**Technical detail of model implemented gBLUP INLA**

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For each trait, the linear mixed model for multiple locations:

y = **1**µ + **X**b + **Z**a + **W**na + e

Where:

**y:** vector of phenotypes (traits);

**b:** vector of random effect for environmental condition (Season+Field), is estimated with ;

**a:** vector of random of additive effects, with ;

**na:** vector of random of non-additive effects, with ;

**e:** vector of residuals from the model ;

**A:** matrix of relationship by inbreds, can be created by Pedigree or Markers (Sweet Corn);

**X:** is the matrix design for random effects for environmental;

**Z:** is the matrix design based on inbred of hybrid incidence;

**W:** is the matrix design based on hybrid incidence;

The model is fitted using INLA (Integrate Nest Laplace Approximation) R Packager, is Bayesian approach for fit.

**Heritability (narrow sense):** the heritability means captures the percentage of the variance of interesting , and related with error variance , this can be defined with intra class correlation too, the formula is:

The values of close to 1, is relatedness with , and this is good, because the genetic effect in this trait is great that error, and selection can be realized with high rate of successes.

**Heritability (broad sense):** the heritability means captures the percentage of the variance of interesting , and related with error variance , this can be defined with intra class correlation too, the formula is:

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**Reliability:** is commonly used when reporting the quality of a random effect estimate in genetic studies. The formula requires the PEV (predictor error variance) of which corresponds to the square of the standard error (SE) of the random effect (, and the formula is:

The reliability is close relatedness with accuracy , and can be expressed in:

According to statistical theory, the values of PEV will range from zero to the . In cases where we have full information about a given genotype, then the PEV will be close to zero as we have little uncertainty in the true additive value of a genotype, hence,  . However, when there is very little information, then the PEV will approximate to . Note that these extreme values of PEV translate invalues of 1.0 and 0.0, respectively. Therefore, values closer to 1.0 are an indication of very good quality of a given additive effect estimate. More detail can be found (Bermann et al. 2023), this metric put more detail in quality of random effect estimated for each genotype, means mode detailed information inside of genetic variance (Gezan 2023).

**References:**

Bermann, Matias, Ignacio Aguilar, Daniela Lourenco, Ignacy Misztal, and Andres Legarra. 2023. “Reliabilities of Estimated Breeding Values in Models with Metafounders.” *Genetics Selection Evolution* 55 (1): 6. https://doi.org/10.1186/s12711-023-00778-2.

Dohm, M.R. 2002. “Repeatability Estimates Do Not Always Set an Upper Limit to Heritability.” *Functional Ecology* 16 (2): 273–80. https://doi.org/10.1046/j.1365-2435.2002.00621.x.

Gezan, Salvador. 2023. “Linear Mixed Models: Obtaining Estimates of Random Effects with ASReml-R.” October 20, 2023. https://vsni.co.uk/case-studies/calculating-accuracy-of-random-effect-estimates-with-ASReml-R.