

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
Endorsement email	:
Keyword 1	: Genomics-assisted breeding
Keyword 2	: Estimation of Variance Components
Keyword 3	: Genomic selection
Title of Entry	: Methods for robust Bayesian analyses of complex genetic experiments
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Breeding programs rely on rich experimental designs to estimate or predict breeding values and advance their populations towards selection goals. Typically, multiple traits at several locations, across multiple years and conditions, are measured on replicated genotypes. Bayesian inference methods can be profitably employed to analyze such data sets, particularly if occasionally unfavorable trial conditions lead to partial data loss, presence of outlier observations, or imbalance in replication. Recent advances in numerical methods and computer infrastructure put Bayesian inference within reach of most public and private sector breeding programs. Although experimental designs may be complicated and vary from program to program, each organization usually employs a consistent approach. Thus, we need a set of methods and software tools that are customizable, yet can be deployed at a given institution and produce reliable results across years without significant adjustments. Unfortunately, current model fitting methods are based on the Metropolis-Hastings algorithm which has severe limitations in this setting. This set of fitting methods relies on proposal distributions that require careful tuning. The simpler to implement variant of this approach, Gibbs sampling, does not require such adjustments, but can be numerically unstable and exhibits convergence problems even when fitting relatively simple models. Worse, these problems are influenced by parameter estimates themselves, in addition to the structure of the experimental design, and thus require constant supervision by experts. A different approach, Hamiltonian Monte Carlo, has been in use for many years in some specialized settings. While it also requires a careful choice of tuning parameters, recent developments have produced methods to derive these adjustments automatically. I have implemented these approaches to analyze genetic experiments. I will show that they produce

numerically robust estimates, with fast and reliable convergence. I will illustrate their application to simulated and real data, with comparisons to the widely-used Gibbs sampling. Software based on these methods will be publicly available. I hope it will empower even resource-limited organizations to deploy state-of-the-art statistical methods and thus accelerate progress in breeding programs world-wide.

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