



# Advanced Proteomics Data Analysis Course

## Description:

In the last years, new paradigms have been emerging concerning mass spectrometry data analysis. The course will set the scene by bringing up the technical concepts behind state-of-the-art algorithms and provide extensive hands-on application of the relevant bioinformatics tools. In addition, the power and the limitations of the currently available software will be examined. Most bioinformatics tools used in this course are open-source and can be freely downloaded for use at one's home institution

The course is designed primarily for mass spectrometrists with some informatics concepts. In addition, informaticians with little proteomics background are also welcome to apply. We also offer a pre-course day addressed to proteomics scientists with little informatics proficiency. Joint lecture sessions and five parallel tutorial tracks will be offered during the five-day course. For the hands-on sections, the students can bring their own data.

**Location:** Parc Científic de Barcelona, Spain

**Number of participants:** max. 25

**Fee:** 450€\*

**Date:** January 25<sup>th</sup> to 29<sup>th</sup> 2010

**Duration:** 5 Days (9:00 to 18:00h)

**Organizer:** Parc Científic de Barcelona, ProteoRed and SEProt

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## C o n t e n t s

- 1) ProteoWizard: project overview
- 2) Structure and update of open source data formats
- 3) MS/MS Database search, Spectral libraries
- 4) Sequences databases
- 5) The Prophets–PeptideProphet and ProteinProphet for database searching validation (TPP)
- 6) Combining multiple database search results and/or multiple experiments with iProphet (TPP)
- 7) msInspect tools for quantification
- 8) Accurate Mass and Time with msInspect  
Software platforms for creating mass spectrometry-based computational tools
- 9) MS1-based quantification with XPress and ASAPratio (TPP)
- 10) MS2-based quantification with Libra (TPP)
- 11) Qurate, a tool for visually assessing quantitative events.
- 12) Label-free quantification with msInspect
- 13) Progenesis LC-MS: Label free MS-based quantification
- 14) Analysis and management of proteomics data (Proteios)
- 15) Statistical analysis with R

## Instructors

**Jimmy Eng**, Proteomics Software Engineer  
Proteomics Resource, University of Washington

**David Shteynberg**, TPP developer  
Seattle Proteome Center, Institute of System Biology

**Damon May**, msInspect developer  
Computational Proteomics Laboratory, Fred Hutchinson Cancer Research Center

**Parag Mallick**  
ProteoWizard, Center for Applied Molecular Medicine

**Fredrik Levander**  
Department of Immunotechnology, Lund University

**David Rossell**  
Institute for Research in Biomedicine, Barcelona

**Pre-course instructors:** Salvador Martínez and Alex Campos

**\*Course enrollment is limited and reserved on a first come first served basis. Please contact with us so that we can send you the registration form**