

Genomics

Code: 42399

ECTS Credits: 12

2025/2026

Degree	Type	Year
Bioinformatics	OT	0

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Teaching groups languages

You can view this information at the [end](#) of this document.

Prerequisites

To carry out this module is necessary to have passed previously both compulsory modules: Programming in Bioinformatics and Core Bioinformatics. Basic notions in genetics are also needed.

It is recommended you have a Level B2 of English or equivalent.

Objectives and Contextualisation

The technological capacity to generate massive genomic and multiomics data grows at a relentless pace without a parallel growth of the bioinformatics expertise to deal with the integration of molecular data.

The purpose of this module is to provide the knowledge and technical skills which are required to successfully meet the current challenges of genomic and multiomics analyses.

Competences

- Analyse and interpret data deriving from omic technology using biocomputing methods .
- Communicate research results clearly and effectively in English.
- Design and apply scientific methodology in resolving problems.
- Identify the biocomputing needs of research centres and companies in the biotechnology and biomedicine sectors.
- Possess and understand knowledge that provides a basis or opportunity for originality in the development and/or application of ideas, often in a research context.
- Propose biocomputing solutions for problems deriving from omic research.
- Propose innovative and creative solutions in the field of study
- Understand the molecular bases and most common standard experimental techniques in omic research (genomics, transcriptomics, proteomics, metabolomics, interactomics, etc.)
- Use and manage bibliographical information and computer resources in the area of study
- Use operating systems, programs and tools in common use in biocomputing and be able to manage high performance computing platforms, programming languages and biocomputing analysis.

Learning Outcomes

1. Communicate research results clearly and effectively in English.
2. Describe and apply the tools of assembly, annotation, storage, display and analysis of the variation in genomes.
3. Describe the operation, characteristics and limitations of first, second and third generation sequencing techniques.
4. Design and apply scientific methodology in resolving problems.
5. Design and interpret studies of association between genetic polymorphisms and phenotype for identifying genetic variants affecting phenotype characters, including those associated pathologies and that confer susceptibility to human diseases or other species of interest.
6. Enumerate and describe the content of databases of relevant information for the different areas of genomics and carry out advanced searches.
7. Establish the corresponding relationships between nucleotide sequencing, structure and gene function using sources of biological data and the bases of biocomputing analysis.
8. Identify and characterize sources and display formats genomes, along with your notes and information about genetic variation, disease association and gene expression.
9. Integrating genomic data in silico reconstruction of cells and organisms (systems biology, synthetic biology).
10. Possess and understand knowledge that provides a basis or opportunity for originality in the development and/or application of ideas, often in a research context.
11. Propose innovative and creative solutions in the field of study
12. Recognise the strategic importance of genetic advances in the area of human health, especially the genomic applications in personalised medicine and pharmacogenomics.
13. Use and manage bibliographical information and computer resources in the area of study
14. Use the latest algorithms of alignment of sequences and generation of evolutive trees as well as sequencing methods and gene prediction.

Content

Lesson 1. Introduction: Genomes and Omics Data

Lesson 2. Making Sense of Genome Data

- 2.1 Genome Assembly
- 2.2 Genome Annotation
- 2.3 Functional Analysis

Lesson 3. Genome Visualization

Lesson 4. Genome Variation

- 4.1 Theory
- 4.2 Data

Lesson 5. Association Studies and GWA

Lesson 6. Transcriptomics

- 6.1 Microarrays
- 6.2 RNAseq

Lesson 7. Systems Genetics: Integrating Omics Data

Lesson 8. Artificial Intelligence and Machine Learning in Genomics

Lesson 9. Epigenomics

Lesson 10. Metagenomics

Student Seminar Session

Module Assessment Exam

Closing Lecture

Activities and Methodology

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Seminars	4	0.16	
Solving problems in class and work in the computing lab	28	1.12	
Theoretical-Practical classes	37	1.48	
Type: Supervised			
Performing individual and team works	120	4.8	
Type: Autonomous			
Regular study	107	4.28	

The methodology combines master classes, solving practical problems and real cases, work in the computing lab, performing individual and team works, readings and discussing papers related to the thematic blocks. As ICT resource we will use the virtual teaching platform of the master.

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

Continous Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Individual theoretical and practical test	45%	4	0.16	1, 3, 2, 4, 5, 6, 7, 8, 9, 11, 12, 10, 14, 13
Soft skills (assistance, arrival on time and active participation in class)	10%	0	0	1, 4, 11, 10, 13
Student's portfolio	45%	0	0	1, 3, 2, 4, 5, 6, 7, 8, 9, 11, 12, 10, 14, 13

The evaluation system is organized in three main activities. There will be, in addition, a retake exam. The details of the activities are:

Main evaluation activities

- Student's portfolio (45%): Work done and presented by the student.
- Individual theoretical and practical tests (45%)
- Soft skills (10%): assistance, arrival on time and proactive participation in class.

Retake exam

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 module. The teacher will inform the procedure and deadlines for the retake process. Please note that soft skills cannot be recuperated.

Not valuable

The student will be graded as "Not Valuable" if the weight of the evaluation is less than 67% of the final score.

Unique assessment

Students who take advantage of the unique evaluation will take a single synthesis test in which the contents of the entire theory program of the subject will be evaluated. The test will consist of theoretical questions and problems and will take place coinciding with the same date set in the calendar for the last continuous assessment exam.

The same evaluation system will be applied as for the continuous evaluation. The grade obtained in this synthesis test will account for 40% of the final grade for the subject.

Seminars and problems (portfolio) are evaluated in the same way and dates as in the continuous assessment. The grade obtained will mean 60% of the final grade for the course.

Use of AI

In this course, the use of Artificial Intelligence (AI) technologies is permitted as an integral part of the assignment, provided that the final result reflects a significant contribution by the student to personal analysis and reflection.

Students must clearly identify which parts were generated with this technology, specify the tools used, and include a critical reflection on how they influenced the process and final outcome of the assignment. Lack of transparency in the use of AI will be considered a breach of academic honesty and will result in a penalty on the assignment grade, or greater penalties in serious cases.

Bibliography

Basic references

- Archibald, J. M. 2018. Genomics: A Very Short Introduction. The *Very Short Introductions* series from Oxford University Press.
- Brown, T. A. 2018. Genomes. 4r edition. Garland Science
- Mäkinen, V.; Belazzougui, D.; Cunial, F. and Tomescu, A.I. 2023. Genome-Scale Algorithm Design: Bioinformatics in the Era of High-Throughput Sequencing. 2nd edition. Cambridge University Press.
- Compeau, P and P. Pevzner. 2015. Bioinformatics Algorithms Volume 1 and 2. 2n edition. Active Learning Publishers LLC
- Gibson, G. and S. V. Muse, 2009. A Primer of Genome Science. Sinauer, Massachusetts. 3rd edition.
- Barnes, M. 2007. Bioinformatics for geneticists (2nd Ed.) Wiley.
- Brown, T. A. 2018. Genomes. 4th edition. Taylor & Francis Inc.
- Lesk, M. K. 2017. Introduction to Genomics. 3rd edition. Oxford Univ. Press.
- MacLean, Dan 2023. R Bioinformatics Cookbook: Utilize R packages for bioinformatics, genomics, data science, and machine learning. Packt Publishing.
- Makinen, V.; A. Belazzougui, F. Cunial, A.I. Tomescu. 2105. Genome-Scale Algorithm Design: Biological Sequence Analysis in the Era of High-Throughput Sequencing. Cambridge Univ Press.
- Marshall, Christina 2019. Bioinformatics and Functional Genomics. Callisto Reference
- Pevnser, J. 2009. Bioinformatics and Functional Genomics (2nd edition). Wiley-Blackwell.
- Pevzner, P. and R. Shamir. 2011. Bioinformatics for Biologists. Cambridge University Press
- Samuelsson, T. 2012. Genomics and Bioinformatics: An Introduction to Programming Tools for Life Scientists. Cambridge University Press.
- Exhaustive Bioinformatics Books List
(<https://www.iscb.org/iscb-publications-bioinformatics-review/35-ISCB%20Publications/ISCB%20Publications>)
- Genomics articles from across Nature Portfolio (<https://www.nature.com/subjects/genomics>)

Recomended Websites

- Course: Gurrent topics in Genome Analysis 2016. NHGRI (<http://www.genome.gov/12514288>)
- National Human Genome Research Institute (USA) (<http://www.genome.gov/>)
- Genomic careers (http://www.genome.gov/genomicCareers/video_find.cfm)
- 1000 genomes project (<http://www.internationalgenome.org/>)
- PopHuman database (<http://pophuman.uab.es>)
- PopLife database (<https://poplife.pic.es/>)
- Genomeonline databases (GOLD) (<https://gold.jgi.doe.gov/>)
- Genome data viewer NCBI (<https://www.ncbi.nlm.nih.gov/genome/gdv/>)
- Ensembl genome browser (<http://www.ensembl.org>)
- UCSC genomebrowser (<http://genome.ucsc.edu/>)
- Genome size databases (<http://www.genomesize.com/>)
- Bioinformatics Barcelona (<https://bioinformaticsbarcelona.eu/es/>)
- Course: Gurrent topics in Genome Analysis 2016. NHGRI (<http://www.genome.gov/12514288>)
- International Society for Computational Biology (<https://www.iscb.org/>)

Software

Software to be used through the module

- R <https://cran.r-project.org/>
- Rstudio <https://www.rstudio.com/products/rstudio/>
- Fastqc <https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>
- bwa <http://bio-bwa.sourceforge.net/>
- vcftools <https://github.com/vcftools/vcftools/zipball/master>
- bedtools <https://bedtools.readthedocs.io/en/latest/>
- GATK <https://software.broadinstitute.org/gatk/>
- IGV <https://software.broadinstitute.org/software/igv/>
- JBrowse <https://jbrowse.org/jb2/>

Groups and Languages

Please note that this information is provisional until 30 November 2025. You can check it through this [link](#). To consult the language you will need to enter the CODE of the subject.

Name	Group	Language	Semester	Turn
(PLABm) Practical laboratories (master)	1	English	first semester	morning-mixed
(SEmm) Seminars (master)	1	English	first semester	morning-mixed
(TEM) Theory (master)	1	English	first semester	morning-mixed