

**Stanford University**  
**Department of Statistics**

DEPARTMENTAL SEMINAR

4:30pm, Tuesday, March 3, 2020  
Sloan Mathematics Center Room 380C

Refreshments served at 4pm in Sequoia Lounge.

**Speaker:** Xiaoquan Wen, *University of Michigan*

**Title:** **Statistical challenges in integrative analysis  
of genetic association data**

**Abstract:**

Integrative analysis of genetic association data from molecular and complex traits has emerged as a practical approach to investigate disease etiology. In this talk, we will focus on two prevailing types of integrative analysis methods: co-localization analysis and transcriptome-wise association study (TWAS). The former method attempts to assess the overlappings of causal genetic variants from different types of traits, and the latter approach aims to identify causal molecular phenotypes leading to complex traits. A critical challenge for both kinds of integrative analysis lies in the effective characterization and incorporation of genetic association evidence and the corresponding uncertainty. By taking advantage of probabilistic summaries from Bayesian multi-variant genetic association analysis, we demonstrate a set of rigorous and intuitive statistical solutions to both types of integrative analyses. Finally, we discuss the promise and limitations of the current integrative analysis, as well as the statistical challenges for future work.