



DEPARTMENT OF BIOSTATISTICS AND
BIOINFORMATICS SEMINAR

**Imaging Mass Spectrometry Based Proteomic
Data Analysis and Biomarkers Discovery**

By

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Abstract:

In proteomics study, Imaging Mass Spectrometry (IMS) is an emerging and very promising new technique for protein analysis from intact biological tissues. Though it has shown great potential and is very promising for rapid mapping of protein localization and the detection of sizeable differences in protein expression, challenges remain in data processing due to the difficulty of high dimensionality and the fact that the number of variables chosen to be used in prediction model is significantly larger than the number of observations. To obtain a complete overview of IMS data and find trace features based on both spectral and spatial patterns, one faces a global optimization problem. In this talk, I would like to present some recent progress we have made on the IMS data processing including the application of a multivariate statistical method called Elastic Net (EN) on IMS cancer data analysis and the development of a new software package called IMSmining using both spectral and spatial information for biomarker selection of IMS data. Experimental data analysis results show that IMSmining produces more concise peak list, confirms new biomarkers, and provides better classification rate.

Thursday, October 28, 2010

12:00 p.m. - 1:00 pm

Rollins School of Public Health

Claudia Nance Rollins Building, Room 1000

http://www.sph.emory.edu/bios/news/Notices/hong_seminar.html