UNIVERSITÀ DEGLI STUDI DI PALERMO

DEPARTMENT	Biomedicina, Neuroscienze e Diagnostica avanzata
ACADEMIC YEAR	2019/2020
MASTER'S DEGREE (MSC)	MEDICAL BIOTECHNOLOGIESD AND MOLECULAR MEDICINE
INTEGRATED COURSE	PROTEOMIC METHODOLOGIES AND BIOINFORMATICS - INTEGRATED COURSE
CODE	19367
MODULES	Yes
NUMBER OF MODULES	2
SCIENTIFIC SECTOR(S)	BIO/13, ING-INF/05
HEAD PROFESSOR(S)	VITABILE SALVATORE Professore Ordinario Univ. di PALERMO
OTHER PROFESSOR(S)	VITABILE SALVATORE Professore Ordinario Univ. di PALERMO FONTANA SIMONA Professore Associato Univ. di PALERMO
CREDITS	9
PROPAEDEUTICAL SUBJECTS	
MUTUALIZATION	
YEAR	1
TERM (SEMESTER)	1° semester
ATTENDANCE	Mandatory
EVALUATION	Out of 30
TEACHER OFFICE HOURS	**FONTANA SIMONA** Thursday 15:30 16:30 Dipartimento di Biomedicina, Neuroscienze e Diagnostica avanzata, Sezione di Biologia e Genetica - Via Divisi, 83. A causa di possibili altri impegni istituzionali o riunioni di lavoro potrebbe non essere possibile ricevere gli studenti nel giorno e alle ore indicate. Per questo e preferibile comunque fissare un appuntamento via e-mail. **VITABILE SALVATORE** Monday 16:30 18:30 Piattaforma Microsoft Teams, Dipartimento di Biomedicina, Neuroscienze e Diagnostica avanzata, Plesso di Radiologia – 1° piano, Stanza n. 108.

PREREQUISITES	The required prerequisites concern the deep knowledge of structure and functions of nucleic acid and proteins as well as the correlated molecular processes (replication, transcription and translation).
LEARNING OUTCOMES	Knowledge and Understanding – Student will be expected to know and understand: (1) Theory of the main experimental methodologies used for analyzing protein structure, function and mechanisms of regulation; (2) the bio-molecular meaning of spatio-temporal analysis of gene expression; (3) main proteomic methodologies; (4) bioinformatics tools and procedures for experimental genetic and protein data analysis; (5) biological database organization and access models and related search strategies; (6) advanced strategies for pairwise and multiple sequence alignments (for both gene and protein). Applying knowledge and understanding – Learning and ability to apply knowledge by the student will be focused to the opportunity to develop adequate skills within the field of bioinformatics and for applying advanced proteomic technologies Making judgments – The teaching activities carried out during the course will allow student to develop the ability to evaluate and integrate in an autonomous and critical manner in order to select the most adequate proteomic strategies and bioinformatics procedures for achieving a specific experimental aim. Communication skills - During the course it will be underlined the importance to communicate in a comprehensible way, even to non-experts, the meaning of proteomic studies, the different areas in which it is possible to apply the experimental techniques and of bioinformatics procedures discussed during the course Learning ability – Student will gain competence and adequate skills to develop future studies through the application of proteomic strategies and the use of bioinformatics tools.
ASSESSMENT METHODS	The evaluation phase is based on a final interview aimed at evaluating both knowledge and full understanding of the issues dealt with during the course as well as the candidate's ability to present and elaborate the main course concepts. The use of the computer is also foreseen in order to verify the ability to select and use the resources contained in the digital biological databases. The vote is expressed in thirtieth, with a positive result when the total final score ranges between 18 and 30. In order to reach a positive evaluation, a candidate will have to answer at least three oral questions concerning the topics of the course, with a reference to the teaching materials provided by the teacher and/ or the suggested texts. The final evaluation aims at assessing both the level of knowledge and understanding gained by a candidate on the topics of the course as well as its acquisition of interpretative competence and autonomy of judgment in the implementation of appropriate experimental procedures in proteomics and bioinformatics domains. The level of sufficiency will be reached when a candidate shows general knowledge and understanding of the main course topics and guidelines and demonstrates minimal skills in appropriate application of proteomics and bioinformatics techniques aimed at the realization of specific examples of experimental studies; he/she has also to exhibit communication skills and arguments for transferring its knowledge and understanding to the examiners. Below this threshold, the examination result will be insufficient. The more a candidate with its arguments and knowledge is able to interact with the examiners and its knowledge and skills emerge in using of appropriate techniques for carrying out proteomic studies and automatic biological data analysis tasks, the higher the evaluation vote will be.
TEACHING METHODS	The course is organized through academic lectures, which take place in the classroom with the help of slides and other teaching materials, and training practices, which take place in laboratories and computer room.

MODULE
PRINCIPLES OF BIOINFORMATICS

Prof. SALVATORE VITABILE

SUGGESTED BIBLIOGRAPHY

Manuela Helmer Citterich, Fabrizio Ferre, Giulio Pavesi, Graziano Pesole, Chiara Romualdo; Fondamenti di Bioinformatica; Zanichelli;
2018

AMBIT	20885-Attività formative affini o integrative
INDIVIDUAL STUDY (Hrs)	51
COURSE ACTIVITY (Hrs)	24

EDUCATIONAL OBJECTIVES OF THE MODULE

In this course, students will learn fundamental concepts and methods in bioinformatics, a field at the intersection of biology and computing. It surveys a wide range of topics including biological databases organization, structure, and search strategies; pairwise and multiple sequence alignment principles; the most common on-line alignment search tools; and microarrays image analysis. The final part of the course will be devoted to the introduction of one of the most used biological inspired model: the Artificial Neural Networks.

SYLLABUS

Hrs	Frontal teaching
4	Course introduction; Information representation and coding; Files and images; Databases.
2	Biological databases organization and structure.
2	Pairwise sequence alignment.
2	BLAST: Basic Local Alignment Search Tool
2	Multiple sequence alignment; Clustal Omega.
2	Microarray image analysis.
2	An introduction to Artificial Neural Networks.

Hrs	Practice
4	Search strategies in biological databases.
4	Sequence alignment.

MODULE
PROTEOMIC METHODOLOGIES

Prof.ssa SIMONA FONTANA

SUGGESTED BIBLIOGRAPHY	
Selezione di articoli scientifici	
AMBIT	50644-Discipline biotecnologiche comuni
INDIVIDUAL STUDY (Hrs)	102
COURSE ACTIVITY (Hrs)	48
EDUCATIONAL OBJECTIVES OF THE MODULE	
This Course has two main aims: 1) to enable students in understanding the molecular-biologic meaning of the spatio-temporal analysis of protein expression. 2) to provide students with the basic theoretical knowledge of proteomic methodologies (electrophoresis and mass spectrometry), the chemical and physical principles on which they are based and to present the recent advances and current applications.	

SYLLABUS

Hrs	Frontal teaching
2	Introduction to proteomics: Expression and funtional proteomics, proteomic Strategies
8	Proteomic techniques: gel-based approach and shot-gun approaches. Gel-based approach: •two-dimensional gel electrophoresis: from sample preparation to 2D-PAGE maps analysis •methods for protein spot identification: N-terminal microsequencing, Mass Spectrometry tecniques (MALDI-TOF and ESI-LC-MS/MS); PMF (Peptide Mass Fingerprinting) and tandem mass spectrometry (MS/MS) analises.
3	Shot-gun approaches: •LC-MS/MS •MudPIT •SELDI-TOF •ICAT
2	Mass Spectrometry for Post-Translational Modifications(PTMs)
2	Experimenta design of a proteomic study using a gel -based approach: statisticl analysis of data (uni and multivariate analysis). Critical analysis of a scientific paper example.
4	Bioinformatics: development and use of biological databases. System Biology.
3	Proteomic applications. 1. Characterization of cell phenotype: the stem cell phenotype
2	Examples of proteomic studies of stem cells.
2	Proteomic applications: 2.Clinical proteomics: meaning and use of biomarkers.
2	Critical analysis of a clinical proteomics paper example.
2	pharmacogenomics, pharmaproteomics and personalized medicine.

Hrs	Workshops
4	Data-dependet acquisition"(DDA) and "data independet acquisition"(DIA) methods. Discovery and targeted proteomics. The SWATH analysis.
6	Description and observation of mass spectrometer coupled with nano-LC system: TripleTof 5600+. Steps for system calibration.
6	Bioinforamtic analysis of mass spectrometry data. Use of specialized softwares for protein identification (discovery proteomics) and for quantitative analysis (targeted protetomics)