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.
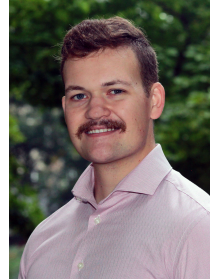
Instructors

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Tulane University	University of Tübingen	University of Wisconsin	Northwestern University

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