Yale SCHOOL OF PUBLIC HEALTH Biostatistics

Presentation

" Joint estimation of multiple precision matrices with sign consistency

with applications in learning multiple gene networks"

Yuan Huang, PhD.

Assistant Professor of Biostatistics, College of Public Health, University of Iowa Ph.D. degree in Statistics at the Pennsylvania State University in 2015

ABSTRACT

The Gaussian graphical model is a popular tool for inferring the relationships among random variables, where the precision matrix has a natural interpretation of conditional independence. With high-dimensional data, sparsity of the precision matrix is often assumed, and various regularization methods have been applied for estimation. Under quite a few important scenarios, it is desirable to conduct the joint estimation of multiple precision matrices. In joint estimation, entries corresponding to the same element of multiple precision matrices form a group, and group regularization methods have been applied, it can be difficult to interpret the results when parameters within the same group have conflicting signs. To tackle this problem, we develop a novel regularization method for the joint estimation of multiple precision matrices. It effectively promotes the sign consistency of group parameters and hence can lead to more interpretable results, while still allowing for conflicting signs to achieve full flexibility.

12:00 noon Wednesday, June 13, 2018 LEPH 216, 60 College Street Lunch will be provided