

## One-Credit Course for **Genome-Wide Association Study (GWAS)**

Instructor: Dr. Zhiwu Zhang

**Why:** This course will introduce strategies for resolving the following problems in GWAS:

- ★ Processing big genotype and phenotype data.
- ★ Insufficient statistical power and/or false positives.
- ★ Excessive costs for experimental design.

**What:** You will learn the following:

- ★ How GWAS works.
- ★ Appropriate experimental design.
- ★ Modeling for better chances of success.
- ★ How to stay away from false positives.
- ★ Use the appropriate strategies to analyze your own data or ours.

**When:** August 24-October 9, 2015, 4:10-5:00 PM

**Where:** Johnson Hall, Room 116

**Registration:** Available through CROPS 512 (Topics in Crop Science). The registrations are limited to 20.

**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.

