Course Guide
33183 Technologies of integrated molecular analysis

COURSE DATA

DATA SUBJECT

Code: 33183
Name: Technologies of integrated molecular analysis
Cycle: Undergraduate Studies
ECTS Credits: 4.5
Academic year: 2026-27

STUDY (S)

Degree	Center	Acad. year	Period
1111 - Grado en Biotecnología	Facultat de Ciències Biològiques	3	Second quarter

SUBJECT-MATTER

Degree	Subject-matter	Character
1111 - Grado en Biotecnología	Technologies of integrated molecular analysis	COMPULSORY

COORDINATION

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FORTE DELTELL ANABEL

SUMMARY

Within the program's Degree in Biotechnology at the University of Valencia, Technologies for Integrated Molecular Analysis is a compulsory subject taught in the third year of the Degree. The course consists of 4.5 ECTS credits with theoretical and practical lectures.

One of the essential features of the Graduate Program in Biotechnology is the multidisciplinary contents, as the realization of many developments in biotechnology requires the interaction of different technologies. In this sense the program has implemented the technologies of genomics and proteomics, which can obtain large amounts of information, and Bioinformatics, to analyze this information

PREVIOUS KNOWLEDGE

RELATIONSHIP TO OTHER SUBJECTS OF THE SAME DEGREE

There are no specified enrollment restrictions with other subjects of the curriculum.

OTHER REQUIREMENTS

Prior knowledge of metabolism, genetics and protein structure

COMPETENCES / LEARNING OUTCOMES

1102 -

Be able to perform an integrated analysis of gene expression at the level of transcriptome, proteome and metabolome.

Design protocols for the separation, purification and characterisation of biological molecules.

1111 - Grado en Biotecnología

Actuar con autonomía en el aprendizaje, tomando decisiones fundamentadas en diferentes contextos, emitiendo juicios en base a la experimentación y el análisis y transfiriendo el conocimiento a nuevas situaciones

Apply analytical, synthetic and critical thinking skills in the application of the scientific method.

Colaborar eficazmente en equipos de trabajo, asumiendo responsabilidades y funciones de liderazgo y contribuyendo a la mejora y desarrollo colectivo

Conocer las características estructurales y funcionales de las macromoléculas

Conocer las potencialidades de las diferentes técnicas ómicas

Contribuir en el diseño, desarrollo y ejecución de soluciones que den respuesta a demandas sociales, teniendo en cuenta como referente los Objetivos de Desarrollo Sostenible

Demostrar razonamiento crítico y autocrítico en el ámbito de la titulación, considerando aspectos tales como la ética profesional, los valores morales y las implicaciones sociales de las diferentes actividades realizadas

Diseñar protocolos de separación, purificación y caracterización de moléculas biológicas

Entender las bases de las tecnologías que se utilizan para analizar los resultados de los análisis ómicos

Identify the molecules that make up a living organism.

Participate in multidisciplinary teams, engaging in teamwork and collaboration.

Propose creative and innovative solutions to complex situations or problems, typical of the area of ¿¿¿¿connection, to donate responses to the various professional and social needs

Que el estudiantado demuestre su capacidad para calcular correctamente los parámetros relevantes de un proceso o un experimento mediante la representación de los datos experimentales

Que el estudiantado demuestre su capacidad para utilizar herramientas matemáticas y estadísticas para la resolución de problemas biológicos

Que el estudiantado demuestre su capacidad para utilizar las diferentes fuentes bibliográficas y bases de datos biológicos y usar las herramientas bioinformáticas

Saber comunicarse de manera efectiva, tanto de forma oral como escrita, adaptándose a las características de la situación y de la audiencia

Ser capaz de realizar un análisis integrado de expresión génica a nivel de transcriptoma, proteoma y metaboloma

Use English to write reports and to interpret information from protocols, manuals and databases.

Work in laboratories, including safety procedures, waste management and accurate activity logging.

DESCRIPTION OF CONTENTS

1. Introduction

Omics Science Concept History: genome sequencing and functional genomics. Strategies for comprehensive study of various biological systems.

2. Sample preparation and analysis in proteomics

Proteome and proteomics. Sample preparation and separation. Mass spectrometry.

3. Protein identification and quantitation

Protein identification procedures. Protein quantitation with and without labeling. Targeted proteomics.

4. Characterization of the proteome

Study of post-translational modifications. Study of protein-protein interactions: interactome and analysis of macromolecular complexes.

5. Metabolomics

Techniques for metabolome analysis. Identification and quantitation of metabolites.

6. Methods of analysis of global gene expression

Comparison of individual analysis methods and global analysis. Serial analysis of gene expression (SAGE) and derived methods. The chips or DNA microarrays: fundamentals and applications. Analysis of the results. Transcriptomic studies with DNA chips. The functional organization of eukaryotic genomes. Ultrasequence for transcriptomic studies

7. Global phenotypic studies: phenomics

Collections of deletion mutants or shut off with iRNA. Collections of gene fusions. Analysis techniques for phenotypic studies

8. Interactomics and other omics

Protein interaction: study methods and genomic scale Interactions between proteins and DNA: ChIP Epigenomics

9. Tools for Statistics bioinformatics

Introduction to R, R-Studio and Bioconductor. Omic data management including access to on-line data. R objects for comic data. Data preprocessing and annotation.

10. Data mining

Tools for describing data. Main component and cluster analyses.

11. Experimental design

Introduction to experimental design and its application to Bioinformatics.

12. Differential expression

Marginal differential expression. Multiple tests. Error control techniques.

13. Analysis of gene groups

Fisher/Multinomial test. Study of the functionalities of differentially expressed genes.

WORKLOAD

PRESENCIAL ACTIVITIES

Activity	**Hours**
Theory	31,00
Laboratory	2,00
Computer classroom practice	12,00
Total hours	**45,00**

NON PRESENCIAL ACTIVITIES

Activity	**Hours**
Attendance at other activities	0,00
Individual or group project	0,00
Independent study and work	20,00
Preparation of lessons	20,00
Preparation for assessment activities	0,00
Resolution of case studies	27,00
Total hours	**67,00**

TEACHING METHODOLOGY

Theory classes: there will be 2 weekly sessions of one hour Basically, you use the lecture model, offering the possibility that the teacher impinges on the most relevant concepts for the understanding of the subject and indicate the most recommended resources for further preparation of the subject in depth Will use the media needed to develop flexible and coherent classes. The teacher will accessible when required, on the platform to support virtual classroom teaching, the material necessary for the proper monitoring of the lectures On some issues, we will use the participatory model, focussing on communication between students and between them and the teacher.Practical session on proteomics. A two-hour session will be held during which students will analyse scientific articles to gain a deeper understanding of the omics methodologies and strategies employed, in connection with the content covered in the proteomics and metabolomics module.Practical classes in computer classroom. Attendance is mandatory. There will be six sessions of 2 hours each of the statistical analysis To use data analysis software in the subject and various R packages, in particular those related to Bioconductor

EVALUATION

The module is structured into 2 main parts: BIOLOGY (Genomics and Proteomics) and BIOINFORMATICS. The BIOLOGY part accounts for 50% of the final module mark (20% Genomics and 30% Proteomics), while the BIOINFORMATICS part accounts for 50%.

The content of the theoretical classes will be assessed by a written exam on the first 8 topics (BIOLOGY). A minimum mark of 3 out of 10 is required in each part (Genomics and Proteomics) to be allowed to average them.

A mark of 40% of the maximum score in each of the parts (BIOLOGY and BIOINFORMATICS) is required to pass. If either part is passed on the first sitting (achieving 50% or more of the marks), the candidate may sit only the other (failed) part in the resit.

REFERENCES

Basic References:

Referencia b1: -C. David O¿Connor & B. David Hames. Proteomics. Scion, 2008.

Referencia b2: - Wim P. Krijnen. Applied Statistics for Bioinformatics using R. GNU Free Document.

Referencia b3: - Jae K. Lee, editor. Statistical Bioinformatics A Guide for Life and Biomedical.Science Researchers. Wiley-Blackwell, 2010.

Referencia b4: - E. Wit and J.D. McClure. Statistics for microarrays: design, analysis, and inference. Wiley, 2004.

Referencia b5: -R Development Core Team. R: A Language and Environment for Statistical. Computing. R Foundation for Statistical Computing, Vienna, Austria, 2008. ISBN 3-900051-07-0.

Referencia b6: W.N. Venables and B. D. Ripley. Modern Applied Statistics with S. Springer, New York, fourth edition, 2002. ISBN 0-387-95457-0.

Referencia b7: -J. Verzani. Using R for Introductory Statistics. Chapman & Hall / CRC, 2005.

Referencia b8: -S.B. Primrose y R.M. Twyman. Principles of Gene Manipulation and Genomics. Balckwell. 2007. ISBN 978-1-4051-3544-3

Referencia b9: -Fernando Corrales y Juan J. Calvete (2014) Manual de proteómica. Sociedad Española de Proteómica

Complementary References:

Artículos de revisión publicados en revistas especializadas en el tema.