#### **COURSE OUTLINE**

## (1) GENERAL

SCHOOL School of Applied Biology and Biotechnology					
ACADEMIC UNIT					
LEVEL OF STUDIES	Undergraduate				
COURSE CODE	279 SEMESTER 8th				
COURSE TITLE	Data Analysis in Genetics				
INDEPENDENT TEACHING ACTIVITIES  if credits are awarded for separate components of the course, e.g. lectures, laboratory exercises, etc. If the credits are awarded for the whole of the course, give the weekly teaching hours and the total credits		WEEKLY TEACHING HOURS	ũ	CREDITS	
,		LECTURES	3		
	PRACT	ICAL EXERCISES	2		
					5
Add rows if necessary. The organisation of teaching and the teaching methods used are described in detail at (d).					
COURSE TYPE general background, special background, specialised general knowledge, skills development	Field of Scien	nce			
PREREQUISITE COURSES:	No				
LANGUAGE OF INSTRUCTION and EXAMINATIONS:	Greek				
IS THE COURSE OFFERED TO ERASMUS STUDENTS	No				
COURSE WEBSITE (URL)	https://mediasrv.aua.gr/eclass/				

## (2) LEARNING OUTCOMES

#### **Learning outcomes**

The course learning outcomes, specific knowledge, skills and competences of an appropriate level, which the students will acquire with the successful completion of the course are described.

Consult Appendix A

- Description of the level of learning outcomes for each qualifications cycle, according to the Qualifications Framework of the European Higher Education Area
- Descriptors for Levels 6, 7 & 8 of the European Qualifications Framework for Lifelong Learning and Appendix B
- Guidelines for writing Learning Outcomes

The course is designed to introduce Next Generation Sequencing methods and Data Analysis Tools. Emphasis will be put on the understanding and utilization of these concepts and algorithms. The objective is to help the students to reach rapidly the frontier of NGS big data analysis and be able to use standard and deep learning tools to solve problems in an interdisciplinary environment. After completing this course, the student will be able to:

- explain the paradigm shift in Biology and the need for Big Data Analysis
- understand sequencing technologies: chain termination method, sequencing by synthesis,
   Single Molecule Real Time sequencing
- describe the structure of FASTQ, SAM, VCF, GFF3, BED files
- explain de novo and reference based assembly
- describe types of genomic variants and how they are determined

- describe structural and functional annotation results
- understand experimental and RNA sequencing design
- understand differential gene expression
- explain metagenomic sequencing, assembly and classification
- understand how to visualize, compare and analyze genomics data

After completing the lab, the student will be able to use Unipro UGENE for:

- PCR In Silico
- Multiple Sequence Alignment
- Phylogenetic Tree
- Quality Control of Next Generation Sequencing Data
- Metagenomic Classification with Kraken
- Data Submission and Metagenomics DataBases

#### **General Competences**

Taking into consideration the general competences that the degree-holder must acquire (as these appear in the Diploma Supplement and appear below), at which of the following does the course aim?

Search for, analysis and synthesis of data and information, with the use of the necessary technology

Adapting to new situations Decision-making

Working independently Team work

Working in an international environment Working in an interdisciplinary environment

Production of new research ideas

Project planning and management Respect for difference and multiculturalism Respect for the natural environment

Showing social, professional and ethical responsibility and

sensitivity to gender issues Criticism and self-criticism

Production of free, creative and inductive thinking

others...

- Search for, analysis and synthesis of data and information, with the use of the necessary technology
- Working independently
- Working in an interdisciplinary environment

# (3)

### **SYLLABUS**

- 1. Introduction
- 2. DNA Sequencing Technology
- 3. Genome Assembly
- 4. Variant Calling
- 5. Genome Annotation
- 6. RNA Sequencing
- 7. Metagenomics
- 8. Genome Data Visualization

### (4) TEACHING and LEARNING METHODS - EVALUATION

DELIVERY	Face to face in the classroom
Face-to-face, Distance learning, etc.	
USE OF INFORMATION AND	Lectures: Power point presentations
<b>COMMUNICATIONS TECHNOLOGY</b>	Labs: Use of biological databases and bioinformatics software
Use of ICT in teaching, laboratory education,	

communication with students
TEACHING METHODS

The manner and methods of teaching are described in detail.

Lectures, seminars, laboratory practice,

Lectures, seminars, laboratory practice, fieldwork, study and analysis of bibliography, tutorials, placements, clinical practice, art workshop, interactive teaching, educational visits, project, essay writing, artistic creativity, etc.

The student's study hours for each learning activity are given as well as the hours of non-

Activity	Semester workload
Lectures	30
Laboratory work	30
Written assignment	20
Autonomous study	45

directed study according to the principles of the ECTS	Course total	125	
STUDENT PERFORMANCE			
EVALUATION	I. Theory: Written Examination (40%)		
Description of the evaluation procedure	Oral Presentation (10%)		
Language of evaluation, methods of evaluation, summative or conclusive, multiple choice questionnaires, short-answer questions, open-ended questions, problem solving, written work, essay/report, oral examination, public presentation, laboratory work, clinical examination of patient, art interpretation, other		(50%)	
Specifically-defined evaluation criteria are given, and if and where they are accessible to students.			

# (5) ATTACHED BIBLIOGRAPHY

Jonathan Pevsner, "Bioinformatics and Functional Genomics". Wiley-Blackwell (2015) ISBN: 978-1-118-58178-0

Lisa A. Seidman, "Basic Laboratory Methods for Biotechnology". Benjamin Cummings (2009) ISBN: 9780321570147