

## **Data Independent Acquisition (Workshop 07)**

Wednesday, June 8, 2022, 5:45-7:00 pm

70<sup>th</sup> Annual Meeting of the American Society of Mass Spectrometry (ASMS)

### **Organizers**

- a. Lindsay Pino, PhD  
Talus Bioscience
- b. Florian Meier, PhD  
Jena University Hospital

### **Invited Panelists**

- a. Seth Just, Seer
- b. Stefan Tenzer, University of Mainz
- c. Oliver Bernhardt, Biognosys AG
- d. Joanna Bons, Buck Institute for Research on Aging

### **Summary of Discussion**

Drs. Lindsay Pino (Talus Bioscience) and Florian Meier (Jena University Hospital) invited a panel of experts in data independent acquisition (DIA) to discuss current topics and future directions in the DIA interest group workshop. The session was very well attended with a mix of experts and beginners. The majority of the audience has tested DIA at least once in their own research, many of them only in the last year, as indicated by an informal show of hands.

Each of the invited panelists listed above represented an area of particular interest in this regard and, following an introduction round, various topics, including the panelists' expertise topics, were discussed amongst the panelists and with the audience. To guide the discussion, we posted a series of questions to stimulate conversation amongst the panelists and the audience. Below we summarize the key points from those questions

- What was the biggest advance in DIA in the last year?

Most panelists responded that advances in PTM detections and incorporation of ion mobility represent the biggest advances in DIA over the last year. Data processing was also highlighted as a very active field of research.

- What is currently the biggest limitation for DIA?

Panelists felt that the biggest limitation was PTMs, ironically, since PTM detection was also cited as one of the advances! The discussion identified the selectivity of the precursor mass, i.e. the assignment of fragment ions to specific precursor ions, as a major bottleneck.

- Is DIA as reliable/believable/correct as more traditional methods? Either way, how do we prove this to the field at large?

The overall sentiment from the panelists was that DIA is just as reliable as traditional methods, and that it was no longer necessary to prove this to the broader proteomics field. However, the audience raised many good counterpoints where DIA could not be used in their own work, or whether they could not convince their collaborators/clients to switch to DIA due to mistrust of the technique over traditional methods. This discussion boiled down to the interpretation of individual fragment mass spectra.

- Will DIA continue to 'disrupt', or are we reaching an equilibrium with other techniques?

The question of "disruption" raised a good conversation about the implementation of open source software for DIA analyses. Some panelists felt that open source was not necessary while others felt passionately that, without open source projects and tools, there was no way for creative, innovative thoughts to "disrupt" the field because everyone was stuck reinventing the wheel, so to speak, due to closed-source, "black box" tools that can't be built upon.

- What would be the biggest breakthrough in the next year that DIA could bring?

Overall, the sentiment from the panel was that "more peptide/protein detections" would be next year's great breakthrough, stemming from increased use of AI/ML in data analysis. Further, it was anticipated that DIA enables biological discoveries as the technology matures, which raised the question whether the number of identified proteins is still a reliable metric or whether quantitative accuracy should be valued more. In the longer term, panelists expected further advances in data acquisition strategies that might somewhat combine the advantages of data dependent and independent modes.