Teaching Guide

Identifying Data			2019/20
Subject (*)	Bioinformatics and Biomolecular models	Code	610441020
Study programme	Mestrado Universitario en Bioloxía Molecular , Celular e Xenética		

Descriptors

Cycle	Period	Year	Type	Credits
Official Master's Degree	2nd four-month period	First	Optional	3

Language	Spanish		
Teaching method	Face-to-face		
Prerequisites			
Department	BioloxíaCiencias da Computación e Tecnoloxías da InformaciónComputación		
Coordinador	Dorado de la Calle, Julian	E-mail	julian.dorado@udc.es
Lecturers	Becerra Fernandez, Manuel Dorado de la Calle, Julian Fernández Lozano, Carlos	E-mail	manuel.becerra@udc.es julian.dorado@udc.es carlos.fernandez@udc.es
Web			
General description	Knowledge management in biology is the field of bioinformatics, and includes both the formalization of the information obtained and its organization in appropriate databases, the extraction of relationships between the scattered information, the modeling of biological processes and the generation of hypotheses to support new experimental approaches. From a technical standpoint, bioinformatics using computational methods (the proper method development in this area is often called computational biology) and receives contributions from mathematics, physics and computer engineering. However, from the point of view of the objectives, bioinformatics is a branch of biology, as they can be biochemistry or microbiology. This interdisciplinary nature of bioinformatics lies both its strength and its weakness: first, the application of ideas brought from other fields consistently produces spectacular advances; but on the other hand, it is difficult to develop appropriate training programs. To realize the importance of bioinformatics in modern biology, it may enough to say that the method most cited publications in this area is Blast, a computational method that searches and identifies sequences of proteins and nucleic acids in databases: ie more technical operations is performed by computational biologists, and no experimental. In fact, the interpretation of any experiment in biology requires complex, almost inevitably, bioinformatic analysis, which is especially obvious in massive experiments.		

Study programme competences / results

Code	Study programme competences / results
A3	Skills of understanding the functioning of cells through the structural organization, biochemistry, gene expression and genetic variability.
A9	Skills of understanding the structure and dynamics of proteins to individual and proteomic level, as well as the techniques that are necessary to analyze them and to study their interactions with other biomolecules.
A11	Skills of understanding the structure, dynamics and evolution of genomes and to apply tools necessary to his study.
B1	Analysis skills to understand biological problems in connection with the Molecular and Cellular Biology and Genetics.
B2	Skills of decision making for the problem solving: that are able to apply theoretical knowledges and practical acquired in the formulation of biological problems and the looking for solutions.
B3	Skills of management of the information: that are able to gather and to understand relevant information and results, obtaining conclusions and to prepare reasoned reports on scientific and biotechnological questions
B9	Skills of preparation, show and defense of a work.
C3	Using ICT in working contexts and lifelong learning.
C6	Acquiring skills for healthy lifestyles, and healthy habits and routines.
C8	Valuing the importance of research, innovation and technological development for the socioeconomic and cultural progress of society.
C9	Ability to manage times and resources: developing plans, prioritizing activities, identifying critical points, establishing goals and accomplishing them.

Learning outcomes

Learning outcomes	Study programme competences / results		
Know access to Channels Bioinformatics Web Resources	AR3	BR3 BR9	CC3
Understand and manage properly the area of Bioinformatics	AR3	BR3 BR9	CC3 CC6
Being able to function independently to find information about the different programs and their changeable parameters and understand the impact on the results of the analysis	AR3	BR2 BR3 BR9	CC3 CC9
To have bioinformatics knowledge of how to make a prediction of the onedimensional characteristics of a protein	AR3 AR9 AR11	BR1 BR2 BR3	CC3 CC6 CC8
To be able to perform a simple prediction of the three dimensional structure of a protein based on available data and programs on the Web	AR3	BR1 BR2 BR3	CC3 CC6 CC8 CC9
Learn the basic methods of molecular simulation and how they are used for the study of proteins	AR3	BR1 BR2 BR3	CC3 CC6 CC8

Contents

Topic	Sub-topic
Bioinformatics	Web Resources and Databases in molecular biology. Analysis and comparison of sequences. Sequence alignment. Location of motives. Search of genes. annotation of genes. Browsers genome project. Examples of applications. Data analysis.
Modeling of Biomolecules	Prediction of the characteristics of the protein structure. Obtaining three-dimensional models. Homology modeling. Modeling by threading or by remote homology design. Ab initio methods. Evaluation of the prediction methods.

Planning

Methodologies / tests	Competencies / Results	Teaching hours (in-person & virtual)	Student?s personal work hours	Total hours
Guest lecture / keynote speech	A3 A9 A11	10	20	30
Seminar	B3 B9 C6 C8 C9	2	7	9
Laboratory practice	B1 B2 C3 C9	9	22.5	31.5
Personalized attention		4.5	0	4.5

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

Methodologies

Methodologies	Description
Guest lecture / keynote speech	Oral presentation complemented by the use of audiovisual media for the purpose of transmitting knowledge and facilitate learning.
Seminar	Working technique that aims to make powerpoint and word documents on a topic proposed by the teacher.
Laboratory practice	Methodology that allows students to learn effectively through practical activities (demonstrations, simulations, etc.) the theory of a field of knowledge through the use of information technology and communications.

Personalized attention	
Methodologies	**Description**
Seminar Laboratory practice	The personal attention that is described in relation to these methodologies are conceived as moments of classroom student work with teacher, this involve mandatory participation for the student. The manner and time in which it was held is indicated in relation to each activity along the course according to the work plan of the course

Assessment			
Methodologies	**Competencies / Results**	**Description**	**Qualification**
Guest lecture / keynote speech	A3 A9 A11	A test will be realized to assess the knowledge acquired in the course of lectures. With this methodology the A5, B2 skillls will be assessed	45
Seminar	B3 B9 C6 C8 C9	The seminar will be evaluated by taking into account the ability to extract the most relevant information obtained for the student, the capacity for teamwork and the ability to expose in public. Whit this methodology B1, B3 and B9 competencies will be evaluated	25
Laboratory practice	B1 B2 C3 C9	Regular attendance and active participation in the lab, as well as the bulletin responses made by students will be assessed. They also perform a test to assess the knowledge acquired. With this methodology the A5 and B2 competencies will be assessed	30

Assessment comments

Students presented in the first opportunity of June will be eligible to get honours.

Students with a part-time assistance or exemption may agree with teachers specific methods for evalaution early in the course .

Also students engaged as "SEMIPRESENCIALES" should contact the teachers in the first weeks.

Sources of information

Basic	BIOINFORMATICS ? Attwood, T.K. & D.J. Parry-Smith. 1999. Introduction to Bioinformatics. Addison Wesley Longman Limited, Edimburgo. ? Baxevanis, A.D. & B.F. Francis Oullette (Eds.). 2002. Bioinformatics. A practical guide to the analysis of genes and proteins. 2nd Ed.Wiley-Interscience.? Bishop, M. 1999. Bioinformatics. Taylor & Francis, UK.? Claverie, J.M. and C. Notredame. 2003. Bioinformatics for dummies. Wiley Publishing, Inc.? Gibas, C. y P. Jambeck. 2001. Developing Bioinformatics Computer Skills. O'Reilly? Higgins, D. y W. Taylor. 2000. Bioinformatics: Sequence, structure and databanks. Oxford University Press.? Higgs, P. & T.K. Attwood 2005. Bioinformatics and molecular evolution. Blackwell Publishing.? Kanehisa, M. 2000. Post-genome informatics. Oxford University Press? Li, W-H. 1999. Molecular evolution. Sinauer Associates Inc., Massachusetts, 2nd. Ed.? Mount, David W. 2001. Bioinformatics. Sequence and Genome Analysis. Cold Spring Harbor Laboratory Press.? Nei, M. y S. Kumar. 2000. Molecular Evolution and Phylogenetics. Oxford University Press.? Pevsner, J. 2003. Bioinformatics and Functional Genomics. John Wiley & Sons, Inc.? Rashidi, H.H. and L.K. Buehler. 2000. Bioinformatics Basics. Applications in Biological Science and Medicine. CRC Press, Boca Raton.? Salzberg, S., D. Searls, and S. Kasif (Eds). 1998. Computational Methods in Molecular Biology. Elsevier Science.? Swindell, S.R., R.R. Miller y G.S.A. Myers. 1997. Internet for the Molecular Biologist. Horizon Scientific Press, Norfolk, UK.? Tisdall, J. 2001. Beginning Perl for Bioinformatics. O'Reilly MODELING OF BIOMOLECULES? Bnaszak,L. J. 2000. Foundations of structural biology. Academic Press. ? Bourne, P. E., Weissig,H. 2003. Structural Bioinformatics. John Wiley & Sons.? Branden,C. & Tooze, J. 1998. INTRODUCTION TO PROTEIN STRUCTURE. 2nd editionGarland Publishing, Inc, New York . ? Creighton,T. E. 1993. PROTEINS: STRUCTURES AND MOLECULAR PROPERTIES, 2nd edition. W.H.Freeman & Company, New York .? Gómez-Moreno,C. & Sancho, J. (Coords). 2003. ESTRUCTURA DE PROTEÍNAS. Ariel Ciencia, Barcelona . ? Lesk, A.M. 2000. INTRODUCTION TO PROTEIN ARCHITECTURE. THE STRUCTURAL BIOLOGY OFPROTEINS. Oxford University Press, Oxford . ? Tramontano,A. 2006. Protein Structure Prediction. Wiley-Vch.
Complementary	<i>Molecular visualization programs:</i> Rasmol: http://www.umass.edu/microbio/rasmol Swiss-PdbViewer: http://www.expasy.ch/spdbv/ MOLMOLhttp://www.mol.biol.ethz.ch/wuthrich/software/molmol Cn3Dhttp://www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml Chime http://www.umass.edu/microbio/chime<i>Modeling and prediction servers:</i> SWISS-MODEL http://expasy.ch/swissmod/ ThePredictProtein Server http://ww.embl-heidelberg.de/predictprotein/predictprotein.html Center for MolecularModeling: http://cmm.info.nih.gov/modeling/ GRAMM: http://reco3.musc.edu/gramm/ PQS(Probable Quat. Structure): http://msd.ebi.ac.uk/services/quaternary/quaternary.htmlMolecular visualization programs: Rasmol: http://www.umass.edu/microbio/rasmol Swiss-PdbViewer: http://www.expasy.ch/spdbv/ MOLMOLhttp://www.mol.biol.ethz.ch/wuthrich/software/molmol Cn3Dhttp://www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml Chime http://www.umass.edu/microbio/chimeModeling and prediction servers: SWISS-MODEL http://expasy.ch/swissmod/ ThePredictProtein Server http://ww.embl-heidelberg.de/predictprotein/predictprotein.html Center for MolecularModeling: http://cmm.info.nih.gov/modeling/ GRAMM: http://reco3.musc.edu/gramm/ PQS(Probable Quat. Structure): http://msd.ebi.ac.uk/services/quaternary/quaternary.html

Recommendations
Subjects that it is recommended to have taken before
Molecular Techniques/610441002
Subjects that are recommended to be taken simultaneously
Protein Structure and Dynamics/610441011 Proteomics/610441013 Genomics /610441014
Subjects that continue the syllabus
Project/610441022
Other comments

(*)The teaching guide is the document in which the URV publishes the information about all its courses. It is a public document and cannot be modified. Only in exceptional cases can it be revised by the competent agent or duly revised so that it is in line with current legislation.