LC-MALDI Training at IBSLor-proteomics

Upcoming training sessions:
March 12, 2019 (register before February 28)
September, 24, 2019 (register before August 30)

Objectives: To understand what mass spectrometry consists in and how it allows protein identification, chemical characterization and quantification from complex mixtures.

Note: One or two samples from the trainees may be used in the training. This requires careful discussions with the trainer prior to sample preparation and may not apply to all sample kinds. If several of the trainees (up to 8 per session) want their samples to be used, the choice will be made on a first come/first served basis.

Program:
8:30 AM : Introduction to the available instrumentation, explanations of their principles; notion of isotopic specie.
10:00 AM: general considerations of proteome analysis and sample preparation for LC-MALDI analysis. Launching automatized sample fractionation and deposition on MALDI plates.
0 :15 PM : Lunch.
1 :15 PM: Sample analysis in MS mode. Notion of Ion chromatogram, peak area and relative quantification (strictly theoretical). Statistical handling of relative quantification data.
2:15 PM: Sample analysis in MS/MS mode. Notion of fragmentation. Automatized data interpretation through database interrogation.
4:30 PM: Discussion.
5:30 PM: End of the training. Depending on the complexity of samples, final data may be sent to trainees afterwards.

For registration details, please contact jean-baptiste.vincourt@univ-Lorraine,fr