

Degree programme	Type	Course
Biotechnology	OB	3

Contact lecturer

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Teaching staff

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Group languages

You can consult this information at the [end](#) of the document.

Prerequisites

There are no prerequisites for this subject, but it is necessary to review the concepts acquired in the subjects of "BiochemistryGenetics and Molecular Biology" and "Recombinant DNA Technology" taught during the first and second year.

Knowledge of English is strongly recommended

Objectives

The material taught in this course provides an introductory overview of bioinformatics. This course is aimed at third-year Biotechnology students (5th semester) and corresponds to a theoretical course of 3 credits. The objectives and contents have been defined the objectives and contents of this course taking into account that within of the same subject area (Molecular Biology of Systems) the course is found of "Genomics, Proteomics e Interactomics".

The main objectives are:

-To provide students with the basic bioinformatics knowledge that enables both the use of tools to search for information in molecular databases and to address the computational analysis of sequences and structures of nucleic acids and proteins.

-To provide a broad perspective of the potential of this discipline both in the field of the research and in the professional field.

Learning outcomes

- CM25 (Work collaboratively in teams to solve problems in the field of systems biology.) Work collaboratively in teams to solve problems in the field of systems biology.
- KM25 (Describe the physical and chemical bases of the methodology and instrumentation used in genomic, transcriptomic, proteomic, interactomic and metabolomic analysis.) Describe the physical and chemical bases of the methodology and instrumentation used in genomic, transcriptomic, proteomic, interactomic and metabolomic analysis.
- SM25 (Analyse information from databases and software necessary for the study of correlations between structure, function and evolution of macromolecules.) Analyse information from databases and software necessary for the study of correlations between structure, function and evolution of macromolecules.

Contents

Topic 1 - Introduction. Databases in Molecular Biology. Search engines: Entrez and SRS. Primary and secondary databases. Searches in specialized databases. Identification of proteins through database searches.

Topic 2 - Analysis of DNA sequence information. Restriction maps for cloning. Design of probes and PCR oligonucleotides for the detection and quantification of a sequence, cloning or site-directed mutagenesis. Secondary structure of RNA.

Topic 3 - Sequence alignments. Concepts of homology and similarity. Pairwise sequence alignment algorithms. Dot plot. Global and local alignment. Scoring matrices. Gaps. Similarity searches in databases: BLAST and FASTA.

Topic 4 - Genome projects and genome browsers. Sequencing, assembly and annotation of genomes. Identification of coding and promoter sequences.

Topic 5 - Multiple alignments. Creation and analysis of multiple sequence alignments. Multiple sequence alignment. Editing and visualization programs. Assessment of conserved protein regions. Design of probes and PCR oligonucleotides from a multiple alignment of protein sequences. Phylogenetic trees.

Topic 6 - Proteins: functional analysis. Identification of homologues, motifs, domains and protein families. Identification of distant homologues using PSI-BLAST. Statistical models that relax the frequency of an amino acid at a specific position: PSSM matrices, profiles and hidden Markov models. Prediction of motifs and domains. Databases of motifs, domains and protein families. LOGO representation of motifs or fingerprints.

Topic 7 - Protein structure: prediction, classification and analysis. Methods for predicting the structure of globular proteins: ab initio methods, homology-based methods and neural networks. Assessment of the reliability of prediction methods. Prediction of the structure of membrane proteins with transmembrane helices and beta barrels. Prediction of coiled coils. Methods for predicting tertiary structure. The PDB structure database. Visualization and comparison of structures. Sequence-based predictions and identification of therapeutic targets. Structure-based predictions. Redesign of protein solubility.

Learning activities and methodology

Title	Hours	ECTS	Learning outcomes
Study	40	1.6	SM25
Tutorials	5	0.2	SM25

Classes in the computer room	20	0.8	CM25, SM25
Theoretical classes	6	0.24	KM25

The teaching methodology includes two different types of activities: theory classes and practical computer-lab classes. Learning will also include independent study and problem solving.

Theory classes

Classes aimed at conveying the basic concepts and the information needed to develop independent learning. Theory classes will be held in person and will be taught using audiovisual support. The content taught in theory classes will be assessed in the written tests.

Computer-lab practical classes or problem-solving sessions

This activity will take place in the Faculty computer rooms and will be carried out in groups of approximately 20 students, over 8 sessions. These practical sessions will be organized around problems set by the teaching staff, which students will have to solve using different bioinformatics tools and analyses. At the end of each session, students must submit the problems they have managed to solve. This submission is compulsory and will be done in pairs through the Virtual Campus.

To make the classes run more smoothly, students will have tutorials and support materials available on the Virtual Campus.

Attendance and submission of assignments in the practical sessions are compulsory.

No changes may be made to the practical-session days and/or groups. Changes of practical group are only allowed if a swap is arranged with another classmate.

Tutorials

Individual or pair sessions for resolving questions related to the course. This type of activity will be held at the request of students.

Note: 15 minutes of one class will be reserved, within the calendar established by the centre/degree programme, for students to complete the surveys evaluating the teaching staff's performance and the course.

Annotation: within the schedule set by the centre or degree programme, 15 minutes of one class will be reserved for students to evaluate their lecturers and their courses or modules through questionnaires.

Assessment

Continuous assessment activities

Title	Weight	Hours	ECTS	Learning outcomes
Written test 1	35%	2	0.08	KM25, SM25
Written test 2	35%	2	0.08	KM25, SM25
Problems done in the sessions on the computer room.	30%	0	0	CM25, SM25

The competences of this subject will be assessed through continuous assessment, based on the following items:

- Written tests

- Submission of the problems completed in the computer-lab sessions
- Submission of the integrative assignment

a) Written tests

These will consist of two partial tests: topics 1-4, part 1; and topics 5-7, part 2. They will include short-answer questions and/or multiple-choice questions aimed at relating concepts and solving problems. They will preferably be held in the Faculty computer rooms, so that students will have access to all the bioinformatics tools needed to answer the questions, as well as a list of the links used during the course.

Each partial test will account for 35% of the final mark.

The mark obtained in the assessment activities may only be averaged with the mark for the problems if the average mark of the two partial exams is equal to or higher than 5.

b) Problem solving in the computer-lab sessions

This assessment will consist of the submission, in pairs, of the practical exercises/problems completed in the laboratory. Practical assignments may only be submitted through the Virtual Campus within the period set by the lecturer. Late submission or failure to submit the practical assignments through the Virtual Campus will be penalized with a mark of 0. The submission of the integrative assignment for the course will also be assessed and will account for 5% of the mark corresponding to the submissions for part 2.

This assessment will account for 30% of the final mark.

Single assessment

The single assessment will not correspond to the resit examination and will consist of two parts: a first part assessing the theoretical and practical content taught during the course, which will account for 60%; and a second part in which students will have to solve problems or comment on cases worked on during the practical classroom sessions, which will account for 40%.

Resit examination

To take part in the resit, students must have been previously assessed in the partial exams and in a set of activities. Therefore, students will receive a "Not assessable" mark when the assessment activities have not been completed as described in the teaching guide.

The resit examination will have the same format as the partial tests, that is, multiple-choice questions and problem solving. It will also be held in the Faculty computer rooms on the scheduled date.

The mark obtained in the laboratory practicals may not be taken into account if the submissions have not been completed within the deadline set by the lecturer.

Formula for weighting the final mark

Final mark = Assessment 1 × 0.35 + Assessment 2 × 0.35 + Problems 1 × 0.15 + Problems 2 × 0.15

General considerations on assessment

To pass the course, students must obtain a final mark equal to or higher than 5. The final mark will be obtained by calculating the weighted average of the three assessment activities. No average will be calculated unless a mark equal to or higher than 5 is obtained in the written tests or in the resit examination. If the mark for the written tests and/or the resit examination is lower than 5, the course cannot be passed.

Students who are unable to attend an individual assessment test for a justified reason, such as illness, the

death of a first-degree relative or an accident, and who provide the corresponding official documentation to the Degree Coordination and the theory teaching staff, will have the right to take the test on another date.

Any irregularity in an assessment activity, including academic fraud, plagiarism or misuse of AI, unless such use is expressly authorized in the teaching guide, that may lead to a significant change in the mark will result in that activity being awarded a mark of 0. If the teaching guide states that passing the course requires a minimum mark in that assessment activity, or if several irregularities occur in assessment activities within the same course, the final mark for the course will be 0. In addition, disciplinary proceedings may be initiated against any student who commits any of these irregularities.

The Degree Coordinator will ensure that this is implemented with the lecturer of the affected course.

Use of AI

In this course, the use of Artificial Intelligence (AI) technologies is not permitted at any stage. Any work that includes AI-generated fragments will be considered a breach of academic honesty and may result in a partial or total penalty in the mark for the activity, or more serious sanctions in severe cases.

Any aspect not covered in this guide will follow the assessment regulations of the Faculty of Biosciences.

Bibliography

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https://bibcercador.uab.cat/permalink/34CSUC_UAB/1fbc57r/alma991010834431706709

- Lesk, Arthur M. (2019). Introduction to bioinformatics. (5th ed.) Oxford University Press.

- Mount, David W. (2004). Bioinformatics : sequence and genome analysis. (2nd ed.) Cold

- Ouellette, B. F. Francis & Baxevanis, Andreas D. (2005). Bioinformatics : a practical guide to the analysis of genes and proteins. (3^a ed.) Wiley-Interscience

- Pevsner, Jonathan. (2015). Bioinformatics and functional genomics. (3rd ed.) Wiley-Blackwell

- St. Clair, Caroline & Visick, Jonathan. (2015). Exploring bioinformatics : a project-based approach. (2nd ed.) Jones & Bartlett Learning

- Wishart, David Scott [i altres]. (2020). Bioinformatics. (4th ed.) Wiley

Software

Program JalView (www.jalview.org). multialignment representation

PyMol

Links of data bases and applications:

NCBI/nucleotide

<https://www.ncbi.nlm.nih.gov/nucleotide/>

NCBI/Gene

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

Uniprot

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

BRENDA

<http://www.brenda-enzymes.org/>

Swiss-2DPAGE

<http://us.expasy.org/ch2d/>

Proteome SD-PAGE database

<http://web.mpiib-berlin.mpg.de/cgi-bin/pdbs/2d-page/extern/index.cgi>

String

<http://string-db.org/>

OMIM

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

Phosphosite

<http://www.phosphosite.org/homeAction.do;jsessionid=117096AF4D54A36677C243A7D586DF45>

Nebcutter

<http://tools.neb.com/NEBcutter2/>

Netprimer

<http://www.premierbiosoft.com/netprimer/>

Primer3plus

<http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi>

PrimerBlast

<http://www.ncbi.nlm.nih.gov/tools/primer-blast/>

ClustalW 2

<http://www.ebi.ac.uk/Tools/msa/clustalw2/>

Jalview

<http://www.jalview.org/download>

Uniprot

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

Paquete T-COFFE

<http://tcoffee.vital-it.ch/apps/tcoffee/index.html>

Predictor NPSA:

http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_server.html

Jalview

<http://www.jalview.org/download>

Prosite:

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

InterProScan 4

<http://www.ebi.ac.uk/Tools/pfa/iprscan/>

PRATT

<http://web.expasy.org/pratt/>

WebLogo

<http://weblogo.berkeley.edu/logo.cgi>

JPred3

<http://www.compbio.dundee.ac.uk/www-jpred/>

Predict Protein

<https://predictprotein.org/>

COILS

http://embnet.vital-it.ch/software/COILS_form.html

Phobius

<http://phobius.sbc.su.se/>

Signal Peptide

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

PRED TMBB

<http://bioinformatics.biol.uoa.gr/PRED-TMBB/input.jsp>

RCSB PDB

<http://www.rcsb.org/pdb/home/home.do>

PDBsum

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

VAST

<https://www.ncbi.nlm.nih.gov/Structure/VAST/vast.shtml>

Dali

http://ekhidna.biocenter.helsinki.fi/dali_lite/start

EXPASY:

www.expasy.org

Aggrescan:

<http://bioinf.uab.es/aggrescan/>

Aggrescan 3D

<http://biocomp.chem.uw.edu.pl/A3D2/>

Course groups and languages

The information provided is provisional until November 30. After this date, you will be able to consult the language of each group through this [link](#). To access the information, you will need to enter the course CODE

Type of teaching	Group	Language	Semester	Shift
(TE) Theory	43	Catalan/Spanish	first semester	morning-mixed
(PLAB) Practical laboratories	431	Catalan/Spanish	first semester	morning-mixed
(PLAB) Practical laboratories	432	Catalan/Spanish	first semester	morning-mixed
(PLAB) Practical laboratories	433	Catalan/Spanish	first semester	morning-mixed
(PLAB) Practical laboratories	434	Catalan/Spanish	first semester	morning-mixed