

Bioinformatics

Code: 100780
 ECTS Credits: 6

Degree	Type	Year	Semester
2500250 Biology	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

Josep Antoni Pérez Pons

Sònia Casillas Viladerrams

Prerequisites

In order to take this subject, it is recommendable that the students have previously acquired enough solid knowledge on subjects like Genetics, Molecular Genetics, Microbiology, Structure and Functions of Biomolecules and Further Cell Biology.

We recommend a basic understanding of English, although it is not mandatory.

Objectives and Contextualisation

The treatment and computer analysis of molecular data has acquired a fundamental role in the modern Biology and the topics that will be taught in this subject are a basic introductory vision of bioinformatics. The main objectives are:

- To provide the basic bioinformatics knowledge that allows the use of search tools to interrogate the main public databases in Life Sciences and the different approaches for the computational analysis of nucleic acid and protein sequences.
- To give a perspective of the potential of this discipline in the field of research as well as in the professional field.

Content

Topic 1. Databases in Health and Life Sciences. Introduction to bioinformatics and molecular databases. Database Search Strategies. Integrated information retrieval and data submission to nucleotide databases. Sequence formats. NCBI databases. Tools for DNA sequence analysis, visualization and edition.

Topic 2. Sequence Alignments. Pairwise sequence alignment tools. Dot-Plot. Local and global alignments. Sequence alignment and dynamic programming. Substitution Matrices: identity and similarity. Scores, gaps and gap penalties. Multiple sequence alignment. Progressive method of multiple alignments. Applications of multiple sequence alignment.

Topic 3. Sequence Similarity Search. Heuristic algorithms. Bioinformatics tools for sequence similarity searching in sequence databases: BLAST and FASTA strategies. Types of BLAST searches and their applications. DNA or genome annotation by homology based search tools.

Topic 4. Introduction to programming for task automation in bioinformatics. The standard bioinformatic analysis. Scripts. Perl. Variables. Modules. Bioperl.

Topic 5. Gene and protein domain annotation. Ab Initio gene prediction. Protein domain annotations with InterProScan. Functional annotations using the Gene Ontology.

Topic 6. Comparative Genomics. Phylogenetic footprinting/shadowing. Identifying orthologs and paralogs. Synteny.

Topic 7. Molecular Phylogenetic Reconstruction. Biological evolution. Molecular phylogenetic. Methods of phylogenetic inference (UPGMA, Neighbor-Joining). Phylogenetic reconstruction: Examples.

Topic 8. Genetic Variation and Natural Selection. Types of genetic variation. Neutral theory of molecular evolution. Test of the neutral model of evolution (Ka/Ks). Examples of natural selection.

Topic 9. Proteins: Sequence Analysis. The sequence-structure-function relationship. Primary sequence database of protein. Sequence-based analysis of proteins and prediction of sub-cellular localization.

Topic 10. Proteins: Functional Analysis. Function prediction. Remote homology detection. Tools and resources for identifying protein families, domains and motifs. Secondary and integrated databases.

Topic 11. Proteins: Structural Analysis. The protein data bank (PDB). Searching for structural homologues. Prediction of structural features. Modeling of 3D Structures. Structural Classification of Proteins.