

BIO-693(b)

Bioinformatic Analysis of RNA-sequencing (Spring)

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Cursus	Sem.	Type
Computational and Quantitative Biology		Opt.
Molecular Life Sciences		Opt.

Language of teaching	English
Credits	3
Session	
Exam	Oral presentation
Workload	90h
Hours	160
Courses	80
Exercises	80
Number of positions	30

Frequency

Every year

Remark

The course is fully booked - no more registration possible

Summary

This course will take place from 2nd to 6th June 2025 in room AAC 1 37. 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.

Content

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

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.

Keywords

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

Learning Prerequisites

Required courses

None

Assessment methods

Oral presentation

Resources

Bibliography

Website: <https://bix.unil.ch/>