



Basic course: Bioinformatics for MS analysis

Organiser: EuPA Education Committee in collaboration with the Swiss Institute of Bioinformatics, the Swiss Proteomics Society and the ProteomeXchange consortium

Course dates: October 15 – 19, 2012

One-week full time at the Swiss Institute of Bioinformatics, Geneva, Switzerland

Course objectives

In accordance with the HUPO/EuPA guidelines, we aim to

- Provide an overview of current software and databases for proteomics
- Illustrate how the above can be applied in modern proteomics studies
- Help students to design their own experiments
- Provide practical instruction in the use of the software and databases
- Provide extensive tutorial/discussion sessions

Course description

The course is part of a series designed to give researchers a thorough basis to understand the new trends in protein expression analysis. The aim is to give an overview on the available software and databases for proteomics and to enable scientists entering the field to evaluate how useful these new techniques are to their own research and how to apply them effectively. The program will span proteomics databases contents, tools for MS interpretation for identification and characterization, MS repositories, tools for MS quantitation and tools for MS validation.

Course outline

Theoretical lectures and Practical classes in

- MS identification
- Protein sequence databases
- MS repositories
- Submission guidelines and data standards
- MS validation and knowledge extraction
- MS quantitation methods

Deadline for registrations: September 15, 2012

Minimum number of students: 5 (if not the course will be cancelled). Maximum 16

Fee: 350 € (not including food, accommodation and travel) payable upon confirmation of participation.

Contact person and registration: Patricia M. Palagi

Swiss Institute of Bioinformatics

Tel.: (+41 22) 379 5831 Email: Patricia.Palagi@isb-sib.ch

Fax: (+41 22) 379 5858 <http://www.isb-sib.ch/education>