Research proposal

Project Name: New mate allocation strategies to accelerate genetic gain in agricultural species.

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**Introduction**

With the critical human population increment and the climate changes, the strategies of agricultural breeding are considered as the key element for ensuring global food supply in the further 30 years (He and Li, 2020). The genomic selection (GS) methods (Meuwissen et al., 2001), has been used as an established methodology in agricultural breeding for accelerating the breeding speed.

The foundation of the GS is the genetic prediction methods based on the classical complex quantitative traits model, and the use of genome-wide genotyping technologies (Bernardo, 2008; Meuwissen et al., 2013). By the description of the classical complex quantitative traits model, the phenotype traits are formed based on an infinite number of infinitesimal genetic effect and the interaction of non-genetic factors such as environmental factor (Bulmer, 1980). The strategy that evaluating the estimated breeding value (EBV) for certain species by the predicted overall genetic effects has been tested to be effective and viable (Goddard, 2009). The major object of the past and the current breeding programs is improving the average genetic gain of the future generations.

*Genomic prediction & Genomic selection*

Genomic selection is a marker-based selection method which introduces genetic markers covering the whole genome so that all quantitative trait loci (QTL) are in linkage disequilibrium with at least one marker. This technology was raised by the discovery of the large amount of single nucleotide polymorphisms (SNP) by the next-gen whole genome sequencing and new efficient genotyping approaches. So far, the Best Linear Unbiased Prediction (BLUP) (Henderson, 1984) is commonly used to calculate breeding values. By fitting based on the given genotypes and phenotypes, a BLUP model could estimate the linkages from genotypes to traits. The standard BLUP model, and many extended GBLUP model (BLUP mixed with other effective matrix such as dominance, epistatic, and genome-wide heterozygosity effects) are tested well with many agricultural species. The upcoming challenges are the hidden and unknown associations in a genomic level would actually increase the difficulties of genetic prediction.

Previous studies have verified that performing during the breeding process can obviously increase the average gain per year in many crop species such as maize (Môro et al., 2019; Vivek et al., 2017) and soybean (Smallwood et al., 2019).

*Machine Learning approach*

As predicting complex traits from dense genomic data has been an engaging topic among breeder and bioinformaticians. While considering the large amount of the genomic data, some machine learning approaches such as Random forests and Neural network could be well candidates as they are designed for solving problems with big data.

Aim

This project aims to import artificial intelligence to improve performance of the current genomic selection strategy.

Methods

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