



UNIVERSITÀ DEGLI STUDI DI PALERMO

DEPARTMENT	Scienze e Tecnologie Biologiche, Chimiche e Farmaceutiche		
ACADEMIC YEAR	2016/2017		
MASTER'S DEGREE (MSC)	BIOETCHNOLOGIES FOR INDUSTRY AND SCIENTIFIC RESEARCH		
SUBJECT	FUNCTIONAL GENOMICS		
TYPE OF EDUCATIONAL ACTIVITY	B		
AMBIT	50596-Discipline biologiche		
CODE	08308		
SCIENTIFIC SECTOR(S)	BIO/18		
HEAD PROFESSOR(S)	FEO SALVATORE	Professore Ordinario	Univ. di PALERMO
OTHER PROFESSOR(S)			
CREDITS	6		
INDIVIDUAL STUDY (Hrs)	102		
COURSE ACTIVITY (Hrs)	48		
PROPAEDEUTICAL SUBJECTS			
MUTUALIZATION			
YEAR	1		
TERM (SEMESTER)	1° semester		
ATTENDANCE	Not mandatory		
EVALUATION	Out of 30		
TEACHER OFFICE HOURS	FEO SALVATORE Monday 12:00 14:00 Via Real Mastranza, Caltanissetta Tuesday 10:00 12:00 Viale delle Scienze Dip. STEBICEF, Palermo Wednesday 12:00 14:00 Via Real Mastranza, Caltanissetta Thursday 10:00 12:00 Viale delle Scienze Dip. STEBICEF, Palermo		

PREREQUISITES	The student to attend this course must have a good knowledge of basic genetics and molecular biology together with a good understanding of the principal cellular process occurring in prokaryotic and eukaryotic cells
LEARNING OUTCOMES	<p>Knowledge of genomics, namely on the organization, function and evolution of genomes, and Proteomics, as a complex expression of genes involved in the regulation of biological processes, at molecular and cellular level.</p> <p>Capacity to apply knowledge and understanding: the use and applications of experimental methods and bioinformatics specific knowledge for the analysis and manipulation of genomes, individual genes and proteins.</p> <p>Being able to work autonomously, also taking on responsibility of management of research projects.</p> <p>Acquire knowledge, written and oral, of the English language with specific reference to the typical technical terminology of field.</p> <p>Ability to search the network, browse and extract information from databases, critically analyze scientific literature and extrapolate its findings</p>
ASSESSMENT METHODS	<p>The tests that contribute to student assessment are: two written tests (one to be held in the middle "test in progress" and the other at the end of the course) and an oral presentation, using power point, in the classroom at the end of course on a topic agreed with the teacher. The written tests, each lasting 90 minutes, consist of thirty multiple choice questions and five open questions.</p> <p>Two pass each of the two quiz tests a minimum of 18 correct answers are required. The final exam grade, out of thirty, will be averaged by the grades obtained in the two written tests and in the oral presentation.</p> <p>The student who gives up or fails at least one of two written tests must undergo an oral examination on the entire program and produces the power point presentation.</p> <p>The tests described above are proposed to assess whether the student has acquired knowledge and understanding of the topics, has attained ability to interpret and to judge independently and has gained adequate analytical and communication skills. Examination is passed with the grade of 18, that corresponds to the acquirement of the minimum knowledge of the course contents limited to the main topics. Progressively higher grade will be assigned on the basis of preparation and ability in carrying out the above tests.</p>
EDUCATIONAL OBJECTIVES	The course aims at providing the student the basic theoretical information on the structure, evolution and organization of genomes, gene expression, and the codification and modification of proteins, linking them to specific methodologies applied to the study of single genes or the entire genome, emphasizing on the different perspective and application fields of the two methodological approaches .
TEACHING METHODS	Lectures and bioinformatic classwork
SUGGESTED BIBLIOGRAPHY	<ul style="list-style-type: none"> - G Gibson, S.V. Muse, Introduzione alla Genomica, Zanichelli - G. A. Caldwell et al., Genomica integrata, Ed. Edises - Articoli ed altro materiale monografico in lingua inglese verra' fornito dal docente durante il corso.

SYLLABUS

Hrs	Frontal teaching
4	Introduction to the course. Principles of the genetic analysis. Model organisms and the organization of their genomes: Yeast, Drosophila, Caenorhabditis, Arabidopsis, Mouse. Using genomic databases: FlyBase, Wormbase, TAIR and MGI.
12	Techniques for the global analysis of genomes and their plasticity (array-CGH, ChIP-on-Chip, exome, new generation sequencing, etc.). The microarray technology: microarrays for the study of SNPs, the global expression (mRNA and miRNA), the CNVs and the DNA-protein interactions. The gene expression database and statistical analysis of data. Their application in the study of tumors.
10	Eukaryotic genomes evolution. Mechanisms of genome evolution: Gene duplication, Whole genome duplication, Transposable elements, Mutation, Pseudogenes, Exon shuffling, Genome reduction and gene loss. Genome evolution and speciation. Classification systems for genes, structure and function, the gene families.
10	Production of recombinant proteins in eukaryotic cells. Expression systems in yeast and insect cells. Baculovirus: life cycle, shuttle vectors, purification of recombinant proteins. Handling of proteins: techniques for "in vitro" and "in vivo" mutagenesis.
Hrs	Practice
12	Computational Systems Biology. An overview and discussion of current bioinformatics resources most relevant to functional genomics investigations will be provided. These will include information on using genome browsers (EMBL-EBI – Ensembl, NCBI – Genome, UCSC – Encode), gene/protein annotation (GenCards), microarray/sequencing data repositories (NCBI-GEO, EMBL-EBI – Array express) and pathway analysis (DAVID, WEBGESTALT). Instruction on the integration of data into interaction and regulatory networks and systems biology approaches to mining and modelling of these data.