

UNIVERSITÀ DEGLI STUDI DI PALERMO

DEPARTMENT					
ACADEMIC YEAR					
ANNO ACCADEMICO EROGAZIONE					
SUBJECT					
CODE					
SCIENTIFIC SECTOR(S)					
HEAD PROFESSOR(S)	CHIODI N	IARCEI	LO	Professore Ordinario	Univ. di PALERMO
OTHER PROFESSOR(S)					
CREDITS					
PROPAEDEUTICAL SUBJECTS					
MUTUALIZATION					
YEAR					
TERM (SEMESTER)					
ATTENDANCE					
EVALUATION					
TEACHER OFFICE HOURS	CHIODI MARCELLO				
	Tuesday	15:00	17:00	stanza del docente (edificio 1	3); eccezionalmente su teams
	Friday	12:00	13:00	stanza del docente (edificio 1	3); eccezionalmente su teams

DOCENTE: Prof. MARCELLO CHIODI

PREREQUISITES	Familiarity with computer programming and computational skills
LEARNING OUTCOMES	The first part of the course focuses on the statistical analysis of gene expression. The statistical methodology will be contextualized within the fields of molecular biology, genetics, and transcriptomics. The student will be involved in the analysis of gene expression data using the R software. The second part of the course focuses on technical aspects related to parallel programming and the use of the computer terminal. These aspects are of fundamental importance for managing and analysing large amounts of data (regardless of the nature of the data of interest). These topics will be accompanied by bioinformatic applications such as genome alignment, prediction of molecular interactions, and estimation of cellular fractions in tissues. The student will become familiar with the main statistical methodologies for gene expression analysis. Furthermore, students can independently connect to a computer server and analyze large amounts of data through remote programming and parallel computing. The student will be able to create an executable R program.
ASSESSMENT METHODS	The exam consists of an oral test about the course topics. The student has to present a statistical analysis of genetics data. Before the exam, the student will receive data analysis instructions. The student must show the data analysis results during the oral test. Evaluation criteria: 30 cum laude: excellent knowledge of the topics, excellent use of technical language, excellent ability to autonomously apply the acquired knowledge. 30: excellent knowledge of the topics, excellent use technical language, good ability to autonomously apply the acquired knowledge of the topics, good use of the technical language, moderate ability to autonomously apply the acquired knowledge of the topics, limited ability to autonomously apply the acquired knowledge. 24-25: Moderate knowledge. 21-23: Knowledge of the course's main topics, but without a thorough understanding. Limited use of the technical language, and poor ability to autonomously apply the acquired knowledge. 18-20: Minimal knowledge of the course's main topics and technical language, very limited ability to autonomously apply the acquired knowledge. 18-20: Minimal knowledge of the course's main topics and technical language, very limited ability to autonomously apply the acquired knowledge. 18-20: Minimal knowledge of the course's main topics and technical language, very limited ability to autonomously apply the acquired knowledge. Insufficient: The student does not possess an acceptable knowledge of the topics covered during the course and has no application skills.
EDUCATIONAL OBJECTIVES	The course aims to introduce students to the main statistical methods for gene expression analysis and provide basic computer skills for analysing and managing large amounts of data.
TEACHING METHODS	Frontal lessons and computer exercises using R software and the computer terminal
SUGGESTED BIBLIOGRAPHY	materiale fornito in aula

SYLLABUS

Hrs	Frontal teaching
2	Introduction to computational biology, genetics, and transcriptomics. Overview of molecular biology; central dogma of biology and protein synthesis.
5	Large scale inference in computational biology Introduction to gene expression data
6	Differential expression analysis: Significant analysis of microarray, moderated t-test, Mann-Whitney test, Kruskal-Wallis one-way ANOVA. Identification of genetic signatures. Gene set enrichment analysis. Gene Ontology, Reactome pathway analysis, GSEA software
6	Gene expression harmonization. Batch effect Analysis, PCA and UMAP clustering and unsupervised cluster analysis The bootstrap approach in hypothesis testing. Bootstrap t-test for differential expression analysis.Analisi di sopravvivenza per valutare il potere prognostico delle firme geniche sulle casistiche di tumori
5	Introduction to bioinformatics applications. Introduction to FASTA and FASTQ files. Introduction to sequence alignment problem. Genome alignment using STAR. Introduction to the mechanisms of gene regulation. Prediction of bonds between messenger RNA molecules and microRNAs In silico estimation of cell fractions in tumor tissues. Use of CIBERSORTX
Hrs	Workshops
8	dvanced computer tools for the analysis of large datasets. Introduction to the terminal. Introduction to remote programming.
6	Running software through the terminal. Creating executable R programs
4	Parallel computing in R. Monitoring processes and RAM usage through the terminal.