BIOENG-519

Methods: omics in biomedical research

Chrast Roman, Garcia Miguel, Guex Nicolas, Iseli Christian, Mangeat Bastien, Pavlou Maria, Pojer Florence

Cursus	Sem.	Type
Life Sciences Engineering	MA1, MA3	Opt.

Language of teaching	English
Credits	4
Withdrawal	Unauthorized
Session	Winter
Semester	Fall
Exam	Written
Workload	120h
Weeks	14
Hours	**4 weekly**
Lecture	1 weekly
Practical work	3 weekly
Number of positions	**24**

It is not allowed to withdraw from this subject after the registration deadline.

Summary

High-throughput methodologies broadly called Omics allow to characterize the complexity and dynamics of any biological system. This course will provide a general description of different methods related to the Omics field followed by hands-on rotations in participating technological platforms.

Content

During the initial part of the course we will provide a general description of different methods related to the "omics" field. The presented techniques will be discussed in terms of their rationale, applicability and limitations. During the second part of the course, students will take part in hands-on rotations in participating technological platforms allowing them to put the theory into practice inside a laboratory environment.
The following topics will be covered during the theoretical and practical parts of the course:
General introduction to Omics
From genes to proteins
- Strategy of cloning for protein expression, production of proteins in different cellular settings.
- Purification of proteins by diverse methods (affinity tag, size exclusion, anion exchange).
- Quantity and quality controls of final protein samples by biophysical techniques such as Dynamic Light Scattering, Circular Dichroism and Multi-angle Light Scattering.
Flow cytometry and cell sorting
- Basics of flow cytometry and cytometer subsystems.
- Principles of Multicolour flow cytometry including fluorescence and fluorochromes and appropriate experimental controls.
- Principles on cell sorting: why and how, technological principle, basic parts of a cell sorter.
Genomics and transcriptomics
Broad overview of genomics/transcriptomics techniques to investigate, at bulk and single cell levels:
- Gene expression (RNA-seq, qPCR).
- Epigenetic control of gene expression (ChIP-seq, ATAC-seq).
- Spatial organization of gene expression (spatial transcriptomics).
Proteomics
- Introduction to proteomics and mass spectrometry.
- Mass spectrometry-based proteomics workflows.
- Data analysis (search engines and databases, statistics, data visualization and result interpretation).
Bioinformatics
- Mission of a bioinformatic facility.
- Experimental design and sample nomenclature.
- Data clustering and its applications: theory and practice.

- Data formats and handling.
- Data QC, analysis and visualization, mapping on reference genomes.
- Variant calling, peak calling, quantification, GSEA.
- Protein and transcript reference databases, nomenclature.
- Biological function knowledge, domains, structures, annotations and visualization.
- Evaluation of genetic mutation impact.

Keywords

Omics (including single cell omics)
Bioinformatics
Quality control
Data analysis
Data interpretation

Learning Prerequisites

Required courses

BSc in Life Sciences and Technology or Bioengineering program

Learning Outcomes

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

- Choose appropriate Omics technique(s) to design relevant experiment
- Apply the concept of data quality control
- Interpret the generated data
- Contextualise theoretical and technical concepts of the covered Omics techniques

Transversal skills

- Use a work methodology appropriate to the task.
- Collect data.
- Plan and carry out activities in a way which makes optimal use of available time and other resources.
- Evaluate one's own performance in the team, receive and respond appropriately to feedback.

Teaching methods

This course will be divided into 3 weeks of common theoretical lectures followed by 11 weeks of rotations in participating scientific platforms including Protein Production and Structure, Flow Cytometry, Gene Expression, Proteomics and Bioinformatics. For the platform rotations part, students will work in small groups (max 6 students per group) and will perform experimental work in Protein Production and Purification, Flow Cytometry, Gene Expression and Proteomics platforms (2 weeks / platform) followed by a common rotation at the bioinformatics platform (all students together, week 12-14).

Expected student activities

Lectures
Hands-on practical work during 5 rotations in participating platforms
Reading articles
Project presentation

Assessment methods

Evaluation (written reports or oral presentations) covering platform rotations and written exam during exam session.

Supervision

Office hours	Yes
Assistants	Yes
Forum	No

Resources

Websites

- https://www.epfl.ch/research/facilities/ptpsp/
- https://www.epfl.ch/research/facilities/cytometry/
- https://www.epfl.ch/research/facilities/gene-expression-core-facility/
- https://www.epfl.ch/research/facilities/proteomics-core-facility/
- https://www.epfl.ch/research/facilities/ptbicc/

Moodle Link

- https://go.epfl.ch/BIOENG-519