

Course Unit	Genomic and proteomic		Field of study	Biology and biochemistry	
Bachelor in	Biology and Biotechnology		School	School of Agriculture	
Academic Year	2022/2023	Year of study	3	Level	1-3
Type	Semestral	Semester	1	ECTS credits	6.0
Code	9029-510-3105-00-22				
Workload (hours)	162	Contact hours	T 30	TP -	PL 30
			TC -	S -	E -
			OT 4	O -	

T - Lectures; TP - Lectures and problem-solving; PL - Problem-solving, project or laboratory; TC - Fieldwork; S - Seminar; E - Placement; OT - Tutorial; O - Other

Name(s) of lecturer(s) Altino Branco Choupina, Joaquina Teresa Gaudêncio Dias

Learning outcomes and competences

At the end of the course unit the learner is expected to be able to:

1. Understand the structure of eukaryotic and prokaryotic genomes.
2. Building physical maps of genes and chromosomes and sequencing and analysis of whole genomes.
3. To know the main techniques available for comparing genomes.
4. Build and analyze genomics and cDNA libraries.
5. To be able to detect transcripts and to study the differential expression of transcripts.
6. Understand the dynamic nature of the proteome.
7. Know the main methodologies used to analyze the proteome: uni and bi-dimensional electrophoresis, mass spectroscopy, chromatography, X-Ray crystallography and bioinformatics methodologies.
8. Develop skills that allow the application of different approaches in the field of Genomics and Proteomics.

Prerequisites

Before the course unit the learner is expected to be able to:

Basic computer science knowledge. Molecular biology and genetics principles. Statistics.

Course contents

Genes and Chromosomes physical mapping and genome sequencing. Eukaryotic and Prokaryotic genome structure. Genomic and cDNA library construction and analysis. Transcript detection and differential expression studies. Proteomics general concepts. Methodologies for the analysis of the proteome: uni and bi-dimensional electrophoresis, liquid chromatography and mass spectrometry. Experimental determination and prediction of protein structures: X-ray crystallography, NMR and homology modeling.

Course contents (extended version)

1. Strategies for genome sequencing:
 - YACS.
 - Cosmids.
 - Frequent cut enzymes.
2. Mapping genomes using physical methods:
 - Cosmids and YACS extremities localization and marking.
 - Fish and Prins.
3. Comparative genetic and genomic annotation.
4. cDNA library construction (conventional, subtractive and normalized).
5. Transcriptome sequencing and analysis: ESTs and ORESTES.
6. Genetic expression evaluation: Differential display, SAGE, RT-PCR, Microarrays, iRNA.
7. General concepts in Proteomics.
8. Principal methodologies using in Expression Proteomics:
 - Sample processing and protein extract preparation.
 - Methods for protein separation: uni and bi-dimensional polyacrylamide gel electrophoresis.
 - Methods for protein gel detection.
 - Methods for protein identification: mass spectrometry and antibodies.
 - Gel Electrophoresis data analysis using bioinformatics tools.
 - Chromatographic methods for protein separation: ionic exchange, molecular exclusion and affinity.
9. Examples of expression proteomics clinical and biotechnology application:
 - Discovery of new protein biomarkers in different pathologies.
 - Discovery of new protein targets for the development of new drugs.
 - Discovery of new protein products of natural origin with increase commercial value.
10. Main methodologies used in Structural Proteomics:
 - Experimental 3D protein structures determination using X-Ray crystallography and NMR.
 - Prediction of 3D protein structures using homology modeling and Ab initio bioinformatics tools.

Recommended reading

1. Ginsburg G. S. and Huntington F. W. (2013). Genomic and Personalized Medicine, Second Edition. Elsevier Inc.
2. Lesk. A. M. (2012). Introduction to Genomics Second Edition. Amazon. com, Inc.
3. Pevsner J. (2015). Bioinformatics and Functional Genomics, Third Edition. Wiley-Blackwell Inc.
4. Lovric J. (2011) Introducing Proteomics: From Concepts to Sample Separation, Mass Spectrometry and Data Analysis. First Edition, Wiley-Blackwell Press, New Jersey, USA.
5. Sallam R. M. (2015) Proteomics in cancer biomarkers discovery: challenges and applications. Disease Markers, Review, 1-12.

Teaching and learning methods

Lectures - 2 lessons per week for 1 hour. Theoretical approach using the multimedia and audiovisual means. Provision of study materials via the e-learning resources. Practical classes - 1 lesson weekly for 2 hours. Realization of practical laboratory work, with the equipment available in the laboratory of Molecular Biology, Biochemistry and Informatics.

Assessment methods

- Alternative 1 - (Regular, Student Worker) (Final, Supplementary, Special)
- Intermediate Written Test - 25% (Theoretical component of Genomics.)
- Final Written Exam - 25% (Theoretical component of Proteomics.)

Assessment methods

- Reports and Guides - 50% (Practical evaluation: written reports about practical laboratory and computational classes.)

Language of instruction

1. Portuguese
2. English

Electronic validation

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20-12-2022	20-12-2022	20-12-2022	20-12-2022