

STUDENT SEMINAR

UW-Madison | Department of Statistics | www.stat.wisc.edu

Title

**Signals Recovery of
Three-dimensional
Chromatin
Interactions:
Statistical
Challenges Lead to
Biological Insights**

Speaker

Ye Zheng

(Ph.D. student in
Statistics, UW-
Madison)

Time & Place

Friday, March 29, 3:00pm,
SMI **133**



Abstract

The recent maturation of chromosome conformation capture (3C) and Hi-C sequencing technologies has given rise to high-throughput profiling of three-dimensional chromatin architecture and revealed transformative insights on long-range regulation of genes. Current Hi-C analysis approaches are unable to account for reads that align to multiple locations, and hence underestimate biological signal from repetitive regions of genomes. We developed and validated mHi-C, a multi-read mapping strategy to probabilistically allocate Hi-C multi-mapping reads.

In this talk, the state-of-the-art genomic technologies will be introduced, and we will show how statistical modeling addresses the sequencing data analysis challenges and recovers the signals from repetitive regions of genomes.