Modeling mass spectrometry proteomics data using nonparametric regression methods

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The amount and complexity of the data collected from the mass spectrometry instruments has outpaced the methodological developments in their processing. We propose a number of approaches to address the issues arising in modeling such data. The methods used include local polynomial kernel regression with adaptive bandwidth selection and wavelet methods. We address the issues of non-stationarity in the variance process and correlated errors. In this talk, we provide the results of preliminary simulation studies and apply the methods to a lung cancer SELDI-TOF MS data set.