

# Statistical Genomics

A Course Focusing on GWAS and Genomic Prediction  
CROPS545, Spring 2018, Lecture: MF, 3:10-4:00PM, Lab: W, 3:10-5:40PM

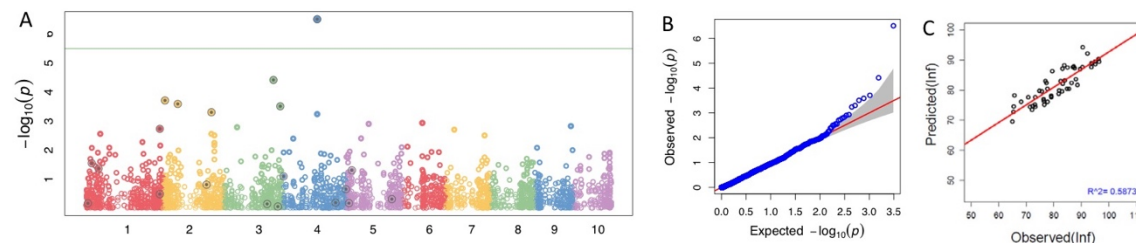
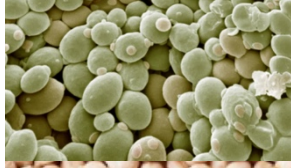


## Typical problems to solve:

- 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 for 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 (<http://zzlab.net>). He published over 50 papers over last ten years on leading journals such as Nature Genetics, PLoS Genetics, BMC Biology and Briefings in Bioinformatics (see [Google Scholar](#)). This is the 2nd round he teaches the course. [Evaluation](#) is available online.