



Bioinformatics course – SEProt - ProteoRed

Title

MS bioinformatics analysis for proteomics

Description

The program will span proteomics databases contents, tools for MS interpretation for identification and characterization, MS repositories, tools for MS quantitation, tools for MS validation, and other helpful bioinformatics tools for proteomics. The course is divided into five parts:

- Protein Databases
- Protein Identification
- Data Validation
- Data integration
- Quantitation

Location: Universidad Complutense de Madrid

Number of participants: max. 20, **Fee:** 50€

Dates: Oct 21st - 23rd 2008

Duration: 18 hours

Organizer: ProteoRed education and training group, SEProt and EuPA

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Contents

Part 1: Protein Databases (2h)

1. Protein databases structure
2. Practical session in databases

Part 2: Protein identification (6h)

3. Introduction
 - 3.1. Mass spectrometry introduction
 - 3.2. Signal processing
 - 3.3. Bioinformatics tools for protein identification
4. Peptide Mass Fingerprinting
 - 4.1. Scores
 - 4.2. Search engines: MASCOT, Aldente
5. Peptide Fragment Mass Fingerprinting (1h 30m)
 - 5.1. Fragmentation
 - 5.2. Ion types in MS/MS
 - 5.3. De novo tools (Peaks, pepNovo, LuteFisk)
 - 5.4. Tools (Mascot, Sequest, Phenyx, X!Tandem)
6. Practical session in MS and MS/MS searches

Part 3: Data validation (3h)

7. Basic statistical concepts
8. Trans Proteomic Pipeline (TPP): Peptide Prophet and Protein Prophet
9. Probability Ratio

Part 4: Data integration (3h 30m)

10. Standards: HUPO-PSI, PRIDE, MIAPE, standard data converters
11. Protein repositories: peptideAtlas, GPMDB, PRIDE, TRANCHE, PROTEIOS
12. Annotations: GO, GOTM, PIKE, Ingenuity

Part 5: Quantitation (3h)

13. Quantitation methods introduction: iTRAQ, SILAC, 18O
14. Quantitation tools
15. Statistics for quantitation

Teaching Staff

Pedro Navarro, CBM-SO, Madrid
Salvador Martínez de Bartolomé, CNB-CSIC, Madrid
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