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by

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## ***Survival Analysis with High-Dimensional Microarray Gene Expression Data***

### ***ABSTRACT***

Analysis of censored survival data with a large number of covariates is an important practical problem, especially now microarrays that can assay tens of thousands of genes are becoming a routine tool in the studies of various types of diseases. How to associate gene expression profiles with clinical outcomes such as patients' survival and identify important genes presents a class of interesting and challenging problems in survival analysis. We propose using the gradient directed regularization method of Friedman and Popescu (2004) in the context of ridge regression for variable selection, parameter estimation, and prediction. This method can be applied to a wide range of survival analysis models which include the Cox proportional hazards model, the accelerated failure time model, and the additive hazards model. We use simulations and a study that investigates the relationship between survival and expression profiles in 92 mantle cell lymphoma patients to illustrate the proposed method. This is joint work with Dr. Shuangge Ma of University of Washington.