Robust genomic prediction in plant breeding

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Genomic prediction (GP) is used in animal and plant breeding to help identify the best genotypes for selection. One of the most important measures of the effectiveness and reliability of GP in plant breeding is predictive accuracy. An accurate estimate of this measure is thus central to GP. Moreover, regression models are the models of choice for analyzing field trial data in plant breeding. However, models that use the classical likelihood typically perform poorly, often resulting in biased parameter estimates, when their underlying assumptions are violated. This typically happens when data are contaminated with outliers. These biases often translate into inaccurate estimates of heritability and predictive accuracy, compromising the performance of GP. Robust statistical methods provide an intuitively appealing and a theoretically well justified framework for overcoming some of the drawbacks of classical regression, enhancing the predictive accuracy of heritability and genomic prediction while alleviating the need for performing outlier detection and/or removal.

In my presentation I will discuss these issues in the context of a recently submitted paper, present some simulation insights and, if time allows, will also present an application to a real crop dataset.

Keywords: Outliers; Genomic prediction; Predictive accuracy; Heritability; Robust estimation.