

BIO-693

Bioinformatic Analysis of RNA-sequencing

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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
Lecture	80
Exercises	80
Number of positions	25

Frequency

Every year

Summary

This course took place from 3rd to 7th June 2024 and should take place in June 2025. It introduced 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 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's 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
- Gene ontology analysis

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: **24 students**. More or less 6 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/>