COURSE DATA

DATA SUBJECT

Code: 43459
Name: Bioinformatics
Cycle: Master's Degree / Doctorate
ECTS Credits: 3
Academic year: 2025-26

STUDY (S)

Degree	Center	Acad. year	Period
2210 - Master's Degree in Research in Molecular, Cellular and Genetics Biology	Facultat de Ciències Biològiques	1	First quarter

SUBJECT-MATTER

Degree	Subject-matter	Character
2210 - Master's Degree in Research in Molecular, Cellular and Genetics Biology	Bioinformatics	COMPULSORY

COORDINATION

PALERO PASTOR FERRAN

SUMMARY

The subject **Bioinformatics** is fundamentally practical and, for that reason, theoretical knowledge will be taught simultaneously with practical work in the computer lab.

Originally, bioinformatics was defined as an interdisciplinary field that included biology, computer science, mathematics, and statistics, and whose goal was to analyze biological sequence data, genome contents and structures, as well as the prediction and function of proteins. With the arrival of "-omics" techniques, bioinformatics has expanded its scope of study to the analysis of large amounts of biological data, or Big Data, including that derived from complete genomes and therefore currently has great importance in biomedical research.

PREVIOUS KNOWLEDGE

RELATIONSHIP TO OTHER SUBJECTS OF THE SAME DEGREE

There are no specified enrollment restrictions with other subjects of the curriculum.

OTHER REQUIREMENTS

Students should have basic knowledge of molecular biology, statistics, and sequence analysis.

COMPETENCES / LEARNING OUTCOMES

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Be able to access the information required (databases, scientific articles, etc.) and to interpret and use it sensibly.

Ser capaz de buscar en la red información sobre secuencias de ácidos nucleicos y proteínas y adquirir la capacidad de manejar software relacionado con el análisis de secuencias.

Ser capaz de procesar y extraer información a partir de los datos proporcionados por un servicio de secuenciación y convertir dicha información a un formato que permita su análisis con diferentes programas de análisis de secuencias.

Ser capaz de recolectar información acerca de un organismo o elemento biológico, a partir de la almacenada en los servidores públicos, organizarla y sintetizarla.

Students should communicate conclusions and underlying knowledge clearly and unambiguously to both specialized and non-specialized audiences.

DESCRIPTION OF CONTENTS

1. Introduction to Bioinformatics with GALAXY (Week 4: 4h)

1. Introduction to computer science and use of GALAXY.
2. Sequencing techniques: quality of sequences and file formats.

2. Databases and sequence search (Week 5: 4h)

3. Introduction to using Genbank and ENA
4. Sequence Search Using BLAST

3. Alignments, genetic distances and phylogenies (Week 6: 2h)

5. Alignment of sequences, importance and most frequent methods. Calculation of genetic distances. Molecular phylogenies.

7. Most frequent concepts and methods/algorithms. Assembly of sequences derived from NGS

4. Genome Assembly (Weeks 6 & 7: 4h)

technologies
8. Evaluation of the assembled genome. Descriptive parameters of the assembly and genomic databases.

5. Annotation of genomes and genomic viewers (Weeks 7 and 8: 4h)

9. Annotation of bacterial and eukaryotic genomes
10. Genomic Viewers

6. Sequence mapping, variant analysis and population genomics (Weeks 8 and 10: 4h)

11. Sequence mapping: main methodologies and concepts. Use of minimap2.
12. Steps involved in variant calling. Types of data formats encountered during variant calling. Use command line tools to perform variant calling.

7. Transcriptome analysis (Week 12: 4h)

13. Introduction to R. Statistical packages for bioinformatics: BIOCONDUCTOR.
14. Analysis of gene expression data. Principal Component Analysis. Cluster analysis.

WORKLOAD

PRESENCIAL ACTIVITIES

Activity	Hours
Other activities	4,00
Computer classroom practice	26,00
Total hours	**30,00**

NON PRESENCIAL ACTIVITIES

Activity	Hours
Attendance at other activities	0,00
Individual or group project	15,00
Independent study and work	15,00
Preparation of lessons	15,00
Preparation for assessment activities	0,00
Resolution of case studies	0,00
Total hours	**45,00**

TEACHING METHODOLOGY

The development of the subject is structured in face-to-face and independent work:

Face-to-face work:

A) Classroom class sessions with a theoretical introduction to the master class system and a practical part based on the resolution of exercises and problems.

B) Tutorials

C) Review

Independent work:

A) Practical exercises and bioinformatic problems solved outside class hours.

B) Study of the contents and prior preparation of the classes.

EVALUATION

The assessment of student learning in the first call will be made by assessing the following sections:

1) An exam in the computer lab that may comprise both knowledge questions on theory and exercises that can be solved using the programs studied in the course. This test will earn up to 7 points and will be made after the end of classes.

2) Continuous Assessment based on class work and in solving exercises and bioinformatics problems. This section will be worth up to 3 points.

In the second call, the student will have two options: 1) an exam where you can collect up to 10 points and 2) if the student has obtained a note for the continuous evaluation on the first call, these points will be added to those of the test, which will be worth up to 7 points.

REFERENCES

- Bioinformatics and Functional Genomics, por Jonathan Pevsner (2015) publicado por Wiley_Blackwell. Tercera edición. Una introducción a la bioinformática y la genómica fácil de seguir y de entender los conceptos. Incluye muchos ejercicios prácticos y direcciones web., y está disponible en línea (https://trobes.uv.es/permalink/34CVA_UV/1b8uv2g/alma991009853672206258).

- Bioinformatics with Python Cookbook : Use Modern Python Libraries and Applications to Solve Real-World Computational Biology Problems (2022), también disponible en línea (https://trobes.uv.es/permalink/34CVA_UV/1bttdu2/alma991009923653906258).

- R Bioinformatics Cookbook : Utilize R Packages for Bioinformatics, Genomics, Data Science, and Machine Learning (2023), disponible en línea (https://trobes.uv.es/permalink/34CVA_UV/1bttdu2/alma991010329590506258)