

Inferring Biological Networks From Genomics Data

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Revealing networks of biological components is one of the key questions in systems biology, and it has potential applications in understanding disease physiology and drug discovery in the area of network medicine. With advances in high throughput biology, we can now measure the expression levels and DNA variations at the genome level, either through microarrays or next generation sequencing. These data offer the opportunity to statistically infer genetic networks from these data. In this presentation, we discuss several approaches for network inference through jointly analyzing gene expression data under diverse conditions in combination of DNA variation data. We provide both theoretical and simulation results to investigate the properties of our procedures. We also demonstrate the usefulness of our approaches through their applications to real data. This is joint work with Hyonho Chun, Bing Li, Ruiyan Luo, Haisu Ma, and Xianghua Zhang.

Key Words: Biological networks, Gaussian graphical models, conditional Gaussian graphical models, hierarchical models, microarrays, eQTL, statistical genomics, computational biology, network inference