

Novel Methods for High Resolution Time-of-Flight Proteomics Experiments

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Abstract:

Proteomics, one of the fastest growing fields of the *omics* revolution, involves detecting and quantifying simultaneous changes in a proteome. To this end, there is a dizzying array of new technologies to facilitate such discoveries. In this talk, we take a closer look at one such technology: surface-enhanced laser desorption and ionization time-of-flight (SELDI-TOF) mass spectrometry. These instruments are capable of quickly generating large amounts of high dimensional autocorrelated data. While undeniably a promising and powerful technology, there has been much controversy in the literature regarding the analysis and reproducibility of SELDI-TOF spectra.

This work focuses on some of the statistical issues encountered when dealing with high resolution SELDI-TOF protein mass spectra and presents novel methods to address these problems. In particular, we demonstrate a wavelet multiscale denoising procedure which also has the added benefit of reducing the dimensionality. We also propose an intuitively appealing peak detection algorithm that accounts for multiple sources of variation. These methods are designed to generate more reproducible and biologically meaningful results. We apply our methods to high resolution SELDI-TOF data from the National Cancer Institute.