

Regularized Estimation for Censored Data Regression and Gaussian  
Graphical Models, with Applications to Genomic Data

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Abstract:

New high-throughput technologies are generating many types of very high-dimensional genomic and proteomic data. These data can potentially be used for predicting clinical outcomes, for studying gene sub networks and for studying inter-individual differences in responses to drugs. In practice, however, the number of independent samples is usually very small as compared to these high-dimensional genomic data. As a result, many standard statistical methods cannot be applied directly or perform poorly in such high-dimension and low-sample size settings. In this talk, I will present several penalized methods for two problems. One is on relating microarray gene expression data to censored survival outcomes, another is on estimating the sparse precision or concentration matrix in the sparse Gaussian graphical model setting. I will demonstrate and evaluate these methods using both simulations and applications to real data sets.