

Bioinformatics

Code: 101909
ECTS Credits: 6

Degree	Type	Year	Semester
2501230 Biomedical Sciences	OB	3	2

Contact

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Use of Languages

Principal working language: spanish (spa)
Some groups entirely in English: No
Some groups entirely in Catalan: No
Some groups entirely in Spanish: No

Teachers

Ramón Guixa González
Arnau Cordomi Montoya
Angel González Wong

Prerequisites

There are no prerequisites.

Objectives and Contextualisation

This course introduces the student to the field of Bioinformatics, an area of research that uses computer databases to store, retrieve and assist in the understanding of biological information. The large genome sequencing projects as well as significant progresses in the determination of three-dimensional protein structures have led to an explosion of genetic sequences and structural data available for automated analysis. The student will learn how genomic analysis and protein structures can lead to a better understanding of the biological processes. Students will be introduced to basic tools of Bioinformatics and Computational Biology. The practical sessions will complement this knowledge, allowing students to become familiar with the details and the use of the most used tools and online resources of the field.

Competences

- Develop critical thinking and reasoning and communicate ideas effectively, both in the mother tongue and in other languages.
- Develop independent learning strategies.
- Generate innovative and competitive proposals for research and professional activities.

Learning Outcomes

1. Develop critical thinking and reasoning and communicate ideas effectively, both in the mother tongue and in other languages.

2. Develop independent learning strategies.
3. Generate innovative and competitive proposals for research and professional activities.

Content

1. Introduction. Databases in Bioinformatics

- NCBI - Entrez
- Bibliographic data bases
- Protein sequences. UniProt
- Nucleotide sequences. GenBank

2. Genomics

- Genome annotations
- Search for genes
- Genome project
- Genomic browsers
- Encode project
- HapMap project
- Catalog of human genes and genetic disorders: OMIM
- Databases of SNPs
- Genome association studies (GWAS)

3. Alignment of sequences

- Sequence comparison methods
- Substitution matrices
- Dynamic programming
- Local and global alignment
- Search by similarity (BLAST)
- Multiple sequence alignment
- Representation of LOGOS of Sequences
- Progressive alignment. ClustalW

4. Phylogenetic analysis

5. Structural bioinformatics

- Protein secondary structure
- Protein tertiary structure. Molecular interactions
- Experimental methods for the determination of the tertiary structure of proteins: X-ray and NMR
- The PDB format
- Protein quaternary structure
- Structural alignment of proteins, molecular cavities, molecular electrostatic potential
- Cell membrane, membrane proteins, prediction of secondary structure of transmembrane segments
- Structural classification of proteins: motifs, domains
- Homology modeling

6. Modes of drug action

- G protein-coupled receptors
- Kinases
- Growth factors

7. Chemoinformatics

- Representation of chemical entities. SMILES and Tanimoto coefficient
- Structure-Activity Relationships. Pharmacophore models

- Protein-ligand molecular docking
- ADME / Tox

Methodology

The orientation of the course is eminently practical with the use of software.

Activities

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Practical classes	24	0.96	1, 3
Research project presentation	5.5	0.22	1
Theoretical classes	24	0.96	1
Type: Supervised			
Consolidation practices and tutorials	10	0.4	1
Type: Autonomous			
Research project	10	0.4	1
Study	71	2.84	2

Assessment

- 2 partial exams of theoretical-practical knowledge and conceptual questions [Tests T1 (32.5%) and T2 (32.5%)]
- Attendance to practical classes and presentation of correspondent reports [AI (15%)]
- Preparation and presentation of a project [PJ (20%)]

Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Attendance to practices and presentation of the corresponding reports	15%	4	0.16	2, 3
Drafting and presentation of a project	20%	1	0.04	2
Practical and theoretical exams	65%	0.5	0.02	1, 3

Bibliography

- Attwood, T.K., Parry-Smith, D.J., Introducción a la Bioinformática, Pearson Education, 2002.
- Baldi, P., Brunak, S., Bioinformatics, MITPress, 1998.
- Baxebanis, A.D., Oullette, F., Bioinformatics, John Wiley & Sons, 1998.

- Lesk, A. Introduction to Bioinformatics. Oxford University Press, 2005.
- Waterman, M.S., Introduction to computational biology maps, sequences and genomes, Chapman & Hall/CRC, 2000.

<http://www.nih.gov/>

<http://www.ncbi.nlm.nih.gov/>

<http://www.pdb.org/>

<http://www.ebi.ac.uk>

<http://www.uniprot.org/>

<http://www.rcsb.org/>

<http://www.genomesonline.org/index>

<http://www.ncbi.nlm.nih.gov/projects/mapview/>

<http://genome.ucsc.edu/ENCODE/>

<http://www.genome.gov/Encode/>

<http://www.nature.com/encode/#/threads>

<http://hapmap.ncbi.nlm.nih.gov>

<http://www.ncbi.nlm.nih.gov/snp>

<http://www.ncbi.nlm.nih.gov/SNP/>

<http://omim.org>

<http://www.1000genomes.org/home>

<http://www.genome.gov/>

<http://www.genome.gov/GWASudies/>

<http://www.embl.de/>

<http://genes.mit.edu/GENSCAN.html>

<http://expasy.org/prosite/>

<http://prodom.prabi.fr/>

<http://pfam.sanger.ac.uk/>

<http://www.cbs.dtu.dk/services/TMHMM/>

<http://scop.mrc-lmb.cam.ac.uk/scop/>

<http://www.cathdb.info/>

http://ekhidna.biocenter.helsinki.fi/dali_server/

<http://www.vcclab.org/lab/edragon/>

<http://matisse.ucsd.edu/itp-bioinfo/links.html>

<http://sites.univ-provence.fr/~wabim/english/logligne.html>

