Course guide
2703129 - OT - Omics Techniques

Last modified: 30/01/2026

Unit in charge: Barcelona School of Informatics
Teaching unit: 1022 - UAB - (ANG) pendent.

Degree: BACHELOR'S DEGREE IN BIOINFORMATICS (Syllabus 2024). (Compulsory subject).

Academic year: 2025 **ECTS Credits:** 6.0 **Languages:** English

LECTURER

Coordinating lecturer: JAIME MARTÍNEZ URTAZA

Others: Segon quadrimestre:
OLGA DOLGOVA KONJUSHENKO - 11, 12
LAURA JIMÉNEZ GRACIA - 11, 12
JAIME MARTÍNEZ URTAZA - 11, 12
SEBASTIAN MARTIN TANCO - 11, 12

PRIOR SKILLS

NA

LEARNING RESULTS

Knowledges:
K1. Recognise the fundamental principles of biology, from the cellular to the organismic scale, and how they relate to current knowledge in bioinformatics, data analysis and machine learning, achieving an interdisciplinary vision with an emphasis on biomedical applications.
K2. Identify statistical and computational methods and mathematical models that can be used to solve problems in molecular biology, genomics, medical research and population genetics.
K3. Identify the mathematical foundations, computational theories, algorithmic schemes and principles of information organisation relevant to modelling biological systems and efficiently solving bioinformatics problems through the design of computational tools.
K7. Analyse sources of valid and reliable scientific information to determine the state of the art of a bioinformatics problem and how to tackle it.

Skills:
S1. Integrate omic and clinical data to better understand and analyse biological phenomena.
S2. Computationally analyse DNA, RNA and protein sequences, including comparative genomic analysis, using computation, mathematics and statistics as the basic tools of bioinformatics.
S3. Solve problems in molecular biology, genomics, medical research and population genetics by applying statistical and computational methods and mathematical models.
S5. Communicate information, ideas, problems and solutions from bioinformatics and computational biology to a general audience.
S7. Implement programming methods and data analysis based on the development of working hypotheses within the area of study.
S8. Make and defend reasoned decisions when solving problems in biology and, in appropriate fields, the health sciences, computer science and experimental sciences.

Competences:
C2. Recognise the complexity of the economic and social phenomena typical of a welfare society and relate welfare to globalisation, sustainability and climate change in order to use techniques, technology and principles of economics and sustainability in a balanced and compatible way.
C3. Communicate orally and in writing with others in English about learning outcomes, thought processes and decision making.
C4. Work as part of a multidisciplinary team, whether as a team member or in a leadership role, to contribute to the development of projects (including business and research projects) with pragmatism, a sense of responsibility and ethical principles, undertaking commitments with due regard to the resources available.

TEACHING METHODOLOGY

- Theoretical classes. Lectures will address the main concepts behind the different topics. They will consist of question-based lectures that promote an active participation of all students in the discussion of different topics/situations/problems/cases that will be presented.

- Practicals. Hands-on problem-based tutorials. They will promote both self-study and teamwork learning strategies. Please bring your laptop computers in class.

LEARNING OBJECTIVES OF THE SUBJECT

1.Acquisition of specific knowledge to apply the different technologies and strategies to generate sequencing data (DNA and RNA)
2.Application of genomic, transcriptomic and proteomic data within different contexts to solve biological problems
3.Understand the experimental and computational methods of genomics, transcriptomics and proteomics

STUDY LOAD

Type	Hours	Percentage
Hours large group	30,0	20.00
Hours small group	30,0	20.00
Self study	90,0	60.00

Total learning time: 150 h

CONTENTS

Sequencing technologies

Description:
Generation of sequencing data. Sanger sequencing; 2nd and 3rd generation sequencing techniques (Illumina, Oxford-Nanopore, PacBio).

Applications of DNA-seq

Description:
Sequencing and processing of DNA sequencing data: genome sequencing, re-sequencing and variant calling.

Metagenomics and microbiome

Description:
Applications of metagenomic and microbiome analysis; pipelines and data analysis to study natural environments and health.

RNA sequencing and analysis of RNA-seq data.

Description:
Analysis of RNA-seq data to understand gene expression and its variations across different conditions: quality control, read alignment, quantification, and differential expression analysis.

Applications of RNA-seq

Description:
Gene expression and splicing variant annotation, metatranscriptomics. Applications in different fields: disease diagnosis, drug discovery, and functional genomics.

Epigenomics and epigenetics

Description:
Epigenomics and epigenetic modifications on the genetic material: data processing and analyses for differential DNA methylation.

Hi-C for 3D genome organization.

Description:
The study the three-dimensional structure of genomes to understand how the spatial organization of DNA influences gene expression and other cellular processes. Hi-C protocols and general processing of Hi-C data.

Single-cell genomics.

Description:
Study of the genetic material (genome, transcriptome) of individual cells: applications and analysis.

Proteomics.

Description:
Methodological foundations of the techniques to study of the protein composition (proteome) within a cell or organism. Special emphasis will be placed on the technologies developed for protein identification, including mass spectrometry and DIGE technology, and their applications in biomedicine.

ACTIVITIES

Theoretical classes

Specific objectives:
1, 2, 3

Full-or-part-time: 60h
Theory classes: 30h
Self study: 30h

Practicals

Specific objectives:
1, 2, 3

Full-or-part-time: 90h
Practical classes: 30h
Self study: 60h

GRADING SYSTEM

The success in meeting the course learning objectives will be evaluated as follows:

- Continuous assessment (40%): may include tests of combined multiple-choice and/or short-answer questions to recapitulate worked contents in each unit, homework, programming exercises, group activities proposed in class, etc.

- Exam (60%) consists of a 2 partial theoretical-practical exams taken at mid term (30%) and final term (30%).

Overall, in order to successfully complete this course, the student must get a minimum final grade of 5 points (out of 10).

Make-up exam: only the students that after the regular evaluation have not passed the course can take a reassessment exam. The grade obtained at the make-up exam will substitute the failed regular grade obtained during the trimester.

BIBLIOGRAPHY

Basic:

- Gibson, Greg; Muse, Spencer V. A primer of genome science. 3rd ed. Sinauer Associates, cop. 2009. ISBN 9780878932368.
- Brown. Terry A. Genomes 5. CRC Press, 2023. ISBN 9780367674076.
- Lesk, Arthur. Introduction to Genomics. Fourth Edition. Oxford University Press, 2025. ISBN 9780198866893.
- Suravajhala, Prashanth N; Bizzaro, Jeff W. Next-Generation Sequencing. 1st Edition. CRC Press, 2025. ISBN 9781003354062.
- Twyman, Richard. Principles of Proteomics. Garland Science, 2013. ISBN 9780815344728.

RESOURCES

Hyperlink:

- http://genome.ucsc.edu/ENCODE/- http://genome.ucsc.edu/cgi-bin/hgGateway- http://www.genomesize.com/- http://www.ncbi.nlm.nih.gov/genome