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The Dantzig Selector for Censored Linear Regression Models: Identifying Predictive Genes for Myeloma Disease Progression

The Dantzig variable selector has recently emerged as a powerful tool for fitting regularized regression models. A key advantage is that it does not pertain to a particular likelihood or objective function, as opposed to the existing penalized likelihood methods, and hence has the potential for wide applications. To our knowledge, almost all the Dantzig selector work has been performed with fully observed response variables. This talk introduces a new class of adaptive Dantzig variable selectors for linear regression models when the response variable is subject to right censoring. This is motivated by a clinical study of detecting predictive genes for myeloma patients' event-free survival, which is subject to right censoring. We establish the theoretical properties of our procedures, including consistency in model selection (i.e., the right subset model will be identified with a probability tending to 1) and the oracle property of the estimation (i.e., the asymptotic distribution of the estimates is the same as that when the true subset model is known a priori). The practical utility of the proposed adaptive Dantzig selectors is verified via extensive simulations. We apply the new method to the aforementioned myeloma clinical trial and identify important predictive genes for patients' event-free survival.