



UNIVERSITY OF
HOHENHEIM

Stephan Bark

A Bayesian Updating Framework for Long-term Multi-Environment Trial Data in Plant Breeding (Bark et al., 2026)

Supervised by Prof. Dr. Hans-Peter Piepho and Prof. Dr. Volker Schmid

"100 Jahre statistische Versuchsplanung: Entwicklungen im landwirtschaftlichen Versuchswesen von R. A. Fisher bis heute" in the BASF Agricultural Center in Limburgerhof

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1 Introduction

- Maximize genetic gain for crop traits of interest.
- Analyze the phenotypic data to support genomic selection decisions.
- Phenotypic performance of genotypes differs across environments.
→ Evaluation of genotypes across multiple locations and years.
- Differentiate the phenotypic performance of genotypes and genotype-environment interactions.



Figure: Field experiment photographed by Florian Gerlach at the University of Hohenheim.

2 The Limitations of the REML Estimation

Buntaran et al., 2022

Definition

The heritability is defined as follows

$$h^2 = \frac{\text{genetic variance}}{\text{genetic variance} + \text{environmental variance}} \quad (1)$$

- Each year genotype effects are obtained contaminated by environmental noise.
→ But genomic selection decisions have to be made based on genomic breeding values (GBV)!
- Separation of GBV and GBV×environment interactions via h^2

Switch statistical perspective to obtain uncertainty in h^2 :

1) Classical mixed model approach provides restricted maximum likelihood (REML) point estimates of the variance components



2) Bayesian updating approach brings historically informed probability distributions of the variance components

→ Unlock probabilistic statements in the context of genomic decision risks:
E.g. "This year $h^2 \leq 0.15$ with a 30 percent probability for e.g. the grain yield trait of rice. We should be careful!"

Breeder: *"How can we access additional information about uncertainty without adding data?"*

Statistician: *"We can not. Bayesian Inference is no magic! However, there are ways to use what we have better!"*

Breeder: *"How!? I thought REML is the best."*

Statistician: *"REML is strong, often sufficient and has the power to borrow strength across genotypes. However, it does not provide uncertainty measures. METs can face abnormal years with special environmental conditions and more ...*

... My question to you is: What will you do when you are confronted with abnormal annual data that cannot be identified as such?"

Breeder: *"Perhaps I need uncertainty information to minimize my selection risk..."*

3 Bayesian Updating Approach

Main Idea of Bayesian Updating for MET Data

- (1) Split up the data into successive multi-year historical windows:

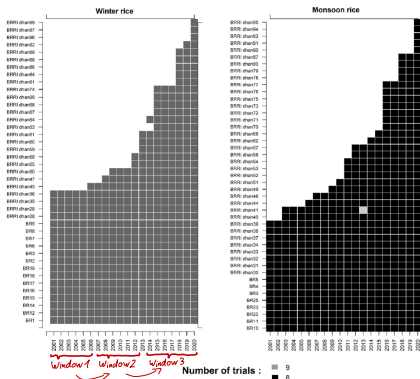
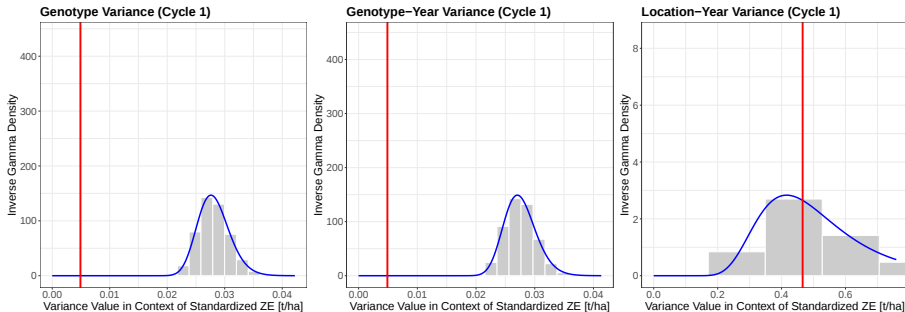


Figure. Classification of genotype-year combinations for the winter rice series (left) and monsoon rice series (right). Gray shading indicates the number of trials conducted in a given year (Rahman et al., 2023).

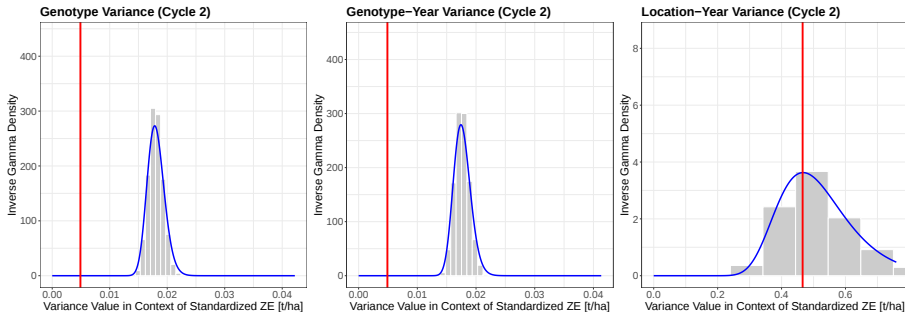
- (2) Introduce prior distributional assumptions for the variance components in the mixed model.
- (3) Update the probabilistic information of the variance components from one data window to the next.

Probabilistic Plot of Variance Components



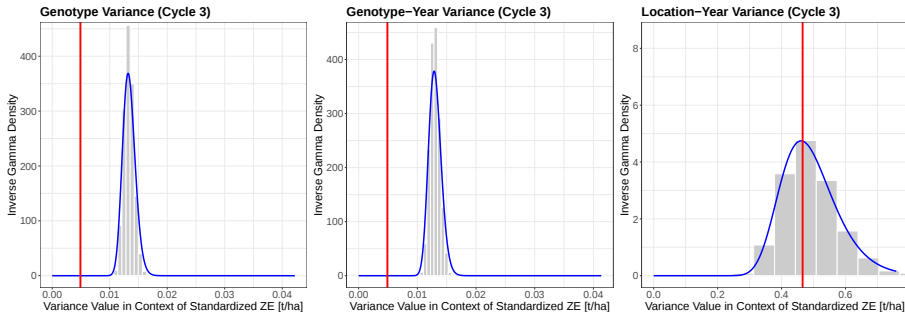
- Maximum Likelihood Estimate
- Posterior Histogram
- Inverse gamma density

Probabilistic Plot of Variance Components



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Probabilistic Plot of Variance Components



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- Mean Squared Error (MSE) wrt. to the posterior predictive distribution of the yield response $\hat{y}^{(d)}$:

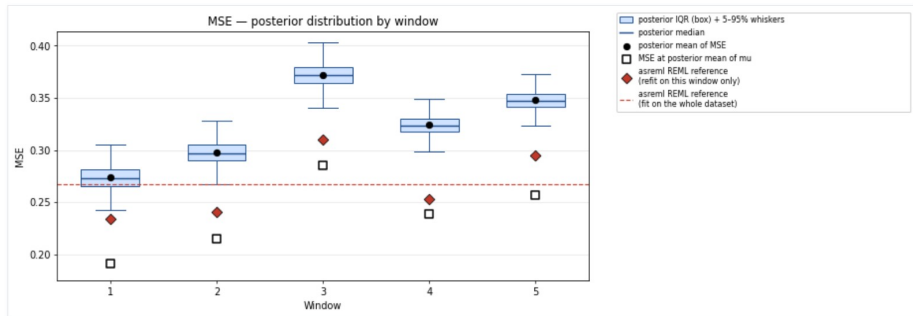
$$\text{MSE}(\hat{y}^{(d)}) = (1/N) \sum_{i=1}^N [y_i^{(d)} - \hat{y}_i^{(d)}]^2,$$

where $d = 1, \dots, D$ corresponds to D draws,
and $i = 1, \dots, N$ corresponds to a dataset with n observed yield values,
and $\hat{y}^{(d)} = (\hat{y}_1^{(d)}, \dots, \hat{y}_n^{(d)})^T$.

- Mathematical note referring to Jensen's Inequality:

$$\mathbb{E}[\text{MSE}(\hat{\mathbf{y}})] \geq \text{MSE}(\mathbb{E}[\hat{\mathbf{y}}]),$$

where $\hat{\mathbf{y}} = (1/D) \sum_{d=1}^D [y^{(d)} - \hat{y}^{(d)}]^2$.



- Refers to the 22-year rice data of Rahman et al. (2023)

4 Conclusion

- (1) Probabilistic statements about heritability and other mixed model based genomic selection criteria!
- (2) Data usage in cycles results in efficiency & stability!
→ Potential to reduce necessary trial sizes...
- (3) Potential to increase model accuracy!

Thank you for your attention!

If you have any further questions, please feel free to contact me at stephan-bark@web.de



Figure: Field experiment photographed by Florian Gerlach at the University of Hohenheim.

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- Studnicki, M., & Piepho, H.-P. (2024). Hierarchical modelling of variance components makes analysis of resolvable incomplete block designs more efficient. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 137(6), 134. <https://doi.org/10.1007/s00122-024-04639-4>

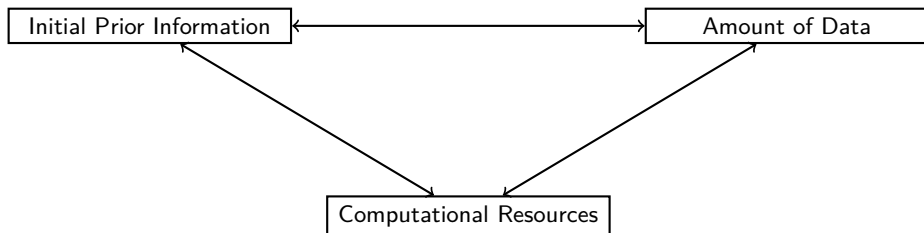
Classical Mixed Model

- + Uses the whole MET data in one go
- Does not consider historical prior information
- Variance component point estimates without uncertainty measures
- REML can estimate variance components to exactly zero (Studnicki and Piepho, 2024) assumed to be non zero by model assumption
- + REML is unbiased for variance components
- + Still less computer intensive
- Less robust and stable estimation process

Bayesian Updating

- Uses the MET data iteratively split into historical subsequent data cycles
- + Does objectively inform probabilistic information of variance components
- + Delivers more accurate estimation, as all variance components by model assumptions are considered and non zero
- Might introduce bias, if priors are not truly objectively informed
- Currently more computer intensive
- + More robust and stable estimation process

Trade Off for Proper Convergence with Bayes



Prior Type	Convergence Risk	Stability	Bias Risk
Strongly Informative	Low	High	High (can over-shrink estimates)
Weakly Informative	Medium	Medium	Low (balances data and prior influence)
Uninformative (flat, improper)	High	Low	None (tends to divergence)

Table: Comparison of prior types and their effects on convergence, stability, and bias risk inspired by Gelman and Yao (2020).