

**Bioinformatics**

Code: 100894  
ECTS Credits: 3

Degree	Type	Year	Semester
2500252 Biochemistry	OB	3	2

**Contact**

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**Use of languages**

Principal working language: catalan (cat)  
Some groups entirely in English: No  
Some groups entirely in Catalan: No  
Some groups entirely in Spanish: No

**Teachers**

Maria Margarita Julia Sape

**Prerequisites**

There are no pre-requisites for this subject.

It is recommended that the student refreshes the core concepts from "Biologia Molecular" and "Química i Enginyeria de Proteïnes" (2nd year).

**Objectives and Contextualisation**

This course provides an introduction to bioinformatics.

Upon completion of the course, the student should be able:

- To master the most important web-based and/or graphical user interface tools for the study of sequences.
- To obtain, align, visualise and compare sequences.
- To infer phylogenetic relationships among sequences.
- To be familiar with the different predictive tools for sequences, and to be able to choose the best suited to each different experimental question.
- To be able to design simple bioinformatics experiments to answer biochemical questions.

**Content**

- Bioinformatics. Biomedical databases, public, centralised repositories, formats, controlled vocabularies and data standardisation for exchange and reanalysis.
- Alignment of two sequences. PAM and BLOSUM matrices. Alignment algorithms.
- "Basic Local Alignment Search Tool" (BLAST). BLAST search algorithm. Parameters and basic BLAST types. Evaluation of BLAST results.

- PSI-BLAST and other advanced types of BLAST searches. The "position-specific scoring matrix" (PSSM).
- Multiple sequence alignment (MSA). MSA strategies: exact, progressive, iterative, consistency-based or structure-based.
- MSA databases: Pfam and "Conserved domain database".
- Phylogenies. Phylogenetic tree types and components. Steps and methods to build and evaluate a phylogenetic tree.
- Domains and motifs. Protein modularity and development of search and/or prediction tools. Bioinformatic tools for predicting the physical properties, location and function of proteins.
- Principles of protein structural prediction. The Chou and Fasman algorithm. Homology-based, fold-recognition or "ab-initio" strategies. Structural visualisation tools. Protein databases (Unoprot, PDB), families, hierarchical categorisation.