Spectronaut® 18

Release Notes

1   Improved Protein Measurement

- Greatly improved quantification (11% more proteins with CV < 10%, 10% more proteins with accuracy error rate < 10% based on ground truth experiment)
- Improved protein identification (5% on average)

2   Linux & Cloud Support

- Direct loading of MS raw data for Bruker & Thermo data via Linux, via HTRMS for Sciex.
- Full Spectronaut support on Linux via command line
- Seamless support on cloud platforms (e.g. AWS)

3   New Options for Analysis Throughput

- New search archive support for directDIA+ allows parallelization or acquisition synchronized processing of MS data for faster throughput
- Greatly expanded command line capabilities
- Added MaxLFQ for SNE-Combine

4   Improved User Interface & Visualization

- Spectronaut starts in Viewer mode when your license expires allowing you to still view your previously analyzed data
- New identifications per cycle plot at run level
- Prominent notification in the GUI for any analysis errors
- Directly use search archives (.psar) in regular DIA analysis, instead of library
- New "Quantified" summary node in analysis overview

5   Other Changes

- Changed all files exported as .xls to .tsv
- New default quantification setting (via DIA analysis → Quantification → Quantification window)