Statistical Genomics

A Course for GWAS and Genomic Prediction

ANIM SCI 545BIOLOGY 545/CROP_SCI 545/HORT 545/PL_P 545
Spring 2020, Lecture: MF, 3:10-4:00PM, Lab: W, 3:10-5:40PM

Typical problems to solve:

- Handle the four common factors leading to false discoveries: population stratification, kinship, skewed distribution and rare variants;
- Justify the discoveries unsatisfied Bonferroni cutoff;
- Design experiment to reduce cost and increase successes;
- Predict phenotypes from genotypes for molecular breeding.

Major Topics:

Advanced programming skills in R, genome wide association study (GWAS), marker assisted selection (MAS), genomic selection (GS), genomic prediction, computer simulation, Bayesian theory, general linear model, mixed linear model, best linear unbiased prediction (BLUP), kinship, type I error, false discovery rate (FDR). Typical graphs include following:
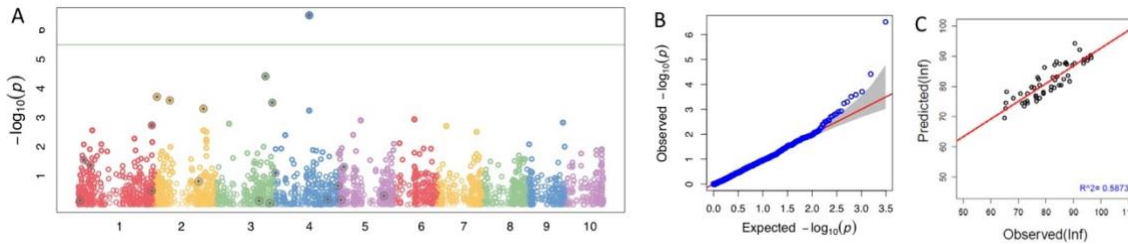
Teaching philosophy:

Active learning through critical thinking, team work, hand-on activities, and RE-inventions.

Instructor:

Dr. Zhiwu Zhang is an Assistant Professor in Department of Crop and Soil Sciences with Endowment of Distinguished Professorship for Statistical Genomics. His research is to develop innovative, cutting-edge statistical methods and computing tools to advance genomic research toward the sustainability of food production and healthcare management. He invented multiple statistical methods for GWAS and genomic prediction and developed several software packages including the widely used GAPIT and FarmCPU. He published over 70 papers over last 15 years resulting over 8,000 citations. This is the 5th round he teaches the course. The teaching documents and previous student evaluations are available online (http://zzlab.net).