UCLouvain

lsinc1332

2026

Biotechnology: omics

5.00 credits	30.0 h + 30.0 h	Q2

This learning unit is not open to incoming exchange students!

Teacher(s)	Branders Vincent ;
Language :	French
Place of the course	Charleroi
Prerequisites	• Molecular biology • Biochemistry • Data visualization • Statistics
Main themes	This course will cover the different biological analysis techniques that generate high-throughput data (so-called “omics” techniques), such as: DNA and RNA sequencing, proteomics, metabolomics... (non-exhaustive list which will be adapted according to the rapid evolution of this field). For each method, the course will introduce: • The operating principle of each method (sequencing, mass spectrometry, etc.) • Analysis, processing and normalization of raw data • Data interpretation and visualization. • The biases and pitfalls related to these techniques (problems of technical and biological variability, reproducibility, experimental design). Generic methods for analyzing biological data will also be covered (clustering, enrichment, ontologies, etc.), in connection with the data analysis course and the statistics course. Finally, the course will include an introduction to the databases that can be used in this field (TCGA, GEO, Encode etc).
Learning outcomes	**At the end of this learning unit, the student is able to :** • understand the operating principle of omics methods; • understand the concepts and principles of omics data analysis; • analyze simple omics data; • understand and critique a publication presenting omics data.
Evaluation methods	The course assessment is based on two components: 1. A final exam (written on paper or, if applicable, on computer), which accounts for 80% of the final grade. 2. A group project, which accounts for 20% of the final grade. • This component is not graded in detail: • the project is awarded full points (5/5) if carried out seriously, • or 0 points in the case of no work or manifestly insufficient work. The project grade is final at the end of the semester: there is no possibility to redo the project in the second session.
Teaching methods	Lectures and supervised practical sessions • The lectures present the fundamental concepts of biotechnology and the associated bioinformatics. • The practical sessions are organized in groups as mini-projects • Each group explores an analysis pipeline (e.g., from the nf-core/Nextflow community) using test datasets provided with the pipelines or retrieved from public databases • The students are required to: • run and document the chosen pipeline, • analyze its main steps and outputs, • present a synthetic report to the whole class.
Content	1. Introduction

	2. Genomics: DNA sequencing • Principles and available technologies • Genomes, exomes, panels • Raw data analysis • Alignment, reference genome, de novo genome assembly, variant calling, quality control, etc. 3. Transcriptomics: RNA sequencing • Principles and available technologies • Gene expression analysis • Differential expression • Enrichment analysis • Variants, isoforms, novel transcripts 4. Proteomics: protein sequencing • Principles and available technologies • Data analysis • Peptide and protein identification • Quantification 5. Biological databases 6. Emerging technologies • Single cell analysis • Spatial omics
Inline resources	https://moodle.uclouvain.be/course/view.php?id=5853
Faculty or entity in charge	SINC

Programmes containing this learning unit (UE)				
Program title	Acronym	Credits	Prerequisite	Learning outcomes
Additional module in life sciences and health for computer scientists	APPSCVS	5		