VNIVERSITAT DE VALÈNCIA

Course Guide
43458 Omic technologies

COURSE DATA

Data Subject	
Code	43458
Name	Omic technologies
Cycle	Master's degree
ECTS Credits	3.0
Academic year	2022 - 2023

Study (s)

Degree	Center	Acad. year	Period
2210 - M.D. in Research in Molecular, Cellular and Genetics Biology	Faculty of Biological Sciences	1	First term
3102 - Biomedicine and Biotechnology	Doctoral School	0	First term

Subject-matter

Degree	Subject-matter	Character
2210 - M.D. in Research in Molecular, Cellular and Genetics Biology	3 - Omic technologies	Obligatory
3102 - Biomedicine and Biotechnology	1 - Complementos de Formación	Optional

Coordination

Name	Department
GIL GARCIA, ROSARIO	194 - Genetics

SUMMARY

The subject "Omics Technologies" is scheduled in the first semester of the Master of Research in Molecular and Cellular Biology and Genetics at the University of Valencia. It is a mandatory subject, so it must be taken by all students.

Omics technologies have occupied since late last century a leading role in many of the scientific discoveries in the biological fields covered by this Master. The term Genomics was coined in 1986 to refer to the subdiscipline of genetics devoted to the study, mapping, sequencing and analysis of complete genomes. Subsequently the suffix "omics" has been extended to many other current disciplines in all fields of Biology that share this globalizing approach. The omics sciences have an important methodological component, and most prospective students must possess basic knowledge on this subject. Therefore, this module focuses mainly on the study of methodologies and applications in current research on 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

OUTCOMES

2210 - M.D. in Research in Molecular, Cellular and Genetics Biology

- 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.
- Be able to make quick and effective decisions in professional or research practice.
- Be able to access the information required (databases, scientific articles, etc.) and to interpret and use it sensibly.
- Students should possess and understand foundational knowledge that enables original thinking and research in the field.
- Be able to access to information tools in other areas of knowledge and use them properly.
- 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.
- Diseñar experimentos para abordar análisis de poblaciones celulares, expresión génica, cuantificación de mRNAs o proteínas.
- Ser capaz de interpretar los resultados derivados de la aplicación de las nuevas técnicas ómicas en biología molecular y celular.

LEARNING OUTCOMES

Knowledge on the foundation of the omics techniques, their applicability in terms of advantages and limitations, understanding their rationale and the interpretation of the results generated.

DESCRIPTION OF CONTENTS

1. The era of the omics sciences

Functional genomics and other omics. Study subject, global approaches and analysis of results.
Professor Rosario Gil

2. DNA sequencing methods for complete genomes

Current high throughput sequencing HTS) methodologies. Third generation sequencing technolgies. Complete genomes assembly. Annotation and functional analysis of genomes. Metagenomics and Metatranscriptomics.
Professor Rosario Gil

3. Methods of analysis of global gene expression

Comparison of methods for individual and global analysis. Serial analysis of gene expression (SAGE) and derivative methods. The chips or DNA microarrays: principles and applications. Analysis of results. Transcriptomic studies with DNA chips. The functional organization of eukaryotic genomes. HTS for transcriptomics. ChIP-chip and ChIP-seq.
Professor José García Martínez

4. Global phenotypic studies

Phenomics. Deletion mutant collections or with iRNA. Gene fusions collections. Analysis techniques for phenotypic studies.
Professor José García Martínez

5. Separation of proteins for proteomics

Preparation of samples for analysis by proteomic techniques. Separation techniques for peptides and proteins. Bottom-up and Top-down Proteomics.
Professor Manuel Sanchez del Pino

6. Mass spectrometry: instrumentation and procedures

Ionization of biological samples and mass analyzers used in proteomics. Fragmentation and de novo sequencing of peptides. Experiments of LC-MS/MS and data acquisition methods.
Professor Manuel Sanchez del Pino

7. Protein identification and quantitation

Protein identification methods. Using search engines. Analysis of macromolecular complexes. Protein quantitation: labeling and label-free methods. Targeted proteomics (SRM / MRM). Analysis of interaction networks and metabolic pathways.
Professor Manuel Sanchez del Pino

WORKLOAD

ACTIVITY	Hours	% To be attended
Theory classes	17,00	100
Classroom practices	7,00	100
Computer classroom practice	3,00	100
Laboratory practices	3,00	100
Preparation of evaluation activities	45,00	0
TOTAL	**75,00**	

TEACHING METHODOLOGY

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

1. Theoretical lectures and case-study sessions.
2. Practical activities in small groups. Visit to the Genomics and Proteomics facilities (SCSIE) to have a first-hand knowledge of the functioning of the sequencing, mass spectrometry and two-dimensional electrophoresis equipment.
3. Presentation of case studies and interpretation of results.
4. Tutorial sessions, in order to assist and guide students regarding problems arising during the development of the course.

EVALUATION

1. Written test with three parts, each one of 45 minutes. One of the questions will correspond to the resolution of a practical case. The final grade of the written test will be the average of all three parts. It will be necessary to achieve at least a score of 3 out of 10 in each part in order to pass the subject. This test will represent 95% of the final course grade.

On the second call, it will be not necessary to repeat the part of the subject in which the student reached a score at or above 5 on the first call, if the student considers it appropriate.

2. Participation in visits to Sequencing and Proteomics Services at SCSIE: 2.5% for each visit.

REFERENCES

Basic

- Bamshad MJ et al. (2011). Exome sequencing as a tool for Mendelian disease gene discovery. Nat Rev Genet 12: 745-755.
- Bunnik EM, Le Roch KG (2013). An Introduction to Functional Genomics and Systems Biology. Adv Wound Care 2: 490498.
- Chee-Seng K et al. (2011). Next generation sequencing technologies and their applications. In: Encyclopedia of Life Sciences (ELS). John Wiley & Sons.
- Corrales F, Calvete JJ (2014). Manual de Proteómica. Sociedad Española de Proteómica.
- Eidhammer I et al. (2008). Computational Methods for Mass Spectrometry Proteomics (Wiley-Interscience).
- Ekblom R, Wolf B W (2014). A field guide to whole-genome sequencing, assembly and annotation. Evo. Appl 7: 1026-1042.
- Gasperskaja E, Ku inskas V. (2017). The most common technologies and tools for functional genome analysis. Acta Med Litu 24: 111. doi:10.6001/actamedica.v24i1.3457
- Goodwin S et al. (2016). Coming of age: ten years of next-generation sequencing technologies. Nat Rev Genet 17: 333351.
- Götz S et al. (2008). High-throughput functional annotation and data mining with the Blast2GO suite. Nucleic Acids Res 36: 3420-3435.
- Gresham D et al. (2008). Comparing whole genomes using DNA microarrays. Nat Rev Genet 9: 291302.
- Haas B J, Zody M C (2010). Advancing RNA-Seq analysis. Nat Biotechnol 28: 421-423.
- Hrdlickova et al. (2017). RNA-Seq methods for transcriptome analysis. Wiley interdisciplinary reviews. RNA 8: 10.1002/wrna.1364. doi:10.1002/wrna.1364
- Kanehisa M et al. (2012). KEGG for integration and interpretation of large-scale molecular data sets. Nucleic Acids Res 40: D109D114.
- Keseler IM et al. (2012). EcoCyc: fusing model organism databases with systems biology. Nucleic Acids Res 41: D605-D612.
- Kulski JK (2015). Next-Generation Sequencing An overview of the history, tools and omic applications. In Next Generation Sequencing - Advances, Applications and Challenges, Kulski J (Ed.), InTech, DOI: 10.5772/61964.
- Kurdyukov S, Bullock M (2016). DNA methylation analysis: choosing the right method. Biology 5: 121.
- Metzker ML (2010). Sequencing technologies the next generation. Nat Rev Genet 11: 31-46.
- Morgan CX, Hutternhower C (2012). Human Microbiome Analysis. PLoS Comp Biol 8: e1002808.

- Myers CL et al., 2005. Discovery of biological networks from diverse functional genomic data. Genome Biology 6: R114.
- Nagarajan N, Pop M (2013). Sequence assembly demystified. Nat Rev Genet 14: 157-167.
- Pérez-Ortín JE et al (2007). Genomics and gene transcription kinetics in yeast. Trends Genet 23: 250-257.
- Richardson EJ, Watson M (2012). The automatic annotation of bacterial genomes. Brief Bioinform. doi: 10.1093/bib/bbs007.
- Teeling H, Glöckner FO (2012). Current opportunities and challenges in microbial metagenome analysis-a bioinformatic perspective. Brief Bioinform 13: 728-742.
- The ENCODE Project Consortium (2012). An integrated encyclopedia of DNA elements in the human genome. Nature 489: 5774

Additional

- Internet:
  1000 Genomes: A Deep Catalog of Human Genetic Variation. http://www.1000genomes.org/
  BioCyC: http://biocyc.org/
  Blast2GO: http://www.blast2go.com/home
  EMBL-EBI (European Bioinfomatics Institute). http://www.ebi.ac.uk/
  ExPASy (Expert Protein Analysis System). http://us.expasy.org/
  Gene Ontology Consortium. http://www.geneontology.org/
  GenomeNet (Kyoto University Bioinformatics Center). http://www.genome.jp/
  GOLD (Genomes Online Database). http://www.genomesonline.org/
  Human Genome Project Information.
  http://www.ornl.gov/sci/techresources/Human_Genome/home.shtml
  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
  National Human Genome Research Institute: http://www.genome.gov/
  NCBI (National Center for Biotechnology Information). http://www.ncbi.nlm.nih.gov/
  Nextprot. https://www.nextprot.org
  NIH Human Microbiome Project. https://hmpdacc.org/
  Saccharomyces Genome Database. http://www.yeastgenome.org/
  STRING. https://string-db.org
  The ENCODE Project: ENCyclopedia Of DNA Elements. http://www.genome.gov/10005107
  The Human Protein atlas. https://www.proteinatlas.org