Course guide
295123 - 295II333 - Bioinformatics

Last modified: 04/06/2026

Unit in charge: Barcelona East School of Engineering
Teaching unit: 707 - ESAII - Department of Automatic Control.

Degree: MASTER'S DEGREE IN INTERDISCIPLINARY AND INNOVATIVE ENGINEERING (Syllabus 2019). (Optional subject).
ERASMUS MUNDUS MASTER'S DEGREE IN ADVANCED MATERIALS SCIENCE AND ENGINEERING (Syllabus 2021). (Optional subject).
MASTER'S DEGREE IN ADVANCED BIOMEDICAL TECHNOLOGIES (Syllabus 2025). (Optional subject).

Academic year: 2026 **ECTS Credits:** 6.0 **Languages:** English

LECTURER

Coordinating lecturer: ALEXANDRE PERERA LLUNA

Others: Primer quadrimestre:
FLAVIO PALMIERI - Grup: T1
ALEXANDRE PERERA LLUNA - Grup: T1

PRIOR SKILLS

Basic Programming Skills

DEGREE COMPETENCES TO WHICH THE SUBJECT CONTRIBUTES

Specific:
CEMUEII-18. Design innovative solutions in biomedicine through the use of computer tools for design, modeling and computational simulation (Specific competence of the Healthcare and Biomedical Applications specialty).

Generical:
CGMUEII-01. Participate in technological innovation projects in multidisciplinary problems, applying mathematical, analytical, scientific, instrumental, technological and management knowledge.
CGMUEII-05. To communicate hypotheses, procedures and results to specialized and non-specialized audiences in a clear and unambiguous way, both orally and through reports and diagrams, in the context of the development of technical solutions for problems of an interdisciplinary nature.

Transversal:
05 TEQ. TEAMWORK. Being able to work as a team player, either as a member or as a leader. Contributing to projects pragmatically and responsibly, by reaching commitments in accordance to the resources that are available.
06 URI. EFFECTIVE USE OF INFORMATION RESOURCES. Managing the acquisition, structure, analysis and display of information from the own field of specialization. Taking a critical stance with regard to the results obtained.
03 TLG. THIRD LANGUAGE. Learning a third language, preferably English, to a degree of oral and written fluency that fits in with the future needs of the graduates of each course.

LEARNING RESULTS

Knowledges:
K8. Demonstrate advanced knowledge of digital and mobile health applications (mHealth).

Skills:
S5. Propose digital biomarkers through advanced analysis of biomedical signals, artificial intelligence techniques and bioinformatics.

Competences:
C6. Integrate the values of sustainability and understand the complexity of systems, with the aim of undertaking or promoting actions that restore and maintain the health of ecosystems and improve justice, thereby generating visions of sustainable futures.

TEACHING METHODOLOGY

The methodology of the course combines theory lessons, laboratory sessions and autonomous learning through the development of projects and the analysis of real applications.

LEARNING OBJECTIVES OF THE SUBJECT

-Properly design a bioinformatics analysis workflow, paying attention to the specific issues of the input data type to be analyzed

STUDY LOAD

Type	Hours	Percentage
Hours large group	21,0	14.00
Self study	108,0	72.00
Hours small group	21,0	14.00

Total learning time: 150 h

CONTENTS

Biology background

Description:
-Basics of genetics
-Genetic variability and genetic diseases
-Genomic data and genomic landscape
-Genome databases and browsers

Specific objectives:
Learn key aspects of genetics: structure and function of nucleic acids and chromosomes.
-Learn the influence of genetics on diseases
-Know current types of functional genomic data: from 1D to 3D genome perspectives.
-Understand basic annotations in a genome. GENCODE project.
-Understand and interpret the information retrieved from a genome browser.

Related activities:
-Home activity 1: Analysis of mRNA sequences using command-line
-Laboratory session 1: Genome databases and browsers

Full-or-part-time: 18h
Theory classes: 4h
Laboratory classes: 2h
Self study : 12h

Sequence alignment

Description:
-Local and global alignment algorithms
-Database similarity searches
-Protein motifs

Related activities:
-Understand the implications of carrying out a local or global alignment.
-Know the family of BLAST algorithms, local alignment tools.
-Get familiar with substitution matrices: PAM and BLOSUM families
-Understand the steps of progressive alignment.
-Identification of conserved motifs given several sequences.

Full-or-part-time: 26h
Theory classes: 4h
Laboratory classes: 6h
Self study : 16h

Analysis of Transcriptomics Data

Description:
-Gene expression and regulation. Techniques and tools
-Processing: normalization, filtering and clustering
-Gene expression databases

Related activities:
-Laboratory 4: microarrays
-Laboratory 5: RNA-sequencing

Full-or-part-time: 26h
Theory classes: 4h
Laboratory classes: 6h
Self study : 16h

Knowledge databases and enrichment analysis

Description:
-Biological pathways: KEGG, Reactome
-Gene ontologies: GO
-Protein interactions: STRINGdb
-Enrichment analysis

Related activities:
-Laboratory 6: Biological pathways and protein interactions
-Laboratory 7: Gene Ontology. Enrichment analysis

Full-or-part-time: 22h
Theory classes: 4h
Laboratory classes: 6h
Self study : 12h

Advanced techniques and applications

Description:
-Proteomics and metabolomics
-Epigenomics
-Machine learning methods

Related activities:
-Laboratory 8: metabolomics analysis pipeline
-Home assignment 2: epigenomics

Full-or-part-time: 20h
Theory classes: 2h
Laboratory classes: 2h
Self study : 16h

GRADING SYSTEM

Any academic fraud, plagiarism or use or possession of unauthorised means in an assessment activity leads to a mark of zero (0) for the affected test or assignment. Furthermore, in accordance with the University's regulations, if disciplinary proceedings are initiated the subject is recorded as "Pending Assessment" until a decision is reached. These incidents are managed in accordance with the **Action Framework for Academic Integrity in Assessment at the UPC**.

Laboratory reports: 40%
Homework assignments: 20%
Final application project: 40%

BIBLIOGRAPHY

Basic:
- Compeau, Phillip; Pevzner, Pavel. Bioinformatics algorithms : an active learning approach (Vol. 1). 2nd ed. La Jolla, CA: Active Learning Publishers, 2015. ISBN 9780990374619.
- Compeau, Phillip; Pevzner, Pavel. Bioinformatics algorithms : an active learning approach (Vol. 2). 2nd ed. La Jolla, CA: Active Learning Publishers, 2015. ISBN 9780990374626.

RESOURCES

Hyperlink:
- KEGG. KEGG: Kyoto encyclopedia of genes and genomes
- Reactome. Reactome
- Bioconductor. Bioconductor
- Gene Ontology. Gene Ontology