Universidad del País Vasco — Euskal Herriko Unibertsitatea

COURSE GUIDE 2024/25

Faculty 310 - Faculty of Science and Technology **Cycle** .

Degree BMYBM204 - Master in Molecular Biology and Biomedicine **Year** .

COURSE

505108 - Omics : Experimental designs and data analysis **Credits, ECTS:** 5

COURSE DESCRIPTION

In this course on the OMICs sciences, Genomics, Transcriptomics and Bioinformatics will be treated within an integrative point of view. The three fields will be jointly developed and a global perspective will be provided. Theoretical aspects, experimental designs, tools for data analysis and possible applications are presented and developed.
The specific aims of this course are:
* to present the main concepts and current experimental approaches for the study of genomes and transcriptomes.
* to illustrate technological developments in the fields of Genomics and Transcriptomics.
* to present to the student real problems on experimental data in order to resolve them by using resources and methodologies presented through the course.

COMPETENCIES/LEARNING RESULTS FOR THE SUBJECT

COMPETENCIAS DE LA ASIGNATURA

Acquisition of knowledge of experimental techniques and designs in Structural and Functional Genomics, and in Transcriptomics.

Ability to carry out bioinformatic analyses of genomic and transcriptomic data, both from microarrays and RNA sequencing.

Management of the necessary tools for obtaining biological information and interpretation from Omics data and drawing conclusions

Gaining information on the various applications of Omics analysis, especially in its translational aspect, according to specialists and researchers in this area.

RESULTADOS DE APRENDIZAJE DE LA ASIGNATURA

Theoretical and Practical Contents

THEORETICAL FRAMEWORK

Unit 1
Introduction to Genomics. Genomes sequencing. The human genome.

Unit 2
Annotation of genomes. Comparative genomics. The genome of model species in Biomedicine. Genes Ontology.

Unit 3
Bioinformatics analysis of sequences. Databases. Comparisons by similarity. Alignments of sequences ang genomes.

Unit 4
Analisis of the genomic variation. Single Nucleotide Polymorphisms (SNPs): Detection and genotyping technologies. Genomic variation in the human species and its relationship with health.

Unit 5
Linkage disequilibrium and Haplotype maps. SNPs technology applications: QTLs mapping and association studies with diseases.

Unit 6
Analysis of genomic expression. DNA microarrays and RNA sequencing. Experimental design and methodologies.Other tools: CGH, Chip on Chip.

Unit 7
Data mining.
Statistical analysis of microarray data.

Unit 8
Advanced topics in Genomics and Transcriptomics

COMPUTER PRACTICES

(1)Topic 1: Databases and tools for the analysis of sequences and genomes.
(2)Topic 2: Analysis of High Througput Sequencing data.
(3)Topic 3: SNPs: detection and genotyping.
(4)Topic 4: Statistical analysis of whole genome expression.
(5)Topic 4: Data mining: biological significance of whole expression results.

METODOLOGIA (ACTIVIDADES FORMATIVAS)

Actividad Formativa	Hours	Porcentaje presencialidad
Drawing up reports and presentations	25	0 %
Working with it equipment	50	50 %
Expositive classes	50	50 %

TYPES OF TEACHING

Types of teaching	M	S	GA	GL	GO	GCL	TA	TI	GCA
Hours of face-to-face teaching	25				25				
Horas de Actividad No Presencial del Alumno/a	38				37				

Legend:
M: Lecture-based
S: Seminar
GA: Applied classroom-based groups
GL: Applied laboratory-based groups
GO: Applied computer-based groups
GCL: Applied clinical-based groups
TA: Workshop
TI: Industrial workshop
GCA: Applied fieldwork groups

Evaluation tools and percentages of final mark

Denominación	Ponderación mínima	Ponderación máxima
Attendance and participation	0 %	50 %
Otros: Trabajos prácticos /Valoración por parte del Tribunal del trabajo escrito	0 %	50 %

ORDINARY EXAMINATION PERIOD: GUIDELINES AND OPTING OUT

Evaluation will be based on three points:
1) Attendance and participation in class. Class attendance is mandatory. Excused absences may be made up with the activity proposed by the professor in charge of the session. Unexcused attendance of less than 80% of the sessions will result in the failure of the course.
2) Presentation and discussion of scientific papers
3) Practical works on experimental data by bioinformatics methods.

The lack of delivery of the practical works will suppose resignation of the call for evaluation and will be recorded as Not Presented.

EXTRAORDINARY EXAMINATION PERIOD: GUIDELINES AND OPTING OUT

The extraordinary call will involve the completion of an exam on the contents of the subject. The exam will consist of the development of a topic covered in the subject and it will be chosen from two topics elected at random.

MANDATORY MATERIALS

The graphic material used in the master classes by each professor will be stored in e-gela, or sent by e-mail to all students.

BIBLIOGRAPHY

Basic bibliography

1. Malconm Campbell, A. & Heder Laurie J.A. 2003. Discovering Genomics, Proteomics and Bioinformatics. Pearson Education, Inc. Benjamin Cummings, San Francisco
2. Gibson G. and Muse, S.V. 2004. A primer of Genome Sciences. Sinauer Associates, Inc.
3. Azuaje, F.,Dopazo, J (Eds.).2005. Data analysis and visualization in Genomics and Proteomics. Wiley
4. Mount DW.2001. Bioinformatics. Sequence and Genome analysis. Applications in Biological Science and Medicine. CDR Press, Boca Raton
5. Baxevanis, A.D., Ouellette, B.F.F. 2001. Bioinformatics. A practical guide to the analysis of genes and proteins. 2nd ed. Wiley interscience.
6. Pevsner J. 2015. Bioinformatics and functional Genomics. Wiley Blackwell. 3rd. ed. ISBN 978-1-118-58178-0
7. Korpelainen E., Tumala J., Somervuo R., Huss M, Wong G. RNA-seq analysis: a practical approach. Chapman and Hall/CRC Computational Biology Series. 2014.ISBN-10:1466595000

Detailed bibliography

Specific bibliography for each unit will be provided through the course by each professor.

Journals

Other papers selected from important journals such as NATURE, SCIENCE, CELL, Molecular cell, EMBO J., NATURE GENETICS will be selected for reading and discussion.

Web sites of interest

(1) NCBI databases https://www.ncbi.nlm.nih.gov
(2) EBI databases https://www.ebi.ac.uk/services
(3) USCS genome browser http://genome.ucsc.edu
(3.1.) UCSC Table Browser (within https://genome-euro.ucsc.edu/)
(4) Ensembl http://www.ensembl.org/
(5) Galaxy https://usegalaxy.org/
(6) SIFT, PolyPHEN (from within Galaxy) and wANNOVAR (wannovar.wglab.org/)
(7)PantherDB http://pantherdb.org/
(8)WebMeV (Multiple Experiment Viewer) http://mev.tm4.org/#/
(9)DAVID https://david.ncifcrf.gov/
(10)Babelomics http://www.babelomics.org/