BIOENG-517

Lab methods : proteomics

Cursus	Sem.	Type
Bioengineering	MA1, MA3	Opt.
Sciences du vivant	MA1, MA3	Opt.

Language of teaching	English
Credits	2
Withdrawal	Unauthorized
Session	Winter
Semester	Fall
Exam	During the semester
Workload	60h
Weeks	14
Hours	**2 weekly**
Project	2 weekly
Number of positions	**12**

Il n'est pas autorisé de se retirer de cette matière après le délai d'inscription.

Remark

Inscriptions sur dossier auprès du responsable de cours, présence aux cours obligatoire pas donné en 2016-17

Summary

Introduction to several mass spectrometry techniques and their application to the proteomics field. Description of bioinformatics tools used to analyze proteomics data. The goal of the course is to provide an overview of main proteomics strategies and their applications in the Life Science context

Content

The course is structured so as to alternate theory and illustrative practical exercise periods in the laboratory.

Day 1:
Morning (theory)

- Introduction to proteomics analysis principles:

- Define what Proteomics is
- Introduction to the Platform
- Mass spectrometry: sampleionization and mass analysis principles (MALDI, electrospray, m/z, resolution, isotopicdistribution)
- Liquid chromatography: sampleseparation principles.

- Instrumentation and methods used in proteomics:

- Distribution and presentation of a selection of representative articles and lab visit

Noon (practical)

- Illustration of what was presentedin the morning
  - Sample preparation (proteindigestion)
  - ESI-MS molecular weight measurement:infusion of diverse samples on Orbitrap instrument (single peptide,

severalpeptides mix, single protein, several proteins mix, show resolution, monoisotopicmass)

- MALDI-MS molecular weightmeasurement: sample preparation and measurements on MALDI-TOF/TOF (same samplesas infusion)

Day 2:
Morning (theory)

- Simple Proteomics Workflows
  - Intact mass measurements
  - Protein identification principles

Noon (practical)

- Illustration of what was presentedin the morning
  - Sample preparation (protein digestionfinalization and sample desalting)
  - Quality control check onMALDI-MS (MW measurements)
  - Infusion-MS/MS to illustratetandem MS fragmentation principles
  - Presentation of LC-MS/MS principlesfor peptide separation and protein identification in front of instruments.

Day 3:
Morning (theory)

- More complex Proteomics Workflows
  - Increasing the depth of analysis: typical workflows for protein and peptide fractionations
  - Increasing the complexity: typical workflows for Post Translational Modifications analysis
  - Increasing the information content: Protein quantification strategies (SILAC, Dimethyl labeling, iTRAQ-TMT, SRM/MRM)

Noon (practical)

- Illustration of what was presentedin the morning

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  - SRM quantification: Triple Quadrupole instrument presentation
  - Hands on introduction on representative bioinformatics tools for MS based protein identification and quantification

- Debriefing about the practical session, Q&A and conclusions

Learning Prerequisites

Required courses

First year of master in Life Sciences & Technology or Bioengineering program.

Learning Outcomes

By the end of the course, the student must be able to:

- Integrate the basic theoretical and technical concepts of mass spectrometry
- Apply these concepts to the analysis of proteins and to the proteomics field
- Describe and explain the different methods and tools presented during the course
- Perform sample preparation for mass spectrometry related experiments
- Analyze and interpret data coming from mass spectrometry and simple proteomics experiments
- Select appropriately approaches and sample preparation methods adapted to the nature of the biological sample analyzed
- Decide between the different methods and tools presented during the course which one could be used in different contexts
- Systematize useful information from a paper and summarize its content

Transversal skills

- Collect data.
- Summarize an article or a technical report.

Teaching methods

Shortex-cathedra lectures to introduce the concepts followed by hands on practicalsessions in the laboratory including sample preparation, analysis by massspectrometry and data interpretation. Deepening of knowledge acquired inpractical sessions by personal work on selected papers representative of thetechnique used in proteomics

Expected student activities

This block course will take place from November 8th to November 11th, 2016.
Practical part will take place in the proteomics core facility.

Assessment methods

Written exam during the semester.

Supervision

Office hours	Yes
Assistants	Yes
Others	Office hours : 8h30-18h Assistants: Jonathan Paz Montoya and Adrien Schmid

Resources

Websites

- http://pcf-ptp.epfl.ch/

Moodle Link

- http://moodle.epfl.ch/enrol/index.php?id=13401