

Degree programme	Type	Course
Microbiology	FB	2

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

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

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.

Learning outcomes

- CM07 (Critically evaluate, in the field of biochemistry, experimental procedures and data analysis, as well as their results, with a gender perspective and with ethical responsibility and respect for fundamental rights and duties, diversity and social and democratic values.) Critically evaluate, in the field of biochemistry, experimental procedures and data analysis, as well as their results, with a gender perspective and with ethical responsibility and respect for fundamental rights and duties, diversity and social and democratic values.
- CM08 (Integrate knowledge and analysis techniques for the study of biomolecules and their functions,

working individually and in groups, to elaborate and present in writing or orally and publicly a scientific work.) Integrate knowledge and analysis techniques for the study of biomolecules and their functions, working individually and in groups, to elaborate and present in writing or orally and publicly a scientific work.

- KM11 (Identify the basic data bases and computer tools to address the computational analysis of nucleic acid and protein sequences.) Identify the basic data bases and computer tools to address the computational analysis of nucleic acid and protein sequences.
- KM12 (Define the basic structure and biological functions of biomolecules and biochemical processes that regulate the vital functions of living beings and their adaptability to the environment.) Define the basic structure and biological functions of biomolecules and biochemical processes that regulate the vital functions of living beings and their adaptability to the environment.
- KM13 (Indicate the theoretical foundations and equipment of the main instrumental techniques to isolate, quantify, characterise and detect biomolecules and metabolites.) Indicate the theoretical foundations and equipment of the main instrumental techniques to isolate, quantify, characterise and detect biomolecules and metabolites.
- SM09 (Use the most common bioinformatics algorithms and programs for the manipulation, comparison, annotation and analysis of genes, genomes and proteins.) Use the most common bioinformatics algorithms and programs for the manipulation, comparison, annotation and analysis of genes, genomes and proteins.

Contents

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

Topic 5. Molecular phylogenetic reconstruction. Molecular phylogeny. Phylogenetic inference methods. Molecular Evolution.

Topic 6. Proteins: Sequence Analysis. The sequence-structure-function relationship. Uniprot Database. Domain identification: PFAM DataBase.

Topic 7. Proteins: Structural Analysis. The protein data bank (PDB). Structural alignments. Structure based search of structural Databases.

Learning activities and methodology

Title	Hours	ECTS	Learning outcomes
Lectures	11	0.44	CM07, KM11, KM12, KM13
Individual reading	10	0.4	CM07, KM11, KM12, KM13
Completion of end-of-unit tests	10	0.4	CM08, KM11, KM12, KM13, SM09
Mentoring	4	0.16	KM11, KM12, KM13, SM09
Computer practices	36	1.44	CM08, KM11, KM12, KM13, SM09

Solving problems	30	1.2	CM07, CM08, KM11, KM12, KM13, SM09
Individual study	35	1.4	CM07, CM08, KM11, KM12, KM13, SM09
Literature search	8	0.32	CM07, KM11, KM12, KM13

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.

Lectures

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.

Computer practices

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.

Since attendance at the practical sessions is mandatory, following the evaluation criteria of the Faculty of Biosciences for integrated laboratories, absence from any of the sessions must be justified and may not exceed 20%. If this value is exceeded, the subject will be graded as Not Assessable.

The use of chat or generative AI assistants will not be permitted during practical classes and exams.

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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Assessment

Continuous assessment activities

Title	Weight	Hours	ECTS	Learning outcomes
Problem-solving in groups	20	0	0	CM07, CM08, KM11, KM12, SM09
Midterm exam #2 (theoretical-practical contents)	35	3	0.12	CM07, CM08, KM11, KM12, KM13, SM09
Continuous assessment (End-of-unit tests)	10	0	0	CM07, CM08, KM11, KM12, KM13, SM09
Midterm exam #1 (theoretical-practical contents)	35	3	0.12	CM07, CM08, KM11, KM12, SM09

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.

During the partial assessments, the final retake and/or grade improvement exam and the single assessment,

the use of chat or generative AI assistants will not be permitted.

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

Main assessment activities

Midterm exams (70%)

Activitie 1. Midterm exam 1. Approximately 35%.

Activitie 2. Midterm exam 2. Approximately 35%.

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 35% and the second one 35%.

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 (30%).

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 (10%).

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 a 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.

In case any student needs to retake all the partial exams (1 and 2), he/she will be subject to a single test. This test will cover the entire subject. The grade obtained in this test must be greater than or equal to 4 points to be

averaged with the rest of the assessment activities.

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.

If the midterm exams are not passed, they may be retaken on the date scheduled at the end of the semester. In this case, the maximum possible grade will be 8.8 out of 10.

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 0.35) + (Midterm exam 2 x 0.35) + (Integrative problem x 0.20) + (End-of-unit tests x 0.10)]

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.

Single assessment

For those students who choose the single assessment system, this will consist of a unique written test in which the contents of the entire program of the subject will be assessed. The test may consist of multiple choice questions, short questions and problems to develop. The grade obtained in this synthesis test will account for 80% of the final grade for the subject. The single assessment test will coincide with the date of the last assessment test. As regards the integrative problem (20% of the final mark), the students will work with a team as in the continuous evaluation system, and the delivery of the work will be within the period indicated at the beginning of the subject. For the single assessment option, the same system for retake and review of the final grade and the same criteria to pass as for the continuous assessment system will be applied.

Restricted use of AI by students is permitted. The use of Artificial Intelligence (AI) technologies is permitted for supporting tasks related to the preparation of work deliveries, such as bibliographic, software or information searches, text correction or translation, and image generation. Students must clearly identify which parts have been generated using this technology, specify the tools used, and include a critical reflection on how these tools have influenced the process and the outcome of the activity. Lack of transparency regarding the use of AI in this assessed activity will be considered a breach of academic honesty and may result in a partial or total penalty in the grade for the activity.

IMPORTANT: Any irregularity committed during an assessment activity (such as academic fraud, plagiarism, or

the improper use of AI, unless such use is expressly authorised in the course guide) that may lead to a significant change in the grade will result in that assessment activity being awarded a grade of 0. If the course guide establishes that obtaining a minimum grade in that assessment activity is an essential requirement for passing the course, or if several irregularities occur in assessment activities within the same course, the final grade for the course will be 0. In addition, disciplinary proceedings may be initiated against any student who commits any of these irregularities

Bibliography

- Bishop, Özlem Taştan. (2014). *Bioinformatics and data analysis in microbiology*. (1st ed.)

Caister Academic Press

[Available](#) online

- Christensen, Henrik. (2018). *Introduction to Bioinformatics in Microbiology*. (1st ed.)

Springer International Publishing

[Available](#) online

- Claverie, Jean-Michel & Notredame, Cedric. (2007). *Bioinformatics for Dummies*. (2nd ed.)

Wiley Pub

[Available](#) in print at the library

- Lesk, Arthur M. (2019). *Introduction to Bioinformatics*. (5th ed.)

Oxford University Press

[Available](#) in print at the library

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 & EMBOSS water (web interface): 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)
- 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/>).

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	72	Catalan/Spanish	second semester	morning-mixed
(PLAB) Practical laboratories	721	Catalan/Spanish	second semester	morning-mixed
(PLAB) Practical laboratories	722	Catalan/Spanish	second semester	morning-mixed
(PLAB) Practical laboratories	723	Catalan/Spanish	second semester	morning-mixed