ASMS workshop 2024

Data Independent Acquisition Interest Group

Data Independent Acquisition: Before and After the Acquisition

Presiders: Qin Fu (Qin.fu@cshs.org); Tejas Gandhi (tejas.gandhi@biognosys.com)
INCOMING PRESIDER: *To be determined* replacing Tejas Gandhi

Panelists:
Shreya Ahuja
Yansheng Liu
Brendan Maclean
Meena Choi

Summary of Discussion

The DIA workshop began with a brief presentation by the presiders on the history of DIA proteomics, including evolution of software. The point was made that the field has progressed a lot over the past decade and contributions of software go hand in hand with hardware. At the same time, the field is still far from its peak and is likely to keep growing in the near future. This was followed by a brief introduction from each panelist, describing how they work with DIA data, from processing raw files all the way through statistical testing and biomarker discovery. We then moved into Q&A to spark discussion.

During the Q&A, there were several topics raised. One of the topic was related to quality control and lack of tools available for performing automated QC. At one point, the question was asked as to how many in the audience is completely new to DIA. Surprisingly, only around a quarter of the audience raised their hands which is markedly lower than the past years. This again highlights that DIA technology has become significantly well known and adopted in the past years.

Another topic of discussion was regarding value of visualization in modern DIA software. There was a discussion here whether it makes sense to look at individual XIC when dealing with hundreds of thousands of peptides. Many people still appreciated that it is possible to look at raw data with different perspectives, instead of blindly trusting the analysis software. However, there should also be automated tests and validations that do not rely on manual inspection.

Another point that came up was whether you need to have the latest MS platform to do DIA. The panelist believe that you can still use an older generation of instrument to get solid and biologically relevant data. In many experiments, the top differentially expressed candidates are likely to be similar across the different MS platforms. Additionally, these days, it is lot easier to start out with DIA as there are a lot of established methods readily available.

Finally, post translational modifications, immunopeptidomics, and quantification were communicated as some of the challenges facing the field.