COURSE CONTENT

(1) GENERAL INFO

SCHOOL	ENGINEERING		
DEPARTMENT	BIOMEDICAL ENGINEERING		
MSc PROGRAM	BIOMEDICAL ENGINEERING AND TECHNOLOGY		
STUDY LEVEL	POSTGRADUATE, MSc		
COURSE CODE	BMET206	**SEMESTER**	B
COURSE TITLE	Bioinformatics		

TEACHING	**HOURS**	**ECTS**
LECTURES AND WORKSHOPS	26	5

COURSE TYPE	SPECIALIZATION
COURSE REUIREMENTS:	-
TEACHING AND EXAMINATION LANGUAGE:	ENGLISH
IS THIS COURSE OFFER TO ERASMUS STUDENTS	YES (IN ENGLISH)
COURSE WEBPAGE (URL)	https://eclass.uniwa.gr/courses/320/

(2) LEARNING OUTCOMES

Learning outcomes

Purpose of the course:
The purpose of the bioinformatics course is to provide students with specialized knowledge and skills needed to analyse, design, and apply computational methods and techniques in the field of biology and medicine. Bioinformatics applications cover a wide range of fields, including genomic data analysis, representation and analysis of protein structures, systems biology, drug development, and other fields of biology and medicine. Students taking this course will gain specialized knowledge of the use of advanced computational methods for the processing, analysis, and interpretation of biological data. It also focuses on the development of new computational methods and tools that can help address the challenges facing biology in the era of big data.

Learning Outcomes:
After the end of the course students:
1. Will know basic concepts of bioinformatics for solving basic and translational research problems.
2. Will develop basic programming principles in the R environment.
3. Will understand and execute Big Data Analysis algorithms at a professional level, selecting correct operating parameters for these tools.
4. Will develop specialized skills in solving complex computational biology problems that can be applied in research fields of Universities, Research Centers and Bio/Pharmaceutical Companies.
5. Develop knowledge mining skills on huge databases of omics data.

Achievement of Course Objectives and Learning Outcomes:
To achieve the above, we will provide students with a systematic introduction to the basic concepts of bioinformatics through lectures, examples and discussions. Lectures may be accompanied by exercises that apply the new knowledge. Practical exercises and workshops will be organized to reinforce programming skills in the R environment. Real biological data will be used to make the course more practical. Students will be provided hands-on experience in running analysis algorithms on large datasets. This will be done through laboratory exercises or programming projects that require the use of bioinformatics tools. Students will be encouraged to participate in complex research projects or simulation environments where they will develop their skills in bioinformatics problem solving. They will be trained in knowledge extraction techniques and the use of tools to retrieve information from large databases.

General abilities

- Searching, analysing and synthesising data and information and making decisions
- Adapting to new situations
- Translating theory into practice
- Promoting free, creative and deductive thinking
- Autonomous work
- Decision-making
- Acquiring the appropriate theoretical background to enable further training at doctoral level
- Design and management of research questions
- Research production
- Working in an interdisciplinary environment
- Adaptation to new technologies
- Working in an interdisciplinary environment

(3) COURSE CONTENT

«Introduction to the R programming language»
Instructions for installing the Rstudio environment and R programming language, creating a project, installing and using R libraries/packages from CRAN and Bioconductor, creating, assigning and deleting variables, using vectors, lists, tables, data frames.

«Reading and loading data»
Set active working directory, read / save data in Comma Separated Value (CSV) format, modify / filter / create data subsets.

«Create graphical images / data visualisation»
Create histograms plots, bar charts, density distribution plots, boxplots, violin plots, piecharts and scatter plots, heatmaps.

«Introduction to bioinformatics»
Definitions, basic concepts, historical background, central dogma of biology, the human genome project, introduction to transcriptomics/sequencing techniques, RNA isolation techniques, sequencing library creation, sequencing process, initial review of sequencing quality/quality control.

«Transcriptomic analysis using R programming language»
Installation and loading of Deseq2 library, loading of transcriptome data, Deseq2 object creation, data quality control/filtering, differential expression analysis, identification and visualization of significantly expressed genes (volcano plots), enrichment analysis of gene sets and visualization of results, writing of results in relevant CSV files.

(4) TEACHING AND LEARNING METHODS - EXAMINATIONS

COURSE DELIVERY	Physical presence, face to face at the auditorium	
USE OF INFORMATION AND COMMUNICATION TECHNOLOGIES	The theoretical part of the course is conducted with a projector (for the presentation of basic theory) and on the blackboard. The laboratory part of the course is carried out in the laboratory using computers.	
TEACHING ORGANIZATION	Activity	Semester workload
	Teaching / lectures	26
	Lecture material study	30

	Unsupervised literature review and preparation of the final project	69
	Total	*125*
STUNDET EVALUATION	30-50% final examination with multiple choice, short answer and problem-solving questions 20-40% hands-on examination in the laboratory with the implementation and solving of a bioinformatics task 20-40% with individual written work on bioinformatics topics	

(5) SUGGESTED LITERATURE

Books, scientific articles and related scientific resources:

[1] Altuna Akalin, Computational Genomics with R.
[2] Vasilis Promponas, Introduction to Bioinformatics, University Cyprus, 2010.
[3] Supratim Choudhuri, Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and Analytical Tools, 1st Edition, Academic Press 2014.
[4] Arthur M. Lesk, Introduction to Bioinformatics, 4th Edition., Oxford University Press, 2013.
[5] Marketa Zvelebil and Jeremy Baum, Understanding Bioinformatics, Garland Science 2007.

Scientific journals:

[1] Bioinformatics, https://academic.oup.com/bioinformatics.
[2] BMC bioinformatics, https://bmcbioinformatics.biomedcentral.com/.
[3] IEEE/ACM Transactions on Computational Biology and Bioinformatics, https://ieeexplore.ieee.org/xpl/RecentIssue.jsp?punumber=8857.
[4] PLOS Computational Biology, https://journals.plos.org/ploscompbiol/.