quantitative trait loci with appropriate mutation probabilities (i.e., 10^{-3} and 10^{-5}, respectively). On average, the full model with all SNP reached a MSE of 1.370 ± 0.004, whereas this parameter reduced until 1.293 ± 0.005 when dropping off between 35% and 47% of the SNP. These results involved a ~6% reduction of MSE when using appropriate SNP for **G** and suggested a very appealing way to improve the statistical performance of gBLUP models when analysing massive genomic data.

SELECTED MARKERS

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The use of marker-enabled predictions in breeding programs can drastically increase the genetic gain per unit of time. However, different genomic selection methodologies may have different predictive abilities depending on the genetic architecture of the trait. In principle, a method might perform better in the prediction of traits that fit the assumptions under which was constructed. When genomic selection is modeled according to a Ridge Regression BLUP (RR-BLUP) approach, the assumptions for the marker variances follows the ones from the infinitesimal model, even though they are applied to a finite set. In this work, we evaluated a small modification of the RR-BLUP method that utilizes a subset of selected markers, and is referred hereafter as RR-BLUP B. The selection of the subset of markers is based in the group that maximizes the predictive ability in a cross-validation scheme. Once this group is defined, a new model is fit, under the same assumptions, but with a reduced number of covariates. To evaluate this approach we report, for an experimental breeding population of the tree loblolly pine (*Pinus taeda* L.), a comparison of GWS predictive models for 17 traits with different heritabilities and predicted genetic architectures. Genome-wide selection models included RR-BLUP B and four traditional methods: RR-BLUP, Bayes A, Bayes Cϖ and the Bayesian LASSO. We show that, for most traits, there is limited difference among these five methods in their ability to predict genetic merit. Nonetheless, out of the four traditional methods tested, Bayes Cϖ performed 15% better for fusiform rust resistance – a disease-resistance trait known to be controlled in part by major genes. However, for the same trait, the proposed method RR-BLUP B increased the accuracy (from 0.24 of RR-BLUP to 0.37) outperforming all the other methods when a reduced number of 100 markers were selected and re-fit.

Poster

P-200
WHOLE GENOME QUANTITATIVE TRAIT PREDICTION BY FUNCTIONAL IDENTITY GENOTYPING AND DIRECT ESTIMATION OF GENE-LEVEL ADDITIVE/DOMINANCE EFFECTS

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Existing methods for predicting genotypic values and breeding values for polygenic traits from whole genome SNP data, such as ridge regression and replicating kernel Hilbert spaces (RKHS) techniques, assign additive effects to individual SNP's or SNP interactions.
Classical quantitative genetics decomposes the genotypic value before epistasis into additive and dominance effects, at each gene, or functionally polymorphic locus.
We seek to reconcile the two approaches by designing a trait prediction model with both additive and dominance effects, as well as a mechanism for mapping from SNP data to common functional variants.