

Bioinformatics

Code: 101000
ECTS Credits: 6

Degree	Type	Year	Semester
2500502 Microbiology	FB	2	2

Contact

Name: Isidre Gibert Gonzalez
Email: isidre.gibert@uab.cat

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

Other comments on languages

The Catalan language is the most used but Spanish and English are also used

Teachers

Daniel Yero Corona
Oscar Conchillo Solé

Prerequisites

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

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.

Competences

- Act with ethical responsibility and respect for fundamental rights and duties, diversity and democratic values.
- Display a capacity for analysis, synthesis, organisation, planning and decision-making.
- Identify and solve problems.
- Know and use -omics tools (genomics, transcriptomics, proteomics, metagenomics, etc.).

- Take sex- or gender-based inequalities into consideration when operating within one's own area of knowledge.

Learning Outcomes

1. Act with ethical responsibility and respect for fundamental rights and duties, diversity and democratic values.
2. Display a capacity for analysis, synthesis, organisation, planning and decision-making.
3. Establish relationships between structure, function and evolution of genes and genomes.
4. Identify and solve problems.
5. Know and use bioinformatics databases and the algorithms and programmes used in the annotation and analysis of genomes, transcriptomes, proteomes and metabolomes.
6. Take sex- or gender-based inequalities into consideration when operating within one's own area of knowledge.
7. Understand the fundamental principles of bioinformatics.
8. Use and interpret sources of data on genomes and macromolecules of any microbial species.

Content

Topic 1. Databases in Health and Life Sciences. Search engines and strategies. Sequence formats. NCBI databases. Tools for DNA sequence analysis, visualization and edition.

Topic 2. Sequence Alignments. Pairwise sequence alignment tools. Local and global alignments. Substitution Matrices: identity and similarity. Scores, gaps and gap penalties. Sequence alignment and dynamic programming. 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. Types of BLAST searches and their applications.

Topic 4. Proteins: Sequence Analysis. The sequence-structure-function relationship. Uniprot Database. Domain identification, profiles and HMM. Analysis and predictions of protein

Topic 5. Proteins: Structural Analysis. The protein data bank (PDB). Structural alignments. Homology modeling. Visualization and representation.

Topic 6. Genomics. Microbial genomes databases and genome browsers. Genome annotation and description tools. Comparative genomics. Genetic exchange detection. Metagenomics.

Topic 7. Molecular phylogenetic reconstruction. Molecular phylogeny. Phylogenetic inference methods. Examples of phylogenetic reconstruction. Selective pressure estimation.

Methodology

The teaching methodology includes two types of differentiated activities: Lectures and practical sessions in the computer classroom. The learning will also have individual and/or collective mentoring of students that will serve as support to solve more specific problems or those requiring it for its complexity or difficulty.

L e c t u r e s

Lectures will address the basic ideas of the different topics and will also increase student motivation to participate actively. Lectures will motivate students to expand and confront autonomously the acquired knowledge as a personal work.

C o m p u t e r

p r a c t i c e s

These practices are organized based on problems proposed by teachers that should be solved using different bioinformatic tools and analysis. These activities are of obligatory attendance.

Mentoring

Individual or small group tutorials to solve questions related to the subject. This type of activity will be carried out at the request of the students.

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.

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Activities

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Computer practices	36	1.44	7, 5, 3, 4, 2, 8
Lectures	11	0.44	7, 5, 3, 4, 2, 8
Type: Supervised			
Mentoring	4	0.16	5, 4, 2, 8
Type: Autonomous			
Completion of end-of-unit tests	5	0.2	7, 5, 3, 4, 2, 8
Individual reading	10	0.4	7, 5, 3, 4, 2, 8
Individual study	40	1.6	7, 5, 3, 4, 2, 8
Literature search	8	0.32	7, 5, 3, 4, 2, 8
Solving problems	30	1.2	7, 5, 3, 4, 2, 8

Assessment

The evaluation schedule is organized into four main assessment activities and there will also be a reassessment test and an optional activity to get a higher mark.

None of the assessment activities will account for more than 50% of the final mark.

The success in meeting the course learning objectives will be evaluated as follows:

Main assessment activities

Midterm exams (60%)

Activitie 1. Midterm exam 1. Approximately 30%.
Activitie 2. Midterm exam 2. Approximately 30%.

Midterm exams are combined tests that can count on theoretical and/or practical questions, combining multiple-choice questions, written answer questions and/or problem solving.

The weights of each one of the exam will depend on the distribution of the sessions in the academic calendar. As a reference, the first evaluation will weigh approximately 30% and the second one 30%.

Each of the two exams (1 and 2) require a minimum grade of 4 points (out of 10) in order to pass the course.

Continuous assessments (40%).

Throughout the course the teachers will pose problems or questions related to the subject taught (or with new content not necessarily introduced by the teachers) that the students will have to solve in the form of tests or sporadic deliveries. There will be two different types of assessments: solving-problem in groups (integrative problem) with periodical deliveries, and continuous assessment of contents through individual questionnaires at the end of each unit.

Activitie 3. Problem-solving in groups (20%).

This integrative problem will consist in the resolution of a problem that will include questions related to the different thematic blocks presented during the theoretical and practical classes.

This integrative problem will be solved autonomously in groups of 3-4 students. The teaching staff will supervise the work and solve doubts and general questions about the strategies to solve problem.

The students will periodically deliver partial results on this problem to the teachers following established guidelines on content, presentation format and deadlines.

This activity requires a minimum grade of 4 points (out of 10) in order to pass the course.

Activitie 4. End-of-unit tests (20%).

Tests of combined multiple-choice, numerical and/or short-answer questions to recapitulate worked contents in each unit. A Moodle platform will be used for questions with feedback. The non-execution of any of the assessment activities is zero in that activity.

This activity requires a minimum grade of 4 points (out of 10) in order to pass the course.

Reassessment attempt

To be eligible for the retake process, the student should have been previously evaluated in a set of activities equaling at least two thirds of the final score of the course.

Reassessment of each midterm exam (1 and 2) can be done separately. The grade obtained at the reassessment exam will substitute the failed regular exam during the trimester and will be used to calculate the final grade according to the percentages reported in this teaching plan. Getting a grade below 4 points in any of the reassessment exams results in failing the course.

The qualification obtained for the End-of-unit tests can be retaken provided that the number of activities carried out is greater than or equal to 50% of the programmed ones. Note however that the grade obtained for the integrative problem cannot be retaken.

Getting a higher mark

In order to get a higher mark, those students who have passed the midterm exams 1 and 2 may opt for a final test. This test will include the whole subject. It is not possible to get a higher grade through a written work or other types of activities.

Exam difficulty level will correspond to the objectives of the subject and, therefore, may be higher than the midterm exams.

The student who takes this exam renounces the previous notes and therefore, the grade of this test will be the one that will prevail in the final grade even if it is lower than the ones obtained in the midterm exams. The new grade obtained cannot be used to obtain "honors".

Calculation of Final Grade

Final grade = [(Midterm exam 1 x 0.30) + (Midterm exam 2 x 0.30) + (Integrative problem x 0.20) + (End-of-unit tests x 0.20)]

Passing the course

Overall, in order to successfully complete this course, the student must get a minimum final grade of 5 points (out of 10) and a minimum grade of 4 points (out of 10) in each of the four main activities.

Not evaluable

The student will be graded as "Not evaluable" if the weighting of all conducted evaluation activities is less than 67% of the final score.

Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Continuous assessment (End-of-unit tests)	20	0	0	7, 5, 3, 4, 2, 8
Midterm exam #1 (theoretical-practical contents)	35	3	0.12	7, 5, 4, 2, 8
Midterm exam #2 (theoretical-practical contents)	25	3	0.12	7, 5, 3, 4, 2, 8
Problem-solving in groups	20	0	0	1, 6, 7, 5, 3, 4, 2, 8

Bibliography

- Christensen, Henrik (Ed.). 2018. Introduction to Bioinformatics in Microbiology. Springer International Publishing. (ISBN 9783319992792) (<https://link.springer.com/book/10.1007%2F978-3-319-99280-8>)
- Claverie, J-M. & Notredame, C. 2007 (2nd ed.). Bioinformatics for dummies. Hoboken, NJ; Wiley, cop. (ISBN 9780470089859).
- Lesk, Arthur M. 2014 (4th ed.). Introduction to bioinformatics. Oxford University Press. (ISBN 9780199651566).
- Taştan Bishop, Özlem (Ed.). 2014. Bioinformatics and Data Analysis in Microbiology. Caister Academic Press. (ISBN 9781908230393).

Software

- 7zip (local installation): Compresses and decompresses files in many formats.
- Artemis (local installation): Genomic browser and annotation tool. <https://www.sanger.ac.uk/tool/artemis/>
- Artemis Comparison Tool (ACT) (local installation): Displays pairwise alignments between two or more genomic sequences. <https://www.sanger.ac.uk/tool/artemis-comparison-tool-act/>
- DALI (web interface): network service for comparing protein structures in 3D (<http://ekhidna2.biocenter.helsinki.fi/dali/>)
- EMBOSS needle i EMBOSS water (interficie web): Pair sequence alignment (<https://www.ebi.ac.uk/Tools/emboss/>)
- MEGAX (local installation): Integrated tool for conducting phylogenetic analysis. <https://www.megasoftware.net/>
- Mendeley (instal-lació local): Reference Manager (institutional account).
- NCBI blast (web interface): Sequence alignment (<https://blast.ncbi.nlm.nih.gov/>)
- Notepad++ (local installation): Computer program designed to edit and visualize text files, also named flat files (ascii i utf8)
- Pymol: (local installation): Allows the user to visualize, analyze an interact in many ways with 3D structures from biological molecules.
- SMS Sequence Manipulation Suite (JavaScript program): Collection of programs for generating, formatting, and analyzing short DNA and protein sequences (<https://www.bioinformatics.org/sms2/>).

- SNAP (web interface): Calculates synonymous and non-synonymous substitution rates based codon-aligned nucleotide sequences. <https://hcv.lanl.gov/content/sequence/SNAP/SNAP.html>.
- Zotero (local installation): Open-Source Reference Manager. (<https://www.zotero.org/>).