

High-dimensional network inference with applications in genomics

Jie Peng
University of California, Davis
CA
95616
`jie@wald.ucdavis.edu`

Abstract

In this talk, we discuss models utilizing sparse constraints for network inference. These models are motivated by reconstruction of genetic regulatory networks using high throughput genomics data. We will discuss integrative analysis of multiple types of genomic data and incorporation of biological knowledge into model building. We will also discuss resampling based methods for model tuning. The performance of these methods are illustrated through simulation studies and real applications.