COURSE DATA

DATA SUBJECT

Code: 42709
Name: Omics techniques for massive data collection
Cycle: Master's Degree
ECTS Credits: 6
Academic year: 2026-27

STUDY (S)

Degree	Center	Acad. year	Period
2116 - Master's Degree in Bioinformatics	Escola Tècnica Superior d'Enginyeria	1	Second quarter

SUBJECT-MATTER

Degree	Subject-matter	Character
2116 - Master's Degree in Bioinformatics	Omics techniques for massive data collection	COMPULSORY

COORDINATION

GIL GARCIA ROSARIO

SANCHEZ DEL PINO MANUEL MATEO

DZUNKOVA - MARIA

SUMMARY

The subject "Omics Techniques" is studied in the second semester of the Master in Bioinformatics at the University of Valencia. This is a compulsory subject, so it must be filed by all students.

Omics technologies have occupied since late last century a leading role in much of scientific discoveries in the fields of biology covered by this Master. The term genomics was coined in 1986 to refer to the subdiscipline of genetics devoted to the study of mapping, sequencing and functional analysis of complete genomes. Subsequently extended the suffix "omics" to many other disciplines have in common be globalizing and used in all fields of biology today. since much of the content of these omics sciences is methodological and most prospective students should already possess them the basics of this subject focuses mainly on the study of the methodologies and applications that have now research in Molecular and Cellular Biology, Genetics and Microbiology.

PREVIOUS KNOWLEDGE

RELATIONSHIP TO OTHER SUBJECTS OF THE SAME DEGREE

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

OTHER REQUIREMENTS

Students must have a sufficient level of knowledge of Molecular Biology and Genetics.

COMPETENCES / LEARNING OUTCOMES

2116 - Master's Degree in Bioinformatics

Be able to access the information required (databases, scientific articles, etc.) and to interpret and use it sensibly.

Be able to access to information tools in other areas of knowledge and use them properly.

Comprender las capacidades y las limitaciones de las técnicas ómicas así como del tipo de información biomédica relevante que se puede obtener de ellas y saber analizar y adquirir una clara visión del futuro.

Desarrollar la iniciativa personal y ser capaces de realizar una toma rápida y eficaz de decisiones en su labor profesional y/o investigadora.

Students should apply acquired knowledge to solve problems in unfamiliar contexts within their field of study, including multidisciplinary scenarios.

Students should be able to integrate knowledge and address the complexity of making informed judgments based on incomplete or limited information, including reflections on the social and ethical responsibilities associated with the application of their knowledge and judgments.

Students should communicate conclusions and underlying knowledge clearly and unambiguously to both specialized and non-specialized audiences.

Students should demonstrate self-directed learning skills for continued academic growth.

Students should possess and understand foundational knowledge that enables original thinking and research in the field.

To be able to assess the need to complete the scientific, historical, language, informatics, literature, ethics, social and human background in general, attending conferences, courses or doing complementary activities, self-assessing the contribution of these activities towards a comprehensive development.

Trabajar en equipo con eficiencia en su labor profesional y/o investigadora y con personas de diferente procedencia.

DESCRIPTION OF CONTENTS

1. General concepts of omics technologies

The era of omics sciences. Functional genomics and other omics (proteomics, metabolomics, fluxomics, etc.). Study subject, comprehensive approaches, and analysis of results.

2. Structural genomics

DNA sequencing methods for complete genomes. Current massive sequencing (NGS) methodologies. Third-generation sequencing. Whole genome assembly. Genome annotation and functional analysis. Genotyping and resequencing. Metagenomics.

3. Functional genomics

Global gene expression. Different types of RNA. Microarrays. RNA-seq library preparation and data analysis. Metatranscriptomics. Eukaryotic and prokaryotic single-cell transcriptomics. Epigenomics. Multi-omics.

4. Proteomics

Sample preparation and separation. Post-translational modifications, macromolecular complexes, and protein interactions. Mass spectrometry. Peptide instrumentation, fragmentation, and sequencing. LC-MS/MS data acquisition methods. Large-scale protein identification and quantification. Applications.

WORKLOAD

PRESENCIAL ACTIVITIES

Activity	Hours
Theory	30,00
Total hours	**30,00**

NON PRESENCIAL ACTIVITIES

Activity	Hours
Attendance at other activities	5,00
Individual or group project	5,00
Independent study and work	74,00
Preparation of lessons	0,00
Preparation for assessment activities	12,00
Resolution of case studies	17,00
Total hours	**113,00**

TEACHING METHODOLOGY

The following teaching methods will be used for activities of this module:

1) Lectures. Method based on the exhibition/lecture and case study

2) Laboratory. In the Genomics Service (SCSIE) the students will see a demonstration of the operation of the sequencing equipment and DNA chips.

3) Presentation of case studies and interpretation of results (in computer room).

4) Personal Tutoring. Assist and guide students in relation to problems arising during the development of activities and non-contact.

EVALUATION

Continuous student assessment based on classroom or laboratory interaction or online activities (15%).

Assessment of submitted reports or papers related to training activities on problems and case studies, cross-curricular activities, or other proposed activities (45%).

Assessment of in-person exams (40%). The final exam for each of the three parts of the course (Structural Genomics, Functional Genomics, and Proteomics) will be conducted independently and will be graded equally. The course assessment system requires passing a minimum overall grade (50%) as well as minimum grades (20%) in each of the three parts.

For the second examination session, all assessment activities will be recoverable except for visits, and the score for the subject sections in which at least a grade of 5 was achieved may be saved (if requested).

REFERENCES

- Chee-Seng, K. et al. (2010). Next generation sequencing technologies and their applications. In: Encyclopedia of Life Sciences (ELS). John Wiley & Sons.
- Metzker, ML (2010). Sequencing technologies the next generation. Nat. Rev. Genet., 11: 31-46.
- Brent, M. R. (2006). Genome annotation past, present, and future: How to define an ORF at each locus. Genome Res., 15:1777-1786.
- Handelsman, J. (2004). Metagenomics: application of genomics to uncultured microorganisms. Microbiol. Mol. Biol. Rev., 68: 669-685.

- Xu, Y., and Gogarten, J. P. (2008). Computational Methods for Understanding Bacterial and Archaeal Genomes. Series on Advances in Bioinformatics and Computational Biology, vol. 7. Imperial College Press, London.

- Pérez-Ortín, J.E.; Alepuz, P. y Moreno; J. (2007). Genomics and gene transcription kinetics in yeast. Trends Genet. 23, 250-257.

- Eidhammer, I., Flikka, K., Martens, L., and Mikalsen, S.-O. (2008). Computational Methods for Mass Spectrometry Proteomics (Wiley-Interscience).

- Bar-Even A. et al. (2006). Noise in protein expression scales with natural protein abundance. Nat. Genet. 38: 636-643.

- Myers, C. L., et al., 2005. Discovery of biological networks from diverse functional genomic data. Genome Biology, 6: R114

- Biological database compilation at NAR: http://nar.oupjournals.org/content/vol29/issue1

- EMBL (European Molecular BIology Laboratory), Bioinformatics. http://www-db.embl.de/jss/servlet/de.embl.bk.emblGroups.EmblGroupsOrg/serv_0?t=0

- ExPASy (Expert Protein Analysis System). http://us.expasy.org/

- GenomeNet (Kyoto University Bioinformatics Center). http://www.genome.jp/

- Gene Ontology Consortium. http://www.geneontology.org/GO.consortiumlist.shtml

- GOLD (Genomes Online Database). http://www.genomesonline.org/

- KEGG (Kyoto Encyclopedia of Genes and Genomes). http://www.genome.jp/kegg/kegg2.html

- MINT: Molecular Interaction Database. http://mint.bio.uniroma2.it/mint/Welcome.do

- NCBI (National Center for Biotechnology Information). http://www.ncbi.nlm.nih.gov/

- Saccharomyces Genome Database. http://www.yeastgenome.org/