West Virginia University

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High-Definition Differential Ion Mobility Separations for Proteomics, Metabolomics, and Structural Characterization Using Isotopic Shifts

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With all the power of modern MS, most biological and environmental analyses require substantial prior separations. The traditional chromatography and electrophoresis are now increasingly complemented by ion mobility spectrometry (IMS) in gases. The nonlinear method of differential or field asymmetric waveform IMS (FAIMS) based on the difference between mobilities at high and low electric fields is much more orthogonal to MS than linear IMS based on absolute mobility, which enables exceptionally specific separations.

We will cover the foundations of high-resolution FAIMS/MS and its exemplary applications. A major focus in proteomics is localization of post-translational modifications in mixtures of isomeric proteoforms (variants), where MS/MS is limited by lack of unique fragments. Variants with various PTMs are effectively disentangled by FAIMS and then identified by ETD. All D-amino acid containing peptides (DAACP) are likewise resolved from L-analogs. A similar challenge in metabolomics is elucidating the isomeric diversity of lipids that comprises multiple types including transacylation, double bond position, and cis/trans geometry. High-definition FAIMS generally resolves over ~80% of lipid isomers across types, and more in conjunction with OzID for double bond localization. Finally, FAIMS can resolve isotopomers and isotopologues with peak shifts dependent on the geometry in a way parallel to NMR, enabling a fundamentally new approach to molecular structure characterization. Substantial orthogonality between FAIMS and Linear IMS enables 2-D separations of exceptional specificity.

Date: Wed, April 4, 2018
Time: 4:30-5:30 pm
Location: 208 Clark Hall

Students, meet the speaker over coffee and cookies in the Bennett Conference room at 3:30 pm