Bioinformatics for MS Workshop, June 3, 2025, Baltimore
Proteomics Data Analysis: From Identification to Quantification

Speakers
Fengchao Yu - University of Michigan, Ann Arbor, Michigan, United States
Daniel Polasky - University of Michigan, Ann Arbor, Michigan, United States
Michael Shortreed - University of Wisconsin-Madison, Madison, Wisconsin, United States

Panel discussion
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Michael Shortreed - University of Wisconsin-Madison, Madison, Wisconsin, United States
Kai Li - University of Michigan, Ann Arbor, Michigan, United States

This year's workshop provided attendees with an insightful exploration into proteomics data analysis, suitable for participants at all levels of expertise. The event featured presentations from leading researchers, followed by an engaging panel discussion.

The workshop commenced with a presentation by Fengchao Yu, who delivered an overview of peptide identification and quantification, particularly emphasizing the use and functionalities of FragPipe. This session effectively established a foundation by discussing fundamental methodologies, enabling attendees to better understand the complexities involved in proteomics workflows.

In the second talk, Daniel Polasky expanded upon specialized applications of FragPipe, highlighting post-translational modification (PTM) peptide and Glycopeptide identification. This session emphasized the intricacies and unique challenges posed by Glycoproteomics, thereby preparing the audience for advanced analytical considerations.

The third presentation, delivered by Michael Shortreed, focused on the MetaMorpheus software, offering insights into its capabilities for advanced proteomics data analysis. This session highlighted MetaMorpheus's utility in addressing specific analytical challenges, broadening the analytical toolkit for participants.

Following the presentations, panelists Fengchao Yu, Daniel Polasky, Michael Shortreed, and Kai Li engaged in a lively and interactive discussion with the audience. The panel explored ongoing challenges and emerging trends, including discussions around software integration, method validation, and best practices for quantitative accuracy. Attendees actively participated, sharing their experiences, posing insightful questions, and fostering dialogue that deepened the collective understanding of current and future proteomics methodologies.

The workshop was successful in providing both theoretical insights and practical advice, equipping participants with valuable knowledge applicable to their research endeavors. Next year's organizers will include Daniel Polasky, who will select the co-coordinator and panelists.


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