

BIOENG-519

Methods: omics in biomedical research

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

Language of teaching	English
Credits	4
Withdrawal	Unauthorized
Session	Winter
Semester	Fall
Exam	During the semester
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 Omics field together with the presentation of relevant bioinformatic tools. 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 followings 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.
- Purifications 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 including principle of fluorescence, cytometer subsystems, principle of compensation and digital world.
- Principles of Multicolour flow cytometry including fluorescence and fluorochromes, stain index, visual paradox and appropriate experimental controls.
- Principles on cell sorting: why and how, technological principle, basic parts of a cell sorter, limits of technology and possible optimizations.

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).
- Genomes 3D organization (Hi-C, 4C).
- Genomes variations (WGS, exome-seq).
- Spatial organization of gene expression (spatial transcriptomics).

Proteomics

- Introduction to mass spectrometry-based proteomics.

- Sample preparation and experimental design (bottom-up proteomics, experimental design, basic sample preparation, fractionation techniques).
- Quantitative proteomics (relative quantification using isobaric-labeling, towards single cell proteomics).
- Data analysis (search engines and databases, statistics, data visualization and results interpretation).

Bioinformatics

- Experimental design and sample nomenclature.
- Data formats and handling - tables and more (fasta, fastq, CSV, BAM, VCF, Excel, R-data, SQL), languages (bash, R, perl, python).
- Data QC and analysis - mapping on reference (genome, peptides, transcripts), variant calling, peak calling, quantification, GSEA.
- External data sources - reference databases and identifiers (Geo, Ensembl, RCSB, RefSeq, SRA, UniPROT, Kegg).
- Visualisation - genome (UCSC, IGV) and interaction (Cytoscape, strings) viewers, plot scripting, BED, WIG, bigWIG.

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 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 5 weeks of theoretical lectures followed by 8 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 two different platforms (platform 1: weeks 6 to 8 and platform 2: weeks 9 to 11) followed by a common rotation at the bioinformatics platform (all students together, week 12-13). Regarding the selection of platforms for rotations: we will try to accommodate as much as possible students preferences. The last week (week 14) will be dedicated to the preparation of the lab reports and to the final exam.

Expected student activities

Lectures
Hands-on practical work during 3 rotations in participating platforms

Reading articles
Project presentations

Assessment methods

Written reports covering 2 rotations in platforms and written exam during the last week of the semester.

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://bix.unil.ch>