Improvement of Mass Spectrometry-based Multi-omics and Applications to Complex Biological Systems

Fri, February 24
3:15 pm
Room 310

Chemistry Seminar

Biological systems contain complex networks of diverse molecules that work together to modulate cellular processes. While many technologies interrogate a single biomolecule class, such as proteins, substantially more information and, potentially value, can be gained from performing multi-omics studies, which profile multiple biomolecule classes simultaneously. Integrated analysis of biomolecules, once a lofty goal, is now feasible and increasingly applied across biological disciplines, in part due to improvements in mass spectrometry (MS) technologies. Evolving MS data acquisition strategies have increased the number of proteins, lipids, and metabolites surveyed; yet, there are still many barriers that exist for performing multi-omics investigations. One major hindrance with multi-omics is the lengthy and wasteful sample preparation process. Current methods to prepare biological samples for MS-based multi-omics are disparate and laborious; they involve copious pipetting, vortexing, incubating, and centrifuging steps and typically take 1-2 days to perform. Here, I present one of my dissertation projects in which we developed a simple, efficient, and unified approach to prepare lipids, metabolites, and proteins for MS analysis. This is achieved through an n-butanol-based monophasic extraction that efficiently recovers both polar and non-polar metabolites. The monophasic extraction is paired with on-bead protein aggregation and accelerated protein digestion. We term this simplified workflow the Bead-enabled, Accelerated, Monophasic Multi-omics (BAMM) method. The BAMM method affords comparable data quality as classic methodologies, yet only requires about three hours of work.

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Laura Muehlbauer is an Analytical Research Scientist at Eli Lilly and Company in Indianapolis, Indiana. She works within the Synthetic Molecule Design and Development organization at Lilly, where she develops and implements analytical methodologies for characterizing and analyzing peptide and small molecule drug candidates. Laura received her BA in Chemistry from St. Olaf College in 2017 and her PhD in Analytical Chemistry from the University of Wisconsin-Madison in 2022. Her graduate research focused on expanding the capabilities and efficiency of biological mass spectrometry, as well as applying the latest mass spectrometry tools to new areas of biology in which global biomolecule profiling has been underutilized.