Research proposal

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

Student Name: Chensong Chen

Principle supervisor: Prof Ben Hayes

Co-supervisor: Dr Elizabeth Ross, Dr Owen Powell, Dr Eric Dinglasan

**Introduction**

With the critical human population increment and the climate changes, the strategies of agricultural breeding are considered as the key technique 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 for years in agricultural breeding for accelerating the breeding speed.

The major object of the breeding programs is improving the average genetic gain of the future generations. 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 foundation of the GS is the genetic prediction. The core theory of the genetic prediction is the classical complex quantitative traits model(Bernardo, 2008; Meuwissen et al., 2013).

*Genomic prediction & Genomic selection*

In 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). Genomic selection 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, which 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 (Goddard and Hayes, 2007). 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 (GBLUP 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. Other GS approach, such as Bayes-A, an extension of GBLUP by calculating the variance of markers separately. Bayes-B is also an extended GBLUP, contain a mixture of a distribution with zero variance and an inverse chi-squared distribution based on the assumption of the existing non-effect markers (Meuwissen et al., 2009). For those advanced GBLUP methods, many studies approved the improvements in GS performance (Habier et al., 2011; Meuwissen et al., 2009).

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. In some traditional machine learning research fields like image/text classification, a large number of studies showed that the CNN approach has outstanding abilities in feature selection and reducing the risk of curse of dimensionality (Guo et al., 2016). Meanwhile, there is a common advantage for almost DL algorithms including multilayer perceptron and Convolutional Neural Network is the capacity to solve predictions that contain some unknown patterns while the conventional statistical methods usually require a designed incidence matrix, especially in the nowadays GS field. For instance, in some polypoid species, the statistical model needs to consider non-additive effects, and associate with an environment-interactive matrix, which could be challenging.

The Convolutional Neural Network (CNN), which is a subtype of the neural network, has been studied to solve genetic prediction problems with dense genotype markers in many plant and animal species (Abdollahi-Arpanahi et al., 2020; Ma et al., 2018; Montesinos-López et al., 2018; Waldmann, 2018). Currently the main challenge of using CNN to predict EBVs is the CNN model tend to ignore epistatic effects and prefer to estimating SNP effects in a global level. The conventional CNN modelling strategy in this case need to be extended for fit the needs of GS.

**Aim**

This project aims to import artificial intelligence to improve performance of the current genomic selection strategy and try to design a platform which could accept vary agricultural species including plants and animals.

*Methods and Materials*

Dense genotyping data for all recorded plant/animal samples

Recording of traits and environmental factors that response to each sample.

Convolutional neural network model based on python.

Random forest model coded by python.

GBLUP by R will be introduced as a competitor.

*Hypothesis:*

In some particular situation, such as traits effected by more non-additive genotypes, machine learning approaches could be competitive methods to improve GS performance.

A specifically modified CNN model abilities to consider biological effects such as epistatic effects for improving performance.

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