

Three-Credit Course for **Statistical Genomics**

Instructor: Dr. Zhiwu Zhang

- Why:** This course is for resolving these problems:
- ★ Processing big genome and phenome data.
 - ★ Insufficient statistical power and/or false positives in Genome Wide Association Study (GWAS).
 - ★ Fake variance explained in genomic selection (GS)
 - ★ Excessive costs for experimental design.

- What:** You will learn the following:
- ★ Fundamentals of statistics, computing, and genomics
 - ★ Concepts and mechanism of GWAS and GS.
 - ★ Critical consideration of factors affecting outcomes.
 - ★ Hand on practice of data analyses
 - ★ Advanced R programming skills
 - ★ State of art methods of GWAS and GS
 - ★ Be comfortable with relevant computing tools

When: January 11-April 29, 2016, WF 3:10-4:25 PM

Where: Johnson Hall, Room 204

Registration: Available through CROPS 545.

Instructor: Dr. Zhiwu Zhang is an Assistant Professor of Statistical Genomics in the Department of Crop and Soil Sciences. His research focuses on developing statistical methods and computing tools for genomic research and applications. He has developed several methods and tools for GWAS, including TASSEL (Bioinformatics, 2007), Compressed Mixed Linear Model (CMLM) and P3D (Nature Genetics, 2010), GAPIT (Bioinformatics, 2012), Enriched CMLM (BMC Biology 2014), and SUPER (PLoS One, 2014). Please see <http://css.wsu.edu/zhiwu-zhang> for more details.

