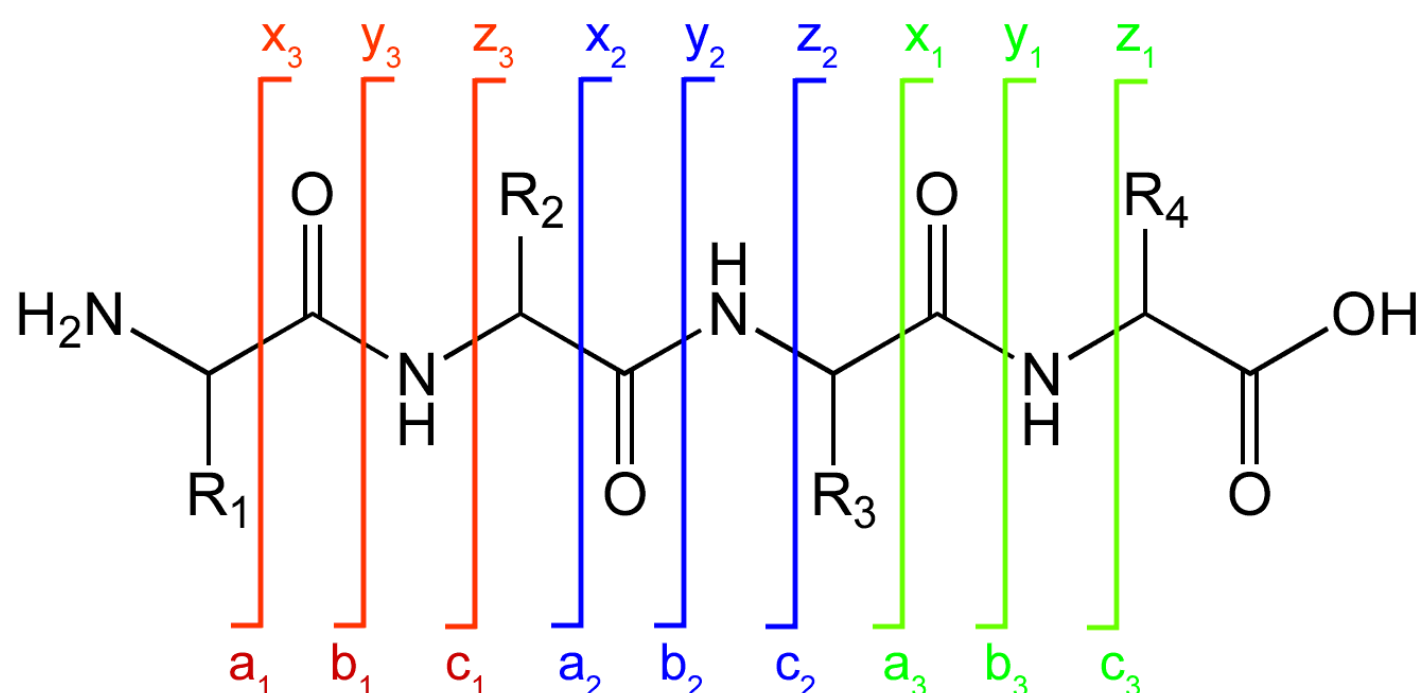


The Gulbenkian Training Programme in Bioinformatics



PDA18

Proteomics Data Analysis

May 28th - June 2nd 2018

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.

In the course, you will also learn how to submit data to the ProteomeXchange online repositories, and how to browse and reprocess publicly available data from these repositories.

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

Note: this is a highly interactive course. It requires that the participants interact with each other and with the course instructors, in order to reach the learning outcomes in full.

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