

Revisiting superiority and stability measures in multi-environment trials using genomic data

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Humberto Fanelli Carvalho

Universidad Politécnica de Madrid

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Genotypes with **high** and **stable** performances over the set of environments are desire targets for a breeding program.

Metrics for **superiority**

- Mean performance

$$Y_{i.} = \frac{1}{J} \sum_{j=1}^J (Y_{ij})$$

- * $Y_{1.} = 12.8$

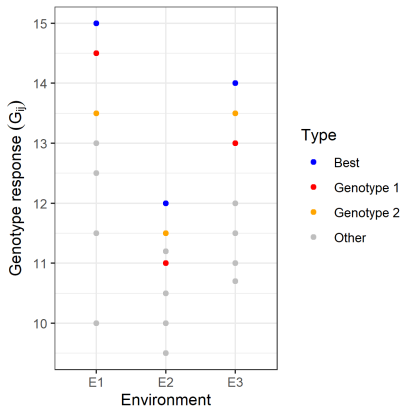
- * $Y_{2.} = 12.8$

- Superiority measure (Lin and Binns 1988)

$$P_i = \frac{1}{2J} \sum_{j=1}^J (Y_{ij} - Y_{\text{Best}_{j,j}})^2$$

- * $P_1 = 0.375$

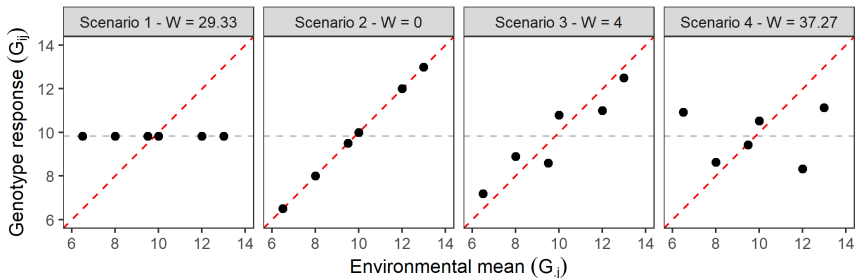
- * $P_2 = 0.458$



Metrics for **stability**

- Ecovalence (Wricke 1962) - $W_i = \sum_{j=1}^J (Y_{ij} - Y_{i.} - Y_{.j} + Y_{..})^2$
 - * Dynamic, partition of GE-interaction, $W_i = 0$ is stable

Ecovalence (W_i)



Metrics for **stability**

- Environmental variance (Roemer 1917)

- * Static, genotypes do not react to the environment, $S_i = 0$ is stable

$$S_i = \frac{1}{J-1} \sum_{j=1}^J (Y_{ij} - Y_{i.})^2$$

- Regression coefficient (Finlay and Wilkinson 1963)

- * Static, genotypes do not react to the environment $B_i = 0$
- * Dynamic, genotypes reacting to the environment $B_i = 1$

$$B_i = \frac{\sum_{j=1}^J (Y_{ij} - Y_{i.})(Y_{.j} - Y_{..})}{\sum_{j=1}^J (Y_{.j} - Y_{..})^2}$$

Stability and superiority measures are generally estimated with phenotypic means (best linear unbiased estimators - **BLUE**)

Drawbacks:

- Metrics are computed using **phenotypes only**
- Difficult to apply when some genotype-environment combinations are **missing**
- Genotypes are assumed **independent**

Most Stability and Superiority measures have the following form:

$$M_i = \sum_{j=1}^J X_{ij}^2$$

Assuming a **genomic prediction model** accounting for $G \times E$, we can compute their **GBLUP**:

$$\mathbb{E}(M_i|y) = \sum_{j=1}^J \mathbb{E}(X_{ij}^2|y) = \sum_{j=1}^J \mathbb{E}(X_i|y)^2 + \sum_{j=1}^J \mathbb{V}(X_i|y)$$

We thus derive two estimators:

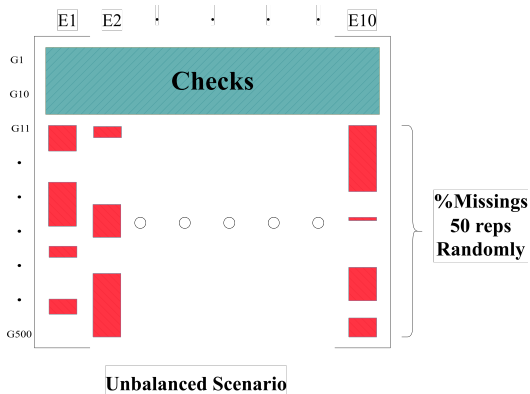
- $M_p : \hat{M}_i = \sum_{j=1}^J \hat{X}_{ij}^2 + \sum_{j=1}^J \text{PEV}_{X_{ij}}$
- $M : \hat{M}_i = \sum_{j=1}^J \hat{X}_{ij}^2$

Simulation: Scenarios

- Total 216 Scenarios

Nº G	200	500		
$SD_{trial_{100}}$	0.1	1	3	10
CORg	0.2	0.5	0.8	
VARg	0.5	1	2	
h2	0.2	0.5	0.8	

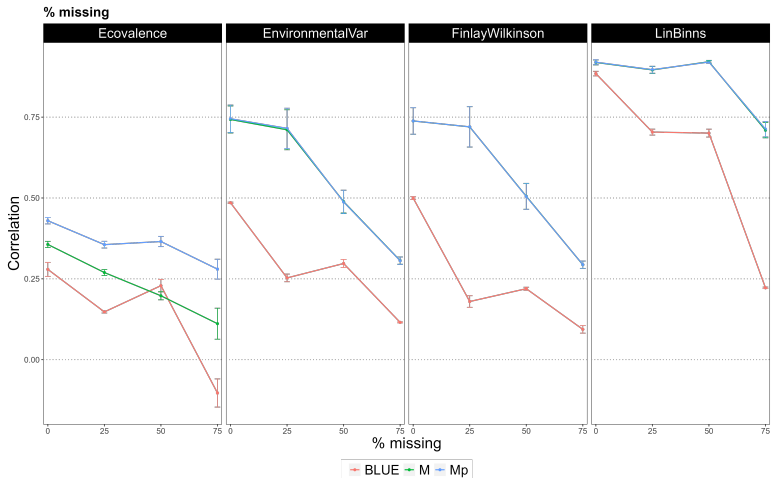
- 0%, 25%, 50%, and 75%



Simulation: Results

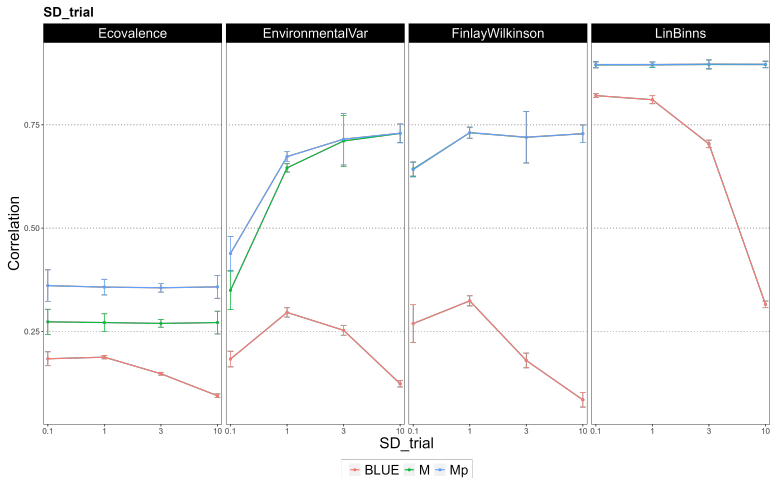
- Instance scenario

($N G=200, SD_{trial100}=3, CORg=0.5, VARg=1, h^2=0.5$)



Simulation: Results

- Instance scenario ($N^{\circ}G=200, \text{CORg}=0.5, \text{VARg}=1, h_2=0.5$, missing = 25%)



The advantage of using genomic information is proven and should be considered by the agronomists/geneticists to compute the genotype-by-environment interaction metrics.

Real data: GBLUP-based estimates of stability/superiority measures

- Use as reference the stability/superiority measures computed using phenotypes only
- Cross-validation using genotypes never observed in the environment

R-package to make methods available to the community





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