy and crossbred population modelling either **homogeneous (HOM)** or **heterogeneous (HET)** SNP (co)variances across the genome

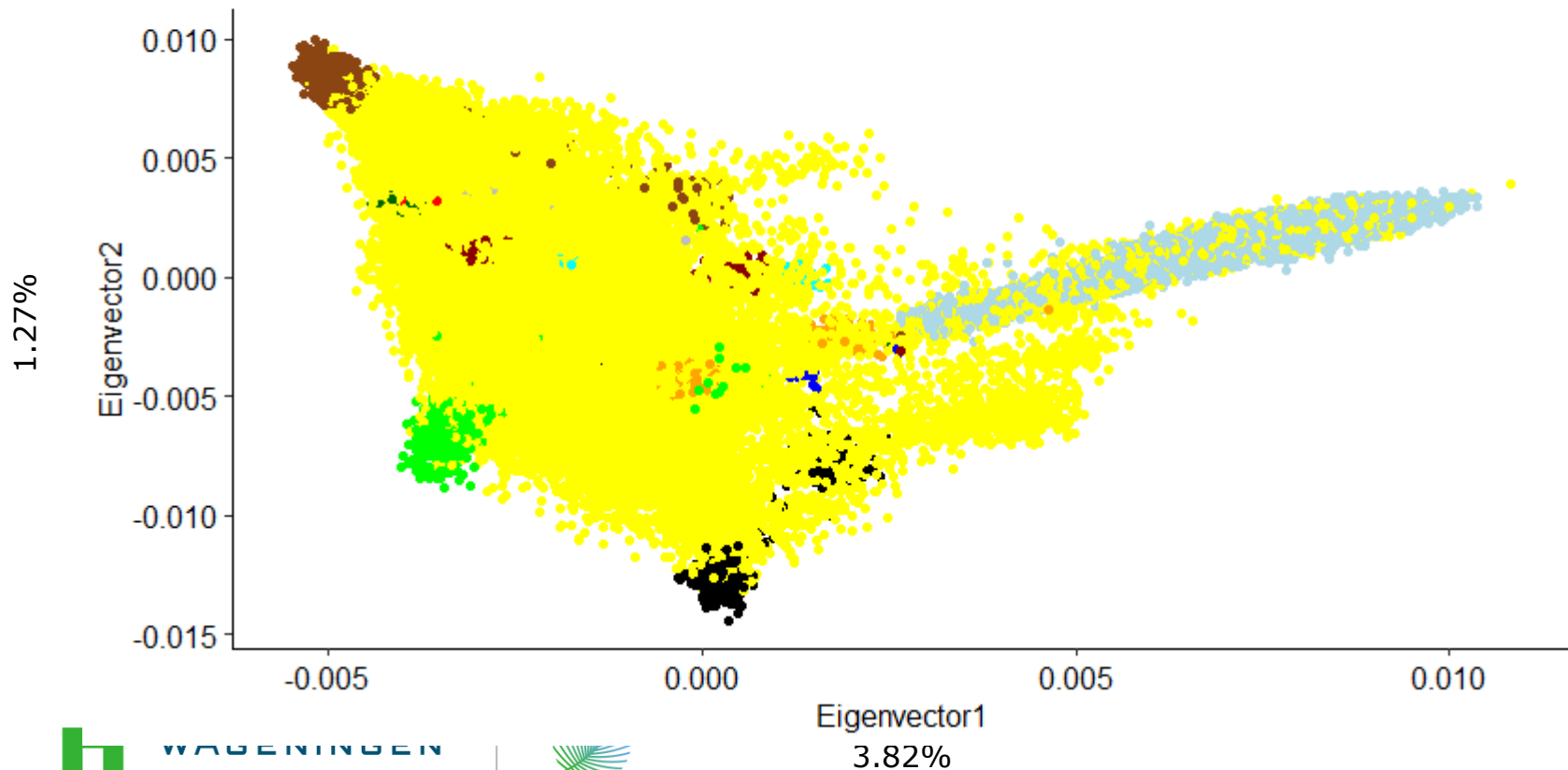
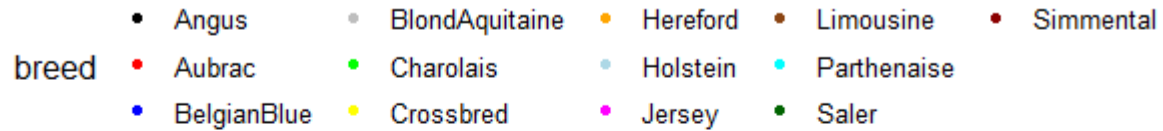
Application in Irish beef crossbred data set

- age at slaughter – novel trait relevant for efficiency and environmental impact of beef production
- 14,193 genotyped bulls, steers, heifers
- HD imputed genotypes (662,011 SNPs)
- Yield deviation as phenotypes for genomic analysis
- CG-effects as continuous descriptor of environment
 - 2783 CG
 - Animals same gender and similar birthday or age purchased into the same herd in close period of time
 - Minimum 3 animals per CG

Breeds: PCA G-Matrix purebred and crossbred animals



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How to define sets for analysis?

- K-means clustering approach (similar Saatchi et al., 2011)
- Applied to genomic relationship matrix of the herds based on average genotypes of the herd
- Distance matrix between herds computed as follows:

$$d_{ij} = 1 - \frac{g_{ij}}{\sqrt{g_{ii} * g_{jj}}}$$

- Number of clusters set to 12 to ensure all main breeds are represented at least by 3 clusters

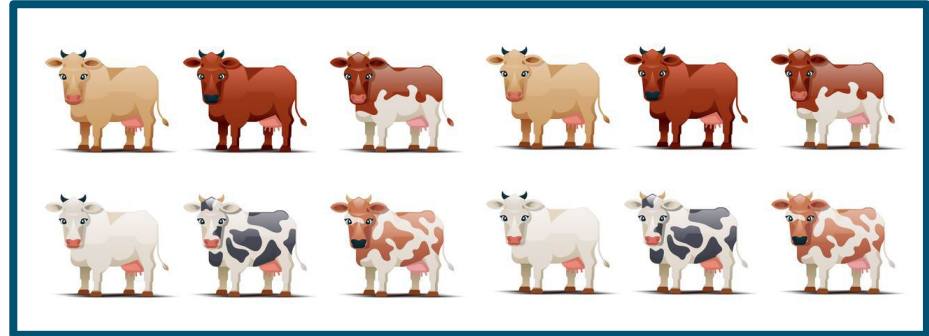
How to define sets for analysis?



Data set 1 4 clusters:

Holstein, Limousine,
Charolais, Angus

$N = 5,196$



Data set 2 7 clusters:

Holstein, Hereford + Belgian Blue,
Limousine + Charolais, Limousine,
Angus + Holstein, Limousine +
Charolais, Charolais + Limousine

$N = 8,997$

Model Data set 1

- Reaction norm model (mtg2)

$$y = \mu + \beta_0 + Q\beta_1 + \tau_0 + \tau_1$$

- Backsolve SNP-effects for intercept and quadratic regression coefficient (calc_grm)
- Calculate weights as:

$$D_{ki} = \sqrt{2p_k(1-p_k)}\hat{\alpha}_{ki}$$

Model Data set 2

- SNP-BLUP (MiXBLUP)

$$y = \mu + Z\gamma_0 + QZ\gamma_1 + e$$

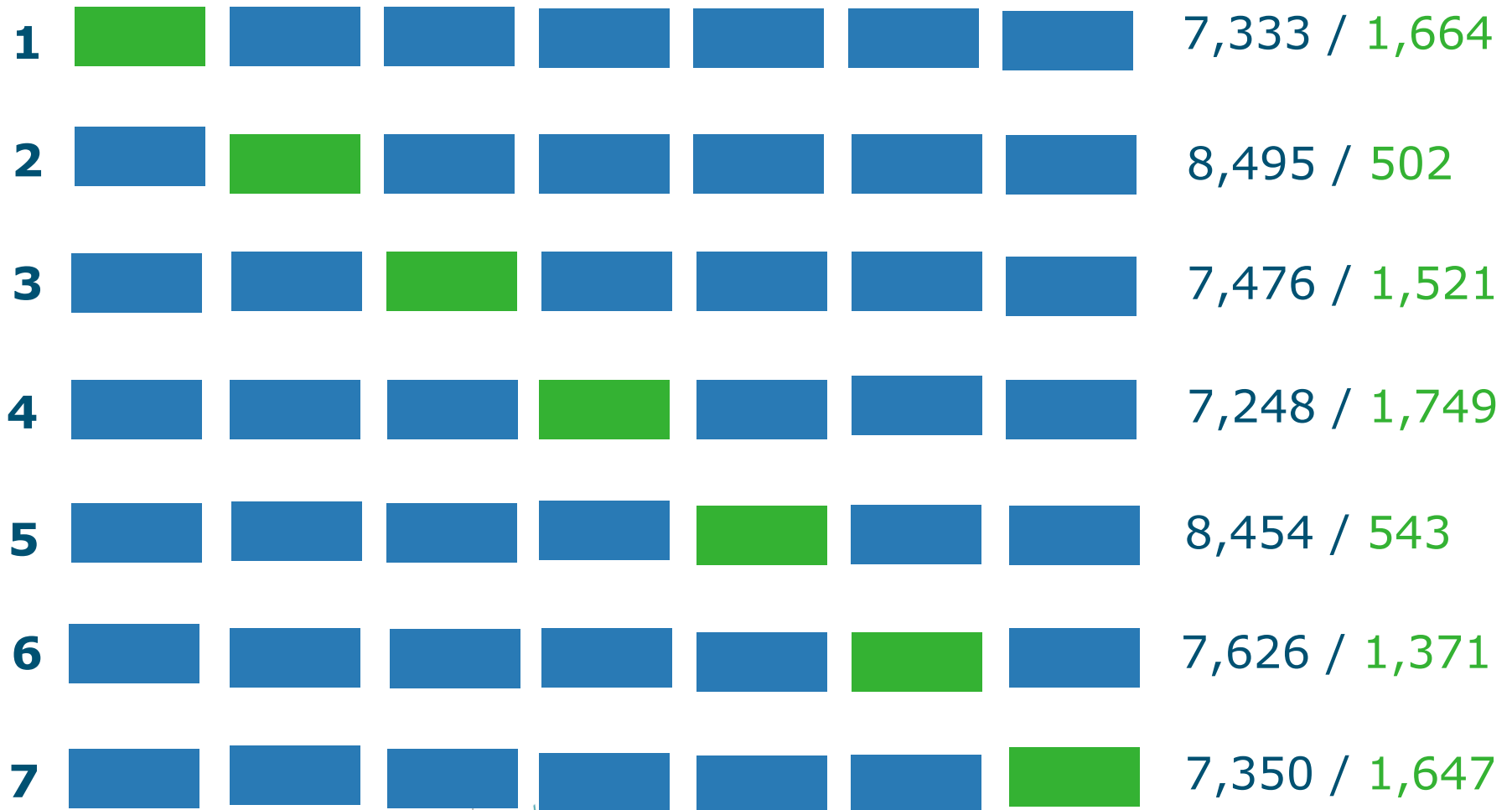
- Apply weights (D) on SNP (co)variance matrix:

$$D_{ki} = \sqrt{2p_k(1-p_k)}\hat{\alpha}_{ki}$$

- $Var([\gamma_0, \gamma_1]') = \sqrt{D_{ki}} \mathbf{G} \sqrt{D_{ki}}$

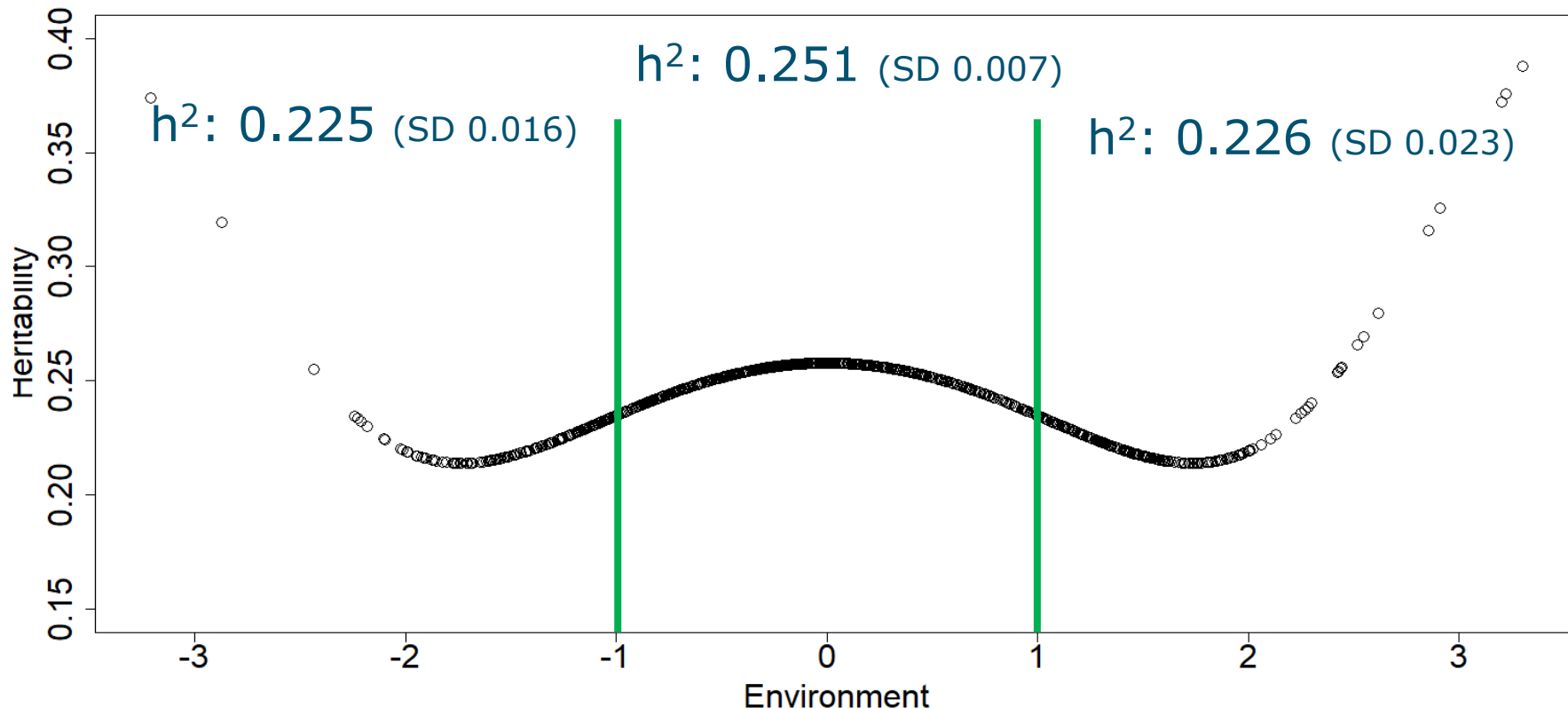
7-fold Cross validation in data set two

Training / validation

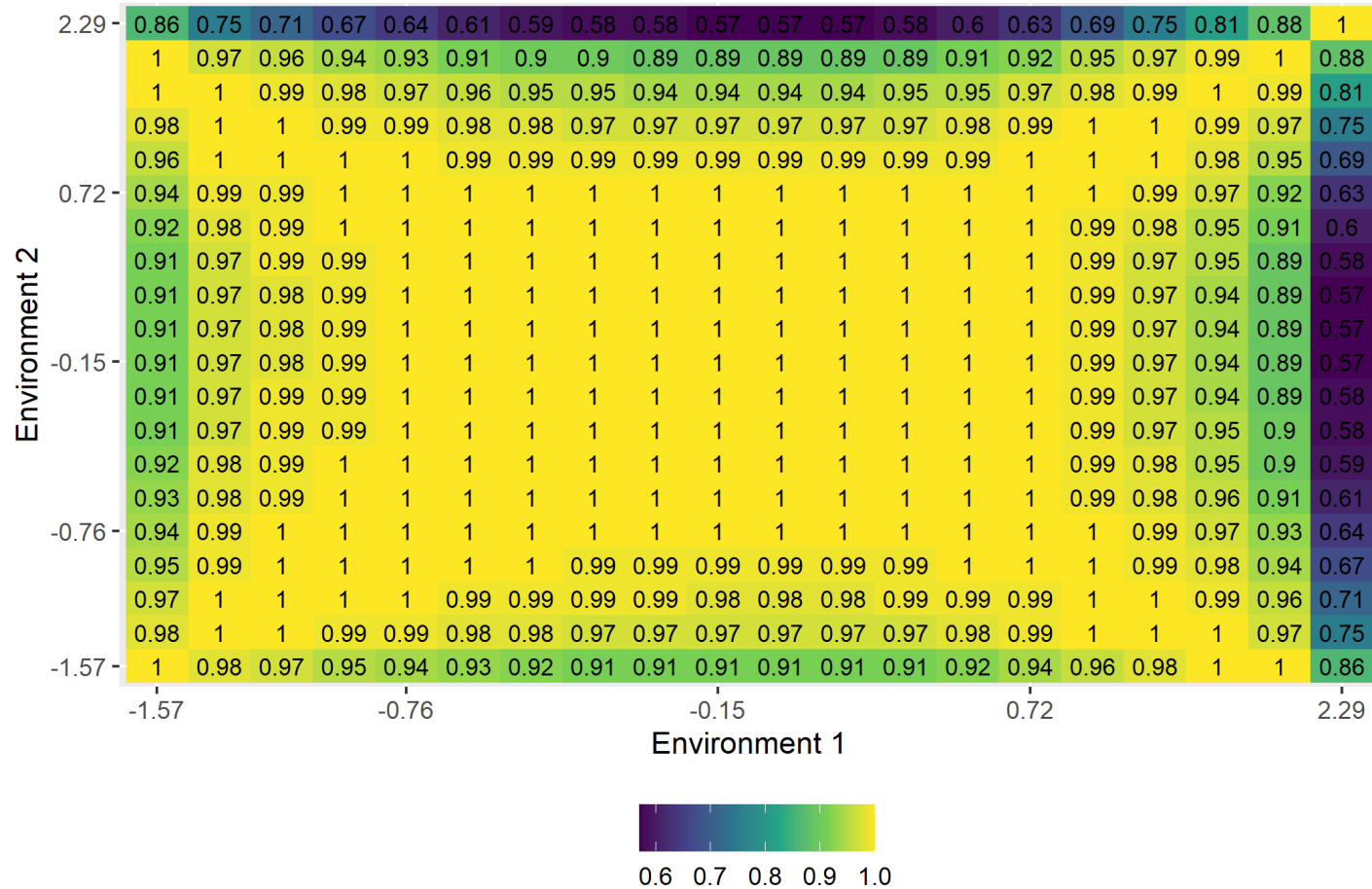


Results – Heritability across environments

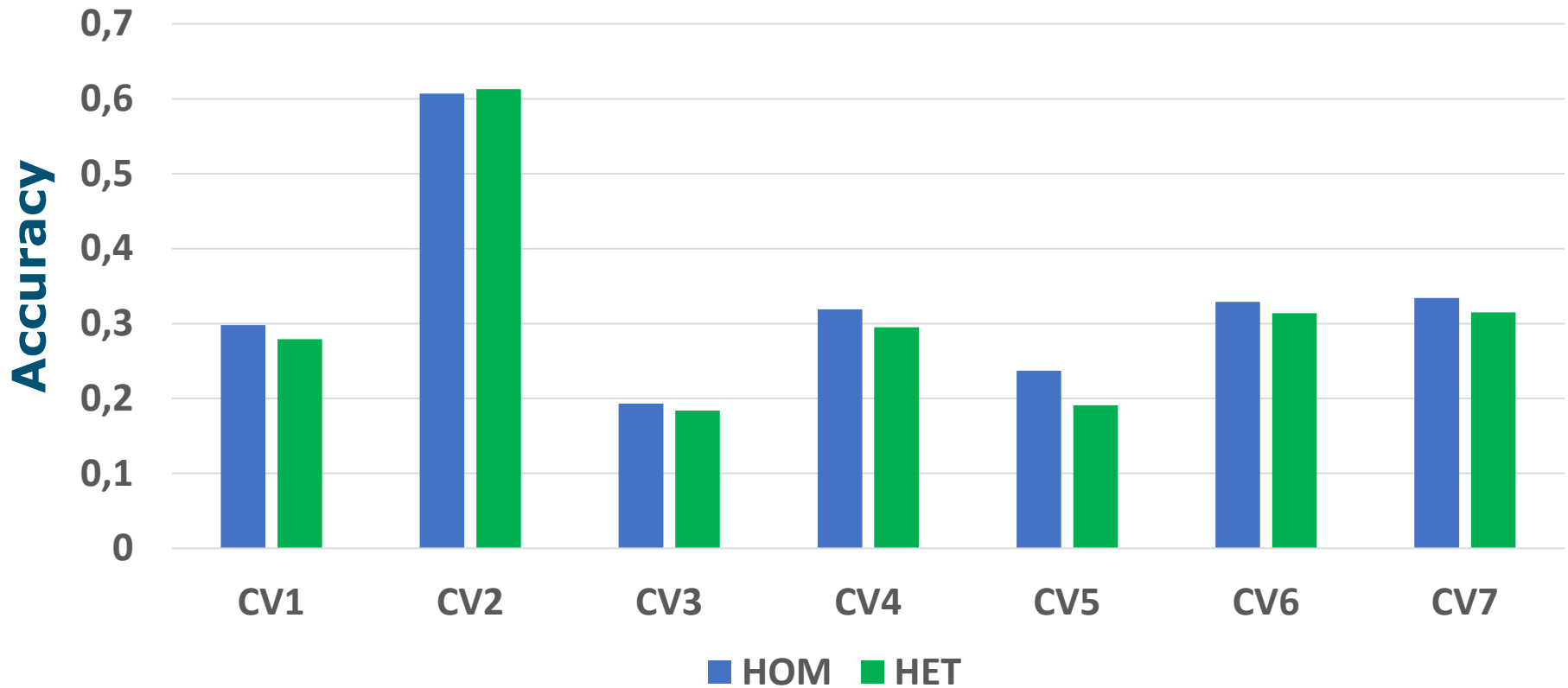
Average heritability: 0.242 (SD 0.017)



Results – genetic correlation across environments



Accuracy of GEBV with HOM and HET



Accuracy of GEBV with HOM and HET

0,7

0,6

The accuracy of selection based on pedigree: 0.13 – 0.23

➔ clear benefit of using genomic information for age at slaughter

0,1

0

CV1

CV2

CV3

CV4

CV5

CV6

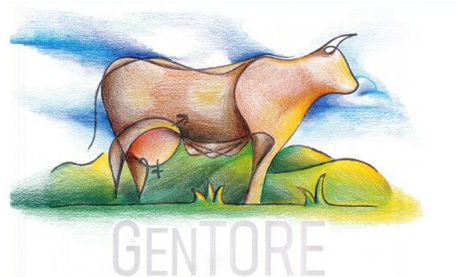
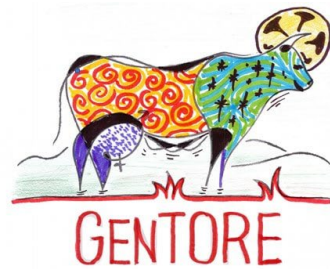
CV7

■ HOM ■ HET

Summary

- Large genetic variation for age at slaughter
- GxE for age at slaughter exists to some extent (extreme environments)
- For majority of environments genetic correlation >0.89
- HOM and HET result in similar accuracies of GEBV
- Genomic reaction norm models results in higher accuracy compared to pedigree information
- Genomic information has potential to increase efficiency and reduce environmental impact of beef production

Thank you!



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