

# Stronger Measures of Genomic Connectedness Enhance Prediction Accuracies across Management Units

World Congress on Genetics Applied to Livestock Production

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Theory to Application 1

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# Genetic connectedness



- BLUP offers meaningful comparison of the breeding values across management units when they are connected

Can we safely compare estimated breeding values or genetic values across management units?

## Connectedness metrics

Prediction error variance of the difference (**PEVD**)

$$\begin{aligned}\text{PEVD}(\hat{u}_i - \hat{u}_j) &= [\text{PEV}(\hat{u}_i) + \text{PEV}(\hat{u}_j) - 2\text{PEC}(\hat{u}_i, \hat{u}_j)] \\ &= (\mathbf{C}_{ii}^{22} - \mathbf{C}_{jj}^{22} - \mathbf{C}_{ij}^{22} + \mathbf{C}_{jj}^{22})\sigma_\epsilon^2 \\ &= (\mathbf{C}_{ii}^{22} + \mathbf{C}_{jj}^{22} - 2\mathbf{C}_{ij}^{22})\sigma_\epsilon^2,\end{aligned}$$

Small PEVD == greater connectedness

Coefficient of determination (**CD**)

$$\text{CD}_{ij} = 1 - \lambda \frac{\mathbf{C}_{ii}^{22} + \mathbf{C}_{jj}^{22} - 2\mathbf{C}_{ij}^{22}}{\mathbf{K}_{ii} + \mathbf{K}_{jj} - 2\mathbf{K}_{ij}}.$$

High CD == greater connectedness

## Choice of **K**

### a) Parametric

- **A**: Pedigree kernel
- **G**: Additive genomic kernel
- **D**: Dominance genomic kernel

**GBLUP**

### b) Non-parametric

- **GK**: Gaussian kernel
- **MK**: Matérn kernel
- **DK**: Diffusion kernel

**RKHS**

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### Question 1

Does genomic information increase measures of connectedness relative to pedigree?



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## Genomic Relatedness Strengthens Genetic Connectedness Across Management Units

Haipeng Yu, Matthew L. Spangler, Ronald M. Lewis and Gota Morota

G3: GENES, GENOMES, GENETICS *Early online August 31, 2017;*

<https://doi.org/10.1534/g3.117.300151>

## Intermediate summary

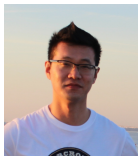
- Genomic relatedness strengthens measures of genetic connectedness relative to pedigree
- 1) Improving the quality of breeding value comparisons vs. 2) Improving the accuracy of genomic prediction

## Intermediate summary

- Genomic relatedness strengthens measures of genetic connectedness relative to pedigree
- 1) Improving the quality of breeding value comparisons vs. 2) Improving the accuracy of genomic prediction

### Question 2

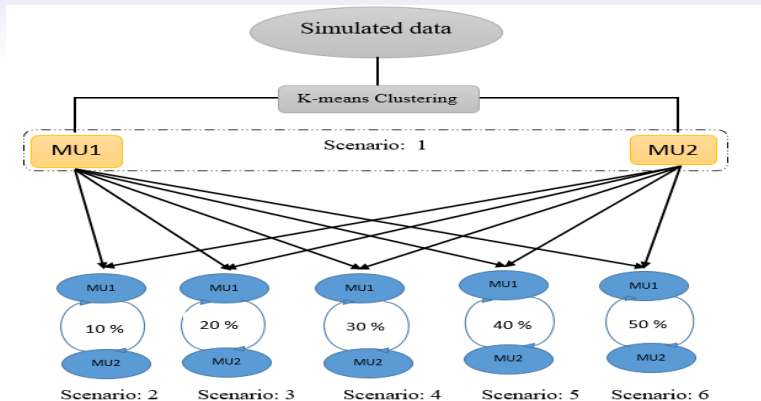
Does increased connectedness observed by genomic relatedness also leads to increased prediction accuracy across management units?



Haipeng Yu

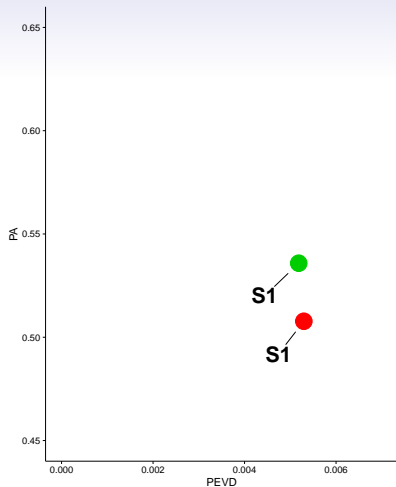


# Management units simulation

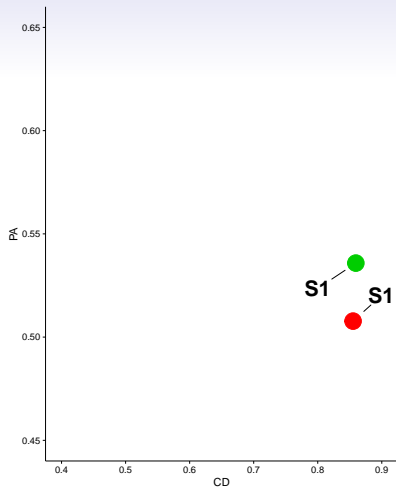


The degree of connectedness was increased by exchanging 10%, (S2) 20%, (S3) 30%, (S4) 40% (S5) and 50% (S6) of randomly sampled individuals between MU1 and MU2.

# Scenario 1



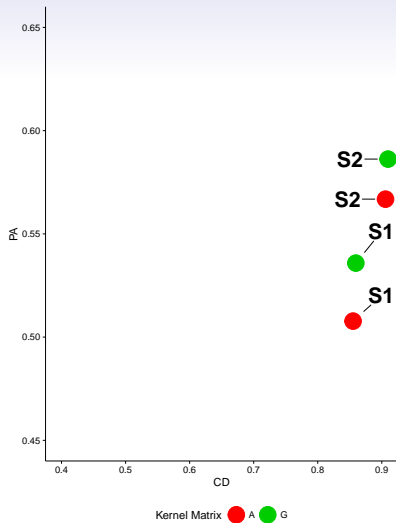
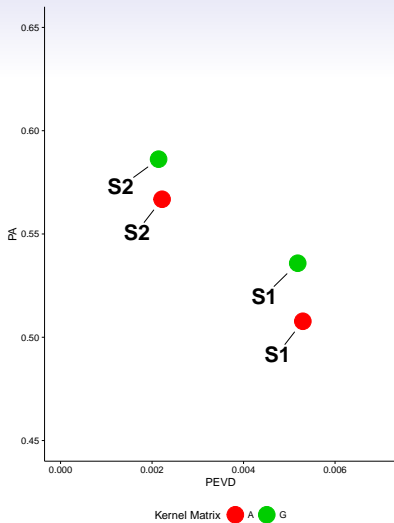
Kernel Matrix ● A ● G



Kernel Matrix ● A ● G

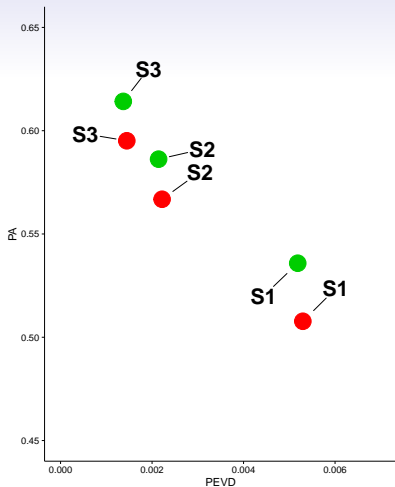
D: 1,015 QTLs and 50,000 markers ( $h^2 = 0.8$ )

## Scenario 2

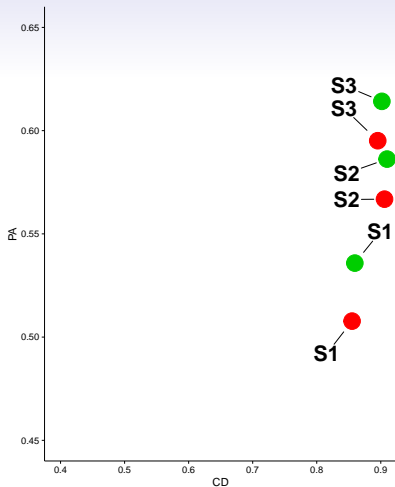


D: 1,015 QTLs and 50,000 markers ( $h^2 = 0.8$ )

# Scenario 3



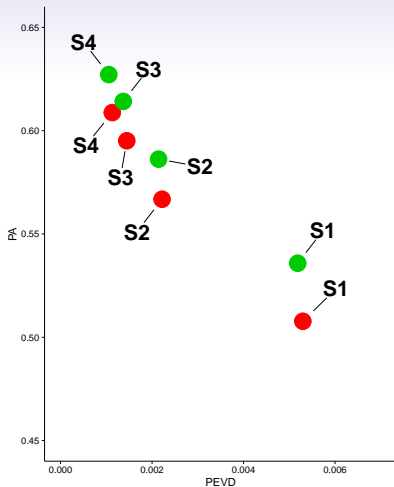
Kernel Matrix ● A ● G



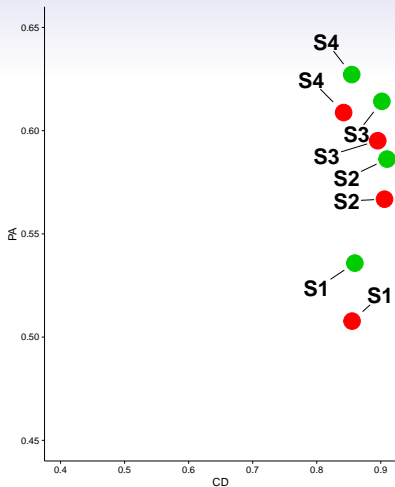
Kernel Matrix ● A ● G

D: 1,015 QTLs and 50,000 markers ( $h^2 = 0.8$ )

# Scenario 4



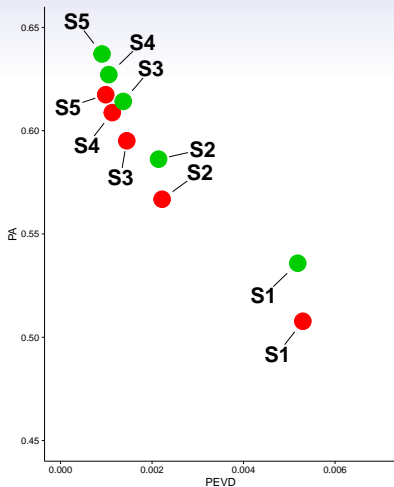
Kernel Matrix ● A ● G



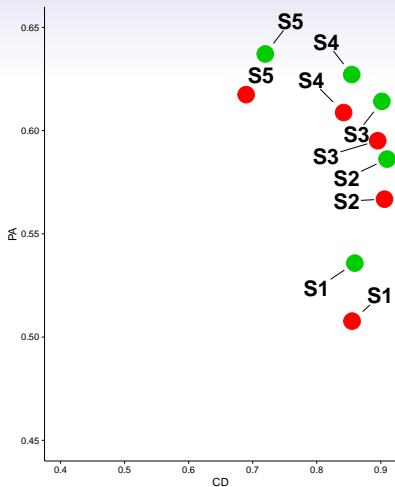
Kernel Matrix ● A ● G

D: 1,015 QTLs and 50,000 markers ( $h^2 = 0.8$ )

# Scenario 5



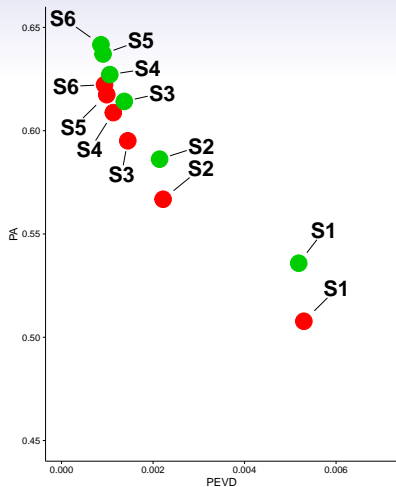
Kernel Matrix ● A ● G



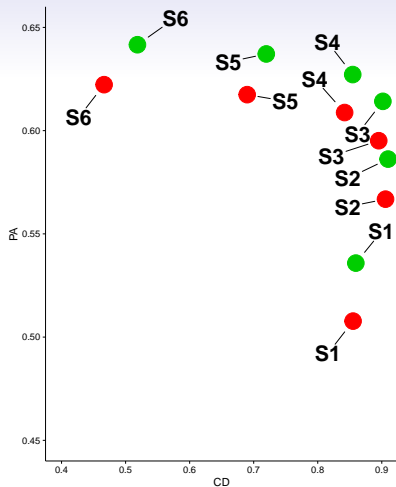
Kernel Matrix ● A ● G

D: 1,015 QTLs and 50,000 markers ( $h^2 = 0.8$ )

## Scenario 6



Kernel Matrix ● A ● G



Kernel Matrix ● A ● G

D: 1,015 QTLs and 50,000 markers ( $h^2 = 0.8$ )

## Summary

- Connectedness across units increased with the proportion of connecting individuals and this increase was associated with improved accuracy of prediction
- Sufficient level of connectedness in terms of prediction accuracy



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### Related project

- Quantifying genomic connectedness from non-additive and non-parametric relationships



Mehdi Momen