

<b>Academic subject: BIOINFORMATICS AND GENOME ANALYSIS</b>			
<b>Degree Class: LM-7</b>		<b>Degree Course:</b> BIOTECHNOLOGIES FOR THE QUALITY AND THE HEALTHINESS OF NUTRITION (CLM BQSA)	
		<b>Academic Year:</b> 2020/2021	
		<b>Kind of class:</b> Mandatory	<b>Year:</b> First
			<b>Period:</b> First Semester
			<b>ECTS: 6</b> divided into <b>ECTS lessons: 5</b> <b>ECTS</b> <b>exe/lab/tutor: 1</b>
<b>Time management, hours, in–class study hours, out–of–class study hours</b> lesson: 150    exe/lab/tutor: 12    in–class study: 40    out–of–class study: 98			
<b>Language:</b> Italian/English (optional)	<b>Compulsory Attendance:</b> no		
<b>Subject Teacher:</b> Claudio Lo Giudice, PhD	<b>Tel:</b> <b>e–mail:</b> <a href="mailto:claudio.logiudice@uniba.it">claudio.logiudice@uniba.it</a>	<b>Office:</b> Department of Biosciences, Biotechnologies and Biopharmaceutics  Room 41    Floor 1	<b>Office days and hours:</b> From Monday to Friday and at the end of each lesson. Timetable to be arranged via e-mail.
<b>Prerequisites:</b> Principles of molecular biology, biochemistry and genetics. Minimal knowledge of the Internet and the major search engines. Minimum knowledge of English.			
<b>Educational objectives:</b> Learning of the structural and functional characteristics of prokaryotic, eukaryotic and organellar genomes. Knowledge of the new sequencing technologies and their applications in genomics and transcriptomics. Use of the main bioinformatics resources for the structural and functional study of genomes.			
<b>Expected learning outcomes (according to Dublin Descriptors)</b>	<p><b>Knowledge and understanding:</b> Acquisition of theoretical and practical knowledge in the field of bioinformatics and genome analysis.</p> <p><b>Applying knowledge and understanding:</b> Application of specific methodologies for accessing the main biological databases and computational algorithms for the comparative and functional analysis of genomes.</p> <p><b>Making judgements:</b> Learn how to critically analyze omics data (e.g. genomics, transcriptomics, proteomics data) with the most common bioinformatics approaches and tools.</p> <p><b>Communication:</b> Acquisition of an appropriate terminology for the description of the fundamental omics data. The achievement of an adequate individual terminological standard will be assessed during the lessons, by means of intermediate tests and during the final exam.</p> <p><b>Lifelong learning skills:</b> Achieve adequate skills for the comprehension of the anatomy and the function of the genomes. Learn how to use the main bioinformatics platforms suitable for studying them.</p>		
<b>Programma del corso</b>			
<ul style="list-style-type: none"> <li>• GENOMES, TRASCRIPOTOMES AND PROTEOMES <ul style="list-style-type: none"> <li>○ DNA <ul style="list-style-type: none"> <li>▪ What is a Gene? Definition, structure and function</li> <li>▪ DNA structure</li> <li>▪ Base pairing and base stacking as stabilizing factors for the double helix</li> </ul> </li> </ul> </li> </ul>			

- Structural flexibility of DNA (A, B and Z forms).
  - RNA
    - RNA and the Transcriptome
    - The RNA content of the cell
    - RNA maturation
    - Transcriptome definition(s)
  - PROTEINS AND PROTEOME
    - Hierarchical levels of protein structure
    - Amino acid diversity underlies protein diversity
    - The link between the transcriptome and the Proteome
    - The genetic code
    - Deviations from the standard genetic code
    - Proteome and biochemical cellular complexity.
- GENOMES OF PROKARYOTES AND EUKARYOTIC ORGANELLES
  - PHYSICAL FEATURES OF PROKARYOTIC GENOMES
    - The traditional view of the prokaryotic chromosome
    - Linear and multipartite prokaryotic genomes.
  - GENETIC FEATURES OF PROKARYOTIC GENOMES
    - Gene organization in the E. coli K12 genome
    - Operons
    - Prokaryotic genome sizes, numbers of genes and biological complexity
    - Genome sizes and numbers of genes vary within individual species
    - Lateral gene transfer
  - EUKARYOTIC ORGANELLAR GENOMES
    - The endosymbiont theory and its molecular bases
    - Most organellar genomes are circular
    - Dimensions of mitochondrial and plastid genomes
    - Genetic content of organellar genomes
- EUKARYOTIC NUCLEAR GENOMES
  - Link between chromosomes dimensions and their DNA content
    - Features of metaphase chromosomes
    - DNA–protein interactions in centromeres and telomeres
  - HOW ARE THE GENES ARRANGED IN A NUCLEAR GENOME?
    - A segment of the human genome and its comparison with other typical eukaryotic genomes
    - The yeast genome and the concept of gene density
    - Gene organization in other eukaryotes
  - HOW MANY GENES ARE IN A NUCLEAR GENOME AND WHAT ARE THEIR FUNCTIONS?
    - Gene numbers can be misleading
    - Gene catalogs
    - GO nomenclature and Gene Ontologies
    - Families of genes
    - Pseudogenes and other evolutionary relics
  - THE REPETITIVE DNA CONTENT OF EUKARYOTIC NUCLEAR GENOMES
    - Minisatellites and microsatellites
    - Genetic profiles based on microsatellites patterns
    - Interspersed repeats
- GENOME SEQUENCING
  - DNA sequencing by the Chemical method (MAXAM–GILBERT)
  - DNA sequencing by the enzymatic chain termination method (SANGER)
    - Chain-termination sequencing in outline
    - Not all DNA polymerases can be used for sequencing
    - Chain-termination sequencing with Taq polymerase

- Strengths and limitations of chain-termination sequencing
- NEXT-GENERATION SEQUENCING
  - Sequencing libraries
  - Next-generation sequencing methods 2<sup>nd</sup> generation (Illumina, Pyrosequencing, Ion Torrent, SOLid)
  - Single Molecule Real Time Sequencing
  - 3<sup>rd</sup>/4<sup>th</sup> generation methods (Pacific Bioscience, Oxford Nanopore).
- BIOINFORMATICS
  - Biological Databases (GENBANK, EMBL-EBI, DDBJ, UNIPROT, PUBMED).
  - Biological databases querying methods.
  - Boolean operators (AND, OR, NOT) for building complex queries.
  - Genomic browsers (Ensembl e UCSC).
  - FASTA format and sequence annotation.
  - Local and global sequence alignment.
  - Database similarity search (BLAST).
  - Bioinformatics methods for gene prediction.

**Teaching methods:** Frontal teaching + PowerPoint presentations.

**Auxiliary teaching:** Practice with the main bioinformatics platforms described in class.

**Assessment methods:** There will be a written test 'in *itinere*' and a final oral exam.

**Bibliography:**

- T. A. Brown “Genomes 4”, Garland Science 2018
- M.H.Citterich, F.Ferri, G.Pavesi, G.Pesole “Fondamenti di Bioinformatica”, Zanichelli 2017

Note: Bibliography must be integrated with lecture notes; PowerPoint presentations are also free available as a “student’s companion”.