



Baylor University

COLLEGE OF ARTS & SCIENCES
Statistical Science

Bayesian Causal Discovery for Reverse-Engineering Gene Regulatory Networks

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Marrs McLean Science Building 301

Abstract: I will present two Bayesian causal discovery approaches. The first approach is motivated by single-cell RNA-seq data. We proposed a zero-inflated Poisson Bayesian network which explicitly accounts for the sparse count nature of single-cell RNA-seq data. The second approach is motivated by breast cancer bulk RNA-seq data. We developed a Bayesian network with latent trajectory embedding to account for the tumor heterogeneity. Both approaches are uniquely identifiable for purely observational, cross-sectional data — a key property that many Bayesian networks do not possess due to Markov equivalence. Efficient parallel-tempered Markov chain Monte Carlo algorithms are designed to explore the multi-modal network space. We illustrate our methods using real RNA-seq datasets.

Bio: Yang Ni is an Assistant Professor in the Department of Statistics at Texas A&M University. His research interests include causal discovery, graphical models, and Bayesian nonparametrics. His research is primarily motivated by microbiome and single-cell multi-omics and electronic health records data.

Please join us in the foyer of the department for refreshments at 3:00 pm