COURSE DATA

Data Subject	
Code	42709
Name	Omics techniques for massive data collection
Cycle	Master's degree
ECTS Credits	6.0
Academic year	2022 - 2023

Study (s)

Degree	Center	Acad. year	Period
2116 - M.U. en Bioinformática 12-V.1	School of Engineering	1	Second term

Subject-matter

Degree	Subject-matter	Character
2116 - M.U. en Bioinformática 12-V.1	4 - Omics techniques for massive data collection	Obligatory

Coordination

Name	Department
GIL GARCIA, ROSARIO	194 - Genetics
PEREZ ORTIN, JOSE ENRIQUE	30 - Biochemistry and Molecular Biology
SANCHEZ DEL PINO, MANUEL MATEO	30 - Biochemistry and Molecular Biology

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 25 years ago 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.

OUTCOMES

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- 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.
- 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.
- Desarrollar la iniciativa personal y ser capaces de realizar una toma rápida y eficaz de decisiones en su labor profesional y/o investigadora.
- Trabajar en equipo con eficiencia en su labor profesional y/o investigadora y con personas de diferente procedencia.
- 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.

LEARNING OUTCOMES

Understanding the foundation of the omics techniques, their rationale and the interpretation fo the generated results.
Knowledge of the capabilities, the implications and limitations of the omics techniques.
Practicing protein identification by analyzing a peptide footprint.
Understanding what relevant biomedical information that can be obtained from these techniques and what is its scope.
Analyze the future of these technologies and the resources / information obtained.

DESCRIPTION OF CONTENTS

1. General concepts in omics technologies

The era of omics sciences. Functional genomics and other omics. Subject, a globalizing approaches and analysis of results

2. DNA sequencing methods for complete genomes

Current methodologies high throughput sequencing (HTS). Third generation of HTS. Whole-genome assembly. Annotation and functional analysis of genomes. Metagenomics and Metatranscriptomics.

3. 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. High throughput sequencing for transcriptomic studies. ChIP-chip and ChIP-seq.

4. Epigenomics and Phenomics

Epigenomics. ChIP-chip and ChIP-seq. Collections of deletion mutants or off with iRNA. Collections of gene fusions. Analysis techniques for phenotypic studies.

5. Sample preparation and separation in Proteomics

Preparation of samples for analysis by proteomic techniques. Separation techniques of peptides and peptides and proteins. Bottom-up and top-down proteomics

6. Mass Spectrometry: Instrumentation and Procedures

Ionization of biological samples and types of mass analyzers. Fragmentation and de novo sequencing of peptides. LC-MS/MS experiments and data acquisition methods in proteomics.

7. Protein identification and quantification

Protein identification methods. Use of search engines. Analysis of macromolecular complexes. Protein quantification: methods with and without labeling. directed proteomics.
Analysis of interaction networks and metabolic pathways.

WORKLOAD

ACTIVITY	Hours	% To be attended
Theory classes	30,00	100
Attendance at events and external activities	2,00	0
Study and independent work	30,00	0
Readings supplementary material	40,00	0
Preparation of practical classes and problem	8,00	0
Resolution of case studies	40,00	0
TOTAL	**150,00**	

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

For the evaluation, the resolution during the academic year of practical questions, a final exam (96%) of theoretical or applied knowledge and the attendance to theoretical or practical sessions (4%). The final exam of each of the 3 parts of the course will be carried out independently and with equal assessment, between the 3 parts (Structural Genomics, Functional and Proteomics). The subject's evaluation system implies passing a global minimum (50%) as well as a minimum (20%) in each of the three parts. For the 2nd examination session (July), the qualifications of visits and practical questions will be saved and the

mark of one or two of the three parts of the subject can be saved (if requested).

REFERENCES

Basic

- 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

Additional

- 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/