

**Genomics, Proteomics and Interactomics**

Code: 100947  
ECTS Credits: 6

| Degree                | Type | Year | Semester |
|-----------------------|------|------|----------|
| 2500253 Biotechnology | OB   | 3    | 1        |

**Contact**

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**Use of Languages**

Principal working language: spanish (spa)  
Some groups entirely in English: No  
Some groups entirely in Catalan: No  
Some groups entirely in Spanish: No

**Teachers**

Marta Puig Font

**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 english reading comprehension ability is required.

**Objectives and Contextualisation**

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.

## Competences

- Design continuation experiments for problem solving.
- Learn new knowledge and techniques autonomously.
- Read specialised texts both in English and one's own language.
- Search for, obtain and interpret information from the principal databases on biology, bibliography and patents and use basic bioinformatic tools.
- Think in an integrated manner and approach problems from different perspectives.
- Use the fundamental principles of mathematics, physics and chemistry to understand, develop and evaluate a biotechnological process.
- Work individually and in teams

## Learning Outcomes

1. Describe the physical and chemical principles behind the methodology and instrumentation used in genomic analysis, transcriptomic analysis, proteomic analysis, interactomic analysis, metabolomic analysis, and metabonomic analysis.
2. Design continuation experiments for problem solving.
3. Learn new knowledge and techniques autonomously.
4. Model a biological process or system and represent it quantitatively.
5. Obtain, interpret and use the information obtained from experiments in genomics, transcriptomics, proteomics, interactomics, metabolomics, metabonomics, etc.
6. Read specialised texts both in English and one's own language.
7. Think in an integrated manner and approach problems from different perspectives.
8. Work individually and in teams

## Content

### GENOMICS

Introduction to genomes

Sequencing, assembly and annotation of genomes

Study of gene expression: Transcriptomics

Genome evolution: Comparative genomics

Genomic variation

### PROTEOMICS AND INTERACTOMICS

Introduction and basic concepts

Proteome diversity

Experimental methods in proteomics

Quantitative proteomics

Structural and functional proteomics

Interactomics

## Methodology

The subject consists of theoretical classes, seminars for the resolution of practical cases and scientific articles, problems and tutoring sessions. The following describes the organization and the teaching methodology that will be followed in these three types of training activities.

### Theory:

The content of the theory program will be taught mainly by the teacher in the form of master classes 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 a support when taking notes. It is recommended that students regularly consult the books recommended in the Bibliography section of this teaching guide in order to consolidate and clarify, if necessary, the contents explained in class.

### Seminars and problems:

The objective of the seminars and the problem sessions is to connect theory sessions with practical work, promoting active learning to develop the ability to analyze and synthesize, critical reasoning, and problem-solving ability. The seminars and problems are sessions with a small number of students (maximum 40 students). Their goal is to deepen or complete the knowledge exposed in the theory sessions by solving problems, discussing case studies and scientific literature. Students will receive periodic readings recommended in English, problems and cases to solve, web addresses to consult, bioinformatics tools, etc.

### Tutoring:

There will be up to 3 tutoring sessions in small group with the teacher. In these sessions the doubts raised by the students about the theoretical program topics will be resolved, and they will facilitate the comprehension of specific aspects of the subject.

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.

## Activities

| Title                            | Hours | ECTS | Learning Outcomes |
|----------------------------------|-------|------|-------------------|
| Type: Directed                   |       |      |                   |
| Seminars and Problems            | 12    | 0.48 | 3, 2, 6, 5, 7, 8  |
| Theory sessions                  | 32    | 1.28 | 3, 2, 6, 5, 7     |
| Type: Supervised                 |       |      |                   |
| Tutoring                         | 3     | 0.12 | 3, 2, 6, 5, 7     |
| Type: Autonomous                 |       |      |                   |
| Recommended reading and problems | 40    | 1.6  | 3, 2, 6, 5, 7, 8  |
| Study                            | 42    | 1.68 | 3, 2, 6, 5, 7, 8  |

## Assessment

The evaluation of the subject will be carried out through a series of activities of continuous assessment, a partial exam and a review of recovery, corresponding to each of the two parts of the subject: Genomics and Proteomics / Interactomics. The weight of each part of the subject is 50% on the final grade. When beginning

the classes of each part of the subject, the corresponding professor will detail how he will carry out the continuous evaluation. Below is the weight of the different tests and activities:

- Genomic Partial test 35%
- Proteomic Partial test 35%
- Genomics problems 10%
- Proteomics seminars 10%
- Joint project 10%

The partial exams will consist of questions of type test and of short answer or problems. These tests will be eliminatory of matter.

The joint project consists of a joint assignment where knowledge and tools corresponding to both parts of the subject must be applied to solve the proposed exercises.

It will only be average with those qualifications that are  $\geq 4.0$ .

#### Retake exam

Those students who do not exceed the minimum qualification of one or both partial tests must present themselves to the retake exam, if they meet the following requirement: To participate in the recovery, the students must have been previously evaluated in a set of activities whose weight equals to a minimum of two thirds of the total grade of the subject or module. Therefore, students will obtain the "Non-Valuable" qualification when the assessment activities carried out have a weighting of less than 67% in the final grade.

#### Grade improvement

The retake exam will also be open to any student who, having passed the partial tests, wishes to improve the score obtained in one or both partial tests. In this case, the student will have to notify the corresponding professors of their interest in presenting themselves to the retake exam and will have to renounce the grade previously obtained. The degree of difficulty of the test grade improvement may be higher than the partial assessments.

#### Qualification

The subject is considered approved if the final grade is equal or greater than 5.0 points.

For the purposes of qualification, the student will be considered as non-evaluable when the assessment activities carried out have a weighting of less than 67% in the final grade.

### Assessment Activities

| Title                 | Weighting | Hours | ECTS | Learning Outcomes      |
|-----------------------|-----------|-------|------|------------------------|
| Joint project         | 10%       | 2.5   | 0.1  | 3, 1, 2, 6, 4, 5, 7, 8 |
| Partial test 1        | 35%       | 7.5   | 0.3  | 1, 2, 5, 7, 8          |
| Partial test 2        | 35%       | 7.5   | 0.3  | 3, 1, 2, 6, 5, 7, 8    |
| Seminars and Problems | 20%       | 3.5   | 0.14 | 3, 2, 6, 4, 5, 7, 8    |

### Bibliography

#### Textbooks:

- Gibson, G. & S. V. Muse, 2009 (3rd edition). A Primer of Genome Science. Sinauer, Massachusetts. USA.
- Brown, T. A. 2017. Genomes 4 (4<sup>th</sup> edition). Garland Science, New York, USA.
- Lesk, A.M. 2017. Introduction to genomics (3<sup>rd</sup> 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.
- Mirzaei, Hamid, Carrasco, Martin (Eds.) Modern Proteomics - Sample Preparation, Analysis and Practical Applications. Springer. 2016. Available in digital format

#### 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

Databases and analysis tools used in this subject are listed below:

#### Databases:

- Animal Genome Size Database, <http://www.genomesize.com/>
- Ensembl Genome Browser, <http://www.ensembl.org>
- Flybase JBrowse, <http://flybase.org/jbrowse/?data=data/json/dmel>
- GOLD Genomes Online Database, <https://gold.jgi.doe.gov/>
- NCBI Genome, <http://www.ncbi.nlm.nih.gov/genome>
- PopHuman Genome Browser, <https://pophuman.uab.cat>
- UCSC Genome Browser, <http://genome.ucsc.edu/cgi-bin/hgGateway>
- Genome Reference Consortium, <https://www.ncbi.nlm.nih.gov/grc/human>
- RepeatMasker, <http://www.repeatmasker.org/genomicDatasets/RMGenomicDatasets.html>
- BioGPS, <http://biogps.org/>
- ENCODE, <http://genome.ucsc.edu/ENCODE/>
- Expression Atlas, <https://www.ebi.ac.uk/gxa/home>
- GENCODE Human, <https://www.gencodegenes.org/human/>
- InterMine, <http://intermine.org/>
- RevTrans, <http://www.cbs.dtu.dk/services/RevTrans-2.0/web/>
- Synteny Portal, [http://bioinfo.konkuk.ac.kr/synteny\\_portal/](http://bioinfo.konkuk.ac.kr/synteny_portal/)
- VISTA Genome Browser, <http://genome.lbl.gov/vista/index.shtml>
- International Cancer Genome Consortium, <https://icgc.org/>
- Open Targets, <https://www.targetvalidation.org/>
- The Cancer Genome Atlas, <https://www.cancer.gov/about-nci/organization/ccg/research/structural-genomics/tcga>
- Human protein Atlas, <https://www.proteinatlas.org/>
- Human proteome map, <http://www.humanproteomemap.org/>
- Uniprot, <https://www.uniprot.org/>
- SWISS-2D, <https://world-2dpage.expasy.org/swiss-2dpage/>
- Phosphosite, <http://www.phosphosite.org/>
- String, <https://string-db.org/>

#### Analysis tools:

- ScanProsite, <http://prosite.expasy.org/scanprosite/>
- Transeq, [http://www.ebi.ac.uk/Tools/st/emboss\\_transeq/](http://www.ebi.ac.uk/Tools/st/emboss_transeq/)
- GeneID, <http://genome.crg.es/geneid.html>
- MASCOT <http://www.matrixscience.com/>
- Protparam <https://web.expasy.org/protparam/>
- Swissmodel <https://swissmodel.expasy.org/>
- Provean <http://provean.jcvi.org/index.php>
- INPS-server <https://inpsmd.biocomp.unibo.it/inpsSuite>