COURSE DESCRIPTION

COURSE DETAILS

Title (of the course): **BIOLOGÍA MOLECULAR DE SISTEMAS**

Code: 101842

Degree/Master: **GRADO DE BIOQUÍMICA**   Year: 4

Name of the module to which it belongs: MÉTODOS INSTRUMENTALES CUANTITATIVOS Y BIOLOGÍA MOLECULAR DE

Field: BIOLOGÍA MOLECULAR DE SISTEMAS

Character: OBLIGATORIA   Duration: FIRST TERM

ECTS Credits: 6.0   Classroom hours: 60

Face-to-face classroom percentage: 40.0%   Study hours: 90

Online platform: http://www.uco.es/amoodle

LECTURER INFORMATION

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PREREQUISITES AND RECOMMENDATIONS

Prerequisites established in the study plan
None

Recommendations
- It is recommended to have knowledge of technical English for the handling of scientific literature, as well as for the use of bioinformatics tools.
- Knowledge of the Linux operating system (Ubuntu or similar) at the user level is recommended. The student must be able to download programs, install them, compile the different binaries, and manipulate files.
- It is advisable to have basic concepts of the statistical program R.
- General computer knowledge of the Windows operating system and access to browsers such as Internet Explorer, Firefox, Chrome, etc. is required.
- A Internet connection is required both, at home and in the University

INTENDED LEARNING OUTCOMES

CB1

CB2

CB4

CB6

CB7

CE24

CE25

CE26

CE27

CE29

OBJECTIVES

- To know the concept and importance of Molecular Systems Biology (MSB) in the Life Sciences environment.
- To know the main techniques of massive biological data collection ("omics") used in Molecular Systems Biology.
- To know the importance of Bioinformatics in current Biology.
- To understand how to integrate and interpret the results of experimental and computational techniques to explain and predict the functioning of biological systems.
- To know the current situation and future perspectives of Molecular Systems Biology.
- To know the applications of BMS in research, biotechnology, diagnostics, personalized medicine, etc.
- Introduction to the analysis of massive genomic sequencing: quality analysis of sequences and assembled genomes, gene expression analysis, etc.

COURSE DESCRIPTION

CONTENT

1. Theory contents

1.- **Introduction to Molecular Systems Biology**. From traditional biology to the integrative study of biological systems. Systems Biology: definition, justification, objectives, procedures. Networks: concept and importance in Systems Biology. Importance of Systems Biology in current science.

2.- **Introduction to experimental and computational techniques**. Background of experimental techniques: from traditional biology to "omics". Experimental techniques of massive analysis ("omics"): genomics, transcriptomics, proteomics, metabolomics, metagenomics. Computational techniques (Bioinformatics). Main bioinformatics platforms in Systems Biology and their applications.

3.- **Proteomics I**: sample preparation and separation techniques. Analysis techniques. Birth and development of Proteomics. Study of the proteome. Preparation of samples for proteomics. Application of electrophoresis, chromatography, and mass spectrometry to proteomics. Main bioinformatics algorithms for the interpretation of mass spectra.

4.- **Proteomics II:** Main applications of Proteomics in Biosciences. Quantification of proteins in proteomic experiments. Proteins as biomarkers and disease diagnosis. Proteomic tools for biomarker discovery and validation. Application in the field of vaccines against infectious diseases.

5.- **Metabolomics**. Introduction to the concepts of metabolome and metabolomics. Levels of analysis of metabolites. Sample preparation for metabolomics. Applications of metabolomics to Molecular Systems Biology.

6.- **Genomics.** Genomic sequencing strategies. Description of the main massive sequencing systems (NGS). Types of sequences or reads. Sequence quality analysis and filtering. Sequencing coverage. *De novo* assembly. Concepts of contigs and scaffolds. Genomic and Transcriptomic annotations. Quality assessment of assembled genomes. Exome sequencing and targeted sequencing. Other applications.

7.- **Transcriptomics.** Approaches to the analysis of gene expression at the transcript level. Transcriptome. Types of cDNA libraries. Mappings with reference genome or transcriptome. Transcriptome assembly. Sequence mapping: mappers and pseudo-mappers. Differential expression analysis by RNA-Seq. Functional and metabolic pathway enrichments. Isoform analysis. Introduction to single-cell genomic and transcriptomic sequencing and spatial transcriptomics methods.

8. **Metagenomics, metatranscriptomics and other techniques of relevance.** Methods for studying microbial diversity. Workflows. Definition of OTUs. Recommended programs. Applications.

9. **Introduction to omics data integration**. Introduction to programs for the integration of different omics data: Cytoscape, paintomics, Mapman and similar.

2. Practical contents

Case studies and readings of selected articles. Topical reviews on Molecular Systems Biology applications that address basic and applied research issues will be selected and presented as seminars by students in the medium group classes.

Forms designed to encourage discussion and establishment of concepts and ideas (whole group classes)

Hands-on practice in the Bioinformatics Classroom (medium group classes):

- Use of databases in public repositories on Proteomics resources.

- Quantitative proteomic analysis of an experiment on surface proteins in Streptococcus pneumoniae.

- Analysis of the quality of reads from massive sequencing systems.

- Sequence filtering of sequences from next-generation massive sequencers.

- De novo assembly of the complete genome of E. coli bacteria with sequences obtained from Illumina equipment. Sorting and scaffolding of the obtained contigs.

- Introduction to RNA-Seq. Mapping of reads with real mappers and pseudo-mappers. Analysis and manipulation of SAM/BAM files. Obtaining quantitative gene expression files.

- Use and applications of programs for viewing sequence alignment with reference genomes or transcriptomes (IGV, IGB or similar).

- Performance of a differential expression study by RNA-Seq using the R platform.

COURSE DESCRIPTION

SUSTAINABLE DEVELOPMENT GOALS RELATED TO THE CONTENT

Unrelated

METHODOLOGY

Methodological adaptations for part-time students and students with disabilities and special educational needs

Adaptations will be discussed and negotiated with interested alumns

Face-to-face activities

Activity	Large group	Medium group	Total
Assessment activities	-	4	4
Case study	-	7	7
Debates	-	9	9
Lectures	27	-	27
Text analysis	-	6	6
Tutorials	6	1	7
Total hours:	*33*	*27*	*60*

Off-site activities

Activity	Total
Analysis	4
Exercises	30
Group work	7
Information search	4
Reference search	5
Self-study	40
Total hours	*90*

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WORK MATERIALS FOR STUDENTS

Exercises and activities
Lessons summary
Oral presentations
References

EVALUATION

Intended learning	Case Studies	Case study/clinical case discussion/scientific work discussion	Exams
CB1	X		
CB2	X		
CB4	X		
CB6	X		
CB7			X
CE24			X
CE25		X	
CE26		X	
CE27		X	
CE29		X	
Total (100%)	20%	20%	60%
Minimum grade	4	4	4

(*)Minimum mark (out of 10) needed for the assessment tool to be weighted in the course final mark. In any case, final mark must be 5,0 or higher to pass the course.

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Attendance will be assessed?:

No

General clarifications on instruments for evaluation:

- There will be an exam with long questions (not test type). The use of class notes will be allowed in the exam.
- If the student takes the exam and decides at that moment not to hand in the exam, he/she will be considered as failed and not as not presented.
- There will be an homework in the proteomics part with which the section "Case studies" will be evaluated.
- There will be an homework in the genomics, transcriptomics and metagenomics part, whose subject will be agreed in advance with the professor.
- The work must be done either individually or in groups of up to 3 people maximum, and this decision must be agreed in advance with the professor responsible for each work.
- The student must have presented and evaluated the work of the course before the exam of long questions.
- The marks of the practical exercises will be respected in the case that the student has to sit for a new exam due to having failed or not having sat for previous exams.
- The marks of the practical exercises of previous courses will also be respected if the student has to be evaluated in subsequent courses. However, the student may redo the work if he/she considers it in his/her best interest.

Clarifications on the methodology for part-time students and students with disabilities and special educational needs:

Cases will be discussed personally with the student involved to take into account all considerations.

Clarifications on the evaluation of the extraordinary call and extra-ordinary call for completion studies:

- In the evaluation of the extraordinary call and in the extraordinary call for completion of studies, the grades of all the instruments of previous and present courses that have been taken will be kept. In addition, it will be evaluated in the same way as in the ordinary exams.

Qualifying criteria for obtaining honors:

A score of 9.5 points must be met or exceeded in order to obtain an honors degree.

BIBLIOGRAPHY

1. Basic Bibliography
- The one included in the official Moodle page.
- The one included in the web page http://www.uco.es/users/bb1rofra/BiologiaSistemas/

2. Further reading

None

COORDINATION CRITERIA

Common evaluation criteria
Tasks deadlines
Tasks performance

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COURSE DESCRIPTION

SCHEDULE

Period	Assessment activities	Case study	Debates	Lectures	Text analysis	Tutorials
1# Fortnight	0,0	0,0	0,0	3,0	0,0	1,0
2# Fortnight	0,0	0,0	0,0	4,0	0,0	1,0
3# Fortnight	1,0	0,0	0,0	4,0	0,0	1,0
4# Fortnight	1,0	0,0	0,0	4,0	0,0	1,0
5# Fortnight	1,0	2,0	3,0	4,0	2,0	1,0
6# Fortnight	1,0	2,0	3,0	4,0	2,0	1,0
7# Fortnight	0,0	3,0	3,0	4,0	2,0	1,0
Total hours:	**4,0**	**7,0**	**9,0**	**27,0**	**6,0**	**7,0**

The methodological strategies and the evaluation system contemplated in this Course Description will be adapted according to the needs presented by students with disabilities and special educational needs in the cases that are required.

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