Data Independent Acquisition (Workshop 10)

Tuesday, Nov 2, 2021, 5:45-7:00 pm

69th Annual Meeting of the American Society of Mass Spectrometry (ASMS)

Organizers

a. Lindsay Pino, PhD
Talus Bioscience
b. Florian Meier, PhD
Jena University Hospital and Max Planck Institute of Biochemistry

Invited Panelists

a. Birgit Schilling, PhD (Buck Institute for Aging): post-translational modifications, hardware developments
b. Fengchao Yu, PhD (University of Michigan): software developments, library-free DIA
c. Mak Saito, PhD (Woods Hole Oceanographic Institution): beyond mainstream proteomics: DIA as a tool for metaproteomics?
d. Philip Seitzer, PhD (Calico Life Sciences): beyond proteomics: DIA in metabolomics/lipidomics
e. Christopher Rose, PhD (Genentech): single cell proteomics; is DIA always the preferred choice?

Summary of Discussion

Drs. Lindsay Pino (Talus Bioscience) and Florian Meier (Jena University Hospital) invited a panel of experts for research using data independent acquisition (DIA) to discuss current topics and future directions in the DIA workshop at ASMS 2021. The room was quite full, with overflow into the hallway and additional virtual attendees listening in from abroad.

Each of the panelists listed above represented an area of particular interest in this regard and, following an introduction round, various topics, including the panelists' expertise topic, were discussed amongst the panelists and with the audience. The panelists and topics this year were geared towards newcomers to the DIA technique rather than "seasoned veterans", which was reflected in the discussion with participants. When polled the audience skewed towards "interested, but have not implemented" as opposed to "I regularly use DIA in my laboratory".

To stimulate discussions, Dr Pino circled the room with a microphone so participants could ask their own questions or give their own experiences and perspective. Several questions from participants focused on the practicalities of setting up DIA methods and analyzing the resulting data, showing that there is much more room for the DIA user base to grow, perhaps incentivizing instrument vendors to create more easily accessible DIA methods, something which was noted as a pain-point for many participants interested in DIA but not yet using it in their laboratories.

Additional topics discussed included the niches where DIA may not be the best acquisition method for a particular sample, pros and cons of LFQ-DIA vs TMT-DDA necessity (or not) of DDA spectral library generation, feasibility of DIA for non-proteomics studies such as lipidomics and metabolomics, incorporation of ion mobility spectrometry into data analysis softwares, and the future directions and applications for DIA technologies.