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COURSE DATA

Data Subject	
Code	33183
Name	Technologies of integrated molecular analysis
Cycle	Grade
ECTS Credits	4.5
Academic year	2022 - 2023

Study (s)			
Degree	**Center**	**Acad. year**	**Period**
1102 - Degree in Biotechnology	Faculty of Biological Sciences	3	Second term

Subject-matter		
Degree	**Subject-matter**	**Character**
1102 - Degree in Biotechnology	87 - Technologies of integrated molecular analysis	Obligatory

Coordination	
Name	**Department**
FORTE DELTELL, ANABEL	130 - Statistics and Operational Research
GARCIA MARTINEZ, JOSE	194 - Genetics
GARCIA MURRIA, MARIA JESUS	30 - Biochemistry and Molecular Biology

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

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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 (RD 1393/2007) // LEARNING OUTCOMES (RD 822/2021)

1102 - Degree in Biotechnology

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

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

LEARNING OUTCOMES (RD 1393/2007) // NO CONTENT (RD 822/2021)

To learn the ability of observation and interpretation of results obtained using genomic and proteomic techniques, applying theoretical knowledge to practice.

Adequate knowledge about the preparation of biological material (bacteria, yeast, animal and plant cells) to be analyzed by integrated molecular analysis techniques

Design experiments and understand the limitations of the experimental approach

To approach problems from different perspectives and differing strategies complemented reductionist and omics

Interpret the results of omics experiments

Using the Internet as a source of information on databases of genes and proteins acquire the ability to manage software related to sequence analysis Manage information.

Analyze and synthesize the results of a specialist and make an oral presentation, written and visual work.

Be able to understand aspects of research in genomics, proteomics and metabolomics.

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. Protein chips.

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

ACTIVITY	Hours	% To be attended
Theory classes	31,00	100
Computer classroom practice	12,00	100
Laboratory practices	2,00	100
Study and independent work	20,00	0
Preparing lectures	20,00	0
Resolution of case studies	27,00	0
TOTAL	112,00	

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 class of Proteomics. There will be a 2-hour session in the computer room to analyze mass spectra and perform a peptide fingerprint search using MASCOT.

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 subject is structured in 2 main parts: BIOLOGY (Genomics and Proteomics) and BIOINFORMATICS. The BIOLOGY part represents 60% of the final grade of the subject (26% Genomics and 34% Proteomics) while the BIOINFORMATICS part represents 40%.

The evaluation of the contents of the theoretical classes will be carried out by means of a written examination of the first 8 units (BIOLOGY). It will be necessary to obtain a minimum of 3 out of 10 in each part (Genomics and Proteomics) to be able to average between them.

The evaluation of the Bioinformatics part will be carried out by means of: (1) The resolution and delivery of practices in R. (35%) (2) A work that will contemplate the comprehension of the statistical part of an article already published. (35 %) (3) An exam that will consist of 3 questions on the subject treated both in practice and theory (30%). The value of this part of the course will be 4 points out of 10.

It will be necessary to obtain 40% of the maximum score in each of the parts (BIOLOGY and BIOINFORMATICS) to get passed. If either of the two parties is approved in the first call (obtaining 50% or more of the mark) it will be possible to choose to present to the other party (failed) in the second call.

REFERENCES

Basic

- Referencia b1:   -C. David OConnor & 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

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Additional

- Artículos de revisión publicados en revistas especializadas en el tema.