



## Title

**Bioinformatics applied to proteomics**

## Description

The aim of the course is to introduce participants into the main bioinformatic tools currently used in proteomics, i.e., strategies in protein identification, search engines, databases, as well as prediction of protein structure or protein PTMs. The course is divided into five parts:

- Introduction to Image analysis
- Mass spectrometry MALDI-TOF
- Mass spectrometry CID
- Data integration and analysis
- Prediction of protein function.

**Location** Facultad de Medicina, USAL, Campus Miguel de Unamuno 37007 Salamanca, Spain

**Number of participants** max. 15, **Fee** 30€

**Date** May 21<sup>st</sup> to 23<sup>th</sup>

**Duration** 3 Days

**Organizer** ProteoRed education and training group

**Contact person** Nieves Ibarrola, Rosa Dégano

**Phone** +34-923294817

**e-mail** [nibarrola@proteored.org](mailto:nibarrola@proteored.org); [romade@proteored.org](mailto:romade@proteored.org)

## Contents

### Day 1

- Part 1:** Introduction and image analysis (3h 30')
  - 1.1. Motivation
  - 1.2. Introduction to the integration of proteomics and bioinformatics
  - 1.3. Principles of image analysis
- Part 2:** MALDI-TOF mass spectrometry (3h 30')
  - 2.1. Introduction
  - 2.2. Principles of MALDI-TOF mass spectrometry
  - 2.3. Peptide mass fingerprinting
  - 2.4. Processing mass spectra
  - 2.5. Database searching with peptide mass fingerprint data
    - 2.5.1. Databases
    - 2.5.2. Search engines
  - 2.6. Search limitations

### Day 2

- Part 3:** Collision Induced Dissociation (CID) mass spectrometry (8 h)
  - 3.1. Introduction
  - 3.2. Principles of peptide fragmentation
  - 3.3. Interpreting fragmentation spectra with classical methods
  - 3.4. Searching fragmentation spectra against databases
  - 3.5. LC-MS/MS
  - 3.6. De Novo sequencing: main tools
  - 3.7. Searching pos-translational modifications

### Day 3

- Part 3.8:** Analysis of quantitative mass spectrometry data (2h)
- Part 4:** Data integration and protein interaction (6 h)
  - 4.1. Introduction
  - 4.2. What is LIMS?
    - 4.2.1. License free tool (Garban)
  - 4.3. Data standards
    - 4.3.1. PEDRO
    - 4.3.2. Proteios
    - 4.3.3. HUPO PSI
    - 4.3.4. Ontologies
  - 4.4. Interactomes and protein networks: data bases (APID). Computational methods for data search and analysis
  - 4.5. Dynamic search for information (PIKE)
  - 4.6. Graphical representation of data

### Teaching Staff

**Rune Matthiesen**, CIC bioGUNE, Vizcaya  
**Alberto Medina**, CNB-CSIC, Madrid  
**Alberto Paradelo**, CNB-CSIC, Madrid  
**Javier de la Rivas**, CIC-CSIC, Salamanca