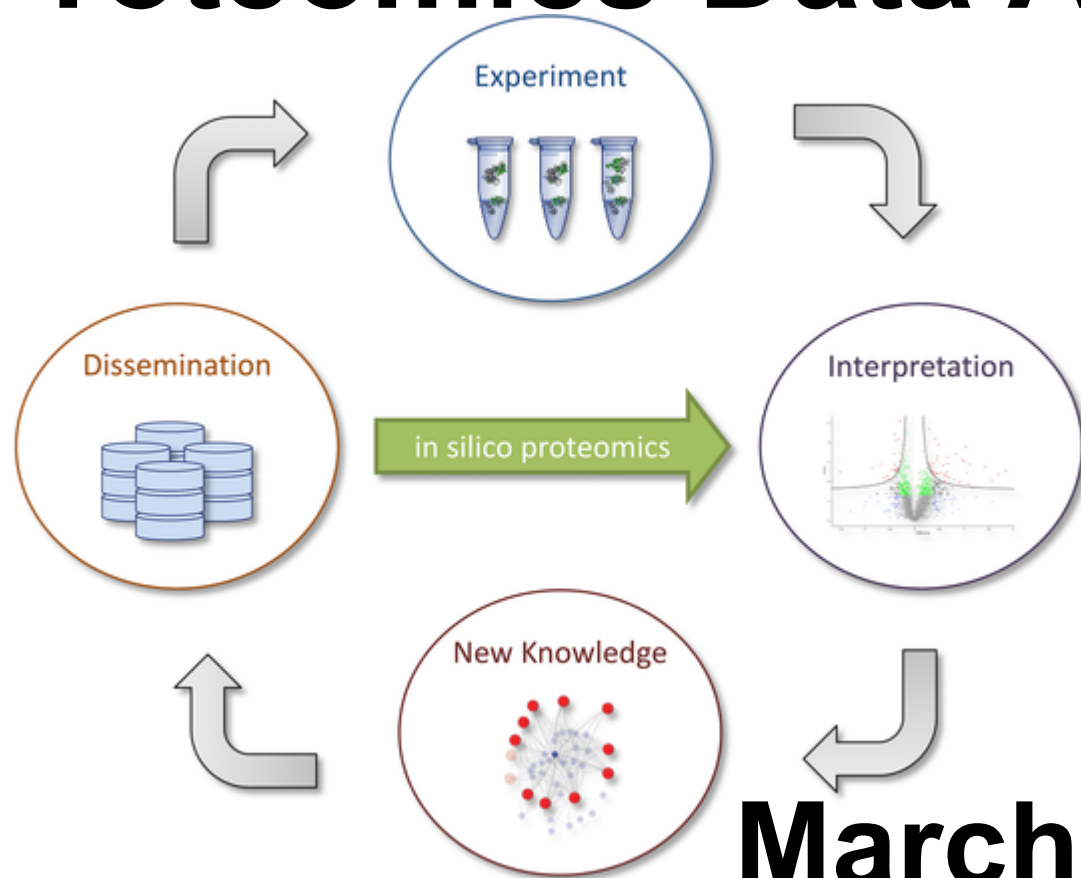


PDA17

Proteomics Data Analysis



March 6th - 10th 2017

Course Description

Mass spectrometry based proteomic experiments generate ever larger datasets and, as a consequence, complex data interpretation challenges. In this course, the concepts and methods required to tackle these challenges will be introduced, covering both protein identification and quantification. The core focus will be on shotgun proteomics data. Quantification through isobaric labels (iTRAQ, TMT) and label-free precursor peptide (MS1) ion intensities will also be introduced. The course will rely exclusively on free and user-friendly software, all of which can be directly applied in your lab upon your return from the course.

An introduction to available online resources and repositories will also be given. Here you will see how to link the results from proteomic experiments with external data to conduct pathway, gene ontology and interaction analyses.

The course will provide a solid basis for beginners, but also new perspectives to those already familiar with standard data interpretation procedures in proteomics.

Instructors:

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Course website:

<http://gtpb.igc.gulbenkian.pt/bicourses/PDA17>

