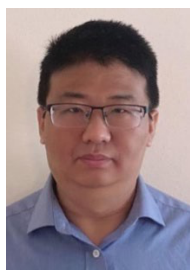


One-Day Course, Sunday only

Top-down Mass Spectrometry Data Analysis and Visualization

People attending this course might also be interested in attending Top-Down Proteomics, so we bundled these two one-day courses as a two-day course (there is a cost savings). The bundled two-day course is listed as *Top-Down Proteomics AND Mass Spectrometry Data Analysis and Visualization* under the one-day course section.



Xiaowen (Kevin) Liu
Tulane University



Kyowon Jeong
University of Tübingen



Boris Krichel
University of Lübeck

Top-down mass spectrometry (MS) has gained increasing attention in the past decade because of its capability to sequence whole proteoforms with combinations of post-translational modifications (PTMs) and other alterations. Because of the complexity of top-down MS data, it is still challenging for MS labs to efficiently use software tools for top-down MS-based proteoform identification, characterization, and quantification. In the short course, we will teach students and researchers several software pipelines for top-down MS data analysis and visualization. We will present computational tools for file format conversion, spectral deconvolution, proteoform identification, PTM localization, proteoform quantification, and visualization of top-down MS data. We will explain the algorithms and statistical methods in the tools and parameter selection for various applications. We will use public top-down MS data to show how to apply the tools to various research problems ranging from modified proteoform identification to proteoform biomarker identification. We will give students and researchers hands-on training to use the tools to analyze top-down MS data sets.

Topics

1. Introduction of top-down MS data
2. Computational methods for top-down MS data analysis
 - Top-down spectral deconvolution
 - Proteoform identification by database search
 - PTM localization
3. Software pipelines for top-down MS data analysis
4. Applications and hands-on demo session