Universitat Autònoma de Barcelona

2017/2018

Bioinformatics

Code: 100948
ECTS Credits: 3

Degree	Type	Year	Semester
2500253 Biotechnology	OB	3	1

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
Susana Navarro Cantero

Prerequisites

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

Objectives and Contextualisation

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

The main objectives are: To provide students with basic bioinformatic knowledge that allows both the use of tools to search for information in molecular databases and address the computational analysis of sequences and structures of nucleic acids and proteins.

Skills

- Interpret experimental results and identify consistent and inconsistent elements.
- Learn new knowledge and techniques autonomously.
- Make an oral, written and visual presentation of ones work to a professional or non-professional audience in English or in one's own language.
- Obtain information from databases and use the software necessary to establish correlations between the structure, function and evolution of macromolecules.
- Reason in a critical manner
- Search for and manage information from various sources.
- Search for, obtain and interpret information from the principal databases on biology, bibliography and patents and use basic bioinformatic tools.

- Use ICT for communication, information searching, data processing and calculations.
- Work individually and in teams

Learning outcomes

1. Establish structural, functional and evolutionary relations based on information in existing biological databases .
2. Interpret experimental results and identify consistent and inconsistent elements.
3. Learn new knowledge and techniques autonomously.
4. Make an oral, written and visual presentation of ones work to a professional or non-professional audience in English or in one's own language.
5. Obtain, interpret and use information from databases on biology, bibliography, patents, markets, etc.
6. Reason in a critical manner
7. Search for and manage information from various sources.
8. Use ICT for communication, information searching, data processing and calculations.
9. Work individually and in teams

Content

1.- Introduction. Data banks in Molecular Biology. Search engines: Entrez and SRS. Primary and secondary data banks. Search in specialized databases. Identification of proteins by means of searches in databases.

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

3- Genome Projects and Genomic Browsers. Sequencing, ensemble and annotations of genomes. Identification of coding sequences and promoters.

4.- Sequence alignments. Concepts of homology and similarity. Algorithms of alignment for sequence pairs. Dot-Plot. Global and local alignment. Punctuation array Gaps Search by similarity in databases: BLAST and FASTA.

5. Creation and analysis of multiple sequences alignments: multiple sequence alignment. Editing and viewing programs. Evaluation of conserved regions of proteins. Design of probes and oligonucleotides for PCR based on a multiple alignment of protein sequences. Phylogenetic trees.

6.-Prediction of protein function: identification of homologues, motifs, domains, and protein families. Identification of distant homologues through PSI-Blast. Statistical models that relax the frequency of an amino acid in a specific position (PSSM matrices, profiles, and hidden Markov model HMM). Prediction of motives and domains. Databases of motives, domains, and protein families. Representation of LOGOS of reasons or emprents.

7. Prediction of the secondary structure of proteins: Prediction methods of globular protein proteins, ab-initio based, based on homology and neural networks. Evaluation of the reliability of the prediction methods. Prediction of the structure of membrane proteins with transmembrane helix and beta barrel. Prediction of "coiled-coil".

8. Analysis and prediction of the three-dimensional structure: Methods of prediction of the tertiary structure.The bank of PDB structures. Visualization and comparison of structures. Structural classification of proteins.

9. Analysisand prediction of the folding and aggregation of proteins. Sequence-based predictions, identification of therapeutic targets. Predications based on structure. Redesign of protein solubility.

Methodology

Theoretical Classes

Classes to transmit the basic concepts and the information necessary to develop an autonomous learning. Promotion of the active participation of students. Support in the form of presentations in PowerPoint that will be available to the student on the Virtual Campus.

Computer classroom practices or Problems

This activity is carried out in the computer rooms of the Faculty and will be held in groups of 30-40 students. These practices will be organized based on problems posed by the teachers and that the student will have to solve using the different tools and bioinformatic analysis. The teacher in each session will present different problems, which will be solved as an example (in the session or shortly before the session), the other problems will have to be solved by the students during the same classroom session. At the end of each session the students will have to hand over the problems that have been resolved. This delivery will be done through the virtual campus.

Tutorials

Individual sessions or small groups for the resolution of doubts related to the subject. This type of activity will be done at the request of the students.

Activities

Title	Hours	ECTS	Learning outcomes
Type: Directed			
Classes in the computer room and problems	20	0.8	3, 8, 7, 1, 4, 2, 5, 6, 9
Theoretical classes	6	0.24	3, 8, 7, 1, 5
Type: Supervised			
Tutorials	5	0.2	8, 7, 2, 5, 6
Type: Autonomous			
Study	40	1.6	3, 8, 7, 1, 2, 5, 6, 9

Evaluation

The competences of this subject will be evaluated through continuous evaluation. There will be two types

Of evaluation:

- written tests

- resolution of the problems in the sessions of the computer room or deliveries via platform MODDLE.

A) written tests,

It will consist of a written test at the end of the subject. This test will consist of short questions to relate concepts and the resolution of problems. They will be made preferably in the computer rooms of the Faculty, so that the student will have at his disposal all the bioinformatics tools necessary to answer the questions and problems raised.

The weight of this test will be 85% of the final mark.

To pass these tests, you must obtain a minimum score of 5 out of 10 points. Students who do not pass this test with a mark equal to or greater than 5 can retrieve it in the recovery test scheduled at the end of the semester.

B) resolution of problems in the sessions of the computer room,

It is a group assessment (2 students per group) that will consist of evaluating the problems given by the students. 2 problems (or sessions) chosen by the teacher will be evaluated for the total number of problems delivered. Deliveries via Moodle server (themes 1-4, and 5-9): The teacher will propose a series of activities to be done and delivered via the Moodle server, over the weeks in which topics 1-4 will be addressed. These activities Moodle will require that students have previously worked out the exercises in the problem classes.

The weight of this assessment will be 15% of the final grade.

The mark obtained in this evaluation activity can only be done with the average mark of the written test if the latter is greater than or equal to 5 out of 10.

Evidence of recovery and improvement of note

The recovery exam will have the same format as the final written test, that is: short questions to relate concepts and problem solving. It will also be held in the computer rooms of the Faculty on the scheduled date.

Students who wish to improve their mark may submit to a final exam at the end of the semester, on the date and place scheduled for the recovery exam. The degree of difficulty of this test will correspond to the objective of the test and, therefore, may be superior to other written tests. The student who presents himself to improve the grade waives the mark obtained previously in the evaluation of the written test.

General considerations on the evaluation

To pass the subject it is necessary to obtain a final grade equal to or greater than 5. The final grade will be obtained by doing the weighted average of the two assessment activities. Average will not be done if you do not get a score equal to or greater than 5 in the written test or proof of recovery (and there is a minimum for each part). If the mark of the written test and / or the proof of recovery is less than 5, the subject can not be exceeded.

The revision of the written tests will be carried out on a concerted day and place, between 1 and 7 working days after the publication of the notes.

It will be considered that a student will obtain the "non-evaluable" qualification if the following assumption was given: "the evaluation of all the assessment activities carried out would not have allowed him to achieve the overall grade of 5 in case he had obtained the highest grade In all of them ". Students who can not attend a written test for a justified cause and provide the official documentation corresponding to the Degree Coordinator will have the right to perform in another date a test that could combine the resolution of problems and the oral response to questions raised by the teacher.

The degree coordinator will ensure the specification of this with the teacher of the subject affected.

Any aspect that is not contemplated in this guide will follow the regulations of evaluation of the Faculty of Biosciences.

Evaluation activities

Title	Weighting	Hours	ECTS	Learning outcomes
Problems done in the sessions on the computer room.	15	0	0	3, 8, 7, 1, 2, 5, 6, 9
Written tests	15	4	0.16	3, 8, 7, 4, 2, 5, 6, 9

Bibliography

Attwood T.K. i Parry-Smith, J. 1999. Introduction to Bioinformatics Longman. UK.

Xiong, J. 2006. Essential bioinformatics. Cambridge Univ. Press.

Sheehan, D.,Physical biochemistry : principles and applications 2nd ed. Chichester: John Wilwy & Sons, 2008.

Dear, P.H., 2007. Bioinformatics, Methods Express.

Prevsner, j, 2015. Bioinformatic and functional genomics, 3rd edition. Wiley-Blackwel. ISBN 978-1-118-58178-0.

Lesk, A. 2014. Introduction to bioinformatics, 4th edition. Oxford University. ISBN: 9780199651566.

Web sources: www.youtube.com/user/NCBINLM

www.youtube.com/user/RCSBProteinDataBank