

Genomic inference and prediction of perennial ryegrass yield and quality traits under spatio-temporal genotype by environment interaction



Conference:



Elesandro Bornhofen^{1*}, Dario Fè^{1,2}, Ingo Lenk², Morten G. Pedersen², Thomas Didion²,

Christian Sig Jensen², Torben Asp¹, Luc Janss¹

¹ Center for Quantitative Genetics and Genomics (QGG), Aarhus University, Aarhus, Denmark

² DLF Seeds A/S, Store Heddinge, Denmark

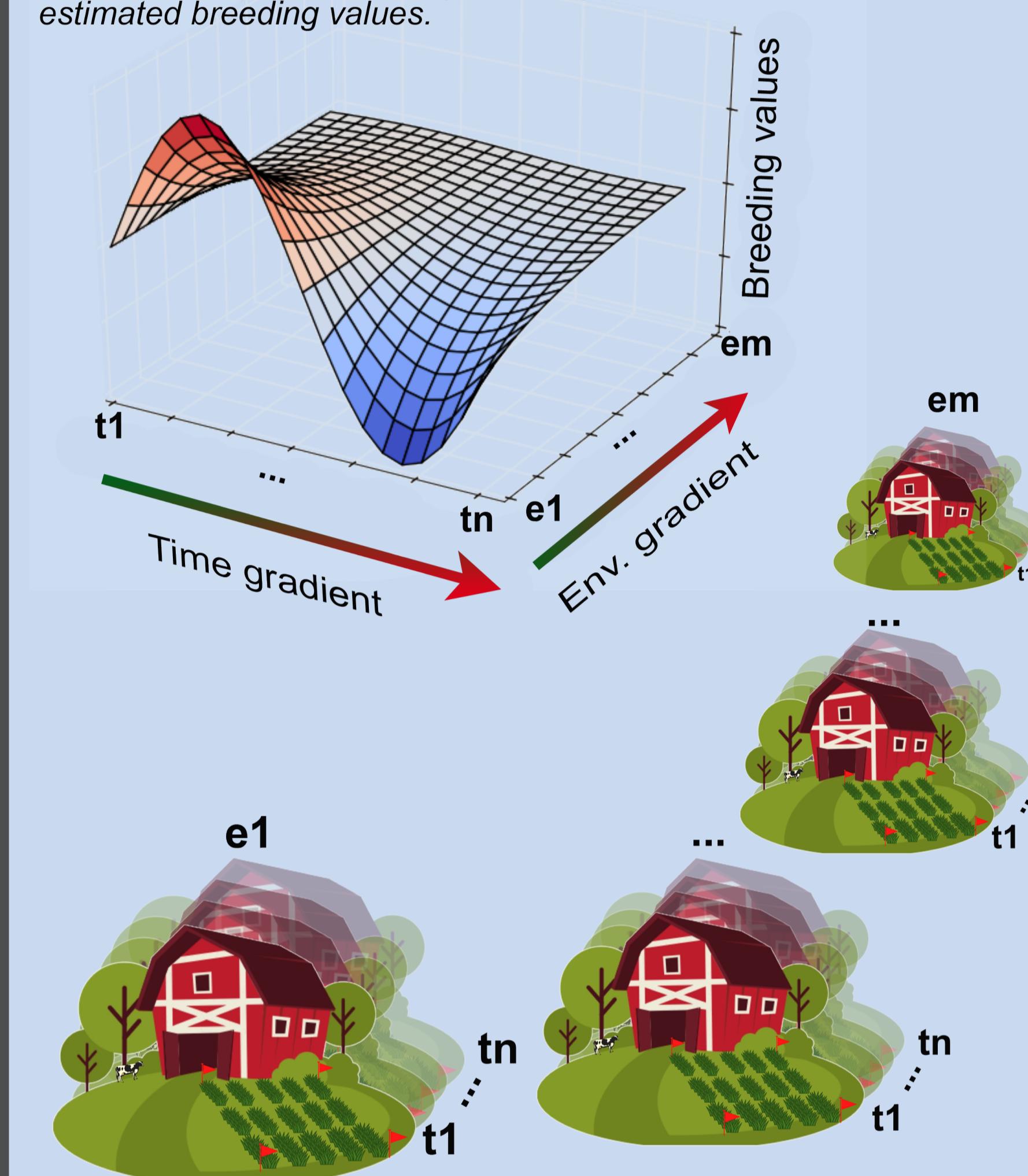
*bornhofen@qgg.au.dk



Introduction

The selection of superior breeding materials of perennial pastures involves recording phenotypes over time-points in multiple locations (Fig. 1). This condition yields a spatio-temporal genetic correlation structure, which is rarely accounted for in inferential studies and prediction settings.

Fig. 1 Representation of multiple harvest-location trials of perennial ryegrass and spatio-temporal estimated breeding values.



The main objective of this study was to model the longitudinal dimension of perennial ryegrass breeding data while accounting for multiple sites and within-trial random spatial variability by leveraging genomic random regression mixed models (gRRMs).

Material & methods

The plant material consisted of 381 bi-parental F₂ family pools from two unconnected sparse diallel crosses and four check varieties of diploid perennial ryegrass evaluated in eight environments for biomass yield and nutritive quality traits. A bias-corrected allele frequency-based genomic relationship matrix (\mathbf{G}) was calculated using 56,645 SNPs. Non-linear additive and residual genetic trends over the temporal dimension (t) were modeled by a second-order Legendre polynomial function while a linear fit was assumed over the environments (e).

$$y_{ijtes} = b_i + \sum_{k=1}^q \alpha_{kj} \phi_k(t) + \sum_{k=1}^q \delta_{kj} \phi_k(t) + \sum_{k=1}^q \beta_{kj} \phi_k(e) + \sum_{k=1}^q \gamma_{kj} \phi_k(e) + \sum_{s=1}^{15} \psi_s + \epsilon_{ijtes}$$

where, b is the fixed effect, α and β are random regression coefficients for the additive genetic effects whereas δ and γ are non-additive genetic effects. The random term ψ accounts for within-trial spatial variation. A simpler reaction norm model was fitted to the data of single cuts to contrast with the full model. Estimations and cross-validations were performed using the DMU package version 6 [1].

Results & discussion

Low values of additive genetic correlations indicated complex GxE interaction across space and time points in early harvest measurements (Fig. 2). The temporal dimension was the main driver of genomic estimated breeding value re-ranking whereas slope-intercept correlation revealed moderate spatial GxE (Fig. 3). Modeling the temporal dimension substantially increases the predictive ability when training-validation relatedness is low (Fig. 4).

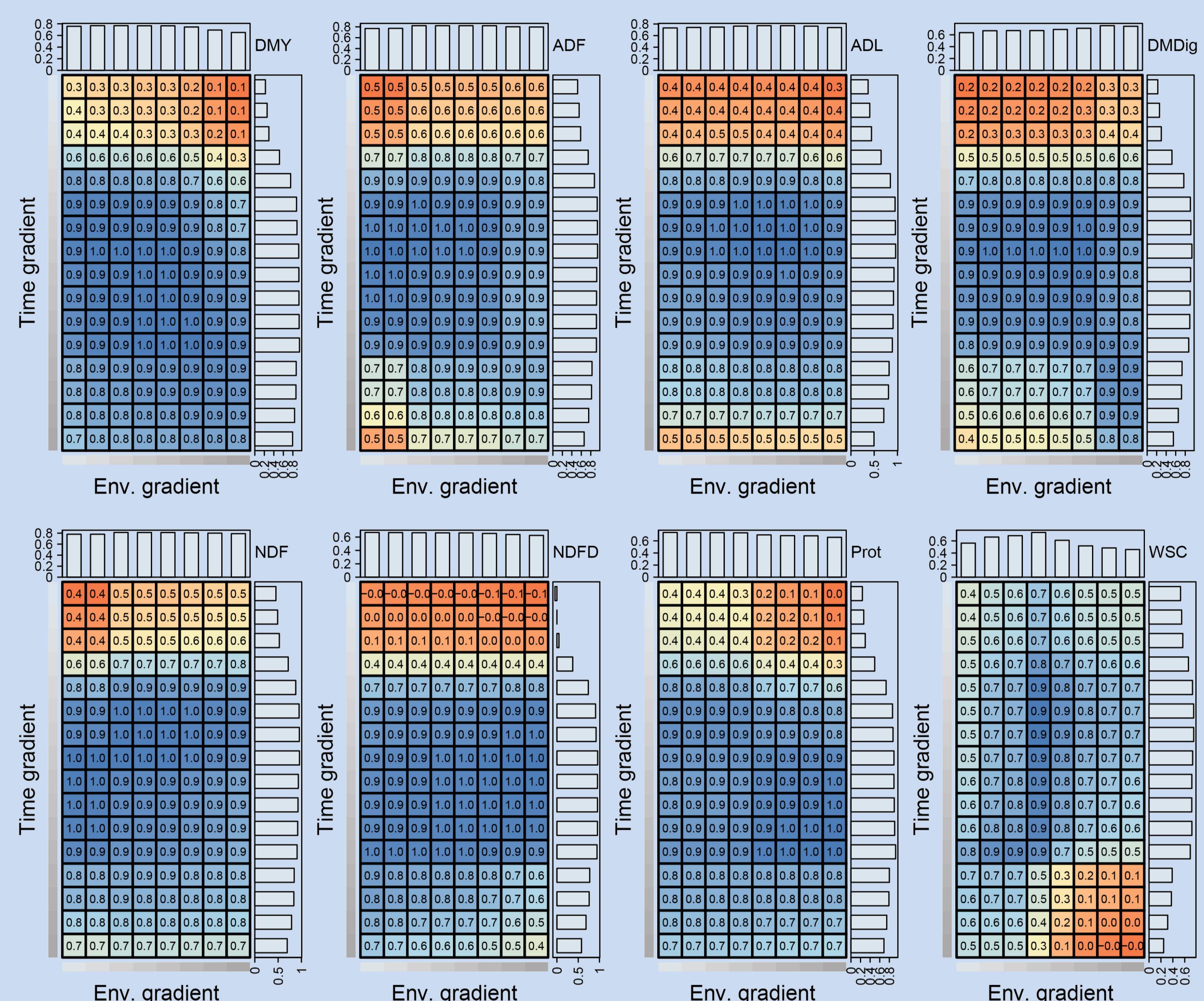


Fig. 2 Additive genetic correlation (ρ_a) between each combination of time and environmental points, estimated via a random regression mixed model for eight ryegrass traits.

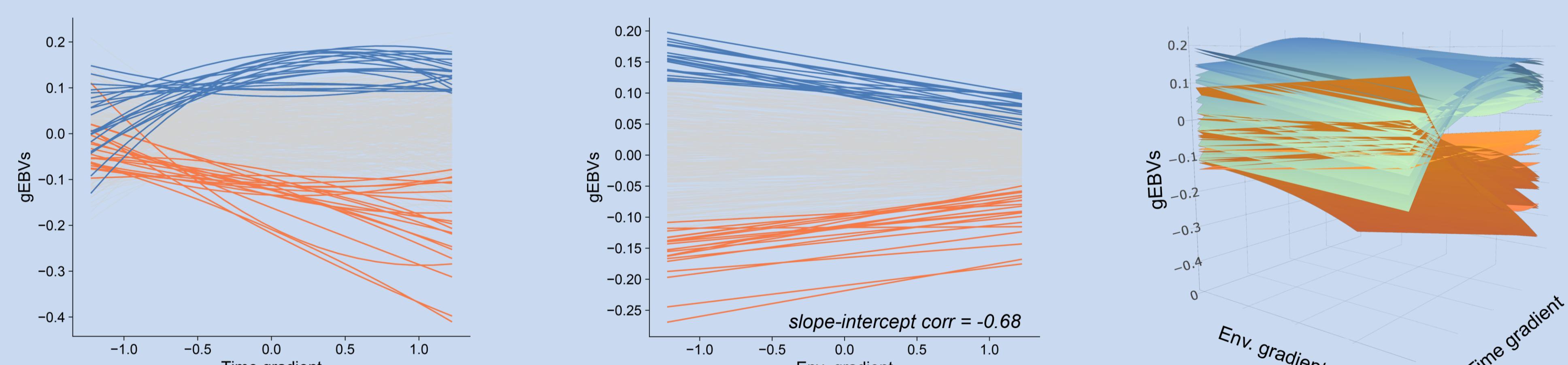


Fig. 3 Families' plasticity is depicted as a reaction norm on different levels of harvest time (left) and environmental (center) gradient for overall environmental and harvest performances, respectively. 3D plot on the right side depicts a gEBV surface for each entry as a function of harvest time and environmental indices.

Covariance functions in the mixed model framework enables covariance structure modeling while alleviating over-parameterization problems of MTM [2].

Across harvest prediction accuracies of dry matter yield were up to 18% higher when fitting the genomic random coefficients model in a condition of low kinship between training and testing sets.

Prediction study

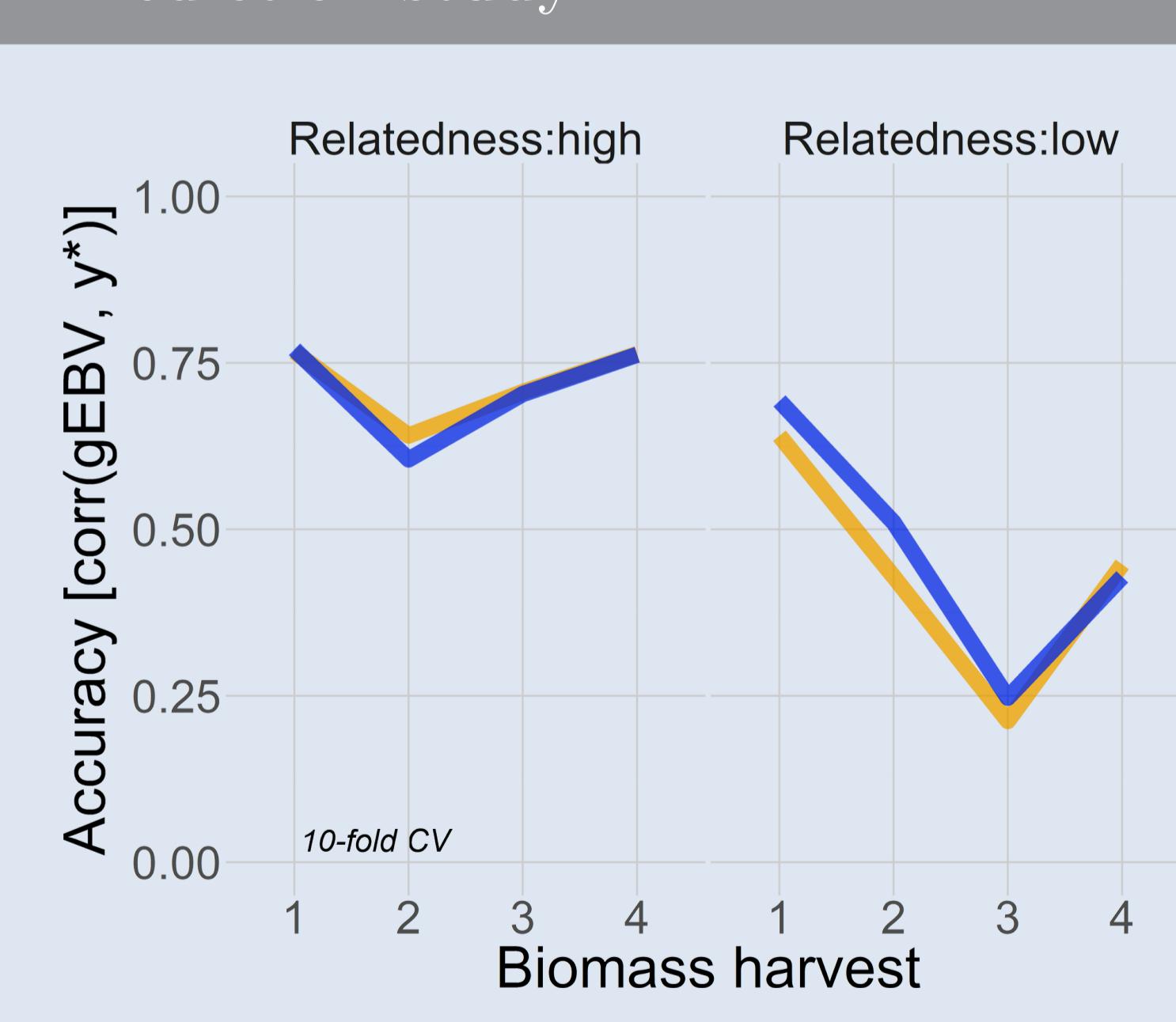


Fig. 4 Prediction accuracy across cuts in two training-testing relatedness conditions.

Acknowledgements

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References

- [1] P. Madsen, J. Jensen. *DMU v.6 package: User guide*, 2013.
- [2] K. Meyer. *Genetics Selection Evolution*, 30, 1998.