Multivariate Genomic Selection Using HAT Method

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Abstract:
Best linear unbiased prediction (BLUP) with mixed model has been applied to genomic selection, called GBLUP, in which all the molecular markers across the entire genome are used to predict genetic values for a trait. In this study, we developed an advanced GBLUP model for the analysis of two or more traits simultaneously. The performance of a genomic selection model must be evaluated by trait predictability which is commonly calculated through lengthy cross validation. To improve computational efficiency, we adopted the recently developed HAT method for an efficient estimation of trait predictability, in which the predicted residual error sum of square (PRESS) can be simply derived without cross validation. We demonstrated the new multivariate genomic selection model with HAT method using a rice dataset which consists of four agronomically important traits and whole-genome SNP markers for 210 recombinant inbred lines. Compared to the single-trait genomic selection, multivariate genomic selection is more desirable because genetic architecture shared by traits, such as genetic covariance between traits, may be dissected. Moreover, multivariate genomic selection has potential to augment the predictability of low-heritability trait by analyzing this trait with a high-heritability trait jointly.

Biography:
Zhenyu (Arthur) Jia is from Wuhan, China. He got his B.S. degree of Biochemistry in Wuhan University. After four years’ study at UC Riverside, he earned a Ph.D. from the Genetics, Genomics and Bioinformatics program and a M.S. from the Statistics Department. He has been a principal biostatistician in the UC Irvine Pathology Department for years, followed by about 2 years’ faculty appointment in the Statistics Department at the University of Akron. Dr. Jia finally returned to his mother school at UCR and joined the faculty at the Department of Botany and Plant Science in 2016. His current research focuses include: (1) chromosomal-length haplotyping using single-cell sequencing data of gametess, (2) next generation GWAS using haplotype data for citrus and pomegranate, (3) statistical genomics and network analysis in crop plants and human diseases (such as prostate cancer).