


	<b>PROCESO PARA EL DESARROLLO DE LAS ENSEÑANZAS DE LA FACULTAD DE CIENCIAS DE LA UEx</b>		 <b>FACULTAD DE CIENCIAS</b> <small>(UEx)</small>
	<b>Curso académico:</b> 2024-25	<b>Código:</b> P/CL009_FC_D002	

### COURSE PROGRAM

Identification and characteristics of the course			
Code	502682	ECTS Credits	6
Course name (English)	<b>Genomics and Bioinformatics</b>		
Course name (Spanish)	Genómica y Bioinformática		
Degree programs	Biotechnology		
Faculty/School	Faculty of Sciences		
Semester	5 <sup>º</sup>	Type of course	Mandatory
Module	Fundamental Biology		
Matter	Genetics		
Lecturer/s			
Name	Office	E-mail	Web page
Francisco Javier Martín Romero	1L5 (University Research Institutes)	<a href="mailto:fimartin@unex.es">fimartin@unex.es</a>	
Felipe Roberto Molina Rodríguez	DG2 (Margarita Salas Bldg)	<a href="mailto:fmolina@unex.es">fmolina@unex.es</a>	
Subject Area	Biochemistry and Molecular Biology / Genetics		
Department	Biochemistry and Molecular Biology and Genetics		
Coordinating Lecturer (If more than one)	Francisco Javier Martín Romero		
Competencies*			
<p>1. Basic Competencies</p> <p>CB1: Students should be able to show that they know and understand facts and contents in a field of study which, based on a previous general secondary school level, have been extended to those included in advanced textbooks and, in some aspects, come from the front line of their field of study.</p> <p>CB2: Students should be able to apply their knowledge professionally in their future jobs or tasks and should have the competencies to develop and defend arguments and solve problems in their field of study.</p> <p>CB3: Students should be able to collect and interpret relevant data (typically within their field of study) to give an educated opinion about relevant social, scientific or ethical issues.</p> <p>CB4: Students should be able to communicate information, ideas, problems and solutions to both specialized and non-specialized audiences.</p>			

\* The sections concerning competencies, course outline, educational activities, teaching methodologies, learning outcomes and assessment systems must conform to that included in the ANECA verified document of the degree program.

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CB5: Students should develop the learning skills required to undertake further studies with a high degree of independence

#### 2. General competencies

CG1: Ability to take advantage of postgraduate courses that specifically empower students to work in teaching, research, or professional fields.

CG2: Ability to autonomously generate, acquire and process information related to Biotechnology.

CG3: Ability to plan, execute and criticize knowledge processes in the field of student activity.

CG4: Ability to apply basic science and technology knowledge to biological and health systems.

CG5: Ability to identify, formulate and solve problems within broad and multidisciplinary contexts, through the integration of knowledge and participation in multidisciplinary teams.

CG6: Ability to analyse and assess the social and environmental impact of technical solutions, understanding ethical and professional responsibility in the field of Biotechnology.

CG7: Ability to solve problems with initiative, decision making, autonomy and creativity.

CG8: Ability to transfer theoretical learning to a practical context.

CG9: Ability to self-evaluate in order to become aware of the need to keep knowledge, skills and attitudes up to date through a continuous training process.

#### 3. Transversal competencies

CT1: To apply the acquired knowledge on the Grade on their job performance in a right and professional way, and to develop with confidence in the lab.

CT2: To use and apply Information and Communications technologies (ICTs) on training and professional field.

CT3: To know and understand the information in advanced textbooks and to have access to the knowledge coming from the front line of their field of study.

CT4: To develop the learning, organization and planning skills, necessary both to continue with further studies with a high degree of independence and to perform professionally.

CT5: To interpret, analyse and synthesize relevant data and information that will enable the student to develop ideas, solve problems and give critical arguments about important social, scientific or ethical issues.

CT6: To transmit effectively results and conclusions to specialized and non-specialized audiences.

CT7: To express oneself correctly orally and in writing in the native language, as well as master a foreign language, preferably in English.

CT8: To lead or work on a team positively adapting to different contexts or situations.



CT9: To respect the fundamental rights and equality of men and women, and to acquire an ethic compromise of respect to life and natural environment.

#### 4. Specific competencies

CE4: To understand the principles that determine the structure of biological macromolecules (including proteins and nucleic acids), as well as biological supramolecular complexes, and be able to explain the relationships between structure and function.

CE7: To understand and know the structure and organization of hereditary material, genomes, and the genetic code, as well as the mechanisms of maintenance, expression and evolution of genomes.

CE8: To understand the main physiological processes of multicellular organisms, their regulation and integration, as well as the molecular bases of these processes.

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CE10: To have an interconnected knowledge of cellular functioning (including metabolism and gene expression), from its regulation to the relationship between different cellular compartments.

CE12: To be aware of the main current problems and future challenges of Biosciences, as well as the ethical and social implications of the practical applications of Biosciences in health and biotechnology sectors.

CE14: To know the techniques and methodologies of recombinant DNA to design genetic engineering strategies.

CE15: To have quantitative skills for experimentation in Biosciences, including the ability to prepare reagents for experiments in an exact and reproducible way.

CE16: To be able to work properly using biological and chemical material, including safety, handling, disposal of biological and chemical waste, and annotated record of activities.

CE17: To know how to apply experimental laboratory protocols in the field of Biosciences.

CE18: To have mathematical, statistical and computer skills in order to obtain, analyse and interpret data, and to understand simple models of biological systems and processes at the cellular and molecular level.

CE19: To be able to find, obtain, analyse and interpret the information from the main biological and bibliographic databases using bioinformatics tools.

CE20: To acquire the ability to transmit information in the field of Biosciences, including mastering specific terminology.

CE21: To comprehensive understand and know the diversity of living organisms, regarding their different levels of organization.

CE23. To understand and know the fundamentals and applications of genetic manipulation of microorganisms, higher cells, animals and plants.

CE24: To acquire the knowledge of usual experimental and computer techniques in Biosciences and know how to interpret the information they provide.

CE26: To identify the possibilities of biotechnological transfer from basic experimentation.

CE27: To assess the socio-economic impact and bioethical implications of biotechnological processes.

CE29: To know and understand the biotechnological aspects of the biochemical, pharmaceutical, food and environmental industries, as well as in biomedicine, animal and plant production.

CE30: To know the main fields of greatest biotechnological demand.

CE31: To be able to develop technical and scientific skills in the context of a research laboratory or a company.



CE36: To identify emerging technologies and evaluate their possible impact on current bioprocesses.

CE39: To know and understand the genomic organization of living organisms, the transmission of genes to offspring, the mechanisms of character inheritance and their variations, and analyse the genetic structure of populations and their dynamics

### Contents

#### Course outline\*

The course comprises a set of topics to be developed in the classroom (large group), as well as practical classes in a computer room with internet connection. Different activities will be developed as an introduction to Bioinformatics and its applications in studies of structure,

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function and biological systems, databases and formats of DNA and protein sequences, sequence search algorithms, pairwise and multiple alignment, introduction to genomic and phylogenetic analysis, protein secondary and tertiary structure prediction, RNA folding prediction, genome annotation, gene prediction, gene and protein classification, functional genomics: "omics" techniques and their integration into networks, as well as an introduction to quantitative modeling of biological function systems.

#### Course syllabus

Name of lesson 1: **Databases of interest in Biotechnology: nucleotides.**

Contents of lesson 1: NCBI platform: Nucleotide sequence search: Nucleotide (GenBank) and Gene databases: characteristics and limitations. Sequence annotation and accession numbers. Genome databases (Entrez Genome). Genome browsers: ENSEMBL.

Description of the practical activities of lesson 1: Interactive introduction to NCBI Gene, Nucleotide, Genomes. Sequence search.

Name of lesson 2: **Databases of interest in Biotechnology: proteins.**

Contents of lesson 2: From the gene to the functional protein. Protein databases: Entrez Protein and UniprotKB/Swiss-Prot. Databases for metabolic pathways: KEGG. Databases for post-translational modifications (PTMs): Phosphosite.

Description of the practical activities of lesson 2: Interactive introduction to NCBI Protein, Uniprot and Phosphosite.

Name of lesson 3: **Tools for working with simple DNA sequences**

Contents of lesson 3: Cleaning of contaminating DNA sequences. Prediction in enzymatic digestion of sequences. Localization of ORFs. Design of PCR primers.

Description of the practical activities of lesson 3: Sequence analysis. Webcutter and PCR primer design.

Name of lesson 4: **Similarity and principles of sequence alignment**

Contents of lesson 4: Identity, conservation, similarity and homology. Safety zones and penumbra. Types of homology. Types of sequence alignments. Point arrays. Data screening and domain identification. Matrices and gap penalty systems. Dynamic programming and heuristic algorithms. Multiple and whole genome alignments.

Description of the practical activities of lesson 4: There are no practical activities in lesson 4.

Name of lesson 5: **Tools for sequence search and comparison.**

Contents of lesson 5: BLAST, BLAST-p, BLAST-n. Execution of searches, advanced parameters, and interpretation of results. Other possibilities: blastx, tblastn, tblastx. PSI-BLAST. E-value: interpretation.

Description of the practical activities of lesson 5: Sequence search and alignment with BLASTn, CLUSTAL Omega and related tools.



Name of lesson 6: **Multiple sequence alignments.**

Contents of lesson 6: Progressive alignments. BLAST, Clustal, Muscle, T-Coffee, M-Coffee, Expresso. Editing and preparation of MSA for publication: Jalview, Boxshade and LOGO-graph.

Description of the practical activities of lesson 6: Sequence search and comparison with BLASTn, CLUSTAL Omega and related tools.

Name of lesson 7: **Structure and dynamics of genomes.**

Contents of lesson 7: Genomes and somatic processing. Genomes vs other 'omes. Mitochondrial genome: gene migration between genomes and genetic ballast in males. Paradoxes and genome size, C and G value. Diversity vs. divergence. Allelic vs. nucleotide diversity. Adaptive landscapes. Genetic creep, selective sweep and its detection in the genome:

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haplotype length and abundance. Evolution of mutation rates. Mutational robustness. McDonald-Kreitman selection test. Molecular clocks. Substitution and saturation. Sequence evolution models.

Description of the practical activities of lesson 7: There are no practical activities in lesson 7.

Name of lesson 8: **Networks and trees**

Contents of lesson 8: Networks, nodes and regulatory circuits. Types of biological networks. Interactome. Trees and topology of networks. Robustness and hysteresis. Anticipative control circuits. Modularity, coherence and incoherence. Phylogeny reconstruction methods.

Description of the practical activities of lesson 8: There are no practical activities in lesson 8.

Name of lesson 9: **Molecular phylogeny.**

Contents of lesson 9: Nomenclature in molecular phylogeny. Construction of phylogenetic trees. Evaluation of the quality of phylogenetic trees.

Description of the practical activities of lesson 9: Making phylogenetic trees with practical examples.

Name of lesson 10: **Tools for working with protein sequences.**

Contents of lesson 10: In silico biochemistry. Prediction in enzymatic digestion of sequences. Analysis and prediction of peptide/protein properties: transmembrane domains, patterns and profiles. Protein domain databases. Protein DataBank. Visualization and modification of PDB files. Molecular modeling with Swiss-Model.

Description of the practical activities of lesson 10: Work with ExPasy, Uniprot, BLASTp. Identification of domains in case studies.

Name of lesson 11: Databases for gene expression studies

Contents of lesson 11: ESTs and messenger RNA. Microarrays as a tool: advantages and disadvantages. Types of microarrays. Design, probe preparation, image and data analysis, and biological confirmation. Databases: Gene Expression Omnibus (GEO): retrieval of experimental data. Analysis with GEO2R. Digital Differential Display.

Description of the practical activities of lesson 11: GEO. Data acquisition and analysis of gene expression results with Gene Expression Omnibus.

Name of lesson 12: **Human genome**



Contents of lesson 12: Human Genome Project: initial strategies. Human chromosomes. Disease categories. Disease databases: OMIM. Variations: SNPS. SNP and disease databases: dbSNP and ENSEMBL.

Description of the practical activities of lesson 12: OMIM. Localization and nature of mutations related to monogenic diseases and complex genomic diseases.

Problems: From bench to the clinic. Identification of new protein functions through bioinformatics prediction, identification of molecular interactors through proteomic assays and genomic editing for application in the treatment of monogenic diseases.

**Educational activities**

Student workload in hours by lesson		Lectures	Practical activities				Monitoring activity	Homework
Lesson	Total	L	HI	LAB	COM	SEM	SGT	PS
1	11	3		1				7
2	12	4		1				7
3	12	4		1				7
4	10	3						7
5	14	4		2				8

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6	13	4		1			8
7	10	3					7
8	10	2					7
9	14	4		2			8
10	16	4		2			8
11	13	4		1			8
12	13	4		2	2		8
<b>Assessment **</b>	2	2					
<b>TOTAL</b>	150	45		13	2		90

L: Lectures (85 students)  
 HI: Hospital internships (7 students)  
 LAB: Laboratory or field practices (15 students)  
 COM: Computer room or language laboratory practices (20 students)  
 SEM: Problem classes or seminars or case studies (40 students)  
 SGT: Scheduled group tutorials (educational monitoring, ECTS type tutorials)  
 PS: Personal study, individual or group work and reading of bibliography



**Teaching Methodologies\***

1. Lectures on theory and problems. Description: expository method consisting of the presentation by the teacher of the contents of the subject matter. It also includes the resolution of example problems by the professor.
2. Resolution, analysis and discussion of proposed practical problems. Description: method based on the presentation of problems by the teacher and their resolution in the classroom.
3. Problem-based learning (PBL). Description: teaching/learning method based on a problem designed by the teacher, which the student solves autonomously or under guidance in order to develop certain previously defined competencies.
4. Learning through experimentation. Description: teaching-learning method based on the scientific method in which the student raises hypotheses, experiments, collects data, searches for information, applies models, contrasts hypotheses and draws conclusions.
5. Cooperative learning. Description: teaching-learning method based on an interactive approach to work organization. The aim is to achieve an effective exchange of information among students, who must be motivated to achieve their own learning as well as that of others.
6. Learning through the virtual classroom. Description: teaching/learning situation in which a computer with a network connection is used as a communication system between teacher and student and even among students and a plan of training activities is developed.

**Learning outcomes**

1. To know the importance of Bioinformatics, its basics and applications.
2. To know how to locate bioinformatics resources on genes, genomes and proteins.
3. To understand the methods of analysis and synthesis of biological information.
4. To manage the information found in biological databases.
5. To discriminate the different levels of algorithmic and effective complexity in different biological entities: genes, genomes, proteins and chromosomes.

\*\* Indicate the total number of evaluation hours of this subject.

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6. To understand and manage the algorithms used in the alignment of DNA and protein sequences.
7. To understand and handle the algorithms used in the reconstruction of molecular phylogenies.
8. To know the methods used in the structural determination of biomolecules, ab initio and homology prediction of protein structures.

#### Assessment systems

For those students who opt for continuous evaluation:

1. Exam (individual test). This test will assess the understanding and acquisition of the knowledge explained by means of a written exam or through the Moodle platform. In any case, the exam will be a combination of multiple-choice questions (true/false or multi-choice) and practical exercises. The grade of this exam, which will be between 0-10 points, will represent 85% of the maximum final grade.
2. Active participation in the classroom and individual or small group tutoring: continuous evaluation method based on the active participation of the student in the activities developed in the classroom and in the guidance and follow-up tutorials, whose grade will represent 5% of the maximum final grade.
3. The activities, tasks and completion of questionnaires and assignments throughout the course will be valued up to 1 total point, which represents 10% of the maximum final grade.
4. In any case, in order to pass the course it will be necessary to obtain a minimum grade of 5 points in the exam (individual test), regardless of the grade obtained in the rest of the items.

For those students who opt for a single global test:

1. Exam (individual test). This test will assess the understanding and acquisition of the knowledge explained by means of a written exam or through the Moodle platform, of 2.5 hours of duration. In any case, the exam will be a combination of multiple-choice questions (true/false or multi-choice) and practical exercises. The grade of this exam will account for 100% of the final grade.

#### Bibliography (basic and complementary)

- "Genomics: Essential Methods". M. Starkey and R. Elaswarapu. Ed. Wiley-Blackwell. ISBN: 978-0-470-71157-6.
- "Genomics, Proteomics and Bioinformatics". 2nd Edition. A. Malcolm Campbell and L.J. Heyer. CSHL Press and Pearson Education. ISBN: 0-8053-8219-4.
- "Bioinformatics and Functional Genomics". 2nd Edition. J. Pevsner. Ed. Wiley-Blackwell. ISBN: 978-0-470-08585-1.

#### Other resources and complementary educational materials

- Virtual site (Moodle) of the course in [campusvirtual.unex.es](http://campusvirtual.unex.es).