When: **Friday 15:00 – 16:00**
Where: **ETB 1003**

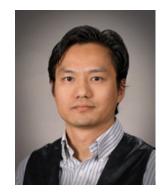**Speaker:**   **Prof. James Cai**

Assistant Professor
Department of Veterinary Integrative Biosciences
Texas A&M University

Title: **Multivariate Multiscale Impacts of Genetic Variants on Gene Expression Variability in Humans**

Date: **01-20-2017**

Abstract: Increasing evidence shows that phenotypic variance is genetically determined, but the underlying mechanisms of genetic control over the variance remain obscure. Here, we conducted variance-association mapping analyses to identify expression variability QTLs (evQTLs), i.e. genomic loci associated with gene expression variance, in humans. We discovered that common genetic variants may contribute to increasing gene expression variance via two distinct modes of action---epistasis and destabilization. To assess the effects of rare and low-frequency variants on gene expression, we established a novel analytical framework based on the identification of outlier individuals that show markedly different gene expression from the majority of a population, and revealed the contributions of rare or private SNPs to the aberrant gene expression in outliers. Together, our findings contribute to the understanding of the mechanisms of genetic control over phenotypic variance and may have implications for the development of variance-centered analytic methods for quantitative trait mapping.

References

1. Epistasis and destabilizing mutations shape gene expression variability in humans via distinct modes of action. Hum Mol Genet (2016) http://www.ncbi.nlm.nih.gov/pubmed/27651397

2. Additive, epistatic, and environmental effects through the lens of expression variability QTLs in a twin cohort. Genetics (2014) http://www.ncbi.nlm.nih.gov/pubmed/24298061

3. Exploiting aberrant mRNA expression in autism for gene discovery and diagnosis. Hum Genet (2016) http://www.ncbi.nlm.nih.gov/pubmed/27131873

4. Aberrant gene expression in humans. PLoS Genet (2015) http://www.ncbi.nlm.nih.gov/pubmed/25617623

Biography: Dr. James Cai's research lies at the interface of genetics, computational statistics, and data science. He maintains diverse research programs that range from theoretical work to laboratory investigations, aimed to advance understanding of genetic control over phenotypic variability toward a more precise and accurate mapping of complex traits in humans and other species.