

## **Variance Function Estimation in Quantitative Mass Spectrometry**

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Improvements in mass spectrometer resolution, accuracy and sensitivity coupled with the development of increasingly sophisticated algorithms for protein identification from spectra have resulted in mass spectrometry becoming the tool of choice in large scale proteomics research. Measurements generated by mass spectrometers are proportional to the concentration of short portions of the proteins (peptides) present in a biological sample. However, the signals are subject to errors that depend on the peptide amounts. The variance function of the errors is an essential parameter for evaluating the results, but estimating it is complicated as the number of nuisance parameters increases with sample size while the number of replicates for each peptide remains small. In this talk, I describe and compare two methods for estimating the variance function associated with iTRAQ isotopic labeling. I then discuss methods for constructing conservative p-values and confidence intervals using the estimated variance function and apply them to several experiments.

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