

## **Statistical trees and networks in clinical expression studies**

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This talk will discuss some of our work on the development and use of statistical classification tree models and Bayesian networks for exploratory and predictive analyses in clinical applications of gene expression profiling.

Topics will include selective commentary on issues of data preprocessing and representation of gene expression data, data reduction, combining clinical factors with gene expression data, issues of variable and model selection, model averaging for prediction, and graphical model determination in assessing and representing expression-based associations among genes using graphical models for exploratory analysis.