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Leveraging historic and modern soybean uniform regional trial results to train genomic prediction models

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Genomic prediction is being utilized by plant breeders in multiple crop species as a method to accelerate genetic improvement. Initial examples of genomic prediction being used for crop improvement focused on large populations with simple family structures and relatively large amounts of phenotypic data per line. In reality, typical breeding programs utilize more complicated breeding designs with varying amounts of phenotypic data per line. In a typical breeding program pipeline, many lines from a family are screened on a limited basis early in development, and only a few lines per family are broadly tested later in development. This data structure leaves breeders with a limited number of lines with the best estimates of phenotypic value, and in addition, these lines often have less direct relatedness to each other, which can make sharing data between individuals challenging. Despite these challenges and limitations, breeding programs need to utilize genomic prediction to accelerate genetic improvement in order to meet future production demands. This project is focused on developing a community resource by utilizing public cooperative regional trial data from MG 00 – IV and genotypic data from available lines to train genomic prediction models. We are interested in analyzing this data using a genomic prediction approach to both help breeders calculate genomic prediction values for selection purposes as well as to help breeders select the best parents to generate populations with favorable population means and variances.