UAB
Universitat Autònoma de Barcelona

Genomics, Proteomics and Interactomics 2026/2027

Code: 100893
Credits: 6

Degree programme	Type	Course
Biochemistry	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

Although no previous formal requirements have been set, basic knowledge is expected on Biochemistry and Molecular biology, Genetics, Microbiology, Cell biology, Methods on recombinant DNA and Statistics.

For certain activities a basic level of understanding for reading english is required.

Objectives

Genomics is the science dealing with the structure, content and evolution of genomes. Is a relatively novel science (we can say that it was born in 1995 with the sequencing of the first bacterial genomes) that developed explosively in the last years. The development of methods for automatic sequencing of nucleic acids has been a key factor about. In 2001 the first draft of the sequence of the human genome was presented, a historic milestone that opened the doors for the studies on comparative genomics and the evolution of the human species, on the biological clues of the human nature, on the genotype-phenotype association studies to find genes or regions of DNA related with diseases, etc.

After the sequencing of genomes appeared the so called "postgenomic" period. Among its tasks are the analyses of genes and genomes expression in a massive way (Transcriptomics and Functional Genomics), the identification and structural-functional analysis of proteins (Proteomics), and of their interactions (and with the other biomolecules) and formation of complexes (interactomics). Together with the identification and quantitation of all the metabolites present in a sample of an organism (Metabolomics), such knowledge provides the basis to try the integration of the whole conjoint and reach a global description of the biology of the cell (Systems biology).

The main formative goals of the subject are : the understanding of the diversity and complexity of genomes and proteomes; the study of the historic and evolutionary character of the genetic information as well as its

nature, the meaning and consequences of the intraspecific and interspecific variability; and finally the potentiality of the applications that come from the genomic, transcriptomic and proteomic information. It is also part of the subject to know the experimental and computational methods that are used in the so-called "omic" sciences.

Learning outcomes

- CM20 (Design experiments that address questions related to genomics, proteomics, interactomics, and other disciplines of systems biology.) Design experiments that address questions related to genomics, proteomics, interactomics, and other disciplines of systems biology.
- CM21 (Make an oral presentation on a topic related to systems biology.) Make an oral presentation on a topic related to systems biology.
- KM24 (Quantitatively illustrate a biological process or system.) Quantitatively illustrate a biological process or system.
- KM25 (Describe the main methods of analysis and prediction used in systems biology.) Describe the main methods of analysis and prediction used in systems biology.
- SM21 (Use digital resources when searching databases, analysing genomic, transcriptomic and proteomic data, and creating models of biological systems.) Use digital resources when searching databases, analysing genomic, transcriptomic and proteomic data, and creating models of biological systems.
- SM22 (Analyse the physical and chemical foundations of the instrumentation and methodology used in the analysis of genomes, transcriptomes, proteomes, etc.) Analyse the physical and chemical foundations of the instrumentation and methodology used in the analysis of genomes, transcriptomes, proteomes, etc.
- SM23 (Examine the molecular processes of living organisms from the perspective of systems biology.) Examine the molecular processes of living organisms from the perspective of systems biology.
- SM24 (Interpret experimental information in the field of systems biology.) Interpret experimental information in the field of systems biology.

Contents

GENOMICS

- Introduction to genomes

- Sequencing, assembly and annotation of genomes

- Study of gene expression: Transcriptomics

- Comparative genomics

- Nucleotide and structural variation

PROTEOMICS AND INTERACTOMICS

- Introduction and Basic Concepts
- Diversity of the Proteome
- Basic Proteomics Techniques
- Quantitative Proteomics
- Structural and Functional Proteomics
- Interactomics

Learning activities and methodology

Title	Hours	ECTS	Learning outcomes
Seminars and problems	16	0.64	CM20, CM21, KM24, KM25, SM21, SM22, SM23, SM24
Study	41	1.64	CM20, KM24, KM25, SM21, SM22, SM23, SM24
Recommended readings and solving problems	40	1.6	CM20, CM21, KM24, KM25, SM21, SM22, SM23, SM24
Theory classes	29	1.16	CM20, KM24, KM25, SM22, SM23
Individual tutorials	3	0.12	

The subject consists of theory classes, seminars for the resolution of practical cases and problems and

tutorials. The following describes the organization and teaching methodology that will be followed in these three types of training activities.

Theory classes:

The contents of the theory program will be taught mainly by the teacher in the form of masterclasses with audiovisual support. Presentations used in class by the teacher will be previously available on the Virtual Campus of the subject. It is recommended that students print this material and take it to class, to use it as support when taking notes. It is advised that students regularly consult the recommended books in the Bibliography section of this teaching guide to consolidate and clarify, if necessary, the contents explained in class.

Seminars and problem classes:

The mission of seminars and problem classes is to bridge between masterclasses and practical work, promoting active learning to develop the ability to analyze and synthesize, critical reasoning, and problem-solving ability. Seminars and problem classes are sessions with a small number of students (maximum 30 students). Its mission is to deepen or complete the knowledge presented in the masterclasses by solving problems and discussing case studies. Students will receive periodic readings recommended, problems and cases to solve, web addresses to consult, etc.

15 minutes of a class will be dedicated to answer the institutional surveys of the UAB

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
Seminars and problems	30	12	0.48	CM20, CM21, KM24, KM25, SM21, SM22, SM23, SM24
Exams	70	9	0.36	CM20, KM24, KM25, SM22, SM23, SM24

Continued evaluation:

The evaluation of the subject will be carried out through a series of continued evaluation activities, a partial exam, and a retake exam, corresponding to each of the two parts of the subject: Genomics and Proteomics/Interactomics. The weight of each part of the subject will be 50% of the final grade. The following details the weight of the different tests and activities corresponding to each of the two parts of the subject:

Genomics 50%: 70% exam + 30% problems-seminars.

Proteomics 50%: 70% exam + 30% problems-seminars.

The partial exams will consist of multiple-choice or short-answer questions or problems. These tests will be eliminatory of matter.

Only those grades that are >=4.0 will be averaged. Students who have obtained a mark of less than 4.0 (out of 10) in the previous exam of one or both of the partials will have to take the recovery exam for the corresponding partial(s) (first partial, second partial, or both).

- To participate in the retake exam, students must have been previously evaluated in a set of activities whose weight is equivalent to a minimum of two-thirds of the total grade for the subject or module. Therefore, the student will obtain the qualification of \"Not Evaluable\" when the evaluation activities carried out have a weighting of less than 67% in the final qualification.

- The students who fail the continued evaluation of the part corresponding to problems and seminars will have the opportunity to make the recovery on the day of the final test.

The final test will also be open to any student who, having passed the partial tests, wishes to improve the mark obtained in one or both partial tests. In this case, the student must notify the corresponding teachers of her interest in taking the final grade improvement test and will renounce the previous grade.

Students who cannot attend an individual evaluation test for justified reasons (such as illness, death of a first-degree relative, or accident) and provide the corresponding official documentation, will have the right to take the test in question on another date.

The course is considered passed if the overall final grade is >=5.0.

At the beginning of the classes of each part of the subject, the corresponding professor will detail how the problems-seminars and the integrating exercise (in the case of the Genomics part) will be evaluated.

Unique evaluation:

There will be an Exam that will include multiple choice or short answer questions or problems from both the genomics and proteomics parts. The grade obtained in this test will account for 70% of the final grade for the subject, half corresponding to the genomics part and the remaining half corresponding to the proteomics part.

The delivery of the activities carried out during the course will follow the same procedure and calendar as in the continued evaluation. Depending on the teacher, they can be individual or group work to be delivered in print, through the virtual campus, or through presentations in the classroom. The delivery will follow the same procedure and calendar as in the continued evaluation. The grade corresponding to this part of classroom practices will mean a final 30%.

For this course, the use of Artificial Intelligence (AI) technologies is permitted exclusively for support tasks such as literature or information searches, text correction, or translations. The student must clearly identify which parts have been generated using such technology, specify the tools used, and include a critical reflection on how these tools have influenced both the process and the final outcome of the activity. Lack of transparency regarding the use of AI in this assessed activity will be considered academic dishonesty and may result in partial or total penalization of the activity's grade, or more severe sanctions in serious cases.

Any irregularity committed during an assessment activity (academic misconduct, plagiarism, or improper use of AI, unless such use is expressly authorized in the course syllabus) that may lead to a significant alteration of the grade will result in that activity being graded as 0. If the course syllabus stipulates that obtaining a minimum mark in this assessment is an essential requirement to pass the course, or if multiple irregularities occur in the assessment activities of the same course, the final grade for the course will be 0. Furthermore, disciplinary proceedings may be initiated against any student who incurs any of these irregularities.

Bibliography

Books:

- Gibson, G. & S. V. Muse, 2009 (3rd edition). A Primer of Genome Science. Sinauer, Massachusetts. USA.

- Brown, T. A., 2017 (4th edition). Genomes 4. Garland Science, UK.

- Lesk, A.M. 2017. Introduction to genomics (3rd edition). Oxford University Press, Oxford, UK.

- Twyman R. M., 2014 (2n edition). Principles of Proteomics. Garland Science, New York & London.

- Lovric J., 2011. Introducing Proteomics. Ed. John Wiley & Sons, Oxford, UK.

Links:

- Campus Virtual de la UAB: https://cv2008.uab.cat/

- Entrez Genome Database: http://www.ncbi.nlm.nih.gov/sites/genome

- Expasy Proteomics Server: http://expasy.org/sprot

Software

None

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	33	Catalan/Spanish	second semester	morning-mixed
(PAUL) Classroom practices	331	Catalan/Spanish	second semester	morning-mixed
(PAUL) Classroom practices	332	Catalan/Spanish	second semester	morning-mixed