

BIO-693(a)

**Bioinformatic Analysis of RNA-sequencing (Fall)**

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Cursus	Sem.	Type
Approches moléculaires du vivant		Opt.
Biologie computationnelle et quantitative		Opt.

Langue d'enseignement	
Crédits	3
Session	
Examen	Exposé
Charge	90h
<b>Heures</b>	<b>160</b>
Cours	80
Exercices	80
<b>Nombre de places</b>	<b>30</b>

**Fréquence**

Tous les ans

**Résumé**

Due to its success, this course will also take place from 1st to 5th September 2025 in room AAC 0 20. It introduces the workflows and techniques that are used for the analysis of bulk and single-cell RNA-seq data. It empowers students to understand and analyze their own data.

**Contenu**

By day (5 days in total):

1. Retrieving raw data from the facility and reference data onto a lab workstation or an HPC cluster and perform mapping
2. Understand the contents of the raw and mapped files, prepare summary data to export to a laptop
3. Get R going with the proper analysis packages on each student laptop, start the analysis of the retrieved data
4. Finalize the analysis, plus start analysis of a selected/assigned dataset per group of students
5. Each group of students prepares a report on their assigned dataset in the morning and presents their results in the afternoon

The course topics will include:

Day 1: Working with data at the command line

- A refresher of bash and R scripting
- Tips and tricks for data reproducibility

Day 2: Sequencing alignments

- Downloading and aligning raw RNA-seq data on HPC clusters
- Quality assessment of sequenced and aligned files

Day 3: Bulk RNA-sequencing workflows

- Getting read counts per gene
- Data quality assessment
- Differential expression analysis and visualization

Day 4: Single cell RNA-sequencing workflows

- Filtering and normalizing single cell datasets
- Cell clustering and cell type assignments
- Differential expression analysis and visualization

Day 5: Prepare and present reports of independent student analysis performed in teams

### Learning Outcomes

By the end of this course, you should be able to:

1. retrieve raw fastq data and process them to derive gene counts
  2. assess quality at several levels (raw read quality, mapping quality, sample quality)
  3. perform a differential expression analysis
  4. gather functional annotation and emit hypotheses on interpreting the results
- By day (5 days total)

### Note

Please do not register by yourself! Send an email to [edms@epfl.ch](mailto:edms@epfl.ch)

Maximum number of participants: **30 students**. More or less 15 slots will be kept for interested UNIL doctoral students.

This course is not open to free auditors.

### Mots-clés

genomics, bulk RNA-seq, single cell RNA-seq

### Méthode d'évaluation

Oral presentation

### Ressources

#### Liens Moodle

- [https://go.epfl.ch/BIO-693\\_a](https://go.epfl.ch/BIO-693_a)