IDENTIFYING DATA
Bioinformatics

Subject	Bioinformatics
Code	V02M074V11111
Study programme	Máster Universitario en Biotecnología Avanzada

Descriptors	ECTS Credits	Choose	Year	Quadmester
	3	Mandatory	1st	1st

Teaching language	Spanish Galician
Department	
Coordinator	Canchaya Sanchez, Carlos Alberto
Lecturers	Arenas Busto, Miguel Becerra Fernández, Manuel Canchaya Sanchez, Carlos Alberto Dorado de la Calle, Julián
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General description	IMPORTANT: The informatic platforms of the educational guides of the two universities, although being similar, they have light differences. In front of any discrepancy between the guides, we will take into account the one published in the web page of the master degree. The realisation of experiments in biology generates every time a greater number of data. The management and analysis of these data would be already impossible without the utilisation of computer tools inside the discipline of the bioinformatics. Bioinformatics is a mixture of knowledge and techniques of the areas of computer science and mathematics applied to life sciences, especially the biology. Within the domain of Bioinformatics, we study the data programming and its storage in databases, access to these databases and the application of distinct algorithms for data processing. In this subject, we will see the application of bioinformatics to distinct fields of the molecular biology from the analysis of sequences to the study of the structure of proteins and nucleic acids.

Training and Learning Results

Code	
B1	Analyses and sinthesis (found the right problems and identify causes and its typology)
B2	Organise and schedule all the resources (human, material, information and infrastructures)
B3	Capacity of information management (with support of TICs)
B4	Planificar y elaborar estudios técnicos en biotecnología microbiana, vegetal y animal
B5	Identify problems, make decisions and apply them in a biotech professional and research contexts.
B10	Work in contexts of sustainability, characterized by: sensitivity to the environment and to different organizations that make it up as well as awareness for sustainable development
B11	Critical reasoning and deep respect for ethics and intellectual integrity
B12	Adapt to new legal situations, or technological innovations as well as exceptionalities associated with situations of emergency
B13	Autonomous Learning
B15	Awareness towards quality, respect for the environment and the responsible consumption of resources and the recovery of waste
C3	Know the biotechnological applications of microorganisms, plants and animals and know how to manipulate them for their biotech application
C7	Search, obtain and interpret information from biological databases: genomics, proteomics, transcriptomics and metabolomics and use the basic tools of bioinformatics

Expected results from this subject

Expected results from this subject	Training and Learning Results

Use the biological databases for obtaining, analysis and interpretation of the information	B1
	B2
	B3
	B4
	B5
	B10
	B11
	B12
	B13
	B15
	C7
Identify the biotechnological applications in microorganisms, plants and animal and learn to manipulate them for their use in the biotechnological sector.	B1
	B2
	B3
	B4
	B5
	B10
	B11
	B12
	B13
	B15
	C3

Contents

Topic	
Introduction to Bioinformatics. Unix	Introduction to the Operative systems. Basic commands. File systems. Management of archives and directories. Other commands.
Molecular evolution	Molecular homology: replacement, insertion and deletion. Multiple Alignment. Models of nucleotide and amino acid substitution. Model selection. Phylogenetic methods. Reconstruction of maximum likelihood. Error and phylogenetic confidence.
Genomic analysis	Researches in databases: BLAST. Genome Projects. Structural genomics. Secuencing. Gene prediction. Functional annotation. Comparative genomics.
Structural biology I	Visualisation of biological macromolecules. Prediction of 1 D characteristics of proteins: sequences, domains. Three-dimensional structure of proteins. Prediction of 3D structure of proteins: modeling by homology and modeling by threading or design by remote homology. Methods ab initio. Molecular docking: Prediction of protein-substrate and protein-protein interactions. Evaluation of the methods of prediction.
Structural biology II	Structure of RNA. Prediction of RNA structures. Databases and servers of programs for the analysis of: sequences, structural motifs and functional structures.

Planning

	Class hours	Hours outside the classroom	Total hours
Lecturing	11	5.5	16.5
Practices through ICT	11	16.5	27.5
Discussion Forum	0	1	1
Seminars	1	0	1
Report of practices, practicum and external practices	0	3	3
Report of practices, practicum and external practices	0	3	3
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Objective questions exam	2	12	14

*The information in the planning table is for guidance only and does not take into account the heterogeneity of the students.

Methodologies

	Description
Lecturing	Classes of content presentation, practical exercises, and discussion. Each student's particular questions will be answered. For students with part-time and academic attendance waivers, the lecturers will adopt the measures they consider appropriate to avoid impacting their grades.

Practices through ICT	Classes of content presentation, practical exercises, and discussion. Each student's particular questions will be answered. For students with part-time and academic attendance waivers, the lecturers will adopt the measures they consider appropriate to avoid impacting their grades.
Discussion Forum	Lecturers will answer individual questions from students.
Seminars	Lecturers will answer individual questions from students.

Personalized assistance

Methodologies	Description
Lecturing	Lecturers will answer each student's questions. For the students with recognition of dedication to partial time and with academic attendance exemptions, the professor will adopt timely measures to avoid harm to the student's grades
Practices through ICT	Lecturers will answer each student's questions. For the students with recognition of dedication to partial time and with academic attendance exemptions, the professor will adopt timely measures to avoid harm to the student's grades
Discussion Forum	Lecturers will answer individual questions from students
Seminars	Lecturers will answer individual questions from students

Tests	Description
Objective questions exam	Lecturers will answer individual questions from students
Report of practices, practicum and external practices	Lecturers will answer individual questions from students
Report of practices, practicum and external practices	Lecturers will answer individual questions from students
Report of practices, practicum and external practices	Lecturers will answer individual questions from students
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Report of practices, practicum and external practices	Lecturers will answer individual questions from students

Assessment

	Description	Qualification	Training and Learning Results	
Report of practices, practicum and external practices	The final reports are based on the computer practical exercises from the first session and will be evaluated by the lecturers. This report should be submitted 24 hours after classes.	15	B1 B2 B3 B4 B5 B10 B11 B12 B13 B15	C3 C7
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Objective questions exam	It will realise one tests type test to evaluate the knowledges purchased during the realisation of the masterclasses and the practices in computer	25	B1 B5 B13	C3 C7

Other comments on the Evaluation

- Part-time enrolled students should contact lecturers to arrange dates for the delivery of their practical reports.

- To be eligible to take the resit exam, it will be necessary to have previously submitted the corresponding five reports.

- Those students who are evaluated in the first opportunity will have priority to obtain the MH.

- For students who apply for the DECEMBER EARLY CALL, current regulations will be applied, according to which the current course teaching guide is in force.

- Implications of PLAGIARISM in the grades: Current regulations will be applied.

- Evaluation will preferably be continuous, however, the student will be able to take a global evaluation exam. The global evaluation exam consist of a written exam (25% of the grade) and the delivery of five reports, one for each of the practical sessions in which the subject is divided, with a weight of 15% each. The papers must be handed in on the official date of the exam.

Sources of information

Basic Bibliography

Complementary Bibliography

Arthur M. Lesk, **Introduction to Bioinformatics**, 4ª, Oxford University Press, 2013

David W. Mount, **Bioinformatics. Sequence and genome analysis**, 2ª, Cold Spring Harbor Laboratory Press, 2004

Recommendations

Subjects that it is recommended to have taken before

Genomics and Proteomics/V02M074V11110

Genetic Engineering and Transgenesis/V02M074V11108

Application techniques in biotechnology/V02M074V11114

Other comments

Since some of the bibliographies recommended for this subject are written in English, it is advisable to know this language,

at least at the level of written comprehension.