

Stage-wise analysis of phenotypic data for cranberry genotypic evaluation

Jeffrey L. Neyhart^{1,2}, Jennifer Johnson-Cicalese², and Juan E. Zalapa^{3,4}

¹USDA-ARS, Chatsworth, NJ.; ²P.E. Marucci Center for Blueberry and Cranberry Research and Extension, Chatsworth, NJ.;

³USDA-ARS, Madison, WI.; ⁴Dept. of Horticulture, University of Wisconsin-Madison, Madison, WI.



Takeaways

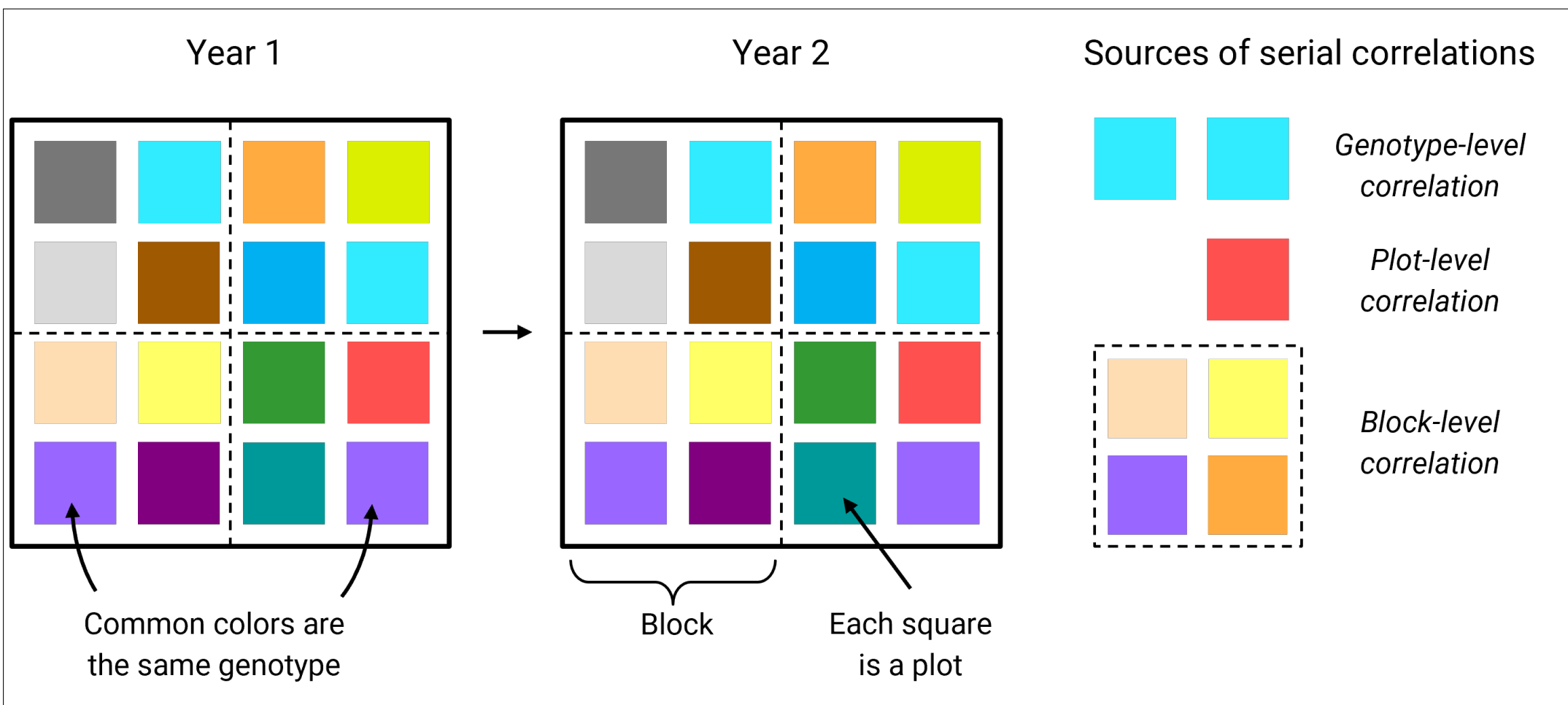
- Takeaway 1
- Takeaway 2
- Takeaway 3

Introduction

Optimal analysis of multi-environment trials (METs) can aid in identifying superior genotypes in breeding programs.

MET data for perennial crops presents statistical challenges:

- **Unbalanced data:** not all genotype-environment combinations are observed
- **Serial correlation:** plots, blocks, and genotypes are not randomized across years
- **Limited replication:** early-stage trials are often single-plant designs



Mixed-effect models are ideal for addressing these challenges to analyze MET data, but have been underutilized in breeding programs of perennial crops such as cranberry

Objectives:

- Determine the best-fitting mixed-effect model for analyzing data from cranberry METs.
- Compare the ability of models to predict genotypic performance for multiple traits in future years.

Materials and Methods

We analyzed phenotypic data from three Rutgers cranberry breeding program trials:

Results

The best test locations are denoted by **larger points in the upper-right corner** of each plot

Some locations are ideal for multiple traits: BTT (Bottineau, ND); PLL (Pullman, WA)

For other locations, only some traits are reliably phenotyped: MRR (Morris, MN); ABR (Aberdeen, ID)

Most test locations are not ideal for phenotyping all traits

Fewer, optimized locations led to similar or better phenotype data quality compared to all or random sets of locations

Optimization generally increased phenotype data quality while reducing the number of locations by 50-75%

Read more / reach out

Read our paper in *Crop Science*

Contact:

- Email: jeffrey.neyhart@usda.gov
- LinkedIn: [linkedin.com/in/jeffneyhart](https://www.linkedin.com/in/jeffneyhart)
- GitHub: github.com/neyhartj

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References