

Meeting: 1004, Bowling Green, Kentucky, SS 5A, Special Session on Advances in the Study of Wavelets and Multi-wavelets

1004-62-38 **Don Hong*** (don.hong@vanderbilt.edu), Biostatistics Shared Resource, 571 Preston Research Building, Nashville, TN 37232-6848, and **Yu Shyr** (yu.shyr@vanderbilt.edu), Biostatistics Shared Resource, 571 PRB, Nashville, TN 37232-6848. *MALDI TOF MS Data Processing Using Wavelets, Splines, and Statistical Techniques*. Preliminary report.

Mass spectrometry (MS) is emerging as a leading technique in the proteomics revolution and it becomes one of the critical components in cancer research recently. However, there are many challenges in both MS data processing and data analysis. In this talk, we present some recent progress on MS data processing using mathematical tools and statistical methods. A novel algorithm for MALDI-TOF MS data processing is developed, which includes the application of splines for data smoothing and baseline correction, wavelets for adaptive denoising, multivariable statistics techniques such as clustering analysis, and signal processing techniques to evaluate the complicated biological signals. A MatLab implementation shows the processing steps consecutively including step-interval unification, adaptive wavelet denoising, baseline correction, normalization, peak detection for biomarkers discovery. (Received January 07, 2005)